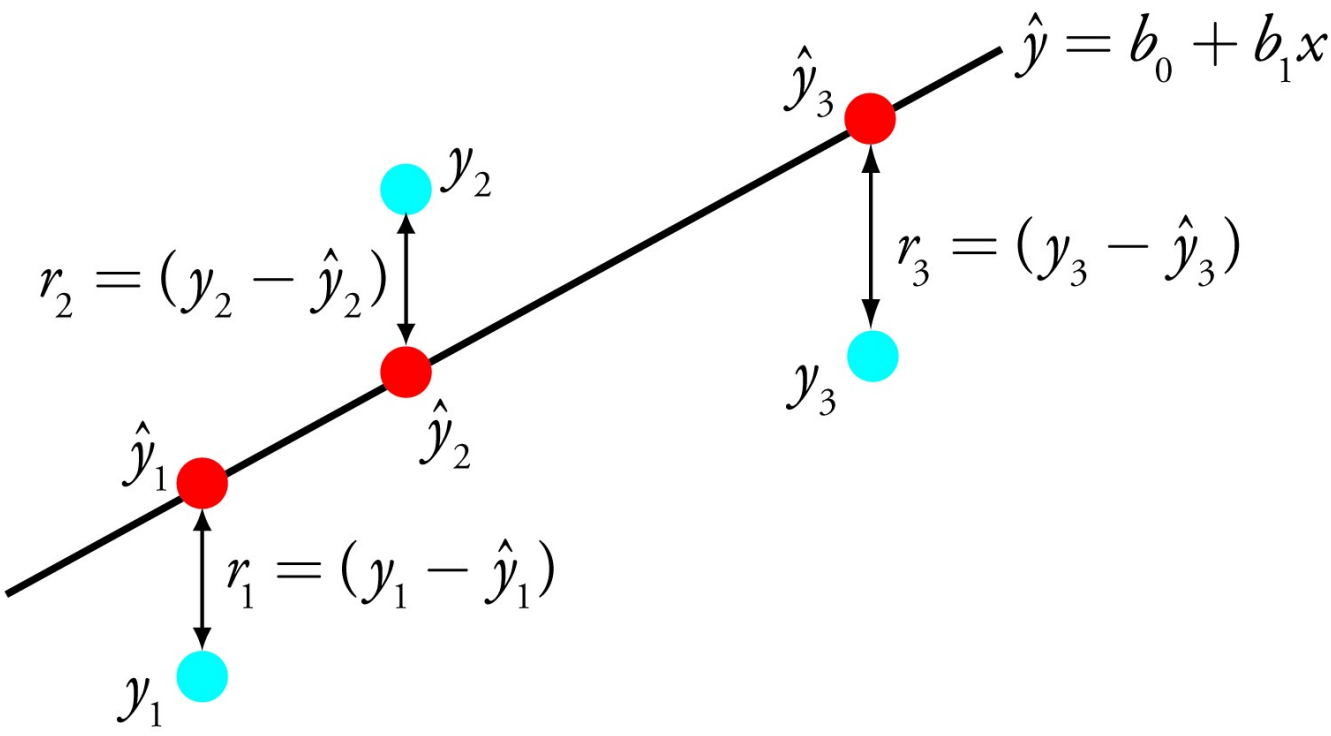
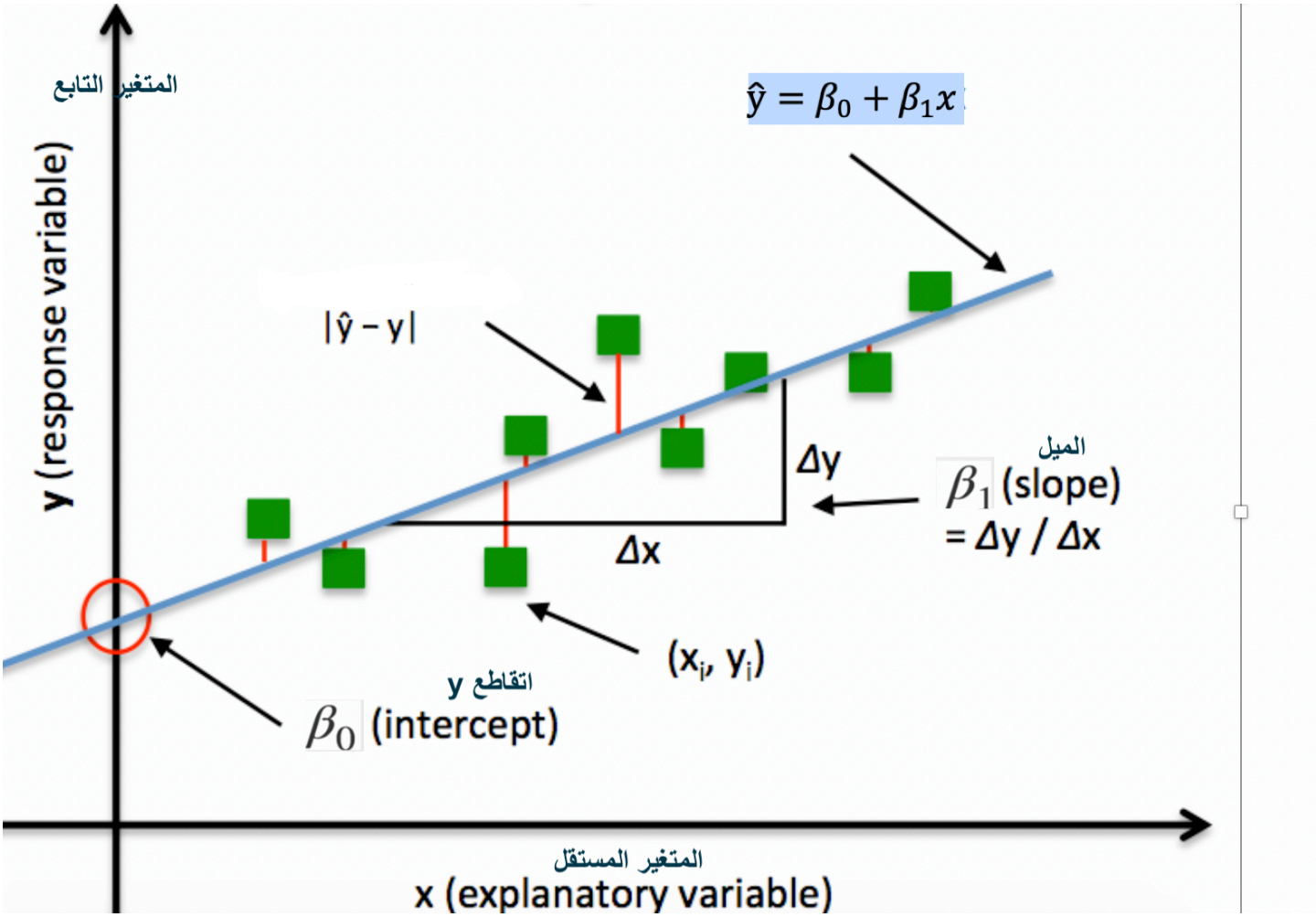
الانحدار الخطي

الأهداف

- وصف النمذجة الإحصائية مع الانحدار البسيط
- شرح الانحدار الخطي البسيط كحل للمعادلة: $\hat{y} = \beta_0 + \beta_1 x$:$\hat{y} = \beta_0 + \beta_1 x$
- رسم خط الانحدار على أساس الميل وتقاطع y y
- التنبؤ بمخرجات نموذج انحدار خطي لبيانات جديدة

المقدمة





$$\hat{y} = \beta_0 + \beta_1 x$$

1 2

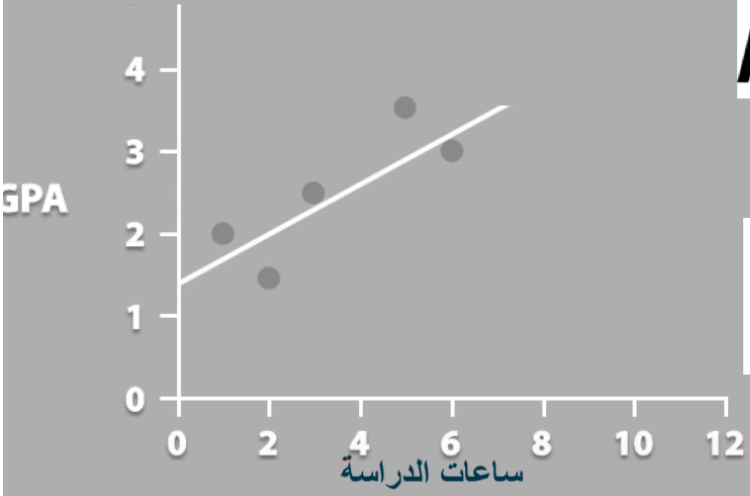
$$\beta_0 = \bar{y} - \beta_1 \bar{x}$$

3 4

7

$$\beta_1 = r \frac{S_y}{S_x}$$

5 6



β_0 : β_0: تقاطع y

β_1 : β_1: الميل

$\bar{y}$: $\bar{y}$: متوسط y

$\bar{x}$: $\bar{x}$: متوسط x

r : r: معامل الارتباط

S_x : S_x: انحدار معياري x

S_y : S_y: انحدار معياري y

In [15]:

```
1 getwd()
```

'/Users/medamin/Projets/DataScience'

In [ ]:

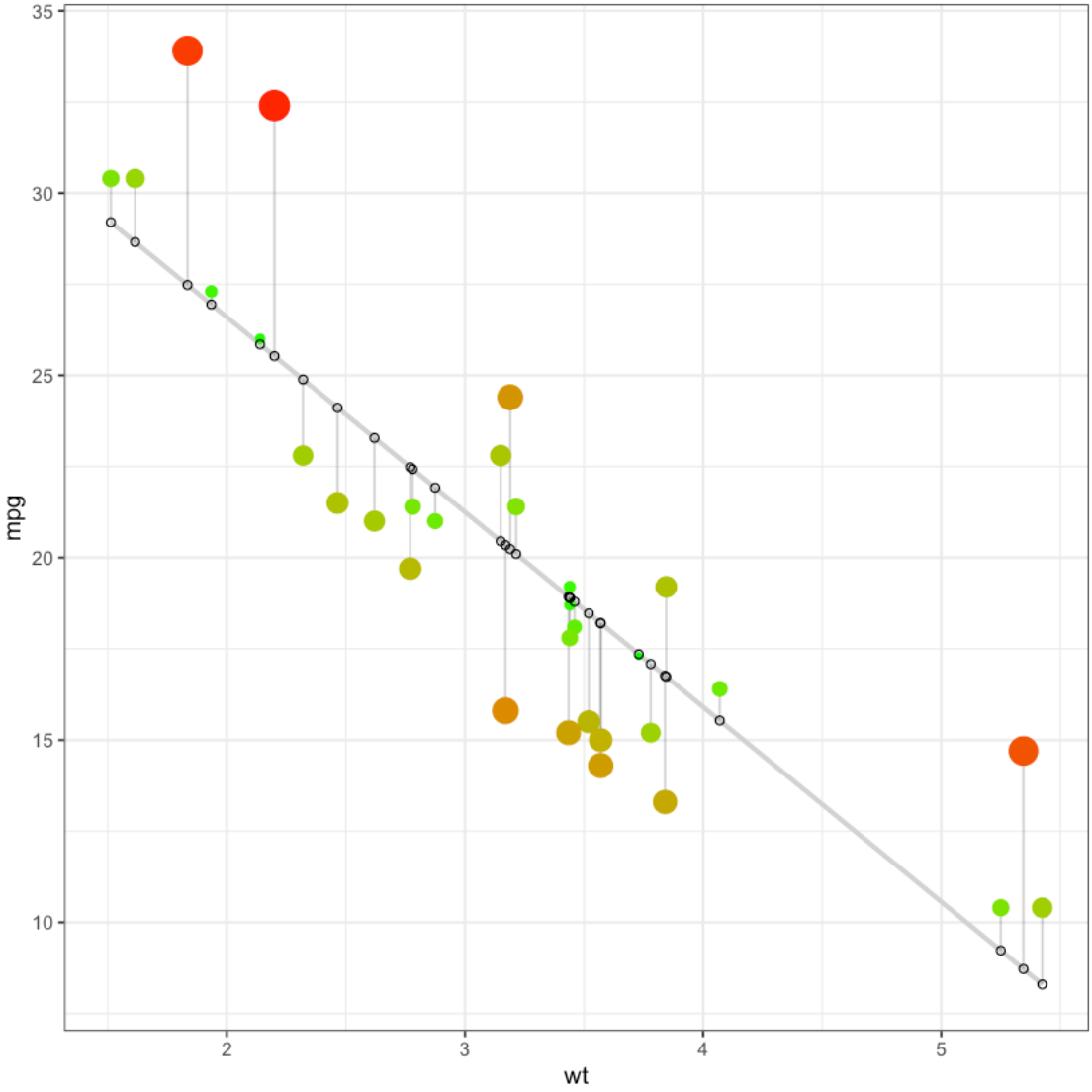
```
1
```

In [165]:

```
1 rm(list=ls())
```

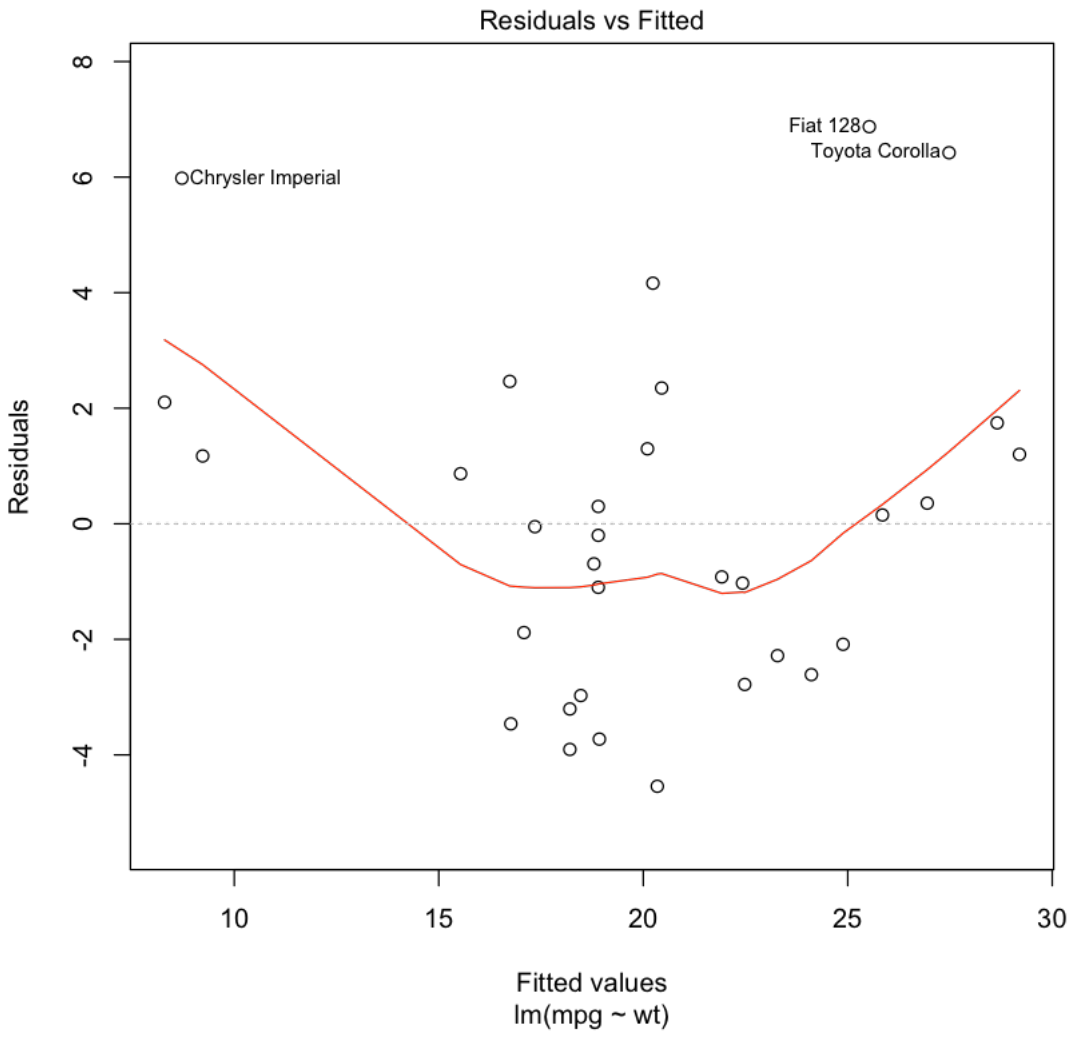
In [130]:

```r
d <- mtcars
fit <- lm(mpg ~ wt, data = d) # fit the model
d$predicted <- predict(fit)   # Save the predicted values
d$residuals <- residuals(fit) # Save the residual values
ggplot(d, aes(x = wt, y = mpg)) +
  geom_smooth(method = "lm", se = FALSE, color = "lightgrey")
  geom_segment(aes(xend = wt, yend = predicted), alpha = .2)
  geom_point(aes(color = abs(residuals), size = abs(residuals
  scale_color_continuous(low = "green", high = "red") +
  guides(color = FALSE, size = FALSE) +
  geom_point(aes(y = predicted), shape = 1) +
theme_bw()
```



In [131]:

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



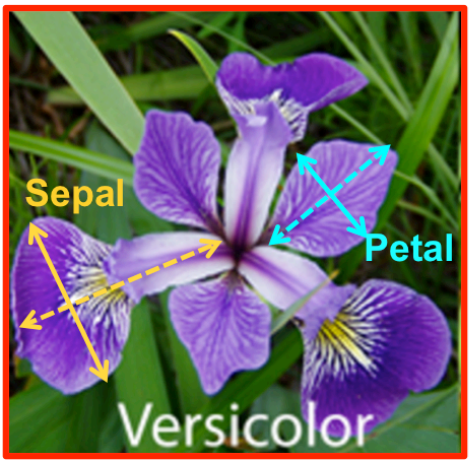
Geogebra Demo.Linear/Multi-linear/Polinomial...etc. عرض

In [ ]:

```
1
```

In [63]:

```
1 library(help="datasets")
```



In [17]:

```
1 unique(iris$Species)
```

setosa versicolor virginica

▶ **Levels**:

In [18]:

```
1 head(iris)
```

A data.frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<dbl>	<dbl>	<dbl>	<dbl>	<fct>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

In [19]:

```
1 glimpse(iris)
```

```
Error in glimpse(iris): could not find function "gli
mpse"
Traceback:
```

In [20]:

```
1 str(iris)
```

```
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.
4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4
2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.
5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.
2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versic
olor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

In [21]:

```
1 levels(iris$Species)
```

'setosa' 'versicolor' 'virginica'

In [22]:

```
1 is.factor(iris$Species)
```

TRUE

In [23]:

```
1 names(iris)
```

'Sepal.Length' 'Sepal.Width' 'Petal.Length' 'Petal.Width'
'Species'

Variables correlations

In [24]:

```
library(ggplot2)
library(GGally)
```

```
Warning message:
“package ‘GGally’ was built under R version 3.4.4”
```

In [25]:

```
1 ggpairs(iris)
```

```
`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.

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th `binwidth`.

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th `binwidth`.

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th `binwidth`.
```
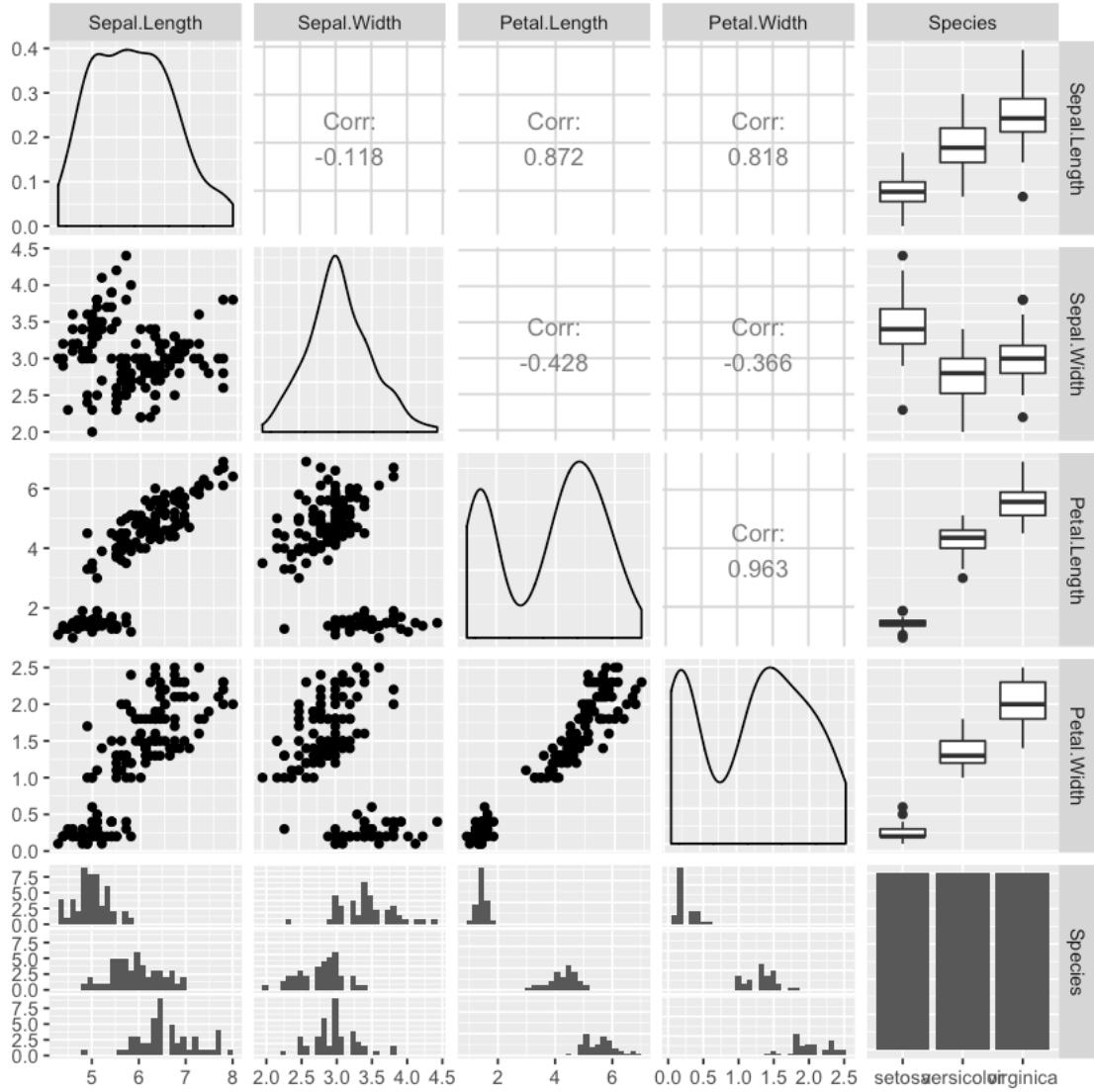



In [33]:

```
(r<-cor(iris$Petal.Length, iris$Petal.Width))
#btw thsiis pearson correlation equation
```

0.962865431402796

$$r = \frac{\sum(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum(x_i - \bar{x})^2}\sqrt{\sum(y_i - \bar{y})^2}}$$

$$r = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2}\sqrt{\sum (y_i - \bar{y})^2}}$$

In [34]:

```
# try pearson, spearman and kendall
cor.test(iris$Petal.Length, iris$Petal.Width, method = "spear
```

```
Warning message in cor.test.default(iris$Petal.Lengt
h, iris$Petal.Width, method = "spearman"):
“Cannot compute exact p-value with ties”

        Spearman's rank correlation rho

data:  iris$Petal.Length and iris$Petal.Width
S = 35061, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.9376668
```

In [35]:

```
(r<-cor.test(iris$Petal.Length, iris$Petal.Width))
# confidence interval determin the correlation figures withir
```

```
        Pearson's product-moment correlation

data:  iris$Petal.Length and iris$Petal.Width
t = 43.387, df = 148, p-value < 2.2e-16
alternative hypothesis: true correlation is not equa
l to 0
95 percent confidence interval:
 0.9490525 0.9729853
sample estimates:
      cor
0.9628654
```

t-statitics

$$t = \frac{r}{\sqrt{1 - r^2}} \sqrt{n - 2}$$

$$t = \frac{r}{\sqrt{1 - r^2}} \sqrt{n - 2}$$

In [36]:

```
names(r)
```

'statistic' 'parameter' 'p.value' 'estimate' 'null.value'
'alternative' 'method' 'data.name' 'conf.int'

```

```

In [37]:

```
r$estimate
```

cor: 0.962865431402796

In [38]:

```
(t_value<-r$estimate*sqrt(148)/sqrt(1-r$estimate^2))
#same as r$statistic
```

cor: 43.3872373820692

In [40]:

```
r$conf.int
```

0.949052459311114 0.972985317378797

$$0.95 \leqslant CorrelationValue \leqslant 0.972$$

$$0.95 \leqslant CorrelationValue \leqslant 0.972$$

In [41]:

```
r$alternative
```

'two.sided'

In [62]:

```
r$p.value
```

4.67500390732856e-86

In [ ]:

```

```

In [44]:

```r
chisq.test(iris$Petal.Length, iris$Petal.Width)
# We have a high Chi-squared value and a P-value of less thar
# So, we reject the null Hyothesis and conclude that. Petal.L
# a SIGNIFICANT relationship
```

```
Warning message in chisq.test(iris$Petal.Length, iri
s$Petal.Width):
“Chi-squared approximation may be incorrect”

        Pearson's Chi-squared test

data:  iris$Petal.Length and iris$Petal.Width
X-squared = 1144.1, df = 882, p-value = 5.143e-09
```

In [45]:

```
# we can even have a btter plot for our iris data
install.packages("PerformanceAnalytics")
```

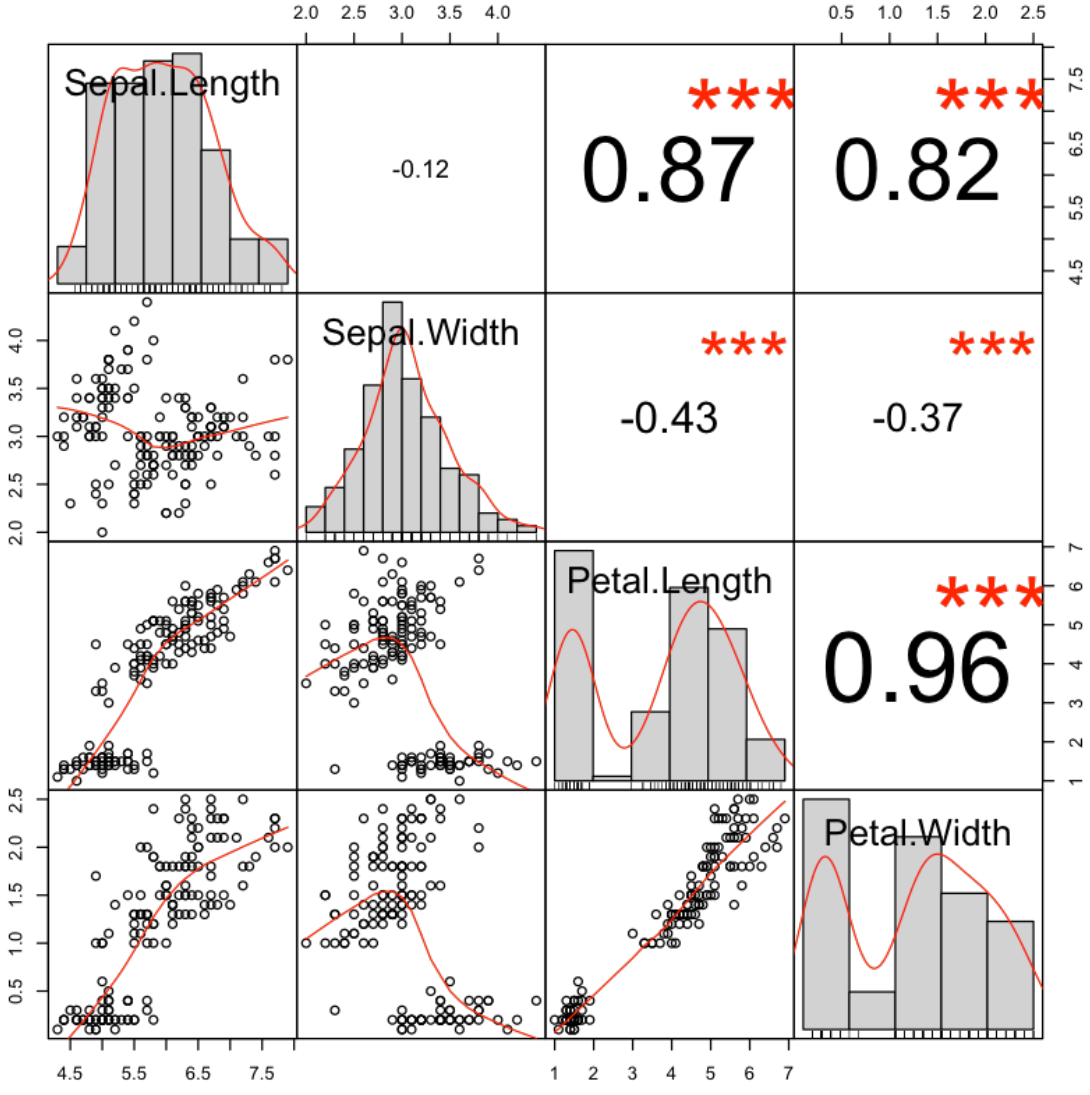
```
also installing the dependencies ‘xts’, ‘quadprog’



  There are binary versions available but the source
versions are later:
                     binary source needs_compilation
quadprog              1.5-5  1.5-7              TRUE
PerformanceAnalytics  1.5.2  1.5.3              TRUE


The downloaded binary packages are in
        /var/folders/hw/83xf1jxs0b58xft1b6ghk0280000
gn/T//RtmpY6bkoz/downloaded_packages

installing the source packages ‘quadprog’, ‘Performa
nceAnalytics’


Warning message in install.packages("PerformanceAnal
ytics"):
“installation of package ‘quadprog’ had non-zero exi
t status”
Warning message in install.packages("PerformanceAnal
ytics"):
“installation of package ‘PerformanceAnalytics’ had
non-zero exit status”
```

In [37]:

```
library(PerformanceAnalytics)
chart.Correlation(iris[,-5], histogram=TRUE, pch=19)
```

```
Loading required package: xts
Loading required package: zoo

Attaching package: ‘zoo’

The following objects are masked from ‘package:base’
:

    as.Date, as.Date.numeric
```

```
Attaching package: ‘PerformanceAnalytics’

The following object is masked from ‘package:graphic
s’:

    legend
```



- is Petal.Width related to Petal.Length really?
- is the relation between the two variables strong enough to claim they are related?
- Can we use the Data from just 150 Observations to make a claim about all the population of ORchedia?

In [46]:

```
# حمّل قاعد بيانات زهرة اوركيد

data(iris)
```

التخطيط البياني

In [47]:

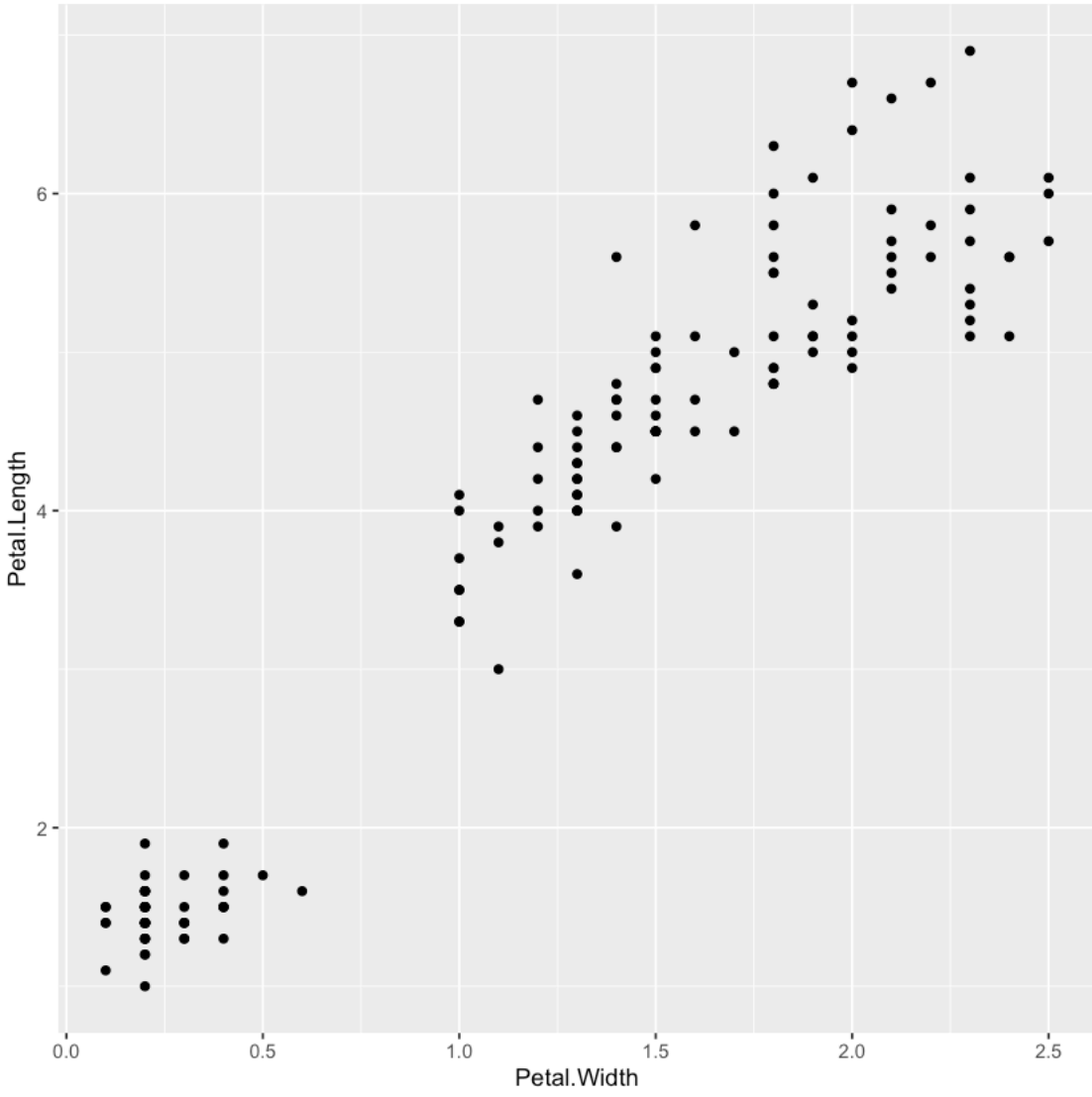
```
# تحميل مكتبة التخطيطيات البيناية
library(ggplot2)


```

In [ ]:

```

```

In [48]:

```
#  Petal.Width, Petal.Length      انجاز تخطيط بياني حول المتغيرين

ggplot(iris , aes(Petal.Width, Petal.Length))+
geom_point()

```



بناء النموذج *Buildthemodel*

بناء النموذج *Buildthemodel*

In [49]:

```
attach(iris)
```

In [50]:

```
lmModel<- lm(Petal.Length ~  Petal.Width, iris)
```

In [51]:

```r
# Get a summary report of the model
summary(lmModel)
```

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
eedom
Multiple R-squared:  0.9271,    Adjusted R-squared:
0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e
-16
```

In [52]:

```
1 library(dplyr)
2 library(broom)
```

```
Attaching package: ‘dplyr’


The following object is masked from ‘package:GGally’
:

    nasa


The following objects are masked from ‘package:stats
’:

    filter, lag


The following objects are masked from ‘package:base’
:

    intersect, setdiff, setequal, union
```

In [53]:

```
1 names(lmModel)
```

'coefficients' 'residuals' 'effects' 'rank' 'fitted.values' 'assign'
'qr' 'df.residual' 'xlevels' 'call' 'terms' 'model'

In [54]:

```
1 names(lmModel$coefficients)
```

'(Intercept)' 'Petal.Width'

In [55]:

```
lmModel %>%
    augment() %>%
head()
```

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [56]:

```
lmModel_Augmented<- lmModel %>%
    augment()
```

In [57]:

```
glance(lmModel)
```

A tibble: 1 × 11

r.squared	adj.r.squared	sigma	statistic	p.value	df	log
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dl
0.9271098	0.9266173	0.4782058	1882.452	4.675004e-86	2	-101.17

In [59]:

```
1 tidy(lmModel)
```

A tibble: 2 × 5

term	estimate	std.error	statistic	p.value
<chr>	<dbl>	<dbl>	<dbl>	<dbl>
(Intercept)	1.083558	0.07296696	14.84998	4.043318e-31
Petal.Width	2.229940	0.05139623	43.38724	4.675004e-86

In [60]:

```
1 var(lmModel_Augmented$`.fitted`)
```

2.88913185794091

In [61]:

```
1
2 lmModel %>%
3     augment() %>%
4     summarise(var_e=var(.resid), var_y=var(Petal.Length)) %>%
5     mutate(R_squared=1-var_e/var_y)
```

A tibble: 1 × 3

var_e	var_y	R_squared
<dbl>	<dbl>	<dbl>
0.227146	3.116278	0.9271098

```
Residual standard error: 0.4782 on 148 degrees of freedom
Multiple R-squared:  0.9271,    Adjusted R-squared:  0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

In [21]:

```
1 r$estimate
```

```
Error in eval(expr, envir, enclos): object 'r' not f
ound
Traceback:
```

In [18]:

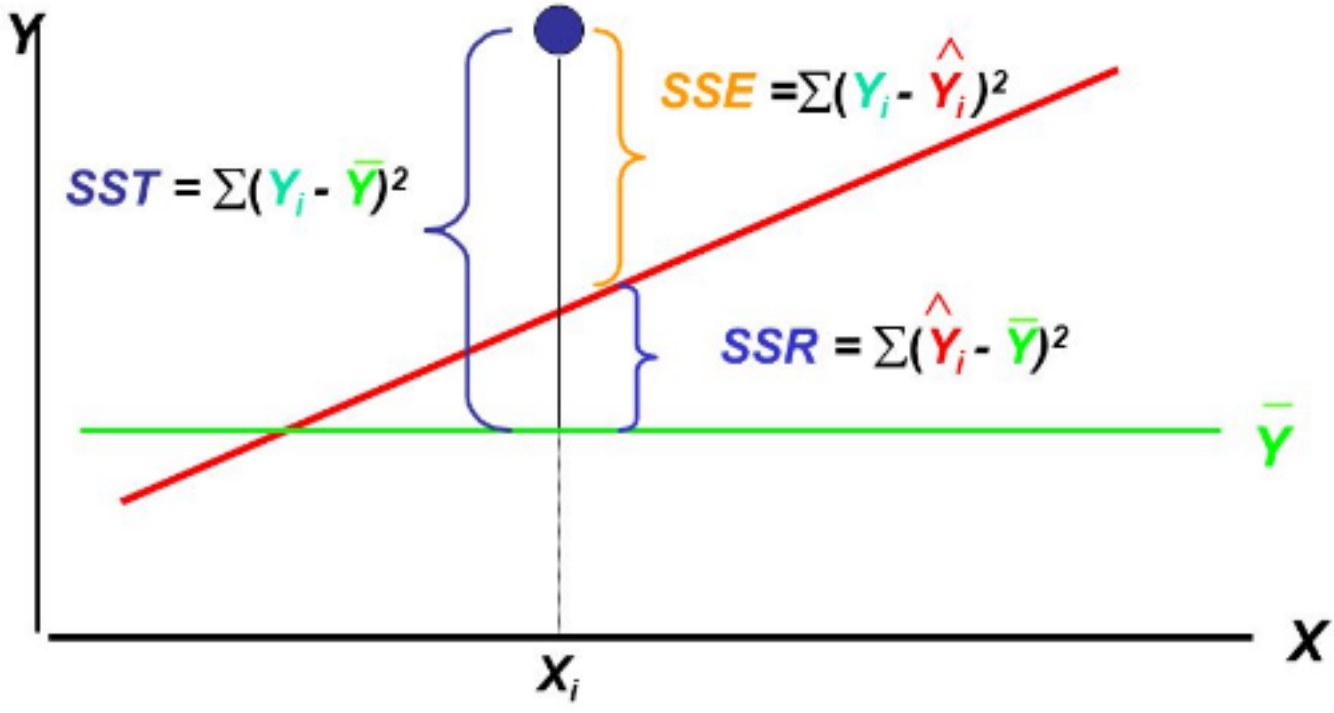
```
1 getwd()
```

'/Users/medamin/Projets/DataScience'

In [27]:

```
1 getwd()
```

'/Users/medamin/Projets/DataScience'



In [22]:

```
1 qchisq(.95,148)
```

177.389749986549

r$estimate^2

In [23]:

```
(t_value<- 2.22994 /0.05140)
```

43.384046692607

It's also known as the residual standard deviation (RSD), and it can be defined as "

Fstatistics

F-value measures the significance of the OverALL model nad not just one variable. And this has more use when there is more than one explanatory variable.

- for one vriable. we have

$$F = t_v^2$$

$$F = t_v^2$$

$$F = \frac{\frac{R^2}{k-1}}{\frac{1-R^2}{n-k}}$$

$$F = \frac{\frac{R^2}{k-1}}{\frac{1-R^2}{n-k}}$$

$$F = \frac{MeanSquareModel}{MeanSquareError}$$

$$F = \frac{MeanSquareModel}{MeanSquareError}$$

$$F = \frac{\frac{SSM}{Df_m.Model}}{\frac{SSE}{Df_e.Err}}$$

$$F = \frac{\frac{SSM}{Df_m.Model}}{\frac{SSE}{Df_e.Err}}$$

Type *Markdown* and LaTeX: α^2 α^2

In [21]:

```
0.9271/(1-0.9271)*148
```

1882.17832647462

In [22]:

```

43.39^2
```

1882.6921

In [ ]:

```

```

In [ ]:

```

```

In [23]:

```
anova(lmModel)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [61]:

```
(F_Value<-430.4806468/0.2286808)
```

1882.45207643143

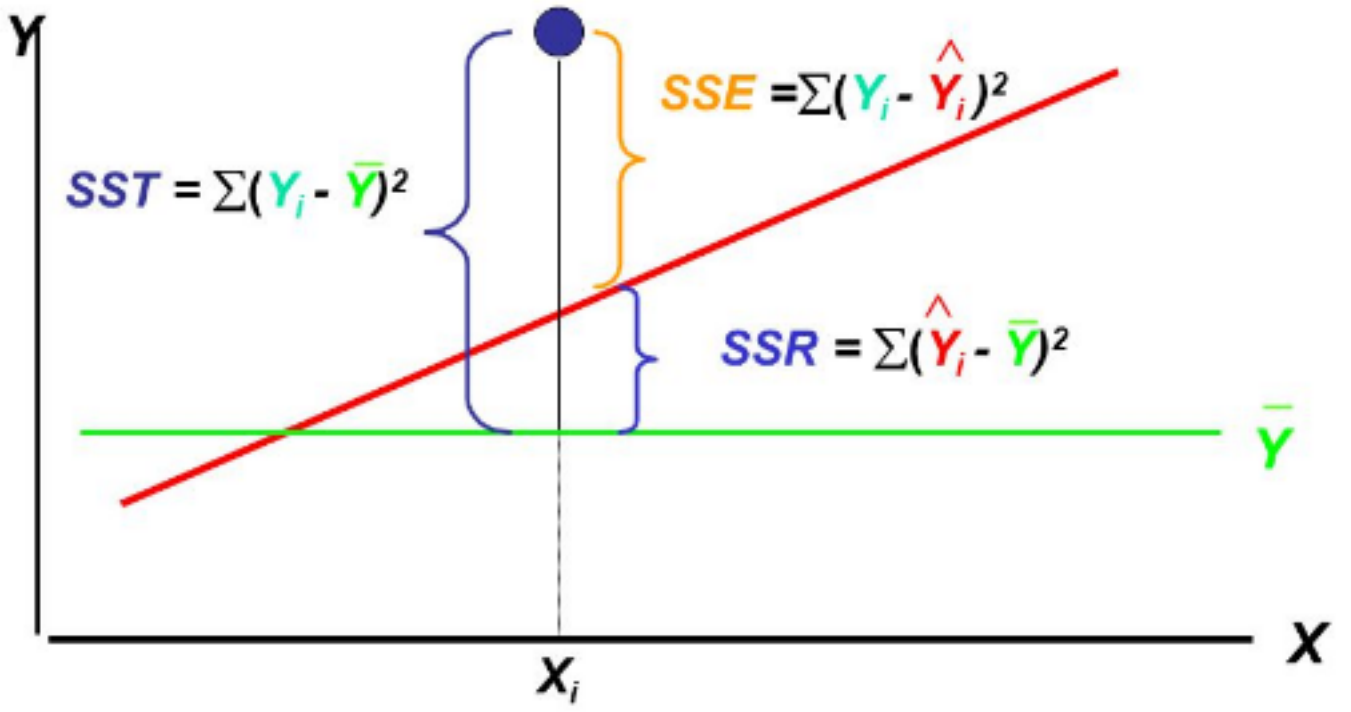
Multiple R-Squared:

Goodness Of Fit

This is percentage of variation in the response variable that is explained by the variation on the explanatory variable.

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST} = \frac{\sum (\hat{y} - \bar{y})^2}{\sum (y_i - \bar{y})^2}$$

$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST} = \frac{\sum (\hat{y} - \bar{y})^2}{\sum (y_i - \bar{y})^2}$



$$0 \leqslant R^2 \leqslant 1$$

$0 \leqslant R^2 \leqslant 1$

$$R^2 = \text{Coefficient Of Determination}$$

R^2 = Coefficient Of Determination

$$R^2 = \text{describes proportion of variance in y that is predictab}$$

R^2 = describes proportion of variance in y that is predictable from x

$$R^2 = \text{Y can not be predicted from x}$$

R^2 = Y can not be predicted from x

Middle values indicate the extent y is predictable.

Middle values indicate the extent y is predictable.

$$R^2 = \text{is correlated to Correlation}$$

R^2 = is correlated to Correlation

For a simple linear regression; = $R^2 = r^2$

For a simple linear regression; = $R^2 = r^2$

$$SST = \sum (y_i - \bar{y})^2$$

$SST = \sum (y_i - \bar{y})^2$

$$SSE = \sum (y_i - \hat{y})^2$$

$SSE = \sum (y_i - \hat{y})^2$

$$SSR = \sum (\hat{y} - \bar{y})^2$$

$SSR = \sum (\hat{y} - \bar{y})^2$

In [43]:

```
1 anova(lmModel)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [ ]:

```
1
```

Adjusted R-Square

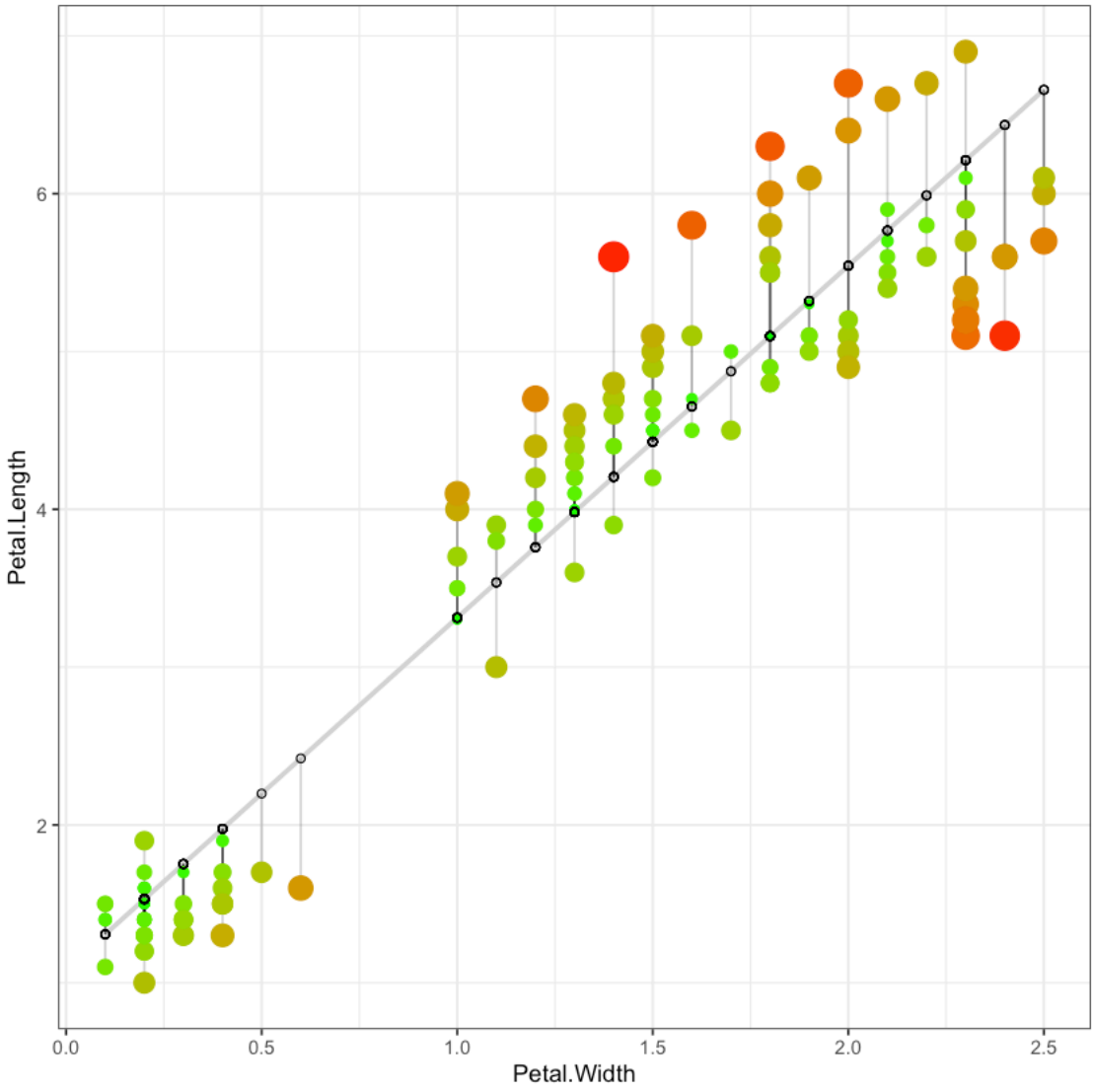
$$\bar{R}^2 = 1 - \frac{\frac{SSE}{n-k}}{\frac{SST}{n-1}}$$

$$\bar{R}^2 = 1 - \frac{\frac{SSE}{n-k}}{\frac{SST}{n-1}}$$

Residual Variation

In [30]:

```
1
2  iris$predicted <- predict(lmModel)   # Save the predicted val
3  iris$residuals <- residuals(lmModel) # Save the residual valu
4  ggplot(iris, aes(x = Petal.Width, y = Petal.Length)) +
5    geom_smooth(method = "lm", se = FALSE, color = "lightgrey")
6    geom_segment(aes(xend = Petal.Width, yend = predicted), alp
7    geom_point(aes(color = abs(residuals), size = abs(residuals
8    scale_color_continuous(low = "green", high = "red") +
9    guides(color = F, size = F) +                              #
10   geom_point(aes(y = predicted), shape = 1) +
11   theme_bw()
```



- Rsiduals.
  - Sum to Zero.
  - randomly distributed above and below Zero

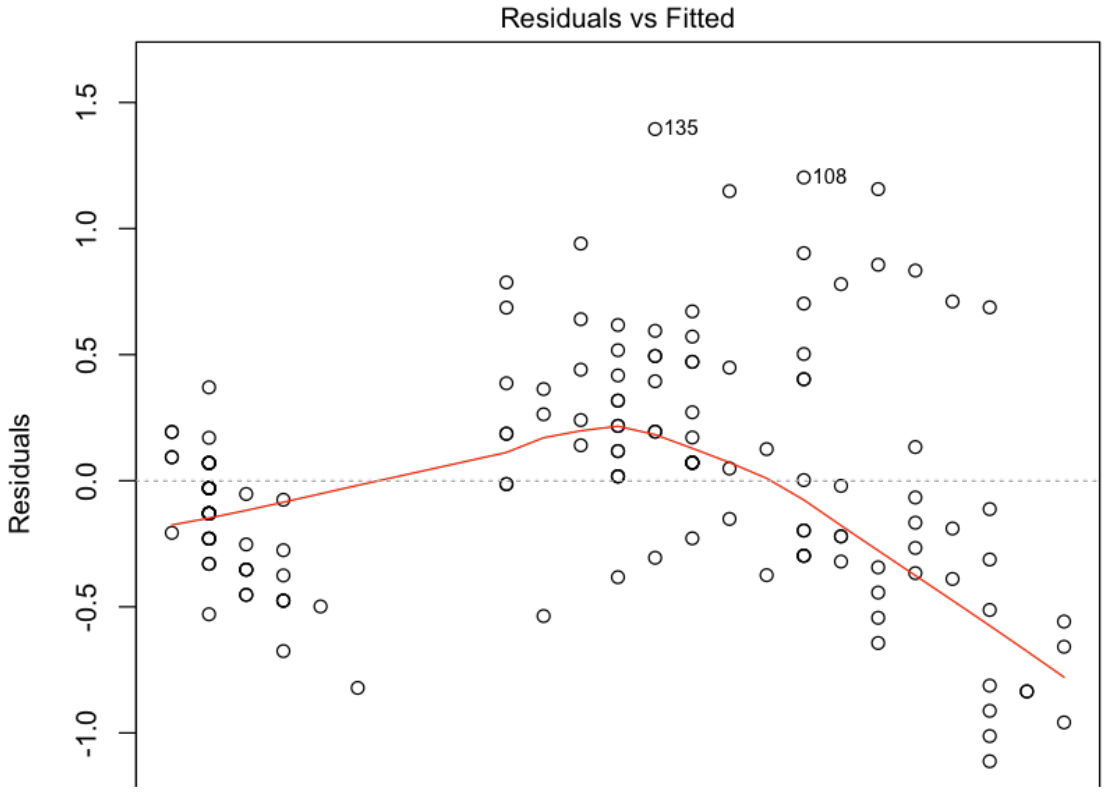
In [26]:

```
1 names(lmModel)
```

'coefficients' 'residuals' 'effects' 'rank' 'fitted.values' 'assign'
'qr' 'df.residual' 'xlevels' 'call' 'terms' 'model'

In [57]:

```
1 par=(mfrow=c(2,2))
2 plot(lmModel)
```



In [32]:

```
1 names(lmModel)
```

```
Error in eval(expr, envir, enclos): object 'lmModel'
not found
Traceback:
```

In [ ]:

```
1
```

In [24]:

```
df <- lmModel %>% augment()
names(df)
head(df)
```

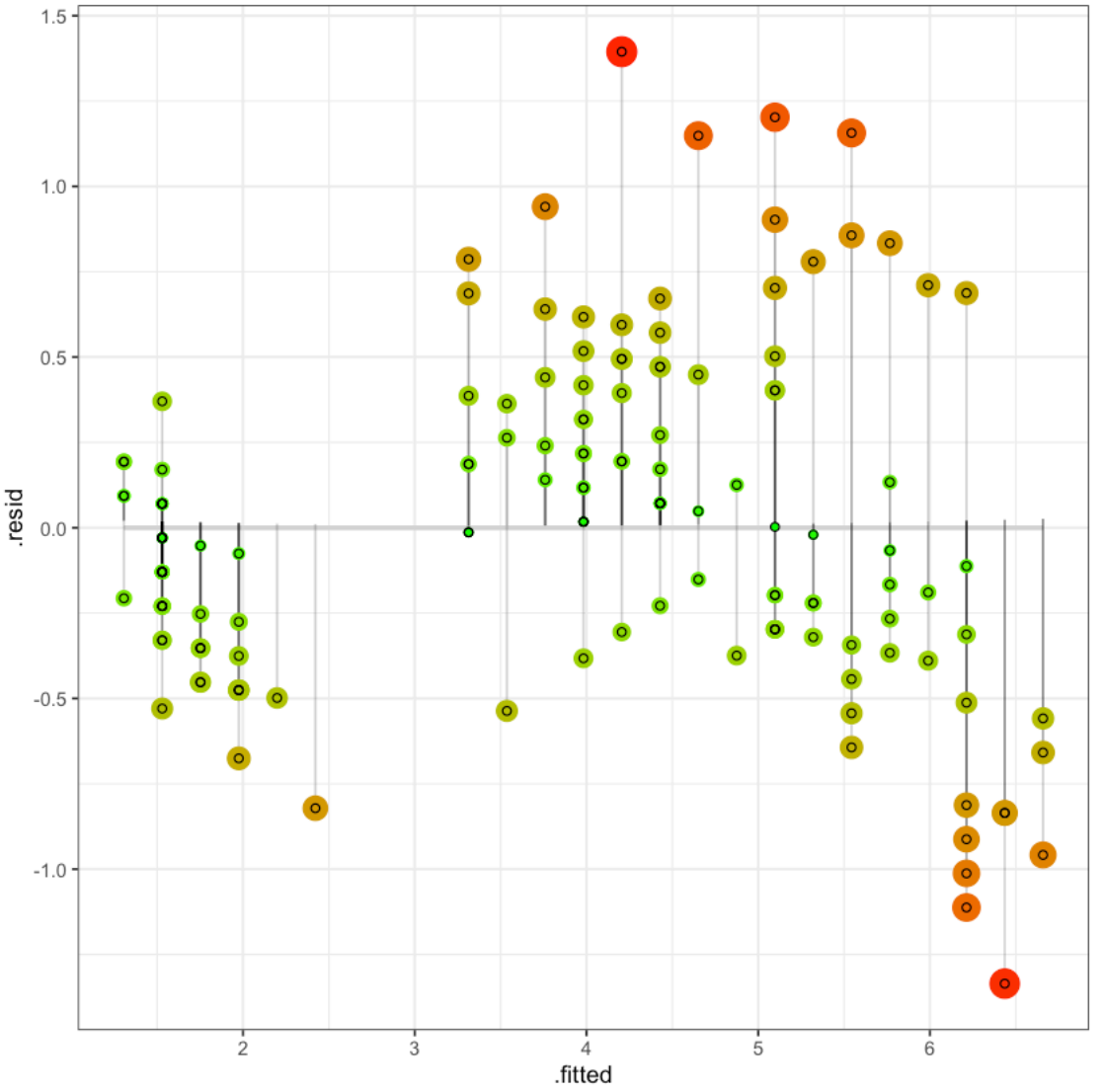
'Petal.Length' 'Petal.Width' '.fitted' '.se.fit' '.resid' '.hat' '.sigma' '.cooksd' '.std.resid'

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [27]:

```
ggplot(df, aes(.fitted, .resid)) +
  geom_smooth(method = "lm", se = FALSE, color = "lightgrey")
  geom_segment(aes(yend = .hat, xend = .fitted), alpha = .2)
  geom_point(aes(color = abs(.resid), size = abs(.resid))) +
  scale_color_continuous(low = "green", high = "red") +
  guides(color = F, size = F) +                                #
  geom_point(aes(y = .resid), shape = 1) +
  theme_bw()
```



In [28]:

```
1 anova(lmModel)
```

A anova: 2 × 5

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
	<int>	<dbl>	<dbl>	<dbl>	<dbl>
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [29]:

```
1 summary(lmModel)
```

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
eedom
Multiple R-squared:  0.9271,    Adjusted R-squared:
0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e
-16
```

In [83]:

```
# mean Square = Sum_Square/Df
# Residual Standard Error = Sqrt(Mean_Sq)
round(sqrt(0.2286808),4)
# which is exactly What was displayed above at Redisual Stand
# Petal length deviate from ht eregression line by approx. 0.
(devationRatio<-0.4782/mean(Petal.Length))
# is 12.72% acceptable for our regression line model
```

0.4782

0.127248536455561

- Typically we have a regression model looks like this: $Y=\beta 0+\beta 1X+\epsilon$ where ϵ is an error term independent of X
- If $\beta 0$ and $\beta 1$ are known, we still cannot perfectly predict Y using X due to ϵ. Therefore, we use RSE as a judgement value of the Standard Deviation of ϵ
- RSE is s just an estimate of the Standard Deviation of ϵ. in other term how the prediction or response deviates from the regression line.

It's also known as the residual standard deviation (RSD), and it can be defined as

$$RSE = \sqrt{\frac{RSS}{n-2}} = \sqrt{\frac{\sum (y_i - \hat{y})}{n-2}}$$

. The smaller the RSE. =>. the model fits the data well

In [84]:

```
0.4782/mean(Petal.Length)
```

0.127248536455561

In [55]:

```
#. R_squared =. cor(x, y ) =r  for our simple linear regtessi
cor(Petal.Length, Petal.Width)
```

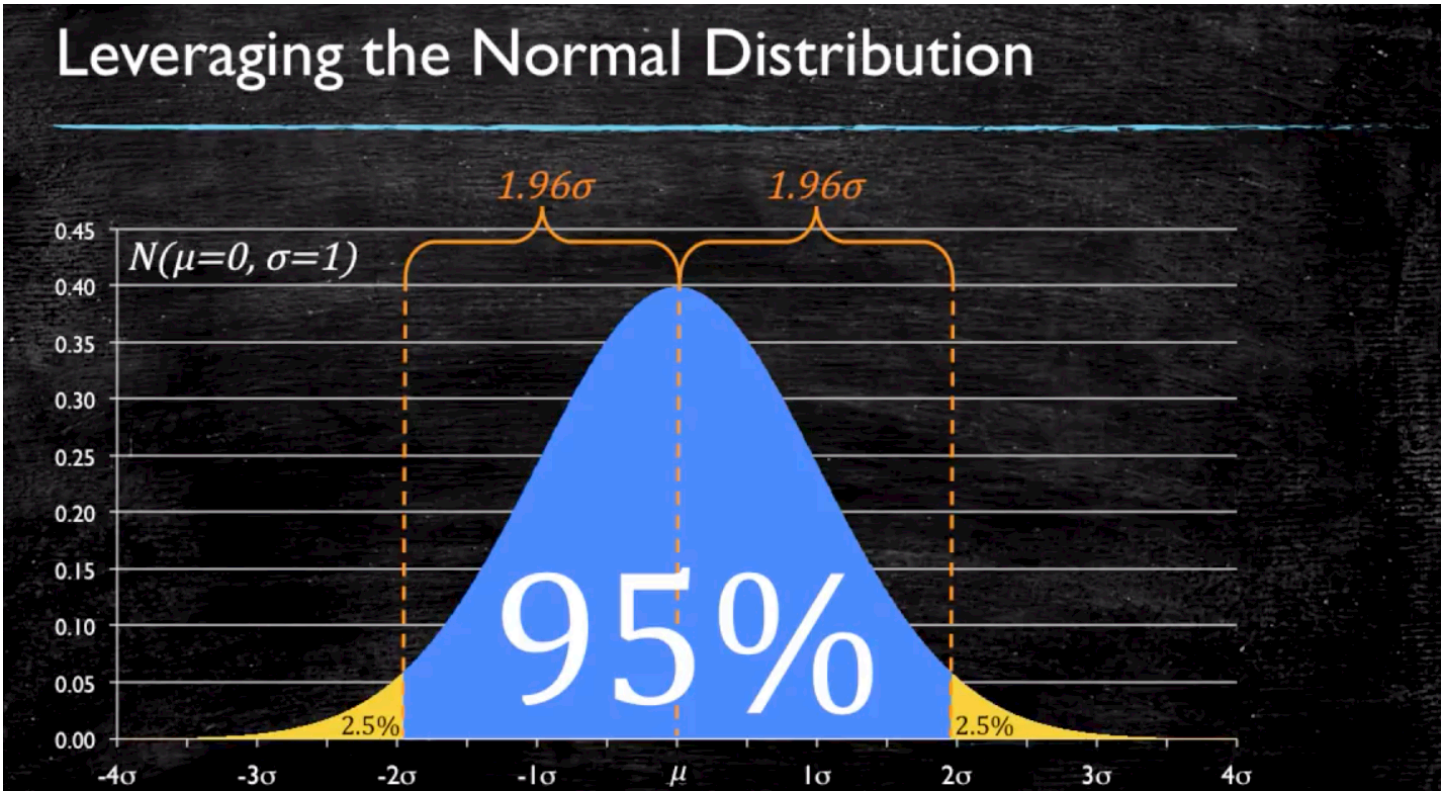
0.962865431402796

$$ln(\frac{p}{1-p}) = b_0 + b_i x$$

the model interpretentation

- Petal.Length= 1.08356 + 2.22994 x + e if Petal.Width increases by 1, Petal.Length will increase by 2.23.
  (is this enough to assess the correlation between the 2 variables) Of course NO.
- we have to recall that we fount this estimate based on a single sample. What's about the whole population. (with a single sample, we have to deal with incertainty)

. it's standard to work with 95% confidence intervals, which means we are 95% certain true values lies wihtin our interval.



In [109]:

```r
# remember the correlation test we have done
cor.test(iris$Petal.Length, iris$Petal.Width)
```

```
        Pearson's product-moment correlation

data:  iris$Petal.Length and iris$Petal.Width
t = 43.387, df = 148, p-value < 2.2e-16
alternative hypothesis: true correlation is not equa
l to 0
95 percent confidence interval:
 0.9490525 0.9729853
sample estimates:
      cor
0.9628654
```

- we are 95% confident that my population mean is bigger than 0.95 and less than 0.973

In [ ]:

```r

```

In [24]:

```r
t.test(iris$Petal.Length)
#conf.int. for  the Petal.Length  mean
```

```
        One Sample t-test

data:  iris$Petal.Length
t = 26.073, df = 149, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 3.473185 4.042815
sample estimates:
mean of x
    3.758
```

In [ ]:

```r

```

In [ ]:

```
1
```

In [111]:

```
1 mean(Petal.Length)
```

3.758

In [112]:

```
1 qt(.95, df=148)*sd(Petal.Length)/sqrt(150)
```

0.238575993390587

In [113]:

```
1
2 mean(Petal.Length) - qt(.95, df=148)*sd(Petal.Length)/sqrt(15
```

3.51942400660941

In [ ]:

```
1
```

In [21]:

```
1 step(lmModel)
```

```
Start:  AIC=-219.33
Petal.Length ~ Petal.Width

             Df Sum of Sq    RSS     AIC
<none>                    33.84 -219.33
- Petal.Width  1    430.48 464.33  171.49

Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Coefficients:
(Intercept)  Petal.Width
      1.084        2.230
```

In [19]:

```
attach(iris)
mean(Petal.Width) + qt(0.95, df=148)*sd(Petal.Width)/sqrt(150
```

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species
```

1.30234800000309

In [115]:

```
attach(iris)
```

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species
```

In [116]:

```
qt(.95, df=148)
```

1.65521450617873

In [ ]:

In [ ]:

In [ ]:

In [ ]:

how to access. the model parameters.

In [118]:

```
1 anova(lmModel)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
```

- Coefficient = 2.23 and the Std Error =0.051. This tell us about typpical variation of this coefficient.The Std Error gives kind of average Expected Error term from this particular sample value.
  (t statistice)Error_t= Estimate / Std_Error
- The higher the t-statistic the more significant the variable is. HIgher in magnitude Petal.Width -> t1= 2.2299/0.05514

P-Value

P-value< 5% P-value gives us an indication how extreme this coefficient if the Petal.Width coefficient equals to Zero. Here we've to Evoque The Null hypothesis where linear regression's coefficient are Zeros. We start at the hypothesis that there is no effect of Petal.width coeficient on the Petal.Length prediction model. briefly, P-value gives the probability of this coefficient occuring just due to random chance. In other term, it tells if the Petal.Width coefficient has no effect ont the Target variable Petal.Length.

At 5% we test wether this variable is significant or not. there’s minimal chance that this predictor is not meaningful for the regression.

F statistic

The F-statistic is equal to 430.48/0.229 = 1882.452. The distribution is F(1, 148), and the probability of observing a value greater than or equal to 1882.452 is less than 0.001. There is strong evidence that \beta_1 is not equal to zero.

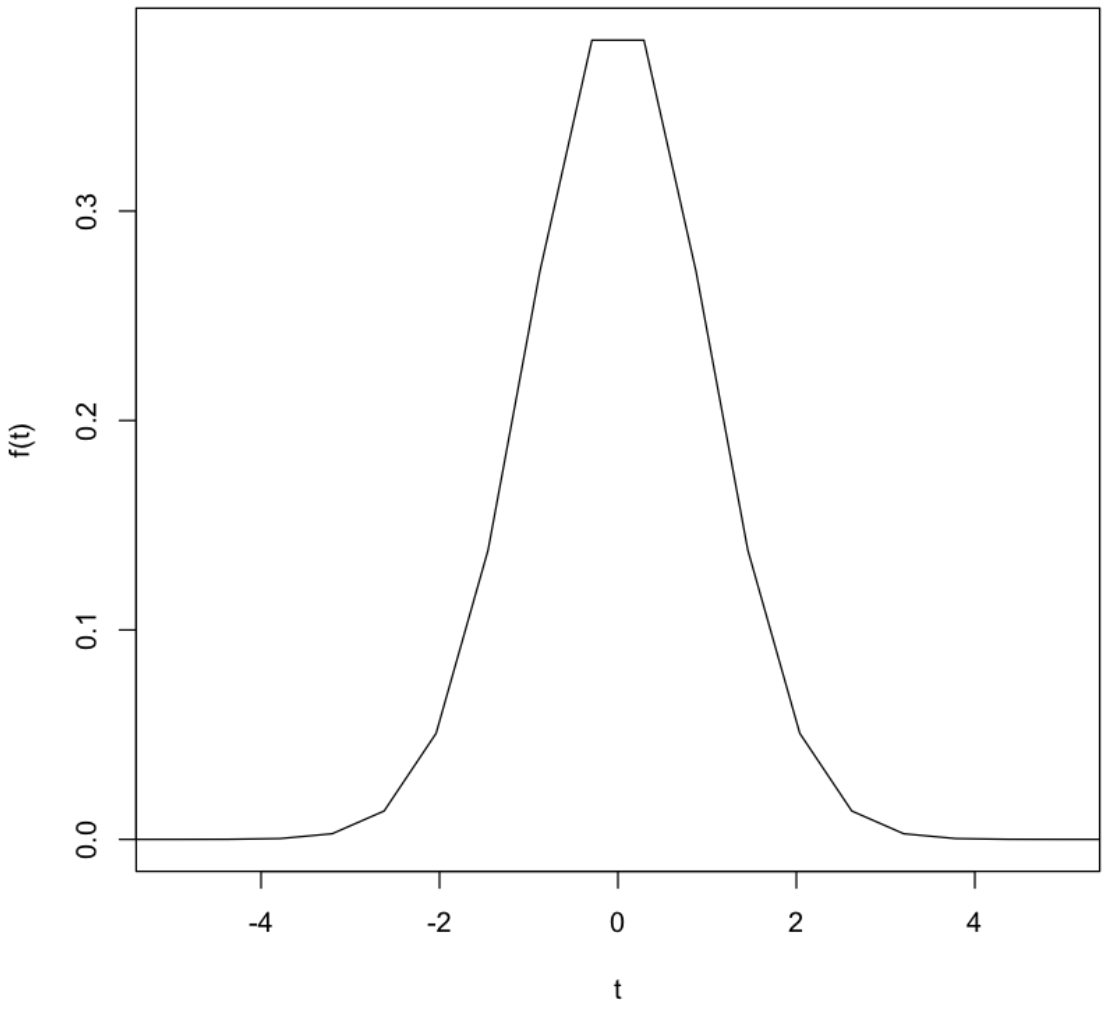
The r^2 term is equal to 0.577, indicating that 57.7% of the variability in the response is explained by the explanatory variable.

In [ ]:

```
1
```

In [119]:

```
t.value=seq(-43.39, 43.39, length=nrow(iris))
plot(x=t.value, y=dt(t.value, 148), type="l", xlim = c(-5, 5)
```



In [121]:

```
confint(lmModel)
```

	2.5 %	97.5 %
(Intercept)	0.9393664	1.227750
Petal.Width	2.1283752	2.331506

In [192]:

```
# R^2 = 1- (Residual sum of squares)/(Total sum of squares)
1- 33.84475/430.48065
summary(lmModel)
```

0.921379160712566

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
eedom
Multiple R-squared:  0.9271,    Adjusted R-squared:
0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e
-16
```

In [122]:

```
anova(lmModel)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [67]:

```
1 t.test(iris$Sepal.Length, iris$Petal.Length)
```

```
        Welch Two Sample t-test

data:  iris$Sepal.Length and iris$Petal.Length
t = 13.098, df = 211.54, p-value < 2.2e-16
alternative hypothesis: true difference in means is
not equal to 0
95 percent confidence interval:
 1.771500 2.399166
sample estimates:
mean of x mean of y
 5.843333  3.758000
```

In [4]:

```
1 2.22994   + 0.05140
```

2.28134

In [ ]:

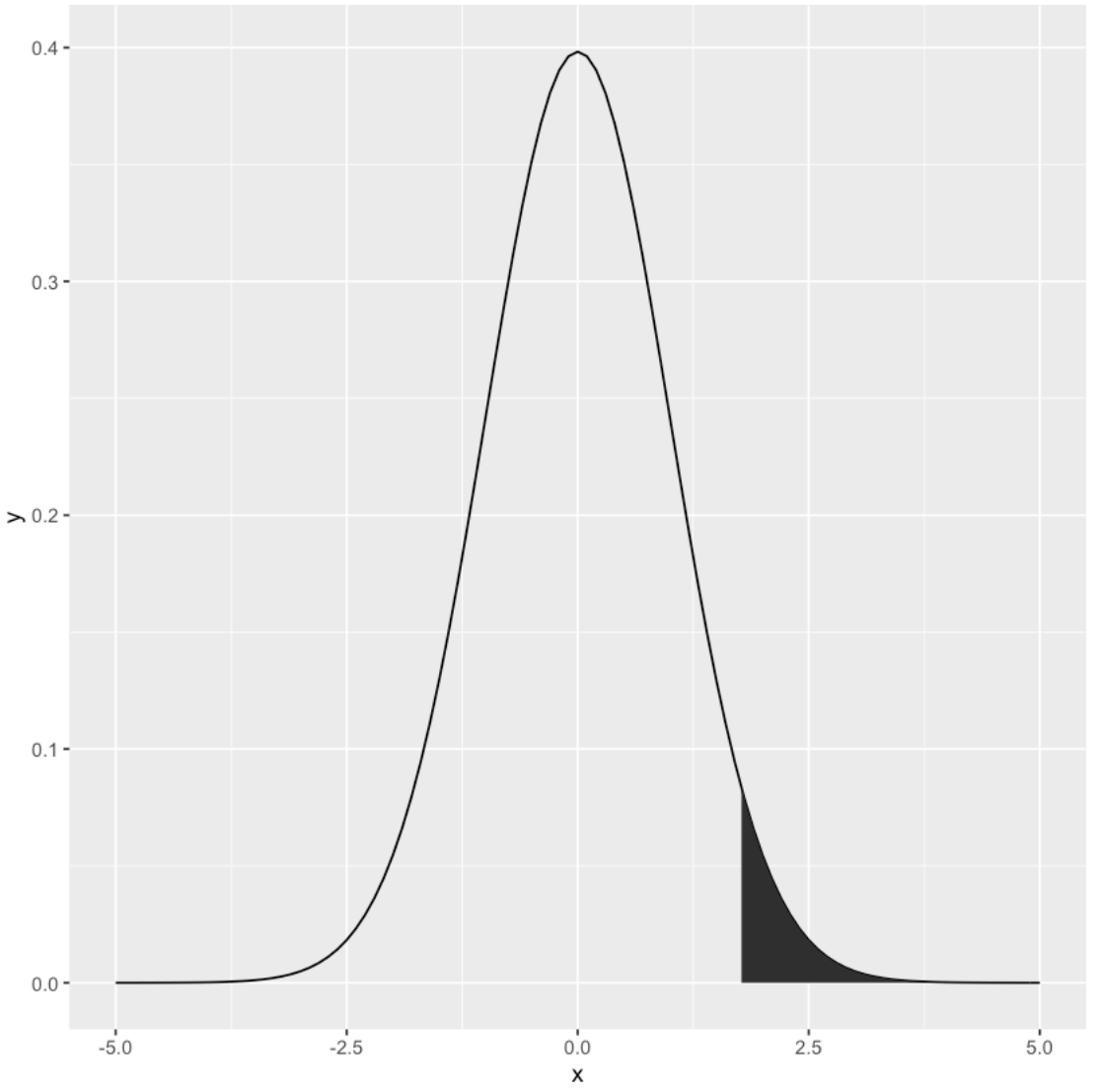
```
1
```

In [ ]:

```
1
```

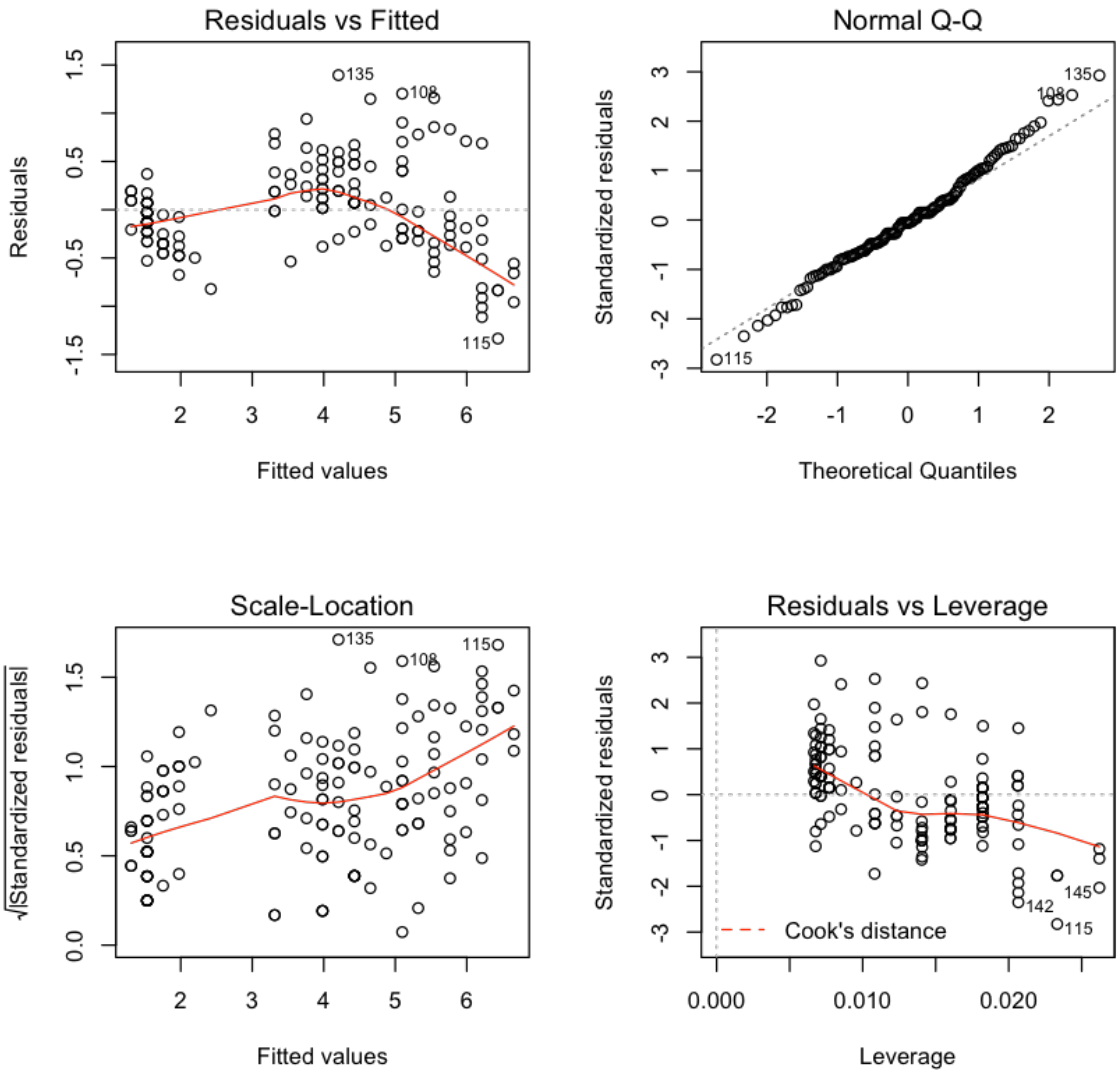
In [66]:

```
ggplot(data.frame(x = c(14.85, 43.39)), aes(x)) +
  stat_function(fun = dt, args =list(df =148)) +
  stat_function(fun = dt,   args =list(df =148),xlim = c(1.77
xlim(-5,5)
```



In [227]:

```
1 par(mfrow=c(2,2)) # Plot in a layout with 2 rows and 2 columr
2 plot(lmModel)
```



In [ ]:

```
1
```

In [ ]:

```
1
```

In [124]:

```
1 length(Residual)
```

```
Error in eval(expr, envir, enclos): object 'Residual
' not found
Traceback:
```

In [127]:

```
1 # residual =  Petal.Length - Predicted_Petal.Length
2 iris$Residual <- Petal.Length- predict(model)
```

In [128]:

```
1 head(iris)
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Resid
5.1	3.5	1.4	0.2	setosa	-0.12954
4.9	3.0	1.4	0.2	setosa	-0.12954
4.7	3.2	1.3	0.2	setosa	-0.22954
4.6	3.1	1.5	0.2	setosa	-0.02954
5.0	3.6	1.4	0.2	setosa	-0.12954
5.4	3.9	1.7	0.4	setosa	-0.27553

In [131]:

```
1 (sem<- sd(iris$Residual)/sqrt(length(iris$Residual)))
```

```
0.0389140929405684
```

In [133]:

```
1 c(mean(iris$Residual)-2*sem, mean(iris$Residual)+2*sem)
```

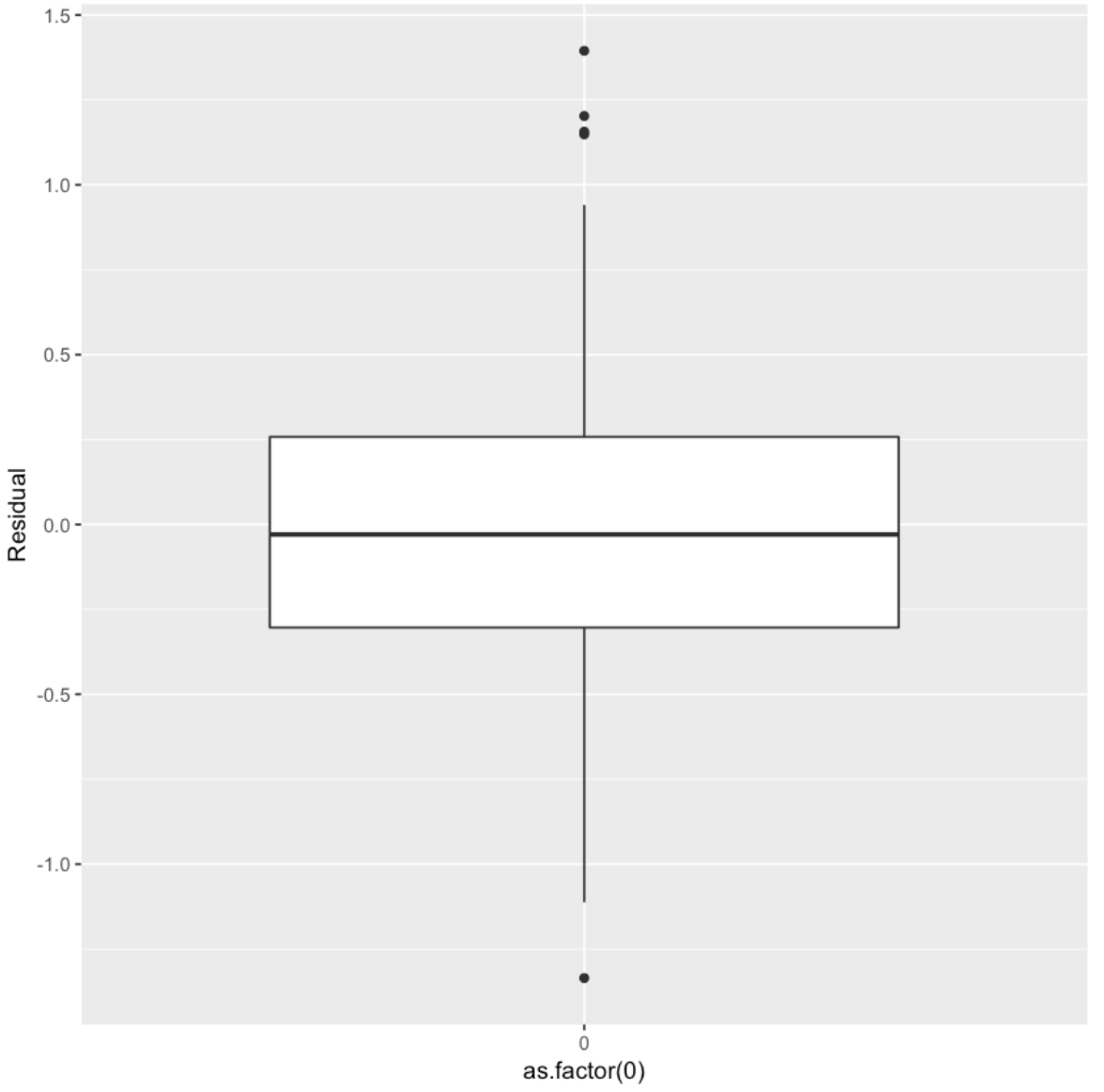
```
-0.0778281858811368  0.0778281858811369
```

In [ ]:

```
1
```

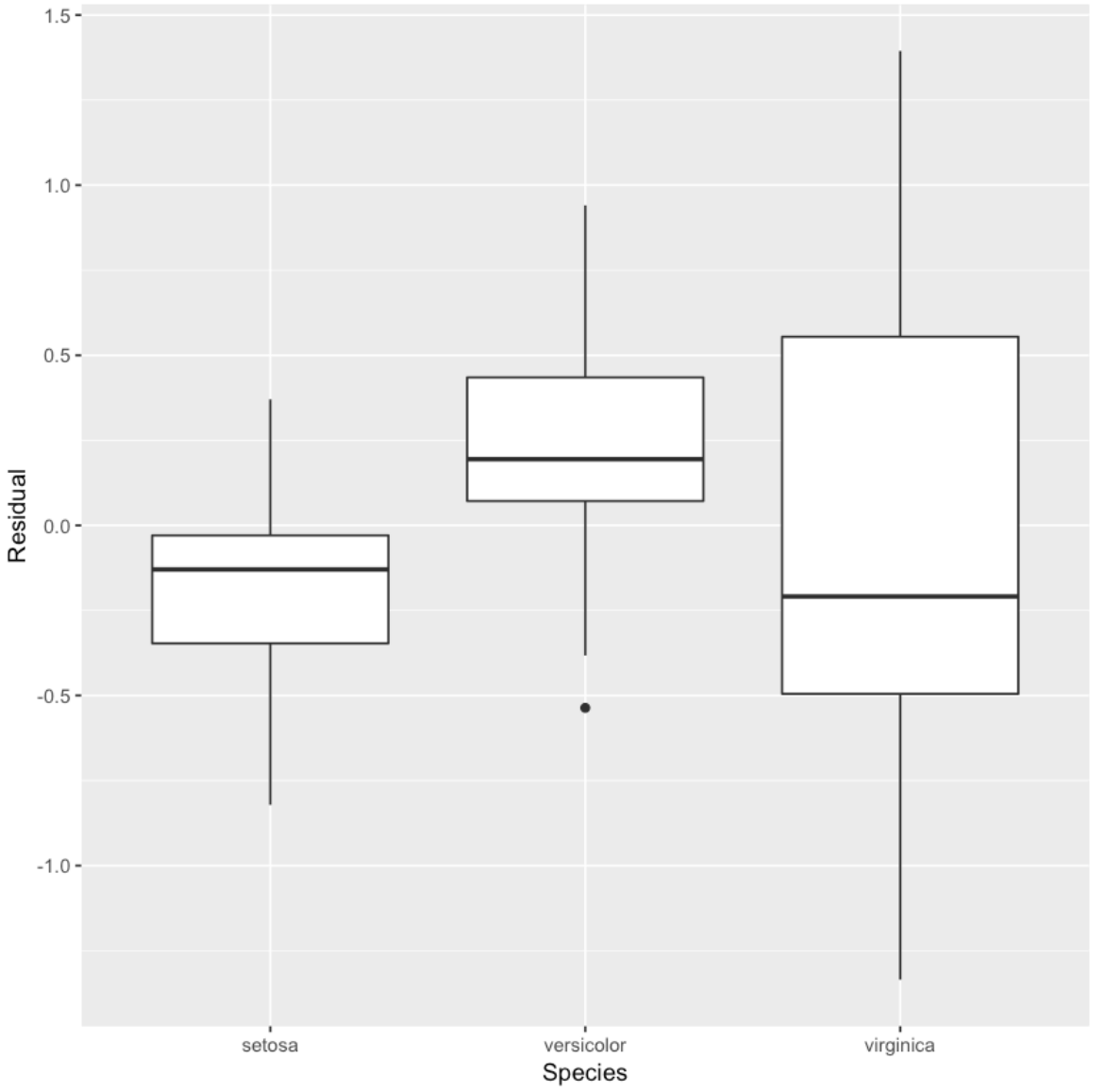
In [134]:

```
ggplot(iris)+
geom_boxplot( aes(as.factor(0), Residual))
```



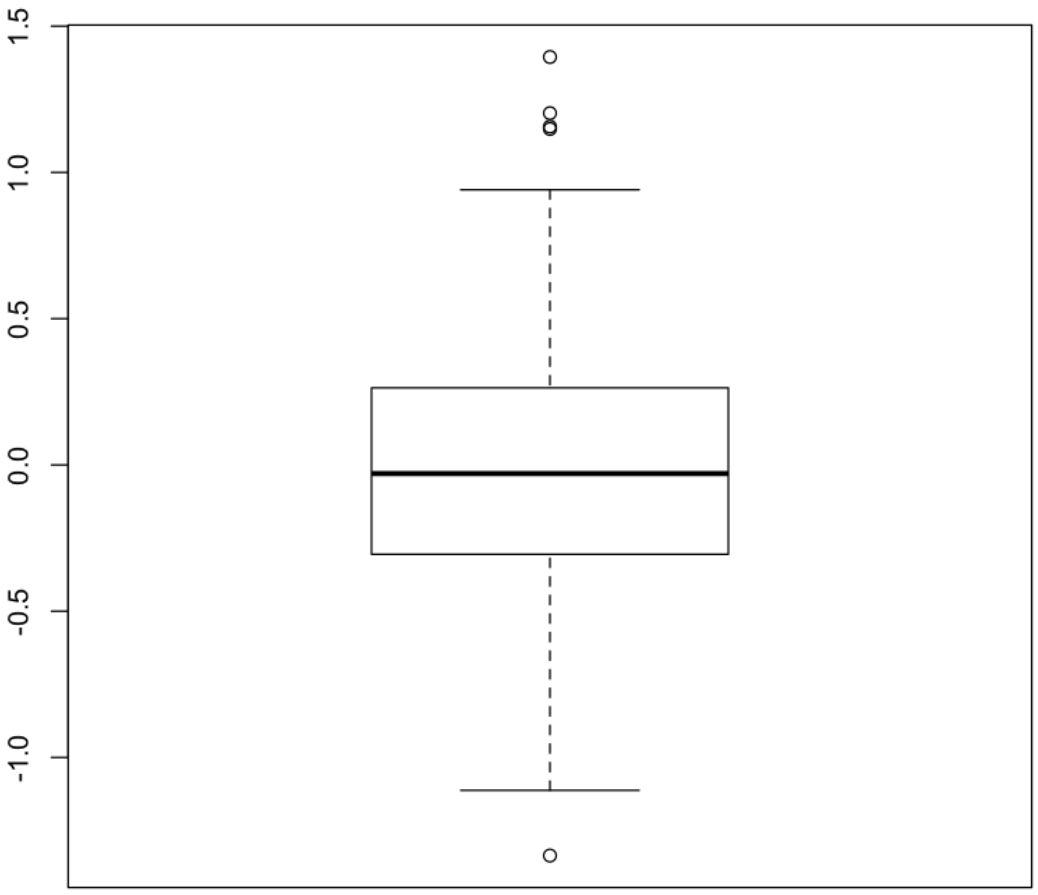
In [135]:

```
ggplot(iris)+
geom_boxplot(aes(Species, Residual))
```



In [136]:

```
1 boxplot(iris$Residual)
```




```
1 # Get a summary report of the model
2 summary(model)
```

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453
```

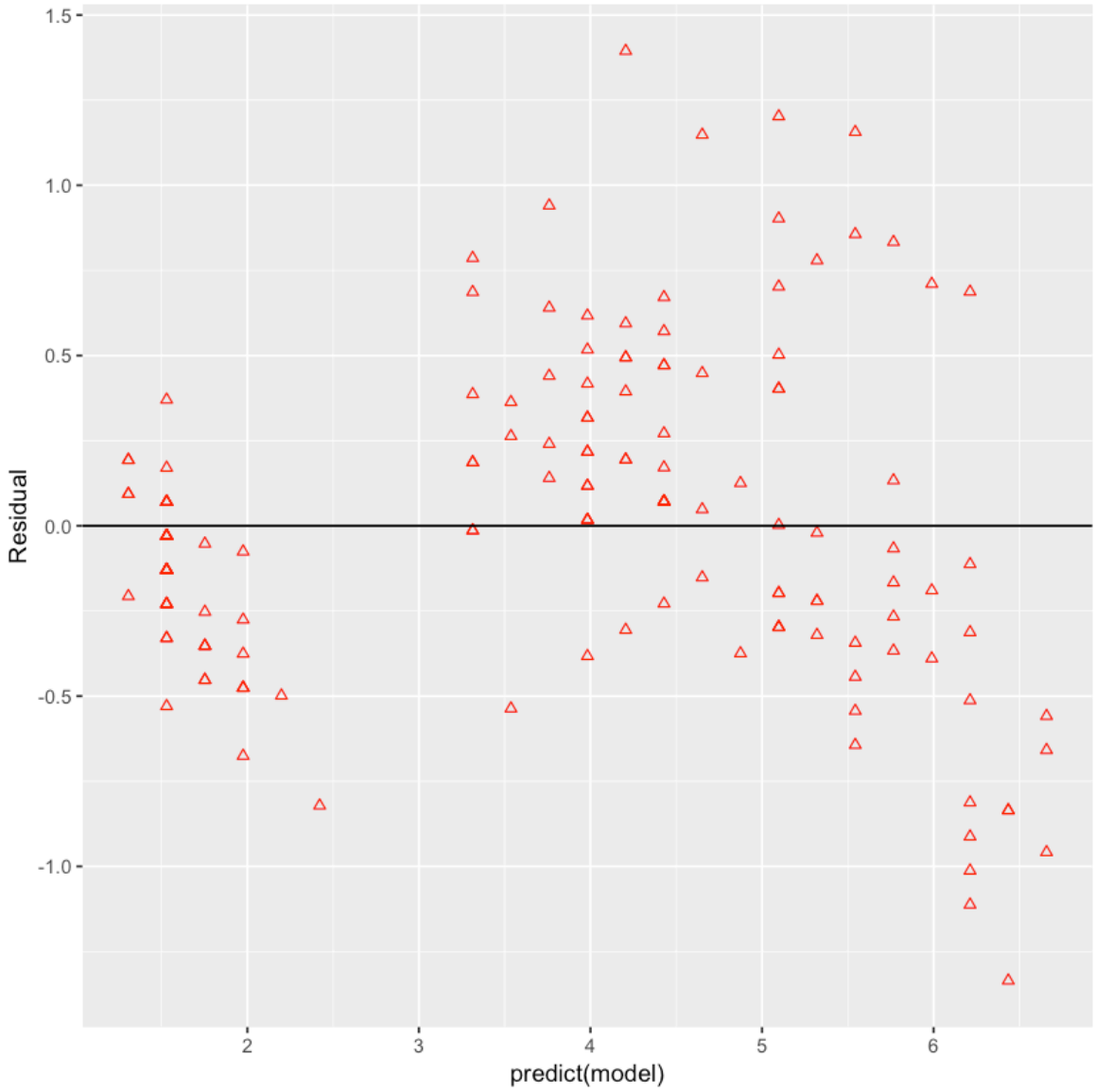
In [137]:

```
summary(iris$Residual)
# same as the one we had above
# Since the median deviance residual is close to zero, this m
#(i.e. the out come is neither over- nor underestimated).
```

```
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max
.
-1.33542 -0.30347 -0.02955  0.00000  0.25776  1.3945
3
```

In [138]:

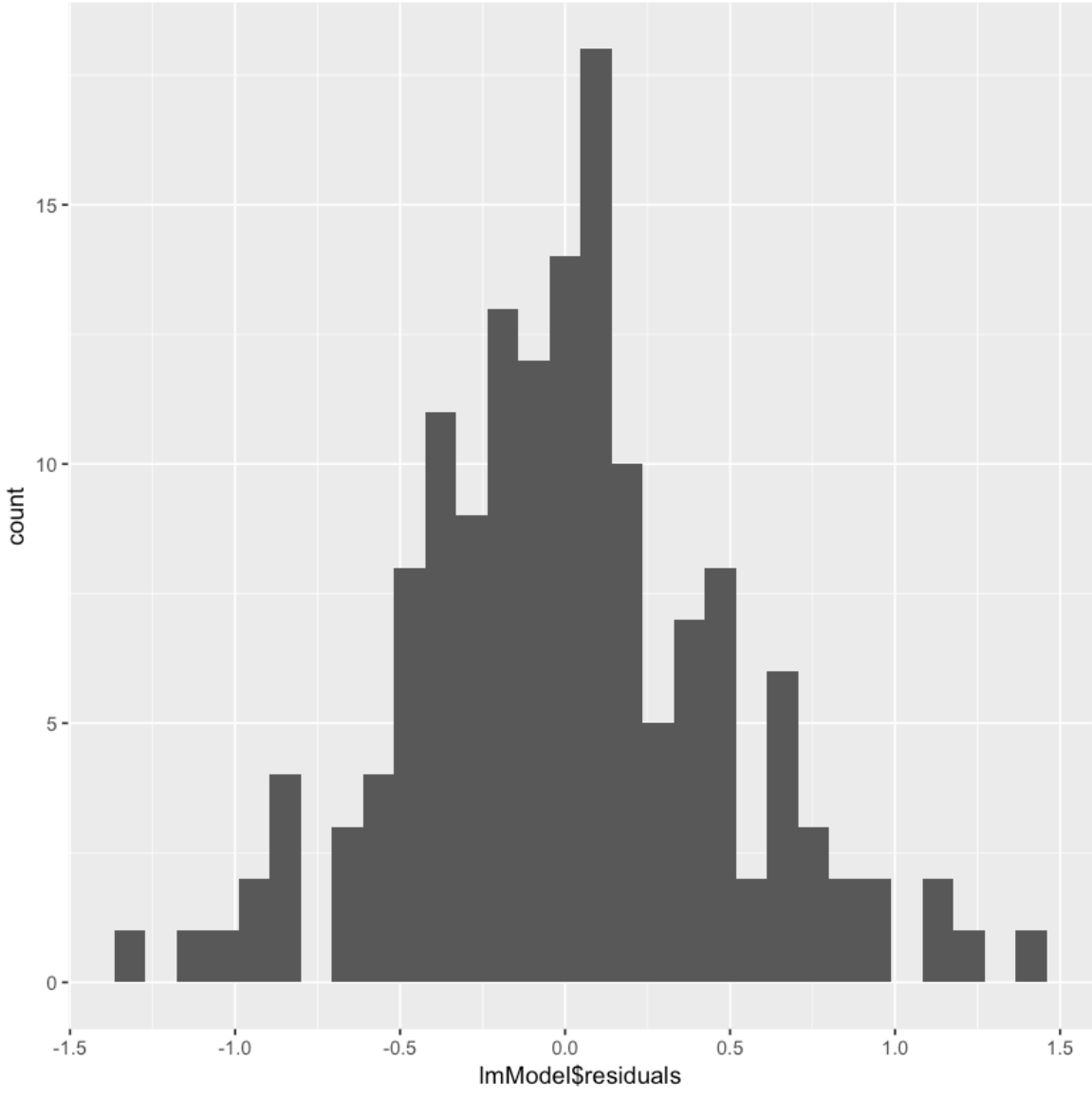
```
# Lets plot these predicted values vs the residuals.
ggplot(iris)+
geom_point( aes( predict(model) , Residual), col="red", pch=2
geom_hline(yintercept=0)
```



In [49]:

```
ggplot() +
geom_histogram(aes(lmModel$residuals))
```

```
`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.
```

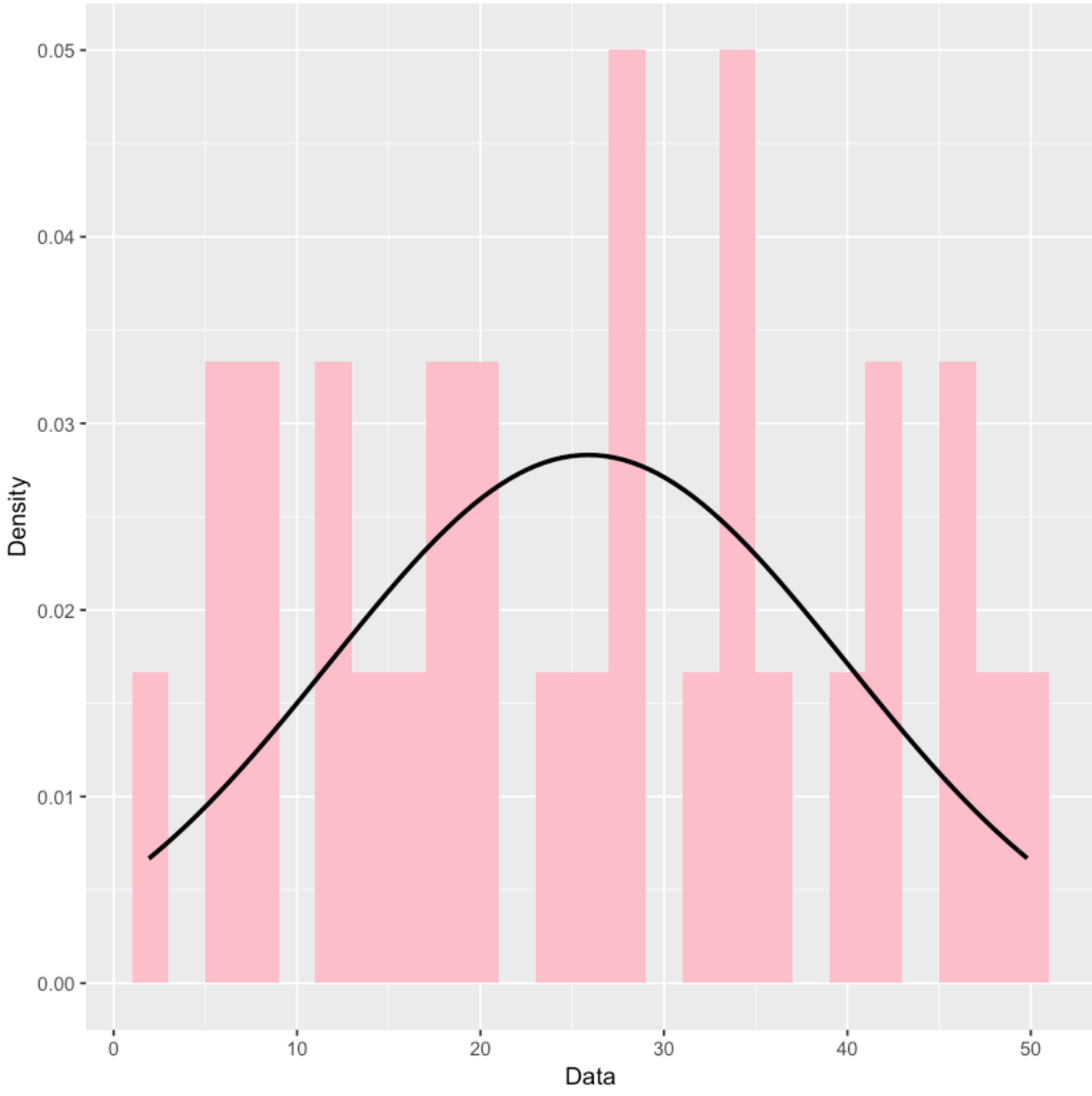


In [ ]:

```

```

In [145]:

```
# exemple de multiple plot on the same graph
data <- data.frame(c(runif(30,1,50)))
ggplot(data, aes(data[,1])) +
    geom_histogram(aes(y = ..density..), binwidth = 2, fill =
    labs(x = 'Data', y = 'Density') +
    stat_function(fun = dnorm,
        args = list(mean = mean(data[,1], na.rm = TRUE),
                    sd = sd(data[,1], na.rm = TRUE)),
        colour = 'black', size = 1)
```



In [152]:

```
names(data)<- "v"
```

In [156]:

```
1 sd(data$v)
```

14.0930419142395

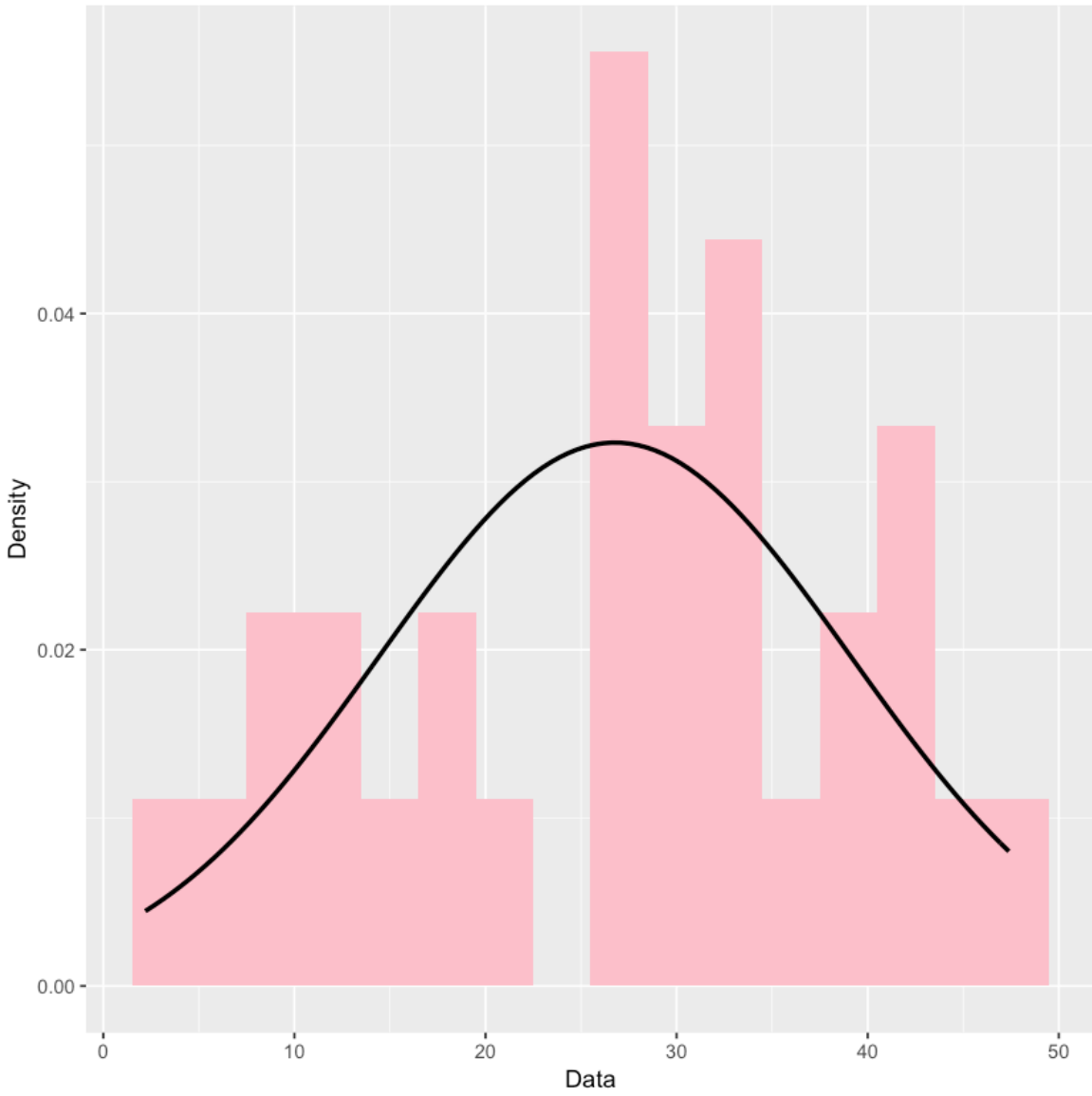
In [157]:

```
1 mean(data$v)
```

25.8732585030841

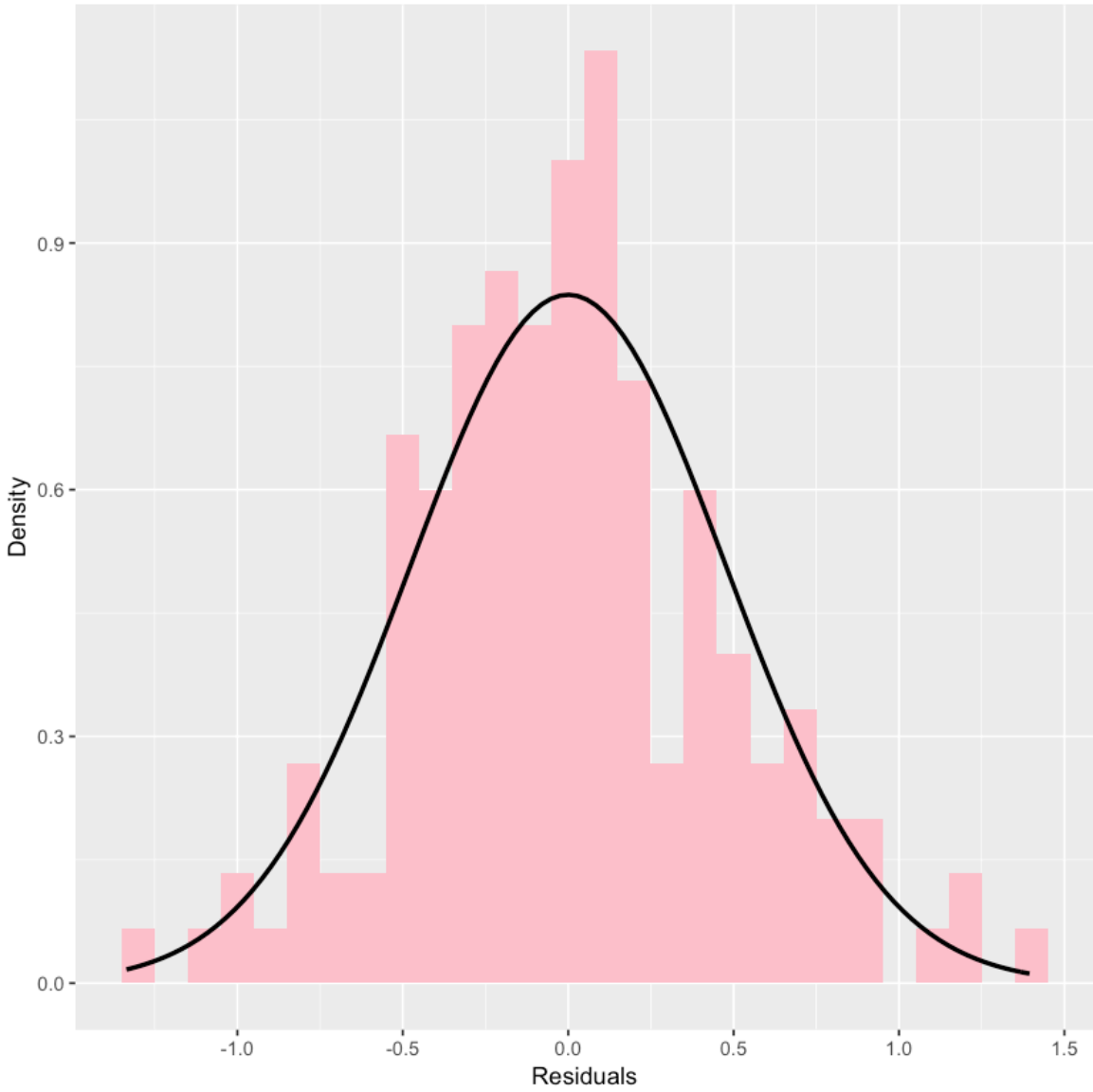
In [166]:

```
data <- data.frame(c(runif(30,1,50)))
ggplot(data, aes(data[,1])) +
    geom_histogram(aes(y = ..density..), binwidth = 3, fill =
    labs(x = 'Data', y = 'Density') +
    stat_function(fun = dnorm,
        args = list(mean = mean(data[,1], na.rm = TRUE),
                    sd = sd(data[,1], na.rm = TRUE)),
        colour = 'black', size = 1)
```



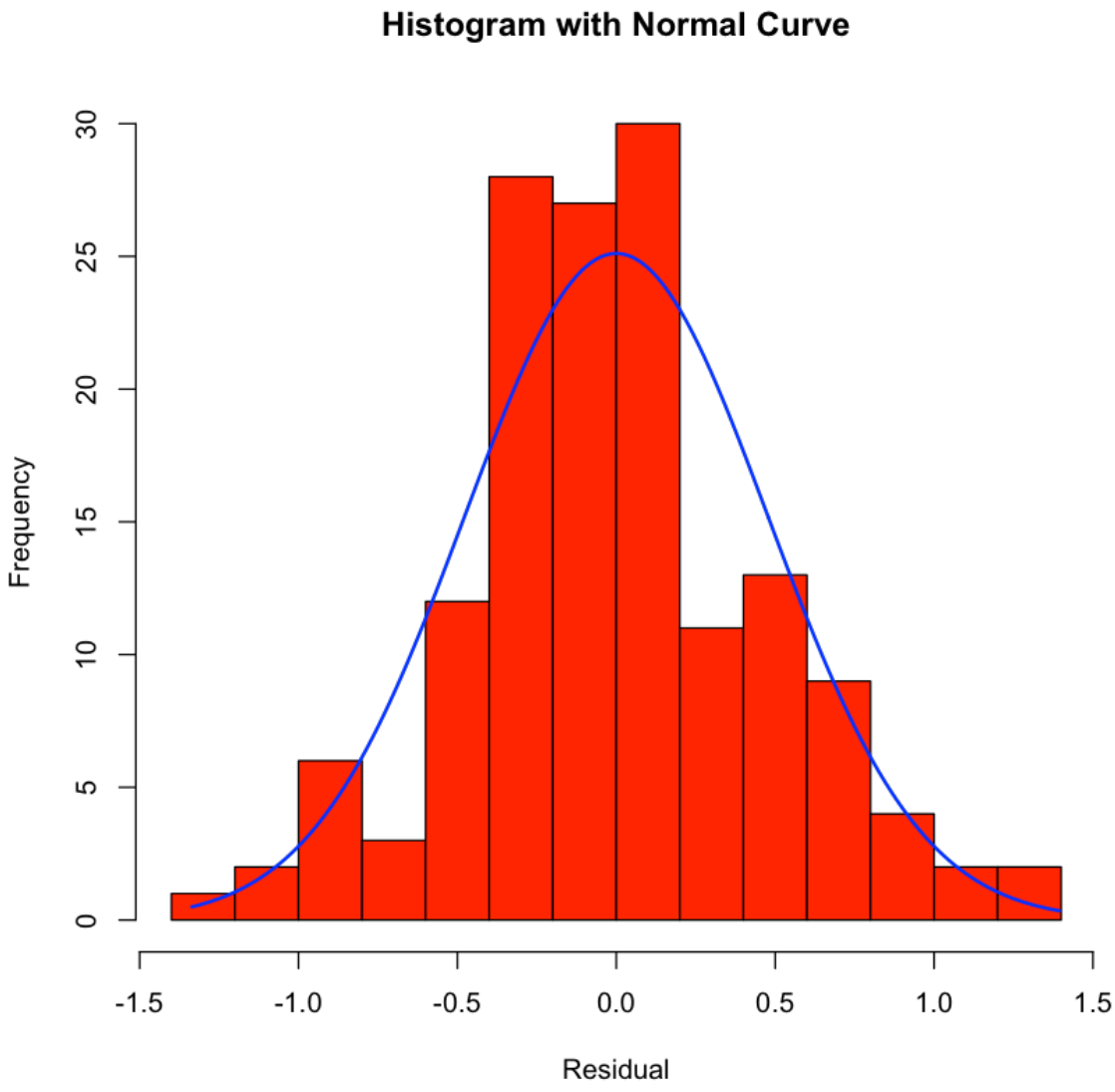
In [52]:

```
ggplot(lmModel, aes(lmModel$residuals)) +
geom_histogram(aes(y=..density..), fill="pink", binwidth = .1
stat_function(fun = dnorm,
        args = list(mean = mean(lmModel$residuals),
                    sd = sd(lmModel$residuals)),
        colour = 'black', size = 1) +
 labs(x = 'Residuals', y = 'Density')
```



In [173]:

```
x <- iris$Residual
h<-hist(x, breaks=10, col="red", xlab="Residual", main="Histo
xfit<-seq(min(x),max(x),length=150)
#dnorm->density of normal dist
yfit<-dnorm(xfit,mean=mean(x),sd=sd(x))
#mids ->the n cell midpoints.
yfit <- yfit*diff(h$mids[1:2])*length(x)
lines(xfit, yfit, col="blue", lwd=2)
```



In [298]:

```
names(iris)
```

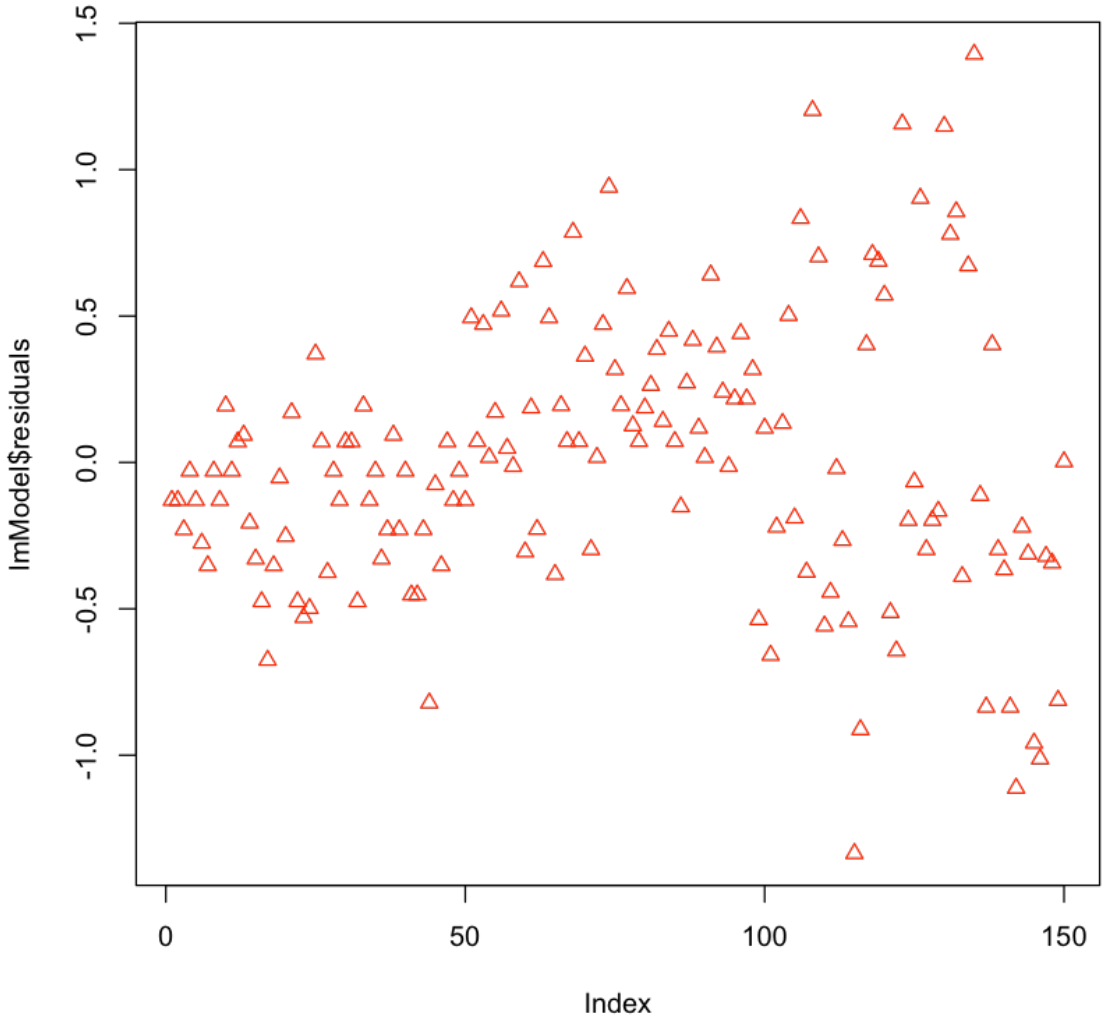
'Sepal.Length' 'Sepal.Width' 'Petal.Length' 'Petal.Width'
'Species'

How to interpret Residuals?

- Residuals follow roughtly normal distribution. We can do so by checking histogram od residuals. If the histogram of residuals looks normal then we have a valid model.

In [16]:

```
#  Simplest way to do previous. Process


plot(lmModel$residuals, col="red", pch=2)

```



In [ ]:

```

```

In [ ]:

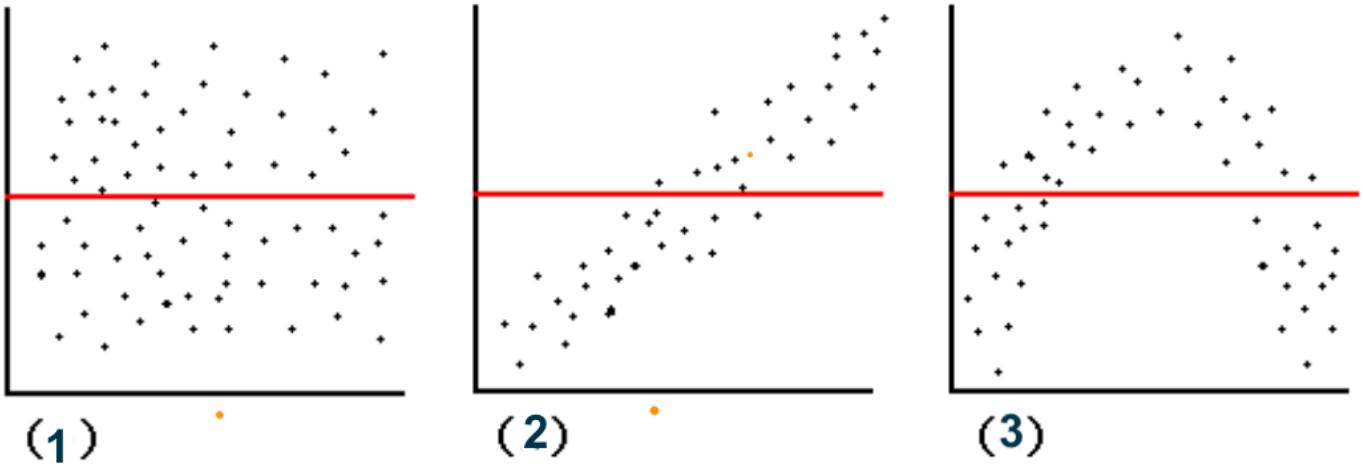
```
1
```

In [ ]:

```
1
```

- A very important point is that we need to check is that our residuals follow roughly normal distribution. We can do so by checking histogram of residuals. If the histogram of residuals looks normal then we have a valid model.

How to interpret Patterns in Residual Plots ?



Residual Plot (a)

- Residuals are randomly distributed around regression line
- Residuals follow normal distribution
- Residuals are Homoscedastic.
- Linear model is valid.

Residual Plot (b)

- Residuals are non randomly distributed around regression line
- Residuals increase as the predicted value increases, which could mean that we might be missing a variable or - two and some predictive pattern is being leaked as a residual.
- Residuals are Homoscedastic.
- Linear model is not valid (if it has intercept), check for explanatory variables which might explain the linear residual or the model has failed to account for intercept
- Or the plot does not belong to a linear model at all another option is that the model might be a model forced to pass through origin i.e a non intercept model

Residual Plot (c)

- Residuals are non randomly distributed around regression line
- Residuals are Homoscedastic
- Residuals have curve pattern to them. -Linear model is not valid. Curved residual pattern might mean that we may have to fit a polynomial of some order to explain the curved pattern of residuals.

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

visualize The Model

In [75]:

```
1 coef(model)
```

(Intercept)
1.08355803285051
Petal.Width
2.22994049512186

In [ ]:

```
1
```

In [115]:

```
ggplot( iris, aes( Petal.Width, Petal.Length))+
geom_point()+
geom_abline(intercept = model$coefficients[1], slope=model$co
```

```
Error in geom_abline(intercept = model$coefficients[
1], slope = model$coefficients[2], : object 'model'
not found
Traceback:

1. geom_abline(intercept = model$coefficients[1], sl
ope = model$coefficients[2],
 .     color = "red", lwd = 2)
```

In [ ]:

```

```

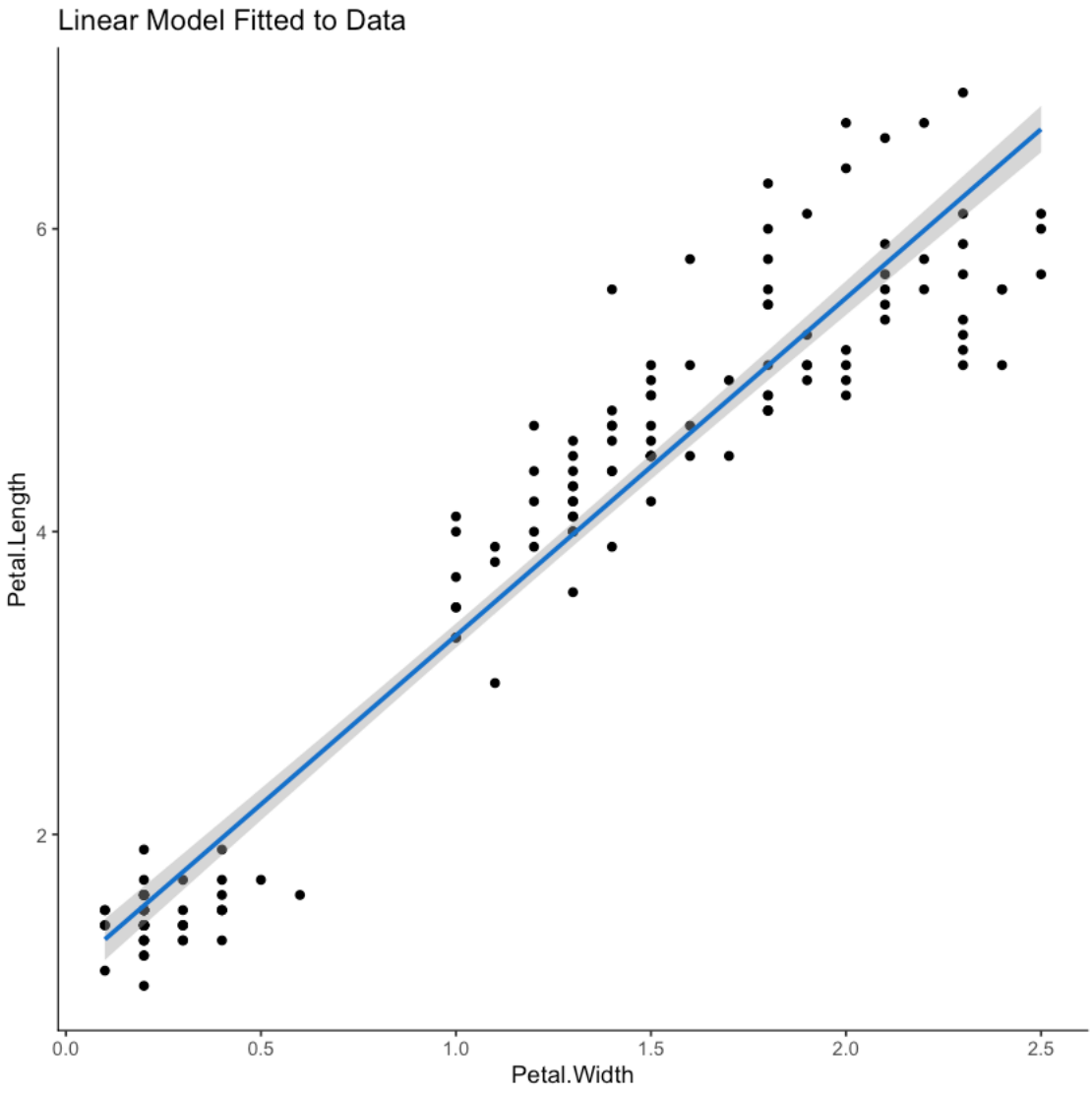
In [114]:

```
eq = paste("y = ", round(model$coefficients[2], 2), "*x ", ro

ggplot( iris, aes( Petal.Width, Petal.Length))+
geom_point()+
geom_abline(intercept = model$coefficients[1], slope=model$co
geom_hline(yintercept = mean(Petal.Length)) +
ggtitle( " LInear Regression ", subtitle = eq)
```

```
Error in paste("y = ", round(model$coefficients[2],
2), "*x ", round(model$coefficients[1], : object 'mo
del' not found
Traceback:

1. paste("y = ", round(model$coefficients[2], 2), "*
x ", round(model$coefficients[1],
 .     2))
```

In [112]:

```
ggplot(iris, aes(Petal.Width,Petal.Length)) +
geom_point() +
stat_smooth(method = "lm", col = "dodgerblue3") +
theme(panel.background = element_rect(fill = "white"),
axis.line.x=element_line(),
axis.line.y=element_line()) +
ggtitle("Linear Model Fitted to Data")
```

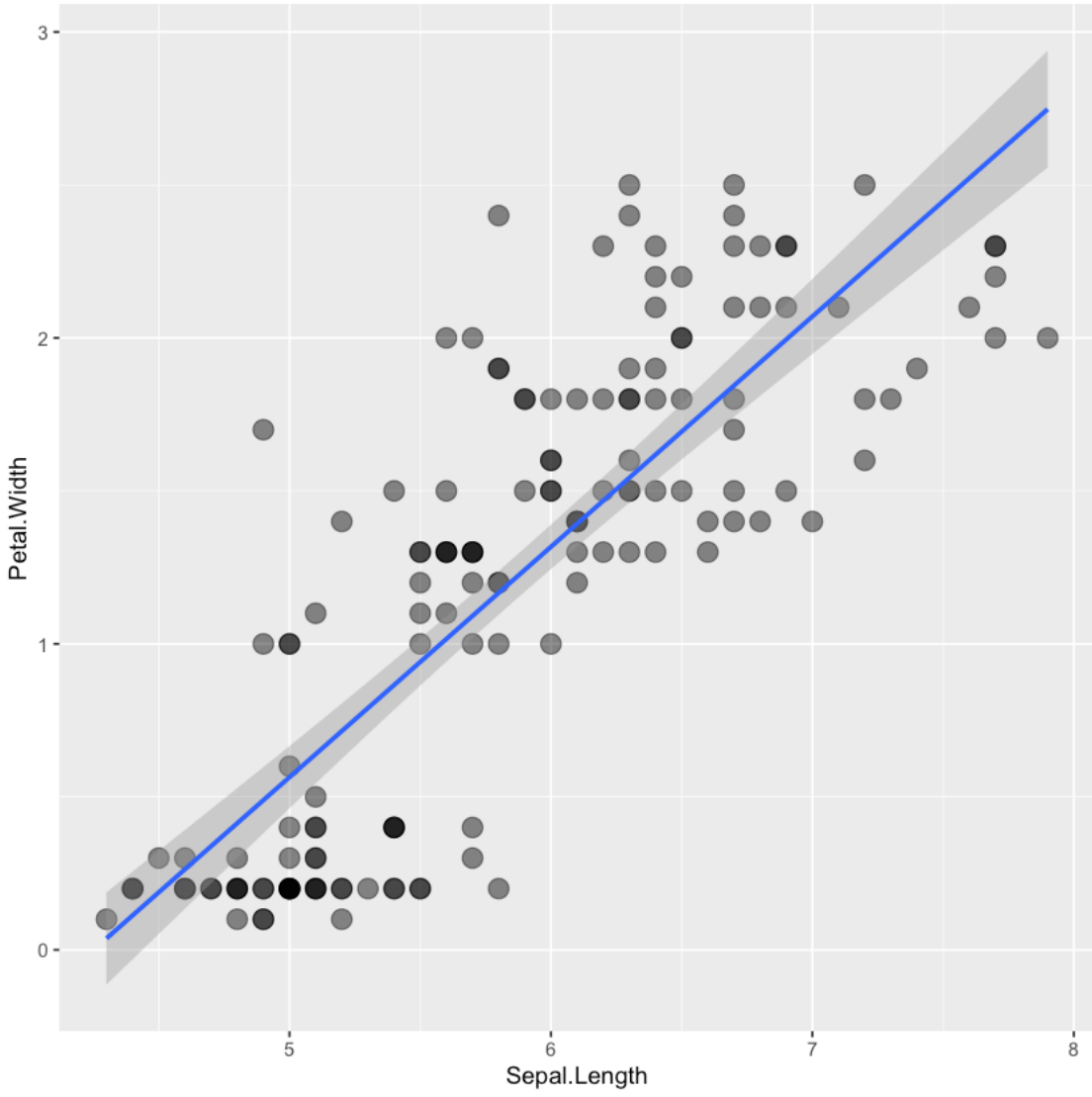


- The gray shading around the line represents a confidence interval of 0.95, the default for the stat_smooth() function, which smoothes data to make patterns easier to visualize. This 0.95 confidence interval is the probability that the true linear model for the girth and volume of all black cherry trees will lie within the confidence interval of the regression model fitted to our data. Even though this model fits our data quite well, there is still variability within our observations.

Another alternative for Sepal Length & Width

In [105]:

```
ggplot(iris, aes(Sepal.Length, Petal.Width))+
  geom_point(size = 4,
             alpha = 0.5)+
  geom_smooth(method = "lm")
```



- here we can either test the ***model*** with a new dataframe using coeficients' model or throught the **predict** instruction

In [106]:

```
newDf<- c(1.5, 3.4, 5)
lmModel$coef[1] +lmModel$coef[2]*newDf
predict(lmModel, data.frame(Petal.Width=newDf))
```

4.42846877553331 8.66535571626484 12.2332605084598

1
4.42846877553331
2
8.66535571626484
3
12.2332605084598

In [107]:

```
library(broom)
```

In [108]:

```
lmModel %>%
    augment() %>% head()
```

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl:
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [109]:

```
1 head(predict(lmModel))
```

1
1.52954613187489
2
1.52954613187489
3
1.52954613187489
4
1.52954613187489
5
1.52954613187489
6
1.97553423089926

In [110]:

```
1 sum(lmModel$residuals)
```

-2.94556046220862e-15

In [111]:

```
1 lmModel %>%
2     augment() %>%
3     summarise(Sum=sum(.resid))
```

A tibble: 1 × 1

Sum
<dbl>
-2.94556e-15

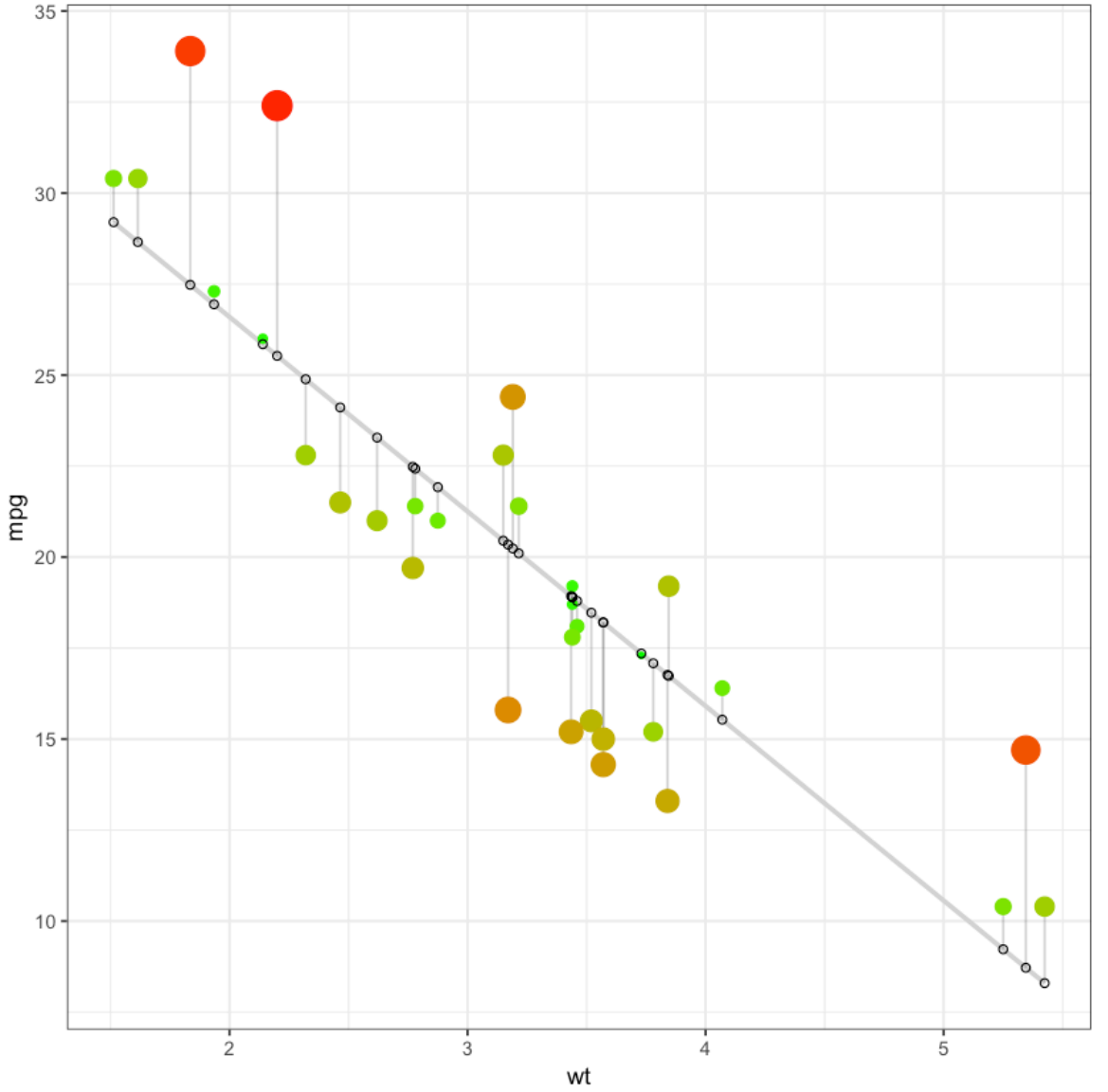
In [ ]:

```
1
```

Residuals

In [75]:

```
cars <- mtcars
lmCarModel <- lm(mpg ~ wt, data = cars) # fit the model
cars$predicted <- predict(lmCarModel)   # Save the predicted
cars$residuals <- residuals(lmCarModel) # Save the residual v
ggplot(cars, aes(x = wt, y = mpg)) +
  geom_smooth(method = "lm", se = FALSE, color = "lightgrey")
  geom_segment(aes(xend = wt, yend = predicted), alpha = .2)
  geom_point(aes(color = abs(residuals), size = abs(residuals
  scale_color_continuous(low = "green", high = "red") +
  guides(color = FALSE, size = FALSE) +
  geom_point(aes(y = predicted), shape = 1) +
  theme_bw()
```



In [76]:

```
summary(lmCarModel)
```

```
Call:
lm(formula = mpg ~ wt, data = cars)

Residuals:
    Min      1Q  Median      3Q     Max
-4.5432 -2.3647 -0.1252  1.4096  6.8727

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  37.2851     1.8776  19.858  < 2e-16 ***
wt           -5.3445     0.5591  -9.559 1.29e-10 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 3.046 on 30 degrees of free
dom
Multiple R-squared:  0.7528,    Adjusted R-squared:
0.7446
F-statistic: 91.38 on 1 and 30 DF,  p-value: 1.294e-
10
```

In [77]:

```
names(lmCarModel)
```

'coefficients' 'residuals' 'effects' 'rank' 'fitted.values' 'assign' 'qr' 'df.residual' 'xlevels' 'call' 'terms' 'model'

In [ ]:

```

```

In [78]:

```
library(dplyr); library(broom); library(ggplot2)


    ggplot(lmCarModel) +
    geom_point(aes( predict(lmCarModel), residuals))
```

```
Don't know how to automatically pick scale for objec
t of type function. Defaulting to continuous.
```

```
ERROR while rich displaying an object: All columns i
n a tibble must be 1d or 2d objects:
* Column `y` is function
Traceback:
1. FUN(X[[i]], ...)
2. tryCatch(withCallingHandlers({
 .     rpr <- mime2repr[[mime]](obj)
 .     if (is.null(rpr))
 .         return(NULL)
 .     prepare_content(is.raw(rpr), rpr)
 . }, error = error_handler), error = outer_handler)
3. tryCatchList(expr, classes, parentenv, handlers)
4. tryCatchOne(expr, names, parentenv, handlers[[1L]
])
5. doTryCatch(return(expr), name, parentenv, handler
)
6. withCallingHandlers({
 .     rpr <- mime2repr[[mime]](obj)
 .     if (is.null(rpr))
 .         return(NULL)
 .     prepare_content(is.raw(rpr), rpr)
 . }, error = error_handler)
7. mime2repr[[mime]](obj)
8. repr_text.default(obj)
9. paste(capture.output(print(obj)), collapse = "\n"
)
10. capture.output(print(obj))
11. evalVis(expr)
12. withVisible(eval(expr, pf))
13. eval(expr, pf)
14. eval(expr, pf)
15. print(obj)
16. print.ggplot(obj)
17. ggplot_build(x)
18. ggplot_build.ggplot(x)
19. by_layer(function(l, d) l$compute_aesthetics(d,
plot))
20. f(l = layers[[i]], d = data[[i]])
21. l$compute_aesthetics(d, plot)
22. f(..., self = self)
23. as_gg_data_frame(evaled)
24. as.data.frame(tibble::as_tibble(x))
25. tibble::as_tibble(x)
26. as_tibble.list(x)
27. lst_to_tibble(x, .rows, .name_repair, col_length
s(x))
28. check_valid_cols(x)
29. abort(error_column must be vector(names_x[is_xd]
```

```
, classes))
```

In [79]:

```
library(dplyr); library(broom)
lmCarModel %>% augment() %>% select(mpg, .fitted, .resid) %>%
```

mpg	.fitted	.resid
21.0	23.28261	-2.2826106
21.0	21.91977	-0.9197704
22.8	24.88595	-2.0859521
21.4	20.10265	1.2973499
18.7	18.90014	-0.2001440
18.1	18.79325	-0.6932545

In [86]:

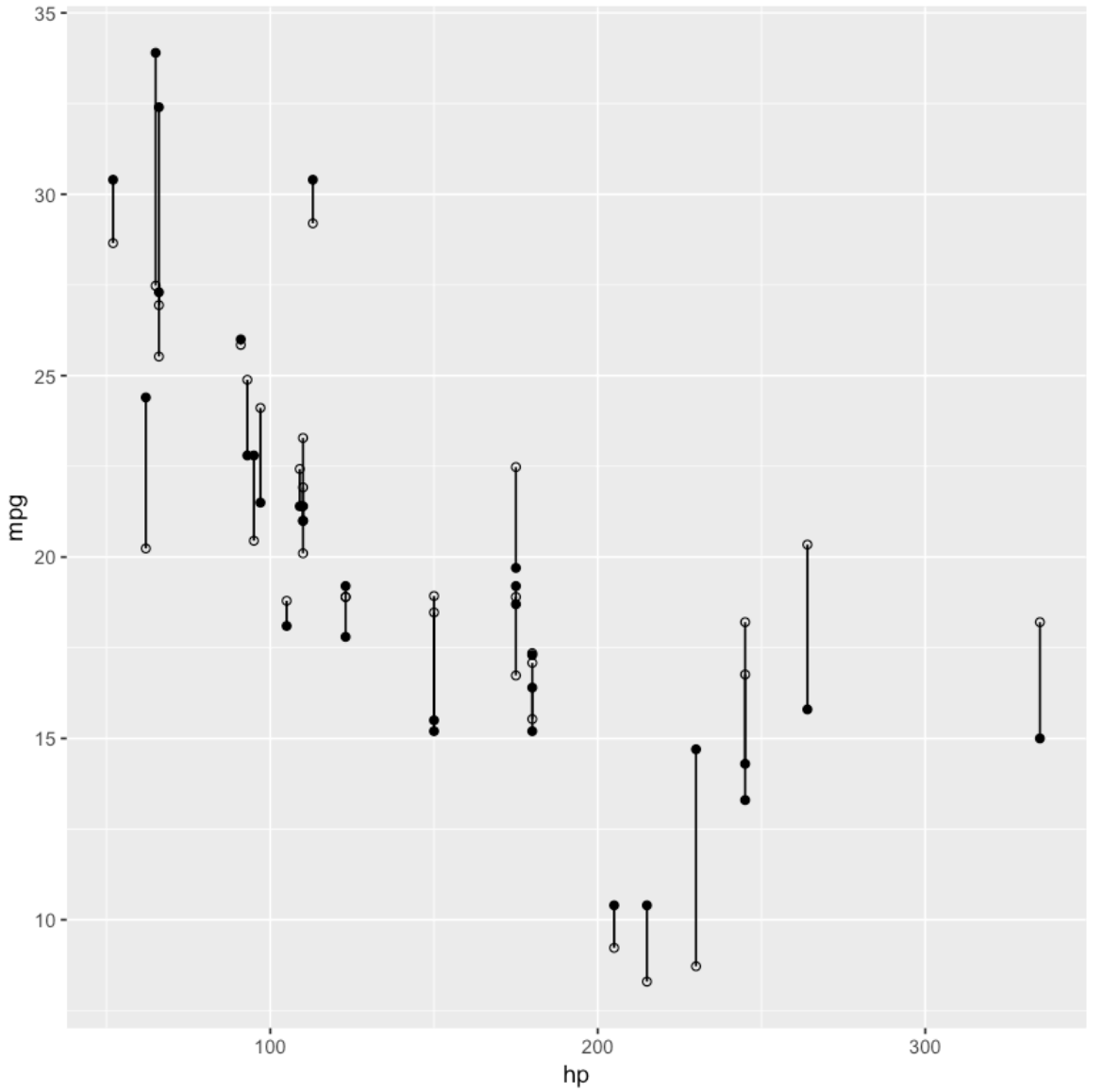
```
1  head(residuals(lmCarModel));  head(predict(lmCarModel))
```

Mazda RX4
-2.28261064680868
Mazda RX4 Wag
-0.91977039576432
Datsun 710
-2.08595211862542
Hornet 4 Drive
1.29734993896137
Hornet Sportabout
-0.200143957176023
Valiant
-0.693254525721567

Mazda RX4
23.2826106468086
Mazda RX4 Wag
21.9197703957643
Datsun 710
24.8859521186254
Hornet 4 Drive
20.1026500610386
Hornet Sportabout
18.900143957176
Valiant
18.7932545257216

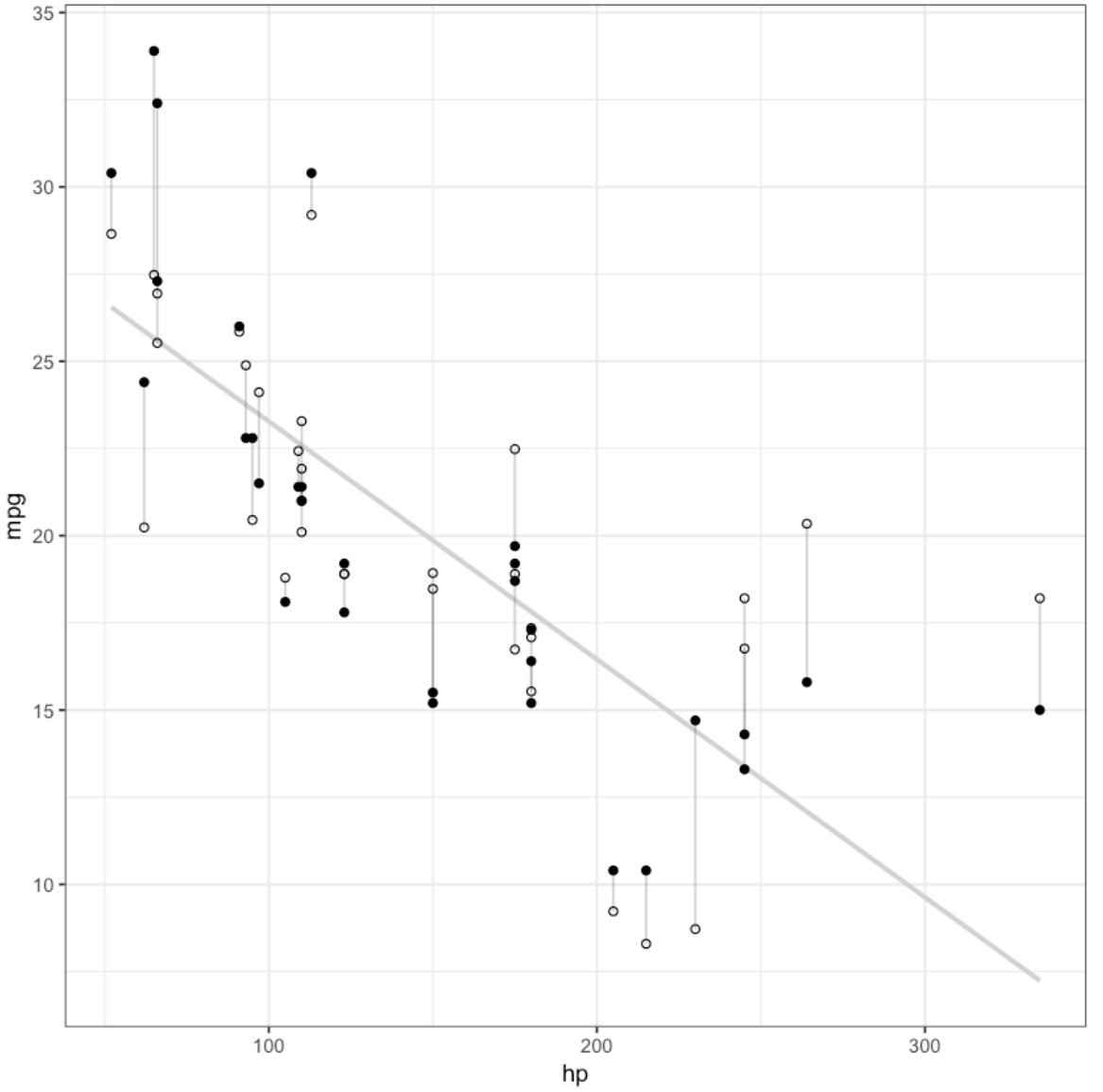
In [88]:

```
df<- lmCarModel %>% augment()
ggplot(mtcars, aes(x = hp, y = mpg)) +
  geom_segment(aes(xend = hp, yend = df$.fitted)) +
  geom_point() +
  geom_point(aes(y = df$.fitted), shape = 1)
```



In [89]:

```
df<- lmCarModel %>% augment()
ggplot(mtcars, aes(x = hp, y = mpg)) +
  geom_smooth(method = "lm", se = FALSE, color = "lightgrey")
  geom_segment(aes(xend = hp, yend = df$.fitted), alpha = .2)
  geom_point() +
  geom_point(aes(y = df$.fitted), shape = 1) +
  theme_bw()
```



In [97]:

```
library(tidyr)
```

In [98]:

```
mtcars %>%
  gather(key = "iv", value = "x", -Sepal.Width) %>%
  ggplot(aes(x = x, y = Sepal.Width)) +
  geom_segment(aes(xend = x, yend = df$.fitted), alpha = .2)
  geom_point(aes(color = df$.resid)) +
  scale_color_gradient2(low = "blue", mid = "white", high = '
  guides(color = FALSE) +
  geom_point(aes(y = df$.fitted), shape = 1) +
  facet_grid(~ iv, scales = "free_x") +
  theme_bw()
```

```
`NULL` must evaluate to column positions or names, n
ot a double vectorTraceback:

1. mtcars %>% gather(key = "iv", value = "x", -Sepal
.Width) %>%
 .     ggplot(aes(x = x, y = Sepal.Width))
2. withVisible(eval(quote(`_fseq`(`_lhs`)), env, env
))
3. eval(quote(`_fseq`(`_lhs`)), env, env)
4. eval(quote(`_fseq`(`_lhs`)), env, env)
5. `_fseq`(`_lhs`)
6. freduce(value, `_function_list`)
7. function_list[[i]](value)
8. gather(., key = "iv", value = "x", -Sepal.Width)
9. gather.data.frame(., key = "iv", value = "x", -Se
pal.Width)
10. unname(tidyselect::vars_select(names(data), !!!q
uos))
11. tidyselect::vars_select(names(data), !!!quos)
12. bad_calls(bad, "must evaluate to { singular(.var
s) } positions or names, \\\n       not { first_type
}")
13. glubort(fmt_calls(calls), ..., .envir = .envir)
14. .abort(text)
```

In [ ]:

```
1
```

In [69]:

```
1 names(lmCarModel)
```

'.rownames' 'mpg' 'wt' '.fitted' '.se.fit' '.resid' '.hat'
'.sigma' '.cooksd' '.std.resid'

In [70]:

```
1 head(lmCarModel)
```

.rownames	mpg	wt	.fitted	.se.fit	.resid	.hat	
Mazda RX4	21.0	2.620	23.28261	0.6335798	-2.2826106	0.04326896	3
Mazda RX4 Wag	21.0	2.875	21.91977	0.5714319	-0.9197704	0.03519677	3
Datsun 710	22.8	2.320	24.88595	0.7359177	-2.0859521	0.05837573	3
Hornet 4 Drive	21.4	3.215	20.10265	0.5384424	1.2973499	0.03125017	3
Hornet Sportabout	18.7	3.440	18.90014	0.5526562	-0.2001440	0.03292182	3
Valiant	18.1	3.460	18.79325	0.5552829	-0.6932545	0.03323551	3

In [71]:

```
1 lmCarModel
```

```
Warning message:
“Unknown or uninitialised column: 'coef'.”

NULL
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

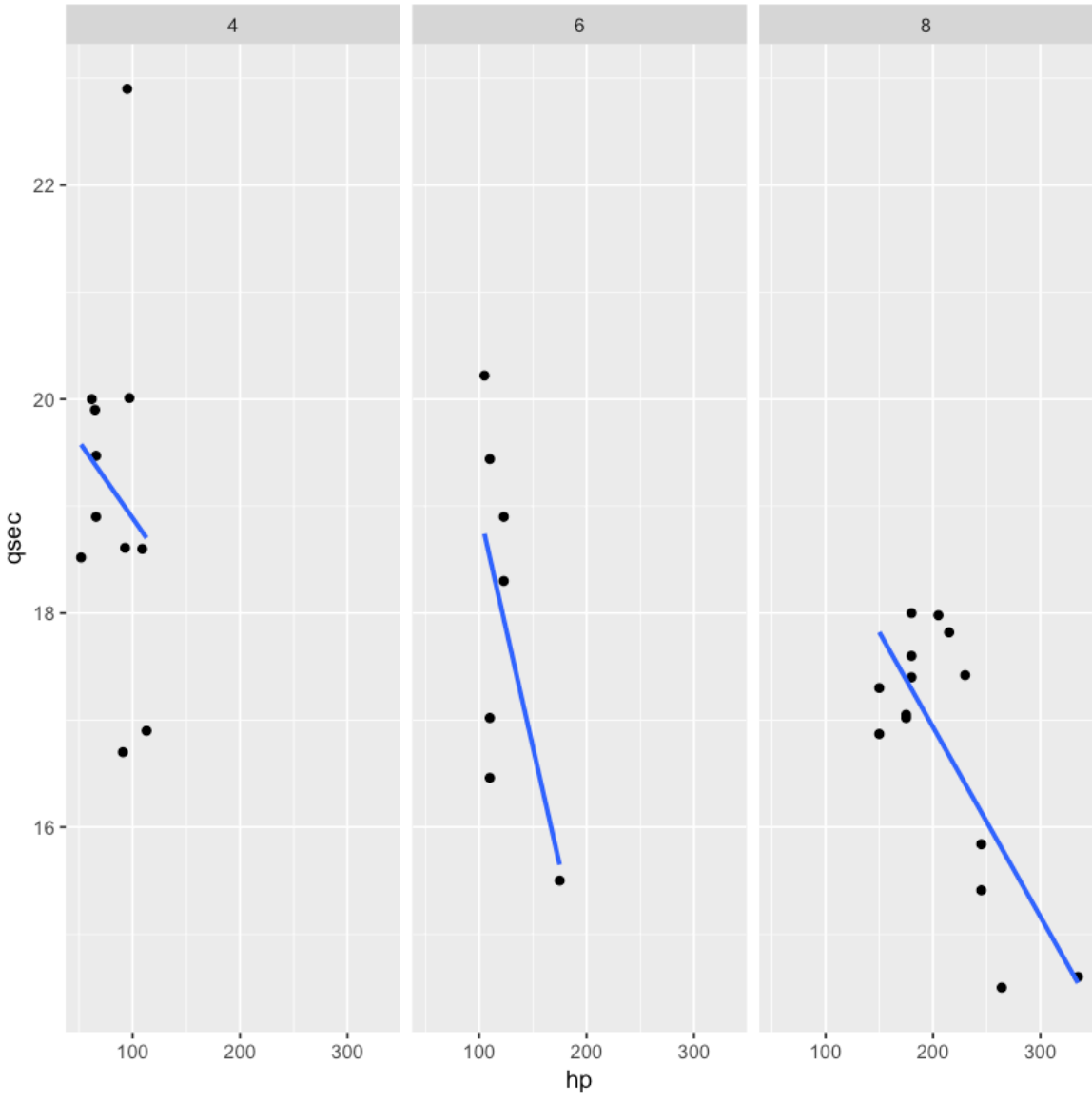
In [12]:

```
1 library(ggplot2)
2 library(dplyr)
```

```
Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats
’:

    filter, lag

The following objects are masked from ‘package:base’
:

    intersect, setdiff, setequal, union
```

In [17]:

```
#Another alternative for lm graph
p <- ggplot(mtcars, aes(hp, qsec)) + geom_point()
 p + geom_smooth(method = "lm", se = FALSE) + facet_wrap(~cyl
```



In [128]:

```
x< as.matrix(cbind(1, Petal.Length, Petal.Width))
y<- as.matrix(Petal.Length)
 solve(t(x)%*%x)%*%t(x)%*%y
```

```
Warning message in x < as.matrix(cbind(1, Petal.Leng
th, Petal.Width)):
“longer object length is not a multiple of shorter o
bject length”
```

A matrix: 150 × 3 of type lgl

	Petal.Length	Petal.Width
TRUE	TRUE	FALSE

TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
FALSE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
⋮	⋮	⋮
TRUE	TRUE	TRUE

TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
FALSE	TRUE	TRUE
TRUE	TRUE	TRUE
FALSE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
FALSE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
TRUE	TRUE	TRUE
FALSE	TRUE	TRUE

```
Error in solve(t(x) %*% x) %*% t(x) %*% y: non-confo
rmable arguments
Traceback:
```

In [ ]:

```
1
```

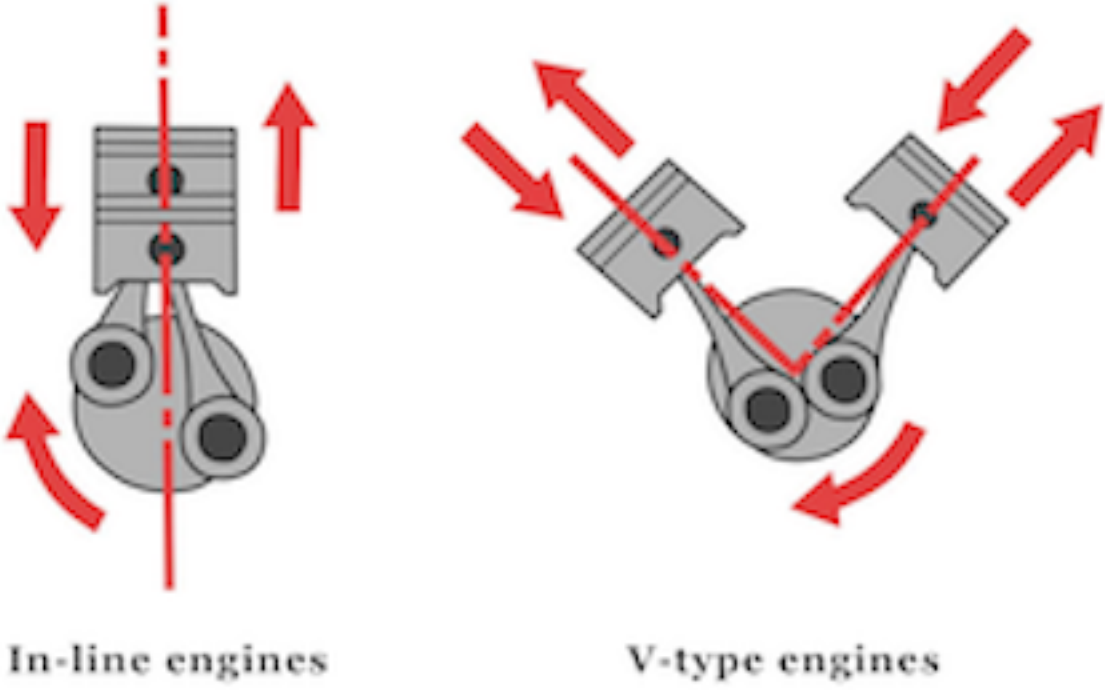
In [ ]:

```
1
```

المسألة

We want to create a model that helps us to predict the probability of a vehicle having a V engine or a straight engine given a weight of 2100 lbs and engine displacement of 180 cubic inches.

نود انشاء نموذج قادر على التنبؤ باحتمال ان V او inline بناء على خاصيتي سعة المحرك disp و وون السيارة wt تكون خصائص محرك سيارة على شكل



First we fit the model:

We use the glm() function, include the variables in the usual way, and specify a binomial error distribution, as follows:

In [ ]:

```
1
```

In [ ]:

```
1
```

In [53]:

```
1 #Generalized Linear Models
2 modelLM<- glm(vs ~ wt +disp, mtcars, family="binomial")
```

In [54]:

```
1 summary(modelLM)
```

```
Call:
glm(formula = vs ~ wt + disp, family = "binomial", d
ata = mtcars)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.67506  -0.28444  -0.08401   0.57281   2.08234

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.60859    2.43903   0.660    0.510
wt           1.62635    1.49068   1.091    0.275
disp        -0.03443    0.01536  -2.241    0.025 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to b
e 1)

    Null deviance: 43.86  on 31  degrees of freedom
Residual deviance: 21.40  on 29  degrees of freedom
AIC: 27.4

Number of Fisher Scoring iterations: 6
```

Deviance

- We see from the estimates of the coefficients that weight influences vs positively, while displacement has a slightly negative effect
- We also see that the coefficient of weight is non-significant ($p > 0.05$), while the coefficient of displacement is significant
- the estimates (coefficients of the predictors weight and displacement) are now in units called logits
- Deviance is a measure of goodness of fit of a generalized linear model.

The null deviance shows how well the response variable is predicted by a model that includes only the intercept (grand mean) where as residual with inclusion of independent variables. Or rather its'a a measure of badness of fit.

```
– higher numbers indicate worse fit.
```

Above, you can see that addition of 2 (31-29 =2) independent variablesdecreased the deviance to 21.4 from 43.86, a significant reduction in deviance.The Residual Deviance has reduced by 22.46 with a loss of two degrees of freedom.

If your Null Deviance is really small, it means that the Null Model explains the data pretty well. Likewise with your Residual Deviance.

```
– The null deviance shows how well the response variable
is predicted by a model that includes only the intercept
(grand mean).
```

Fisher's Scoring

```
 – the Fisher's Scoring Algorithm needed six iterations t
o perform the fit. This doesn't really tell you a lot tha
t you need to know, other than the fact that the model di
d indeed converge, and had no trouble doing it.
```

Information Criteria

The Akaike Information Criterion (AIC) provides a method for assessing the quality of your model through comparison of related models. It's based on the Deviance, but penalizes you for making the model more complicated. Much like adjusted R-squared, it's intent is to prevent you from including irrelevant predictors.

In [ ]:

```
1
```

Remember, our goal here is to calculate a predicted probability of a V engine, for specific values of the predictors: a weight of 2100 lbs and engine displacement of 180 cubic inches.

To do that, we create a data frame called newdata, in which we include the desired values for our prediction.

In [63]:

```
1 dataPred<- data.frame(wt=2.32, disp=108)
```

Now we use the predict() function to calculate the predicted probability. We include the argument type="response" in order to get our prediction.

In [64]:

```
1 predict(modelLM, dataPred, type="response")
```

1: 0.840625522555481

The predicted probability is 0.24.

In [59]:

```
1 install.packages("ResourceSelection")
```

```
Updating HTML index of packages in '.Library'
Making 'packages.html' ... done
```

In [60]:

```
1 library(ResourceSelection)
```

```
ResourceSelection 0.3-5          2019-07-22
```

In [61]:

```
hoslem.test(mtcars$vs, fitted(modelLM))
```

```
        Hosmer and Lemeshow goodness of fit (GOF) te
st

data:  mtcars$vs, fitted(modelLM)
X-squared = 6.4717, df = 8, p-value = 0.5945
```

- Our model seems to fit well because we have no significance difference between the model and the observed Data since P-value is above 0.05.

In [62]:

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	car
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	

In [ ]:

```

```

In [ ]:

```

```

In [10]:

```
A <- structure(list(numeracy = c(6.6, 7.1, 7.3, 7.5, 7.9, 7.9
8.2, 8.3, 8.3, 8.4, 8.4, 8.6, 8.7, 8.8, 8.8, 9.1, 9.1, 9.1, 9
9.5, 9.8, 10.1, 10.5, 10.6, 10.6, 10.6, 10.7, 10.8, 11, 11.1,
11.2, 11.3, 12, 12.3, 12.4, 12.8, 12.8, 12.9, 13.4, 13.5, 13.
13.8, 14.2, 14.3, 14.5, 14.6, 15, 15.1, 15.7), anxiety = c(13
14.6, 17.4, 14.9, 13.4, 13.5, 13.8, 16.6, 13.5, 15.7, 13.6, 1
16.1, 10.5, 16.9, 17.4, 13.9, 15.8, 16.4, 14.7, 15, 13.3, 10.
12.4, 12.9, 16.6, 16.9, 15.4, 13.1, 17.3, 13.1, 14, 17.7, 10.
14.7, 10.1, 11.6, 14.2, 12.1, 13.9, 11.4, 15.1, 13, 11.3, 11.
10.4, 14.4, 11, 14, 13.4), success = c(0L, 0L, 0L, 1L, 0L, 1L
0L, 0L, 1L, 0L, 1L, 1L, 0L, 1L, 0L, 0L, 0L, 0L, 0L, 1L, 0L, 0
1L, 1L, 1L, 0L, 0L, 0L, 1L, 0L, 1L, 0L, 0L, 1L, 1L, 1L, 1L, 1
1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L)), .Names = c(
"anxiety", "success"), row.names = c(NA, -50L), class = "data
```

In [19]:

```
attach(A)
names(A)
```

```
The following objects are masked from A (pos = 3):

    anxiety, numeracy, success

The following objects are masked from A (pos = 4):

    anxiety, numeracy, success


'numeracy'   'anxiety'   'success'
```

In [21]:

```
1 head(A)
```

numeracy	anxiety	success
6.6	13.8	0
7.1	14.6	0
7.3	17.4	0
7.5	14.9	1
7.9	13.4	0
7.9	13.5	1

In [15]:

```
1 mean(A$numeracy)
```

10.722

In [22]:

```
1 model1 <- glm(success ~ numeracy * anxiety, binomial)
```

In [23]:

```
summary(model1)
```

```
Call:
glm(formula = success ~ numeracy * anxiety, family =
binomial)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.85712  -0.33055   0.02531   0.34931   2.01048

Coefficients:
                 Estimate Std. Error z value Pr(>|z|
)
(Intercept)       0.87883   46.45256   0.019    0.98
5
numeracy          1.94556    4.78250   0.407    0.68
4
anxiety          -0.44580    3.25151  -0.137    0.89
1
numeracy:anxiety -0.09581    0.33322  -0.288    0.77
4

(Dispersion parameter for binomial family taken to b
e 1)

    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 28.201  on 46  degrees of freedom
AIC: 36.201

Number of Fisher Scoring iterations: 7
```

In [40]:

```
df.residual(model1)
```

```
46
```

In [41]:

```
1 anova(model1)
```

	Df	Deviance	Resid. Df	Resid. Dev
NULL	NA	NA	49	68.02920
numeracy	1	17.73804731	48	50.29115
anxiety	1	22.00552914	47	28.28562
numeracy:anxiety	1	0.08491994	46	28.20070

In [29]:

```
1 model_numeracy<- glm( success ~ numeracy, binomial)
```

In [30]:

```
1 model_anxiety<- glm( success ~ anxiety , binomial)
```

In [27]:

```
1 range(numeracy)
```

6.6 15.7

In [28]:

```
1 range(anxiety)
```

10.1 17.7

In [ ]:

```
1
```

In [35]:

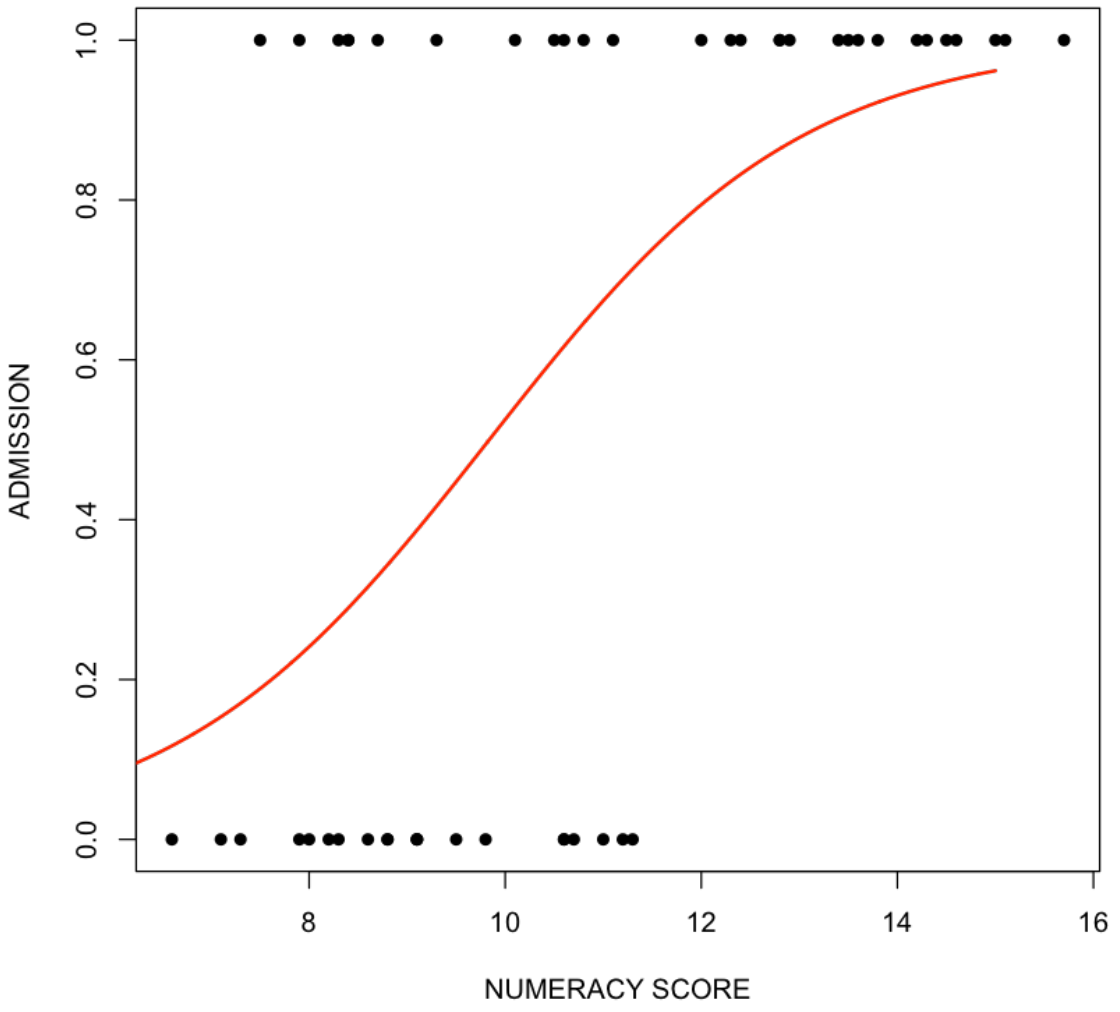
```
1 xnumeracy<- seq(0, 15, .01)
2 ynumeracy<- predict(model_numeracy, list(numeracy=xnumeracy),
```

In [ ]:

```
1
```

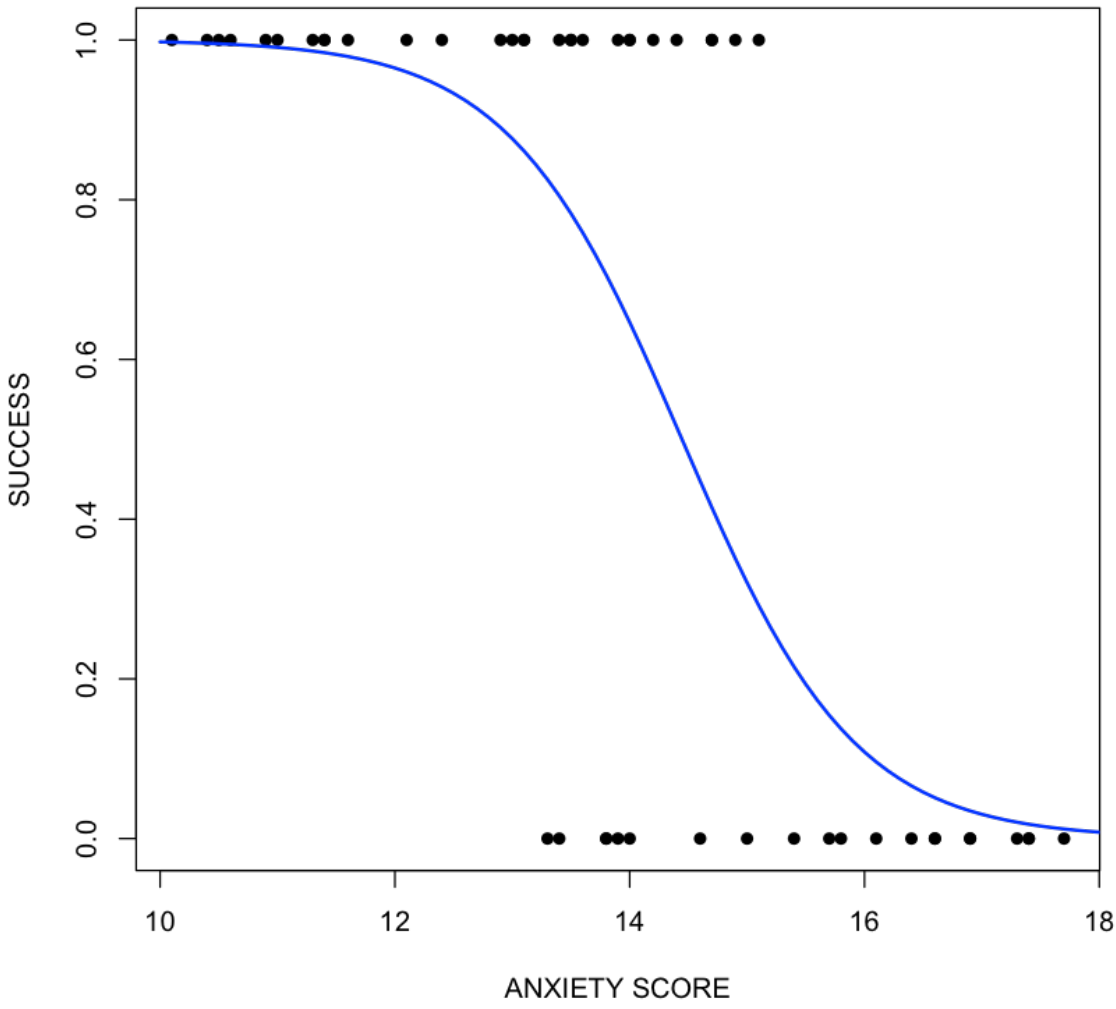
In [36]:

```
plot(numeracy, success, pch = 16, xlab = "NUMERACY SCORE", y
lines(xnumeracy, ynumeracy, col = "red", lwd = 2)
```



In [37]:

```
xanxiety <- seq(10, 20, 0.1)

yanxiety <- predict(model_anxiety, list(anxiety=xanxiety),typ

plot(anxiety, success, pch = 16, xlab = "ANXIETY SCORE", ylab

lines(xanxiety, yanxiety, col= "blue", lwd = 2)
```



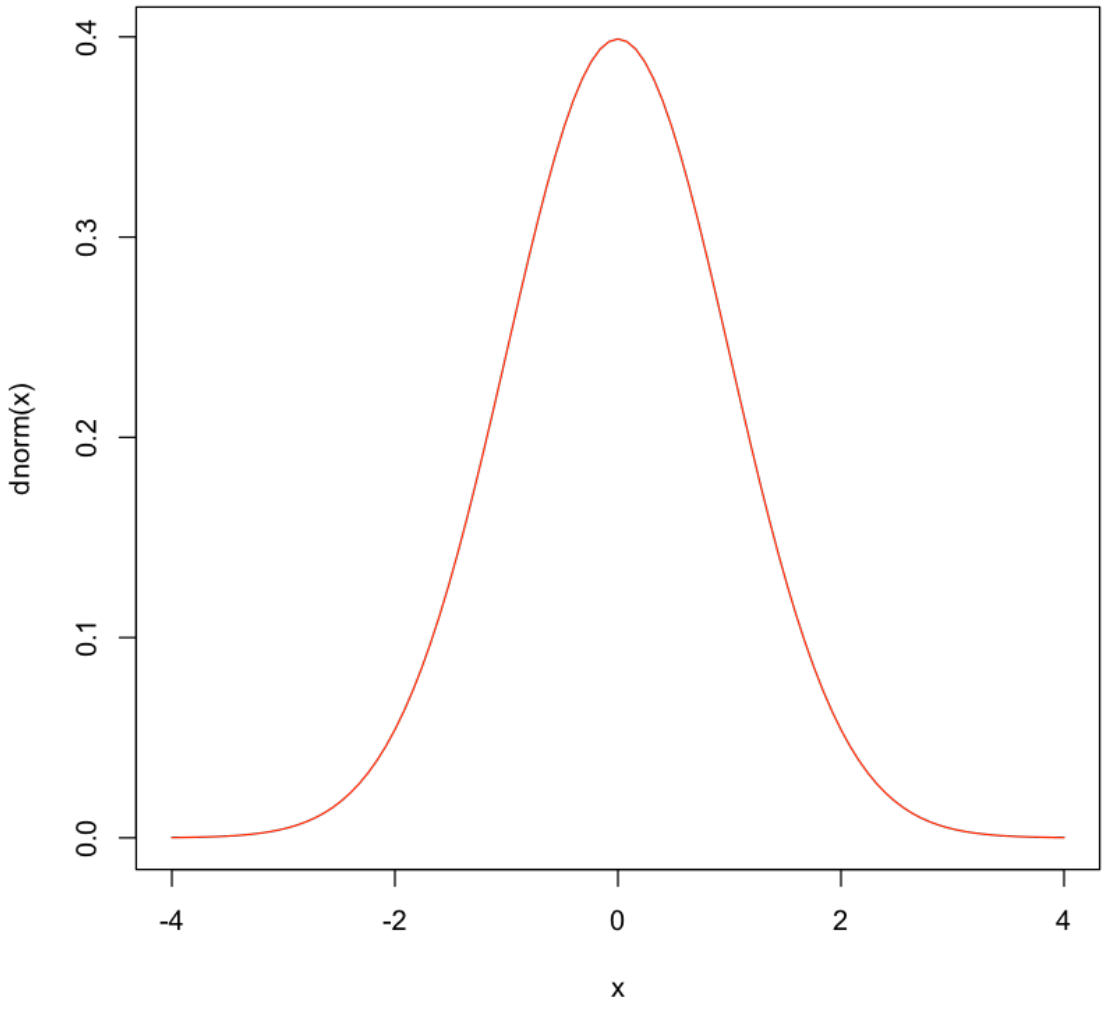
In [39]:

```
ggplot(cars,aes(x=as.factor(0),y=speed))+geom_boxplot()
```

```
Error in ggplot(cars, aes(x = as.factor(0), y = spee
d)): could not find function "ggplot"
Traceback:
```

In [1]:

```
curve(dnorm(x), -4, 4, col = "red")
```



In [2]:

```
ggplot(data.frame(x = c(-2, 4)), aes(x)) +
  stat_function(fun = dt, args =list(df =23)) +
  stat_function(fun = dt,   args =list(df =23),
                xlim = c(1.78,4),
                geom = "area")
```

```
Error in ggplot(data.frame(x = c(-2, 4)), aes(x)): c
ould not find function "ggplot"
Traceback:
```

هذا هو الجدول

In [151]:

```
#  santosa و Iris  هذا جدول لعدد اصناف
table( iris$Species)
```

```
    setosa versicolor  virginica
        50         50         50
```

In [152]:

```
(i.am.number<- 12)
```

12

In [153]:

```
data()
```

In [154]:

```
head(iris)
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Resid
5.1	3.5	1.4	0.2	setosa	-0.129546
4.9	3.0	1.4	0.2	setosa	-0.129546
4.7	3.2	1.3	0.2	setosa	-0.229546
4.6	3.1	1.5	0.2	setosa	-0.029546
5.0	3.6	1.4	0.2	setosa	-0.129546
5.4	3.9	1.7	0.4	setosa	-0.275534

In [155]:

```
1 tail(iris)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	
145	6.7	3.3	5.7	2.5	virginica	-0.9
146	6.7	3.0	5.2	2.3	virginica	-1.0
147	6.3	2.5	5.0	1.9	virginica	-0.3
148	6.5	3.0	5.2	2.0	virginica	-0.3
149	6.2	3.4	5.4	2.3	virginica	-0.8
150	5.9	3.0	5.1	1.8	virginica	0.0

In [156]:

```
1 str(iris)
```

```
'data.frame':   150 obs. of  6 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.
4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4
2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.
5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.
2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versic
olor",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Residual    : num  -0.1295 -0.1295 -0.2295 -0.029
5 -0.1295 ...
```

In [157]:

```
1 levels(iris$Species)
```

'setosa' 'versicolor' 'virginica'

In [158]:

```
1 ?iris
```

In [160]:

```
1 nrow(iris)
```

150

In [161]:

```
1 attach(iris)
2 table(Species)
```

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species


Species
    setosa versicolor  virginica
        50         50         50
```

In [238]:

```
1 library(corrplot)
```

```
corrplot 0.84 loaded
```

In [241]:

```
1 cor<- cor(Petal.Length, Petal.Width, Sepal.Length, Sepal.Widt
```

```
Warning message in if (is.na(na.method)) stop("inval
id 'use' argument"):
“the condition has length > 1 and only the first ele
ment will be used”

Error in cor(Petal.Length, Petal.Width, Sepal.Length
, Sepal.Width): invalid 'use' argument
Traceback:

1. cor(Petal.Length, Petal.Width, Sepal.Length, Sepa
l.Width)
2. stop("invalid 'use' argument")
```

In [243]:

```
corr <- cor(iris)
```

```
Error in cor(iris): 'x' must be numeric
Traceback:

1. cor(iris)
2. stop("'x' must be numeric")
```

In [249]:

```
x<-1:3; y<-101:103
mean(x); mean(y)
sd(x); sd(y)
```

2

102

1

1

In [255]:

```
cor(Petal.Length, Sepal.Width)
```

-0.42844010433054

In [ ]:

```

```

In [ ]:

```

```

In [232]:

```
set.seed(1); n = 50; x1 = rnorm(n, 10, 3); x2 = rnorm(n, 15,
    dataframe = data.frame(x1,x2,x3)   # Three columns

```

In [233]:

```
(datalong = stack(dataframe) )       # Two columns (long
boxplot(dataframe, col=c("wheat4", "tan", "tan3"))
```

values	ind
8.120639	x1
10.550930	x1
7.493114	x1
14.785842	x1
10.988523	x1
7.538595	x1
11.462287	x1
12.214974	x1
11.727344	x1
9.083835	x1
14.535344	x1
11.169530	x1

In [272]:

```
names(dataframe)
```

'x1' 'x2' 'x3'

In [271]:

```
(anov = aov(values ~ ind, datalong))
```

```
Call:
   aov(formula = values ~ ind, data = datalong)

Terms:
                    ind Residuals
Sum of Squares  2141.158  1075.764
Deg. of Freedom        2       147

Residual standard error: 2.705203
Estimated effects may be unbalanced
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [2]:

```
1 str(mtcars)
```

```
'data.frame':   32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22
.8 19.2 ...
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 .
..
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69
3.92 3.92 ...
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

In [ ]:

```
1 attach(mtcars)
```

In [ ]:

```
1  plot(jitter(cyl, .2),  mpg, pch=19, col="darkgrey")
```

In [ ]:

```
1 (cyls<- unique(cyl))
```

In [9]:

```
(n_groups<- length(cyl))
```

3

In [17]:

```
sample_mean<- rep(NA, n_groups)
cis<- matrix(nrow=n_groups, ncol=2)
```

In [ ]:

```

```

In [78]:

```
for(i in 1:n_groups)  {
    #extract relevant Data
    rows<- which(cyl==cyls[i])
    observation<- mpg[rows]
    sample_mean[i]<-mean(observation)
    stdev<- sd(observation)
    n<- length(observation)
    se_mean<- stdev/sqrt(n)
    cis[i, 1]<- sample_mean[i]- 2*se_mean
    cis[i, 2]<- sample_mean[i]+ 2*se_mean
}
```

```
Error in 1:n_groups: NA/NaN argument
Traceback:
```

In [23]:

```
sample_mean
```

21 21 22.8

In [100]:

```

```

In [ ]:

```
1
```

In [ ]:

```
1
```

In [85]:

```
1  ts = replicate(1000,t.test(rnorm(10),rnorm(10))$statistic)
```

In [86]:

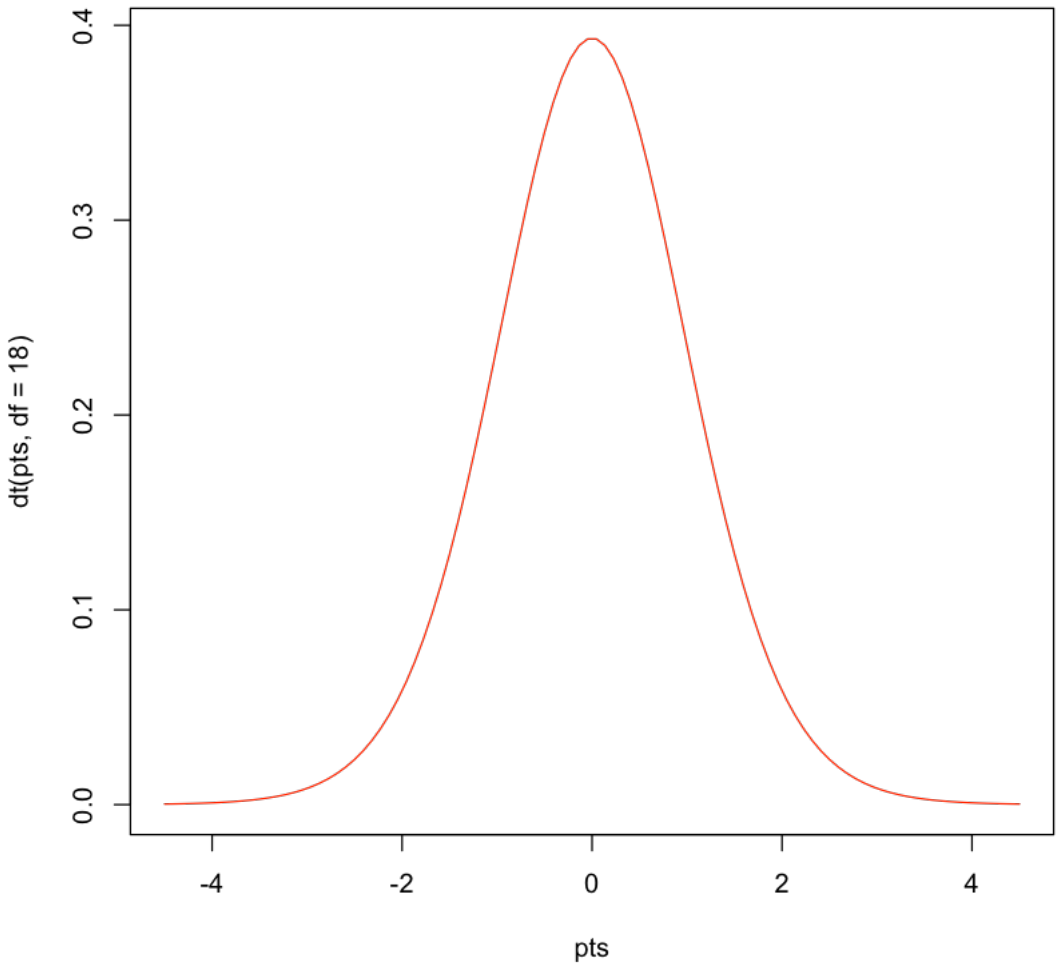
```
1 range(ts)
```

-4.38142823082222 3.12398526076645

In [77]:

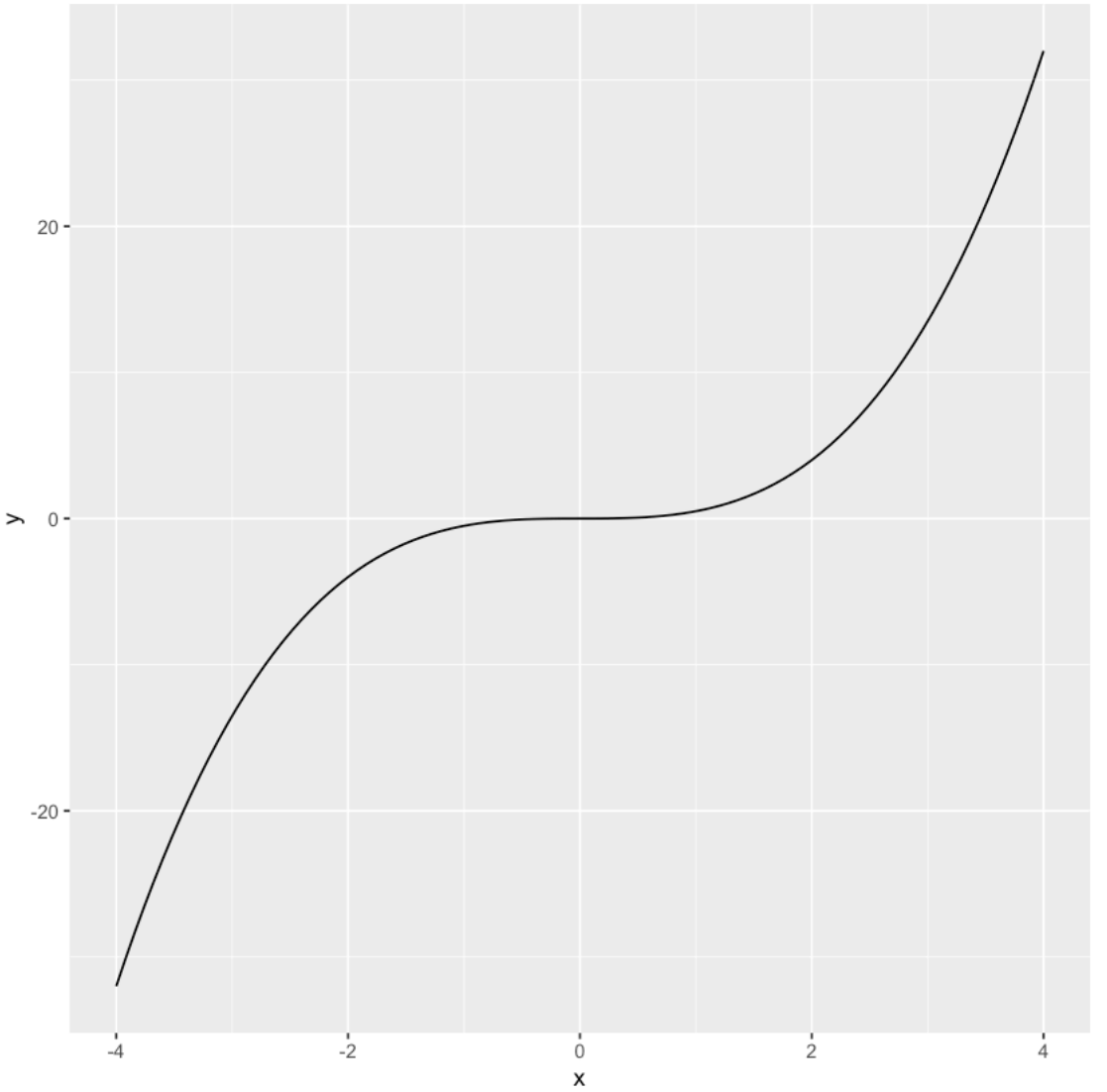
```
pts<-seq(-4.5, 4.5,length=100)
plot(pts,dt(pts,df=18),col='red',type='l')
lines(density(ts))
```

```
Error in density.default(ts): argument 'x' must be n
umeric
Traceback:

1. lines(density(ts))
2. density(ts)
3. density.default(ts)
4. stop("argument 'x' must be numeric")
```



In [79]:

```
cubeFun <- function(x) {
    x^3 * 0.5
}

 ggplot(data.frame(x = c(-4, 4)), aes(x = x)) +
        stat_function(fun = cubeFun)

```

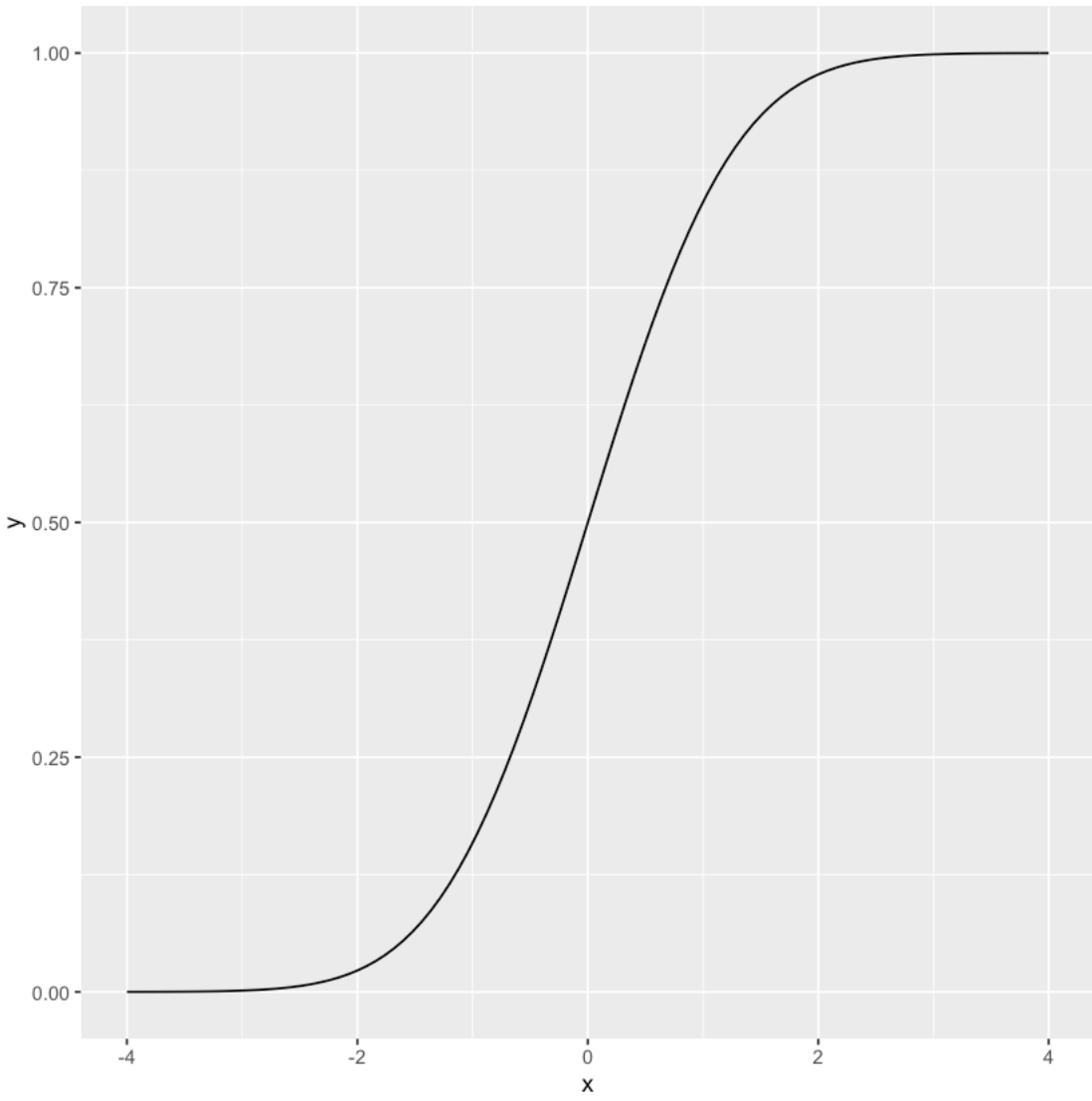


In [ ]:

```
<video controls src="imgs/Introduction.mp4" />
```

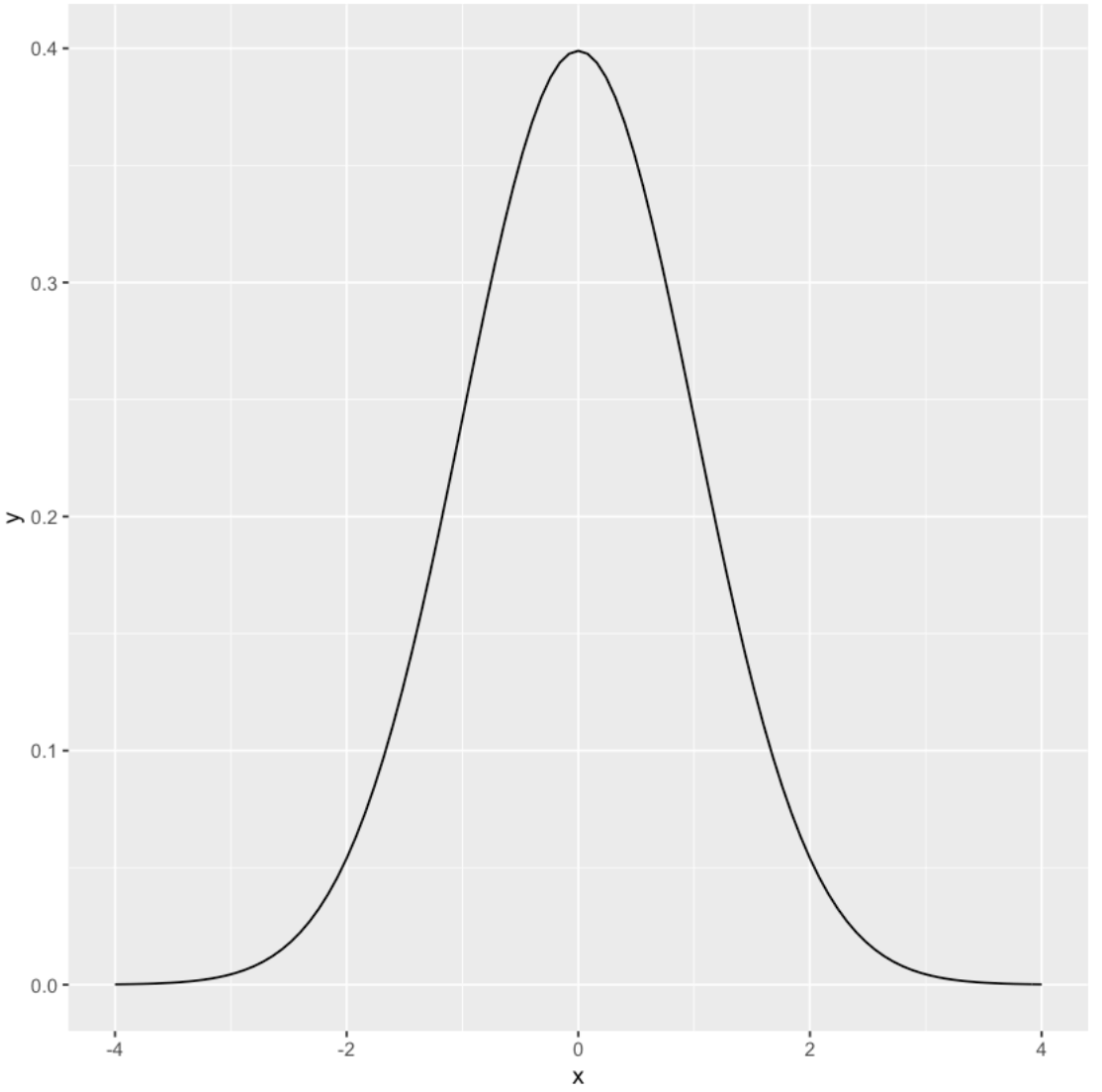
In [74]:

```
ggplot(data.frame(x = c(-4, 4)), aes(x )) +
        stat_function(fun = pnorm)
```



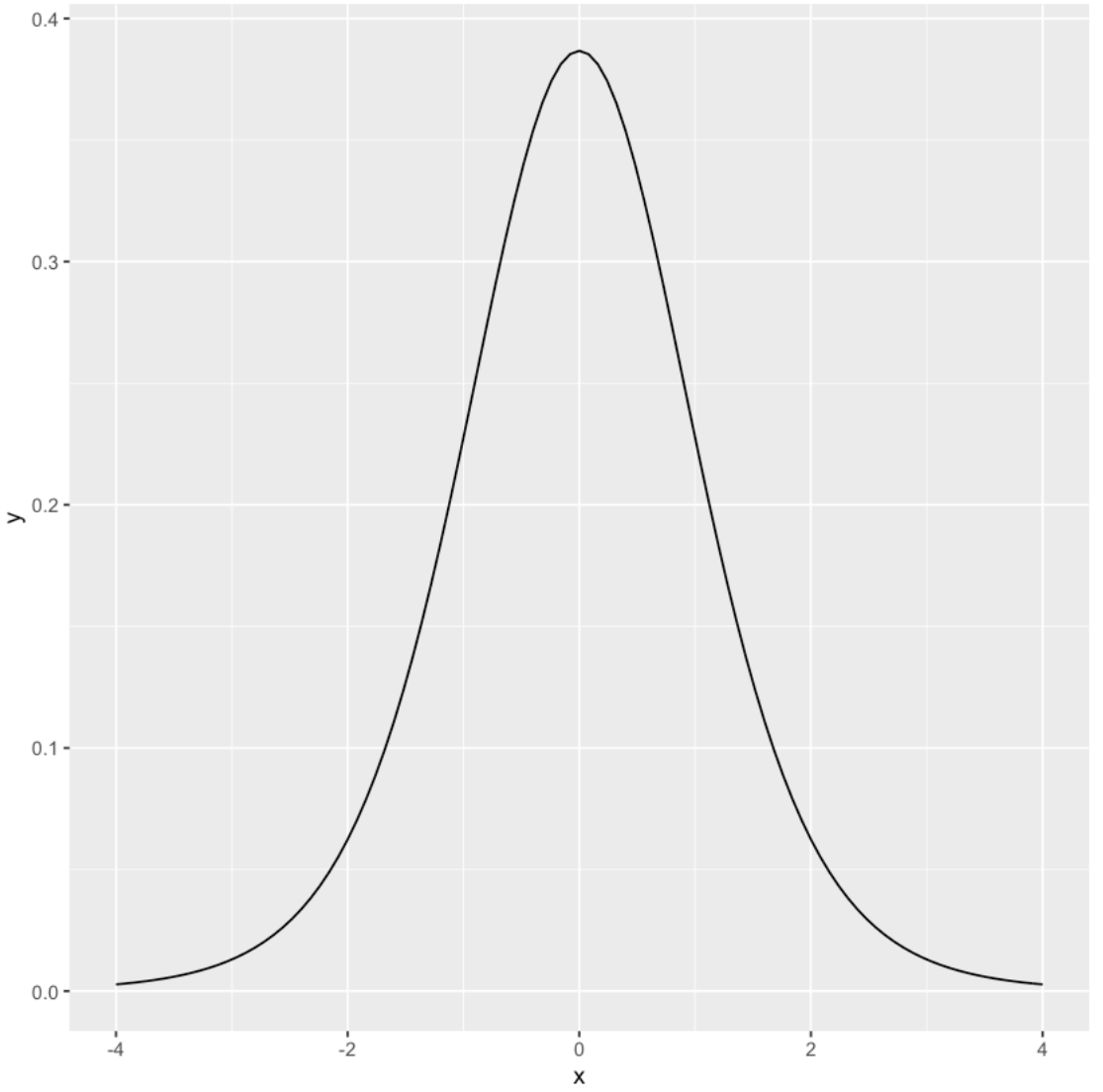
In [76]:

```
ggplot(data.frame(x = c(-4, 4)), aes(x )) +
        stat_function(fun = dnorm)
```



In [75]:

```
ggplot(data.frame(x = c(-4, 4)), aes(x = x)) +
       stat_function(fun = dt, args = list(df = 8))
```



In [84]:

```
1 head(iris)
```

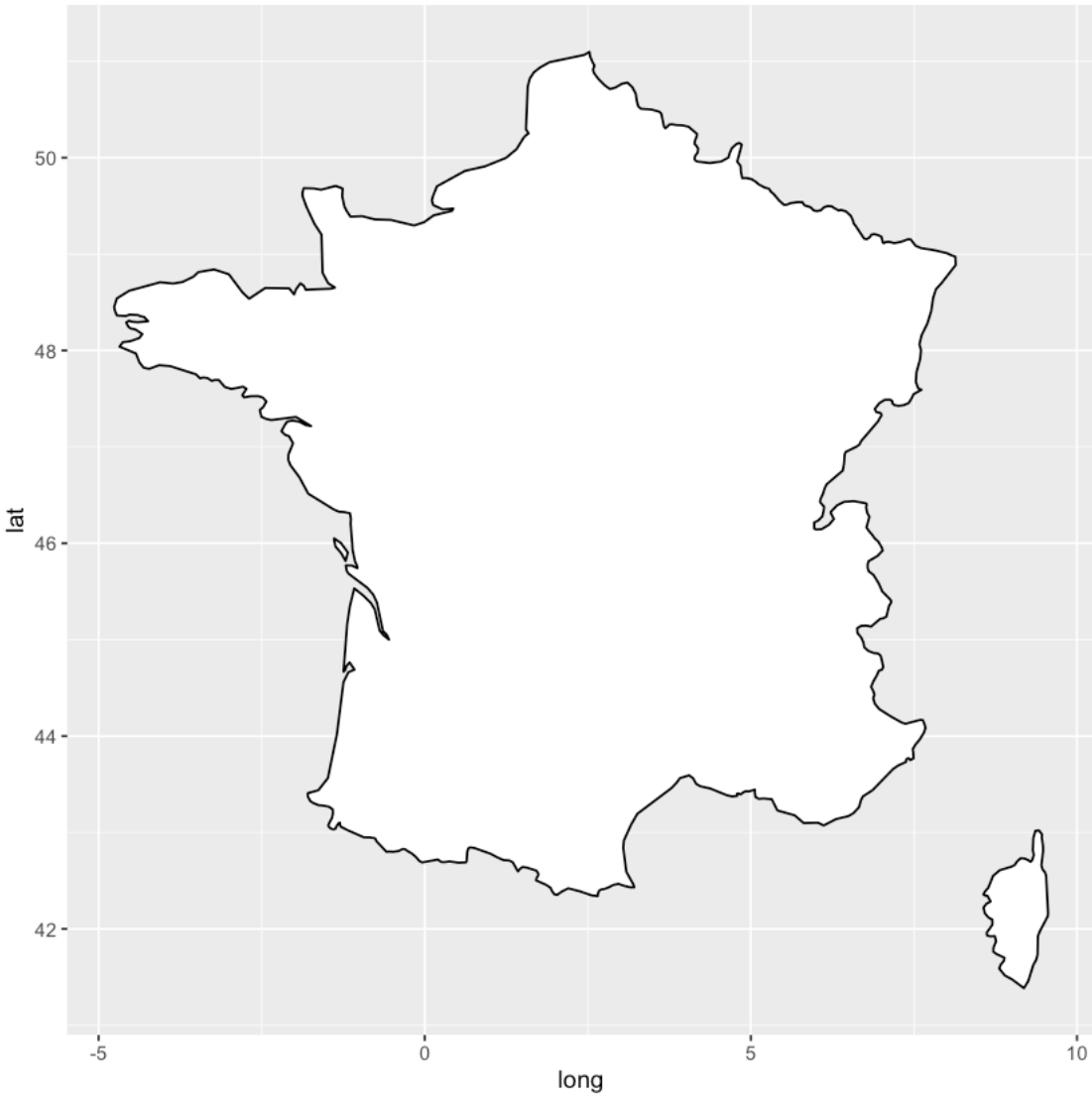
A data.frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<dbl>	<dbl>	<dbl>	<dbl>	<fct>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

In [92]:

```
require(maps)
france = map_data('world', region = 'France')
ggplot(france, aes(x = long, y = lat, group = group)) +
  geom_polygon(fill = 'white', colour = 'black')
```

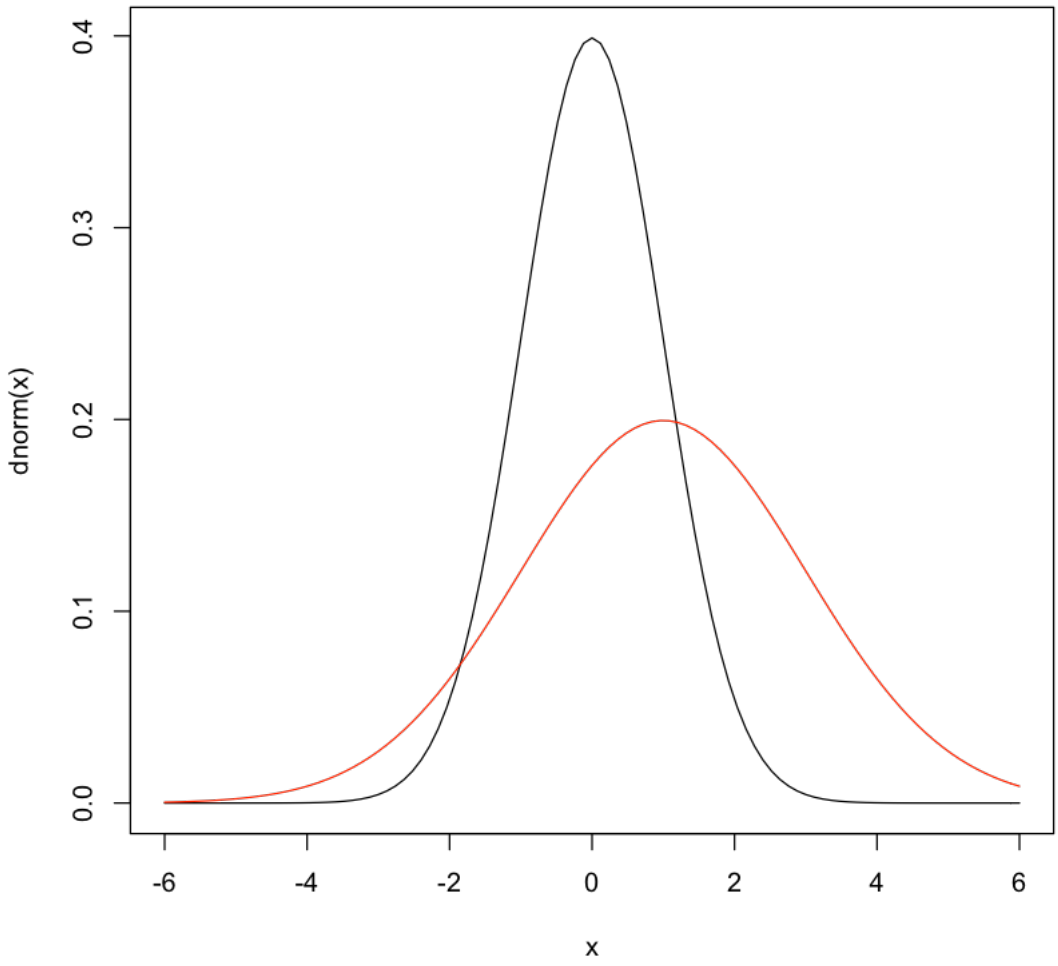
```
Loading required package: maps

Warning message:
“package ‘maps’ was built under R version 3.4.4”
```



In [98]:

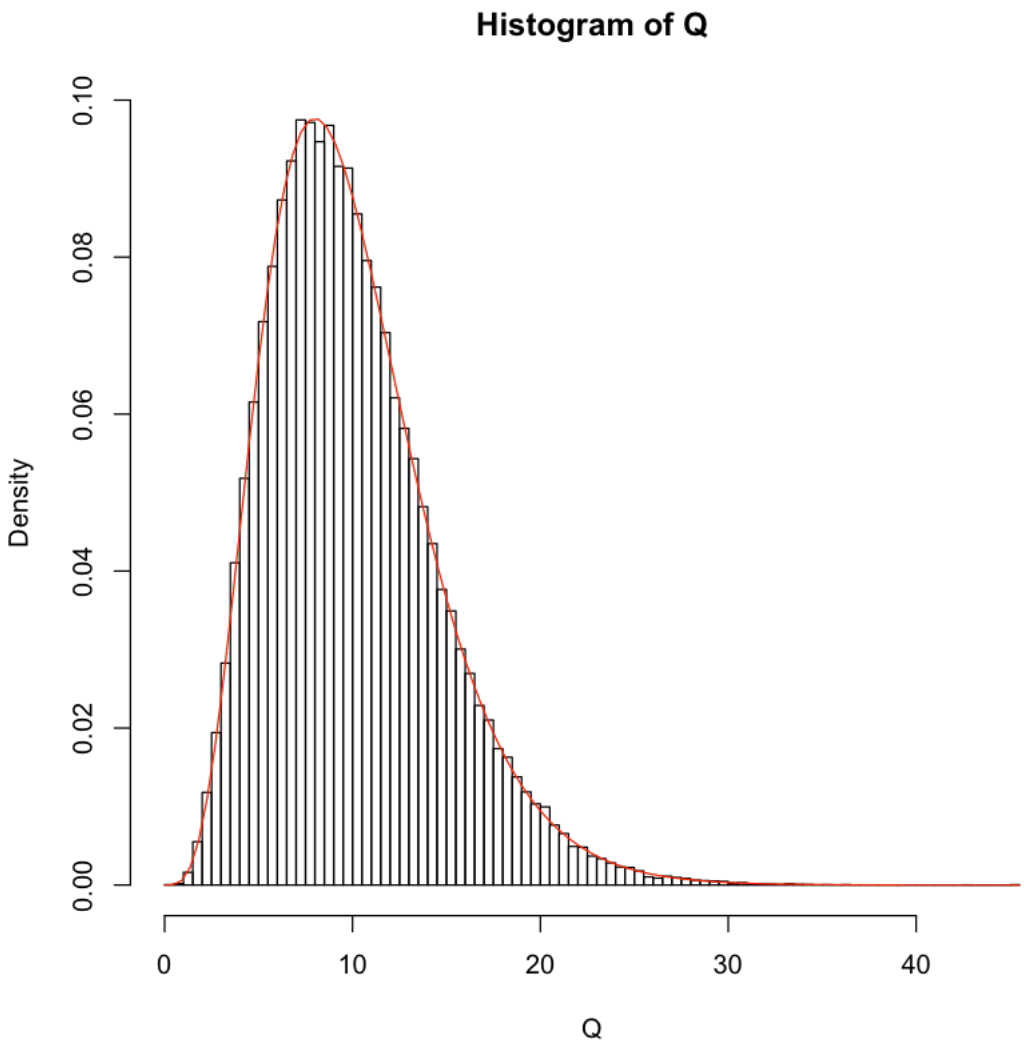
```
curve(dnorm(x), xlim=c(-6,6))
curve(dnorm(x, mean=1, sd=2), col="red", add=TRUE)
pnorm(1.65)
```

0.950528531966352



In [99]:

```
set.seed(90546723)
Q <- rchisq(1e5,10)
hist(Q, freq=FALSE, breaks=100)
curve(dchisq(x,10),col="red",add=TRUE)
```



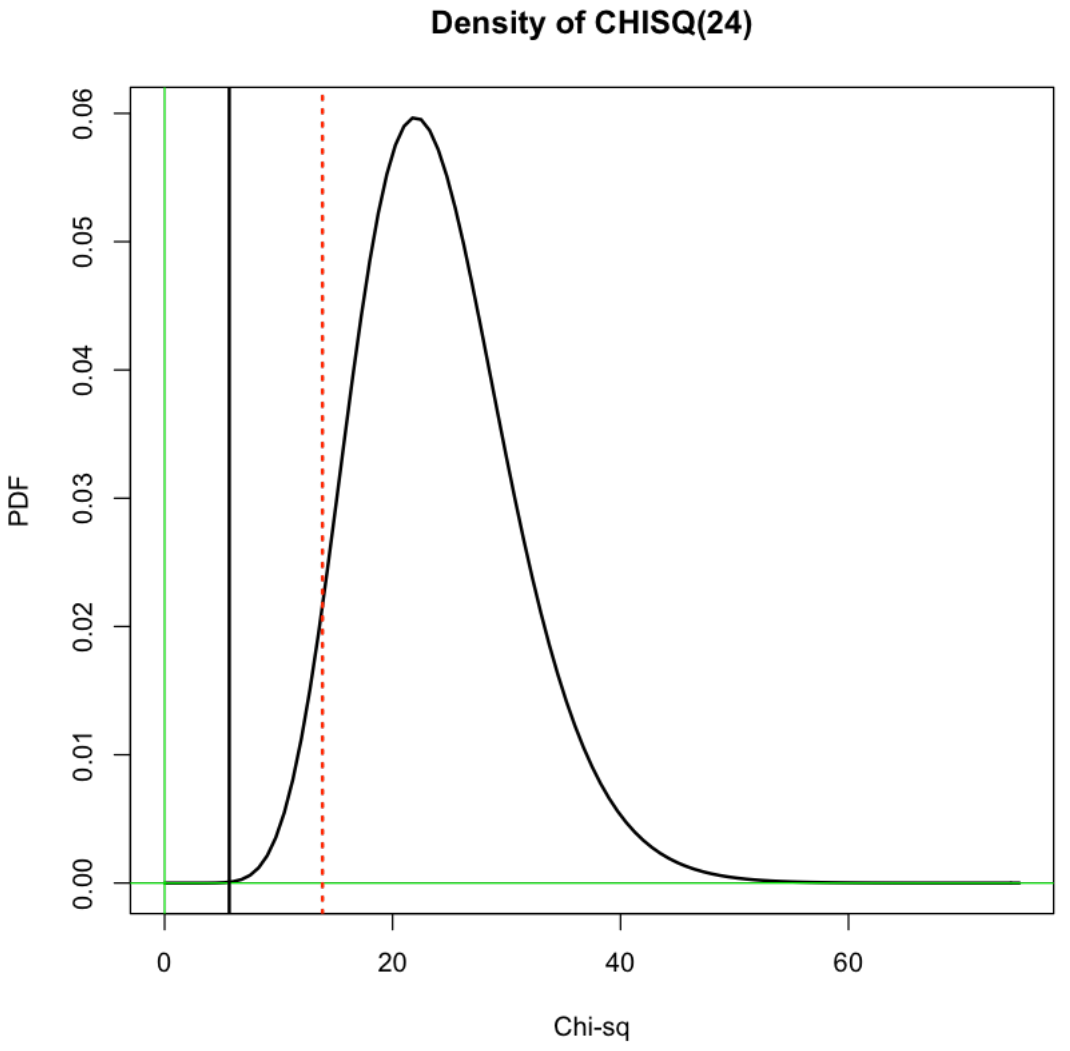
In [100]:

```
pchisq(21.78,10,lower.tail=FALSE)
```

0.0162654403357515

In [104]:

```r
curve(dchisq(x, 24), 0, 75, lwd=2,
    ylab="PDF", xlab="Chi-sq", main="Density of CHISQ(24)")
 abline(h=0, col="green2"); abline(v=0, col="green2")
 abline(v=13.85, col="red", lwd=2, lty="dotted")
 abline(v = 5.67, lwd=2)
```



In [ ]:

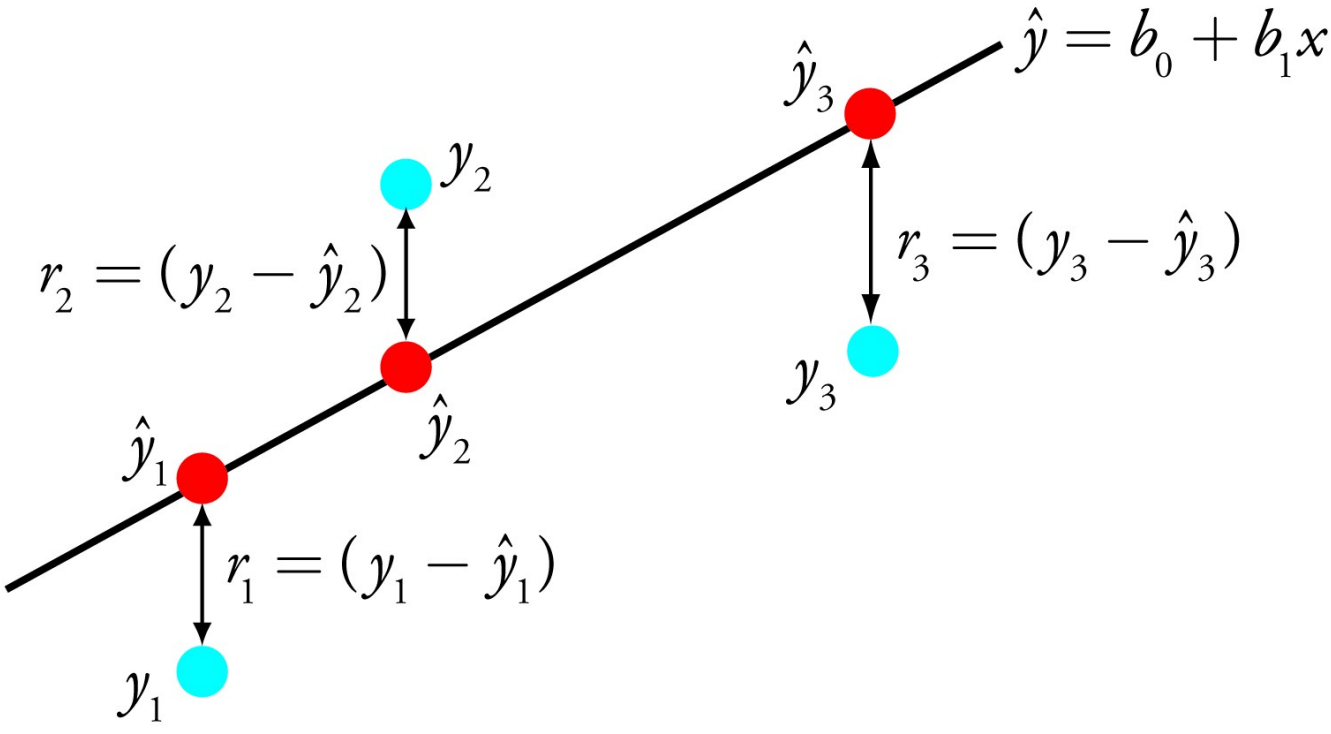
```r

```

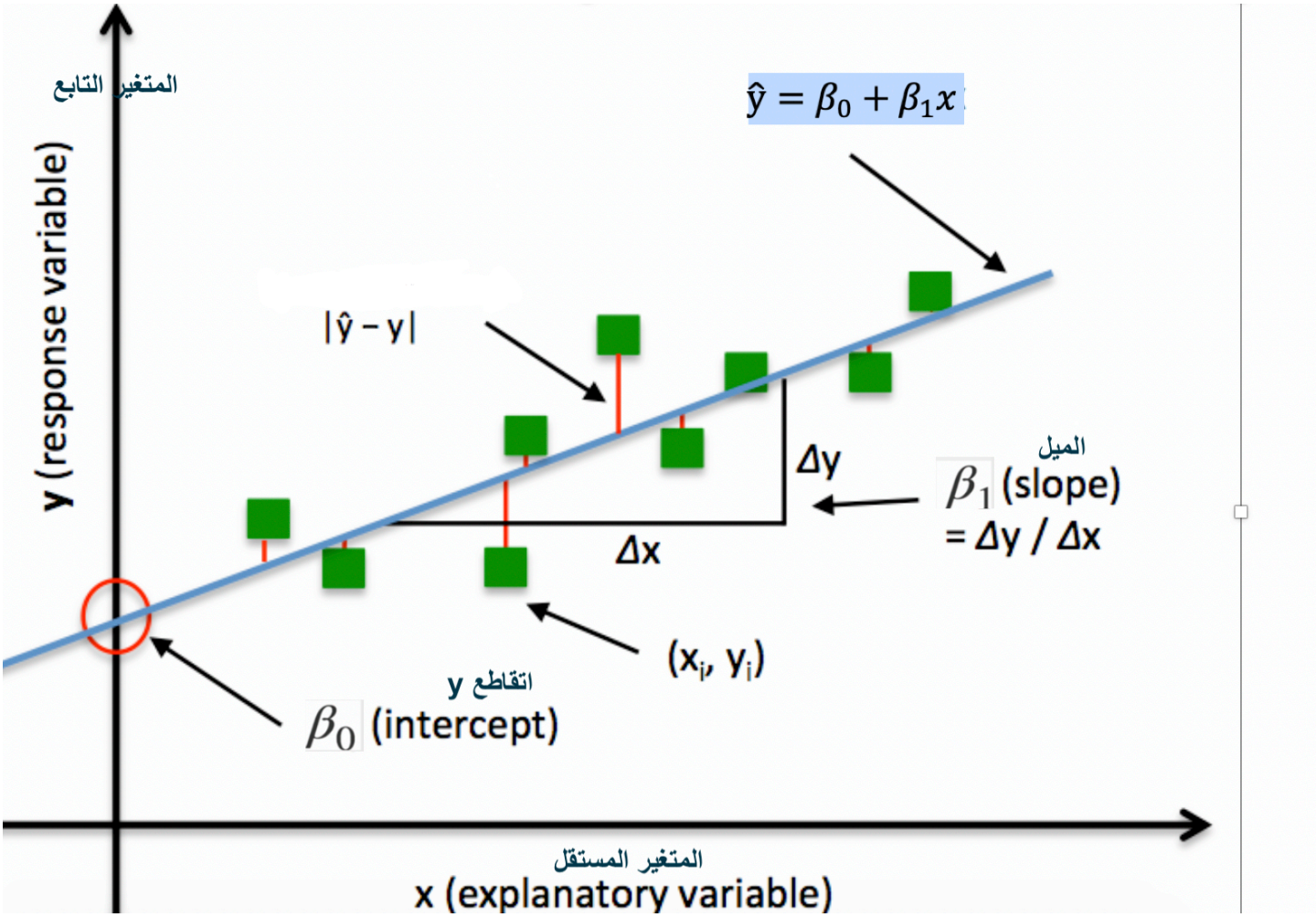
الانحدار الخطي

الأهداف

- وصف النمذجة الإحصائية مع الانحدار البسيط
- شرح الانحدار الخطي البسيط كحل للمعادلة: $\hat{y} = \beta_0 + \beta_1 x$
- رسم خط الانحدار على أساس الميل وتقاطع y
- التنبؤ بمخرجات نموذج انحدار خطي لبيانات جديدة

المقدمة





$$\hat{y} = \beta_0 + \beta_1 x$$

1 2

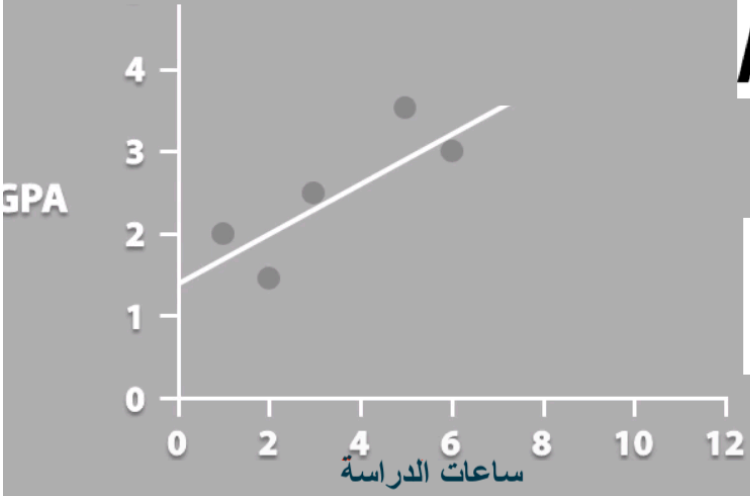
$$\beta_0 = \bar{y} - \beta_1 \bar{x}$$

3 4

7

$$\beta_1 = r \frac{S_y}{S_x}$$

5 6



β_0: تقاطع y

β_1: الميل

$\bar{y}$: متوسط y

$\bar{x}$: متوسط x

r: معامل الارتباط

S_x: انحدار معياري x

S_y: انحدار معياري y

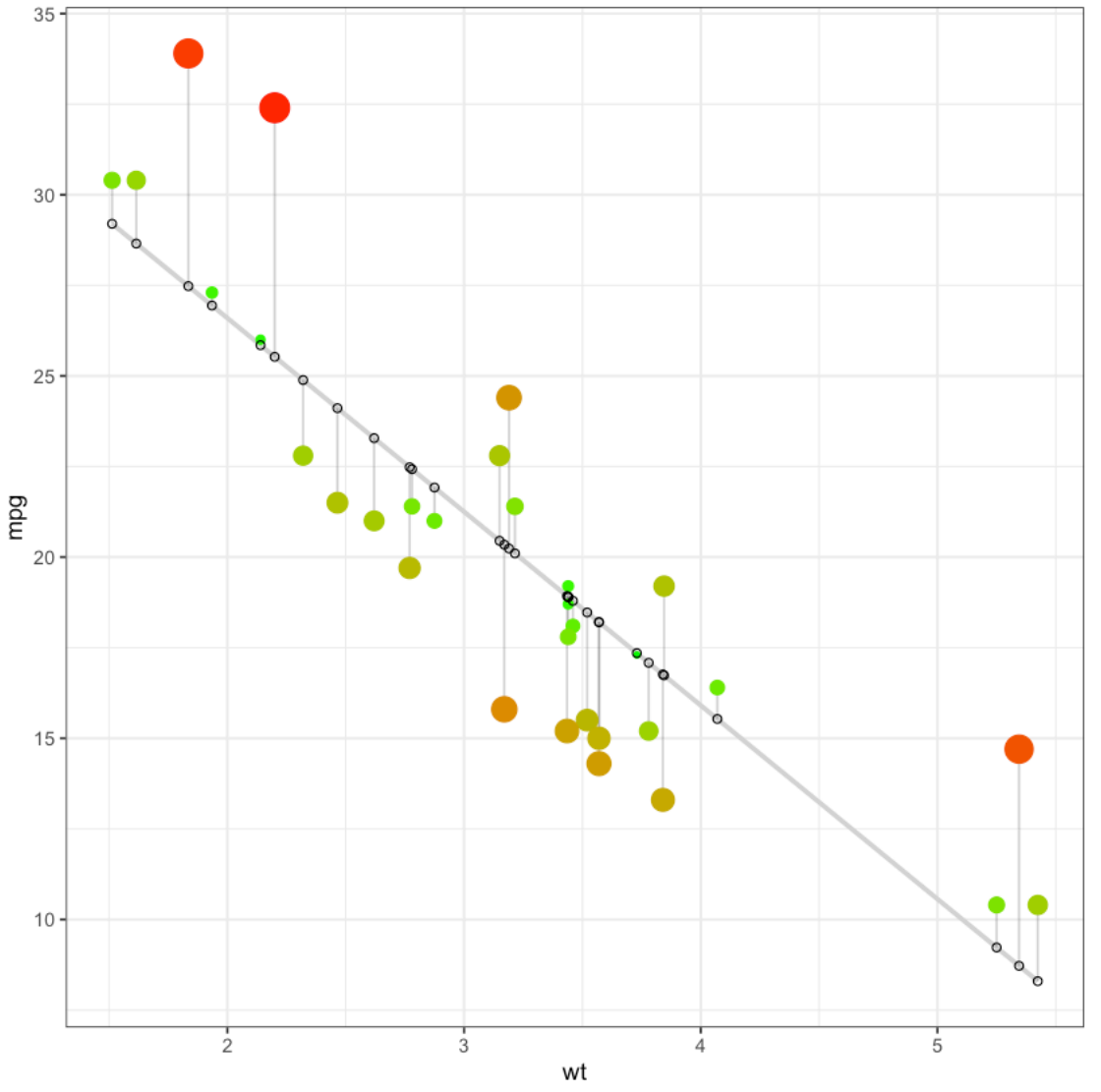
In [15]:

'/Users/medamin/Projets/DataScience'

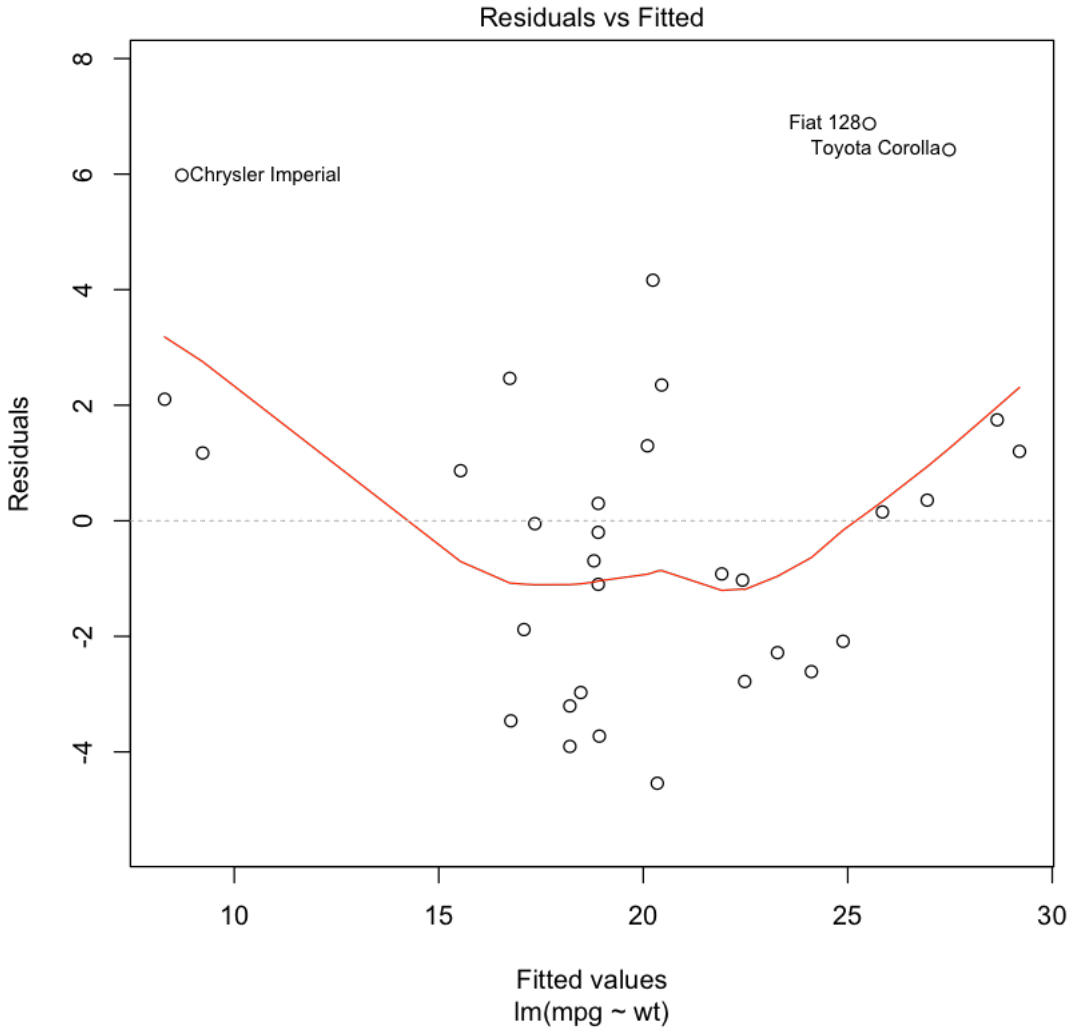
In [ ]:

In [165]:

In [130]:



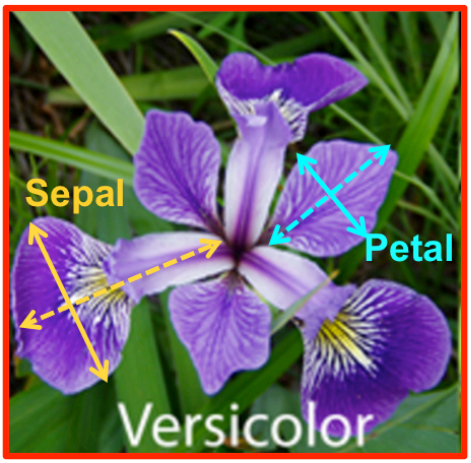
In [131]:



Geogebra Demo.Linear/Multi-linear/Polinomial...etc. عرض

In [ ]:

In [63]:



In [17]:

setosa versicolor virginica

▶ **Levels**:

In [18]:

A data.frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<dbl>	<dbl>	<dbl>	<dbl>	<fct>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

In [19]:

```
Error in glimpse(iris): could not find function "gli
mpse"
Traceback:
```

In [20]:

```
'data.frame':   150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.
4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4
2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.
5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.
2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versic
olor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

In [21]:

```
'setosa'    'versicolor'    'virginica'
```

In [22]:

```
TRUE
```

In [23]:

```
'Sepal.Length'    'Sepal.Width'    'Petal.Length'    'Petal.Width'
'Species'
```

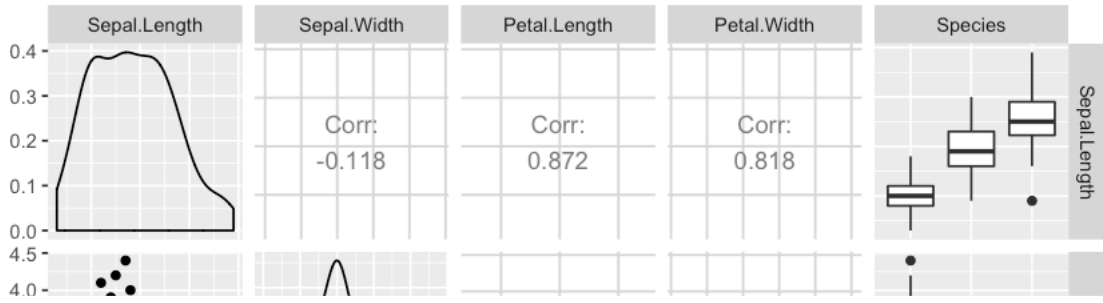
Variables correlations

In [24]:

```
Warning message:
“package ‘GGally’ was built under R version 3.4.4”
```

In [25]:

```
`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.

`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.

`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.

`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.
```



In [33]:

0.962865431402796

$$r = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2}\sqrt{\sum (y_i - \bar{y})^2}}$$

In [34]:

```
Warning message in cor.test.default(iris$Petal.Lengt
h, iris$Petal.Width, method = "spearman"):
“Cannot compute exact p-value with ties”


        Spearman's rank correlation rho

data:  iris$Petal.Length and iris$Petal.Width
S = 35061, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.9376668
```

In [35]:

```
        Pearson's product-moment correlation

data:  iris$Petal.Length and iris$Petal.Width
t = 43.387, df = 148, p-value < 2.2e-16
alternative hypothesis: true correlation is not equa
l to 0
95 percent confidence interval:
 0.9490525 0.9729853
sample estimates:
      cor
0.9628654
```

t-statitics

$$t = \frac{r}{\sqrt{1 - r^2}} \sqrt{n - 2}$$

In [36]:

'statistic' 'parameter' 'p.value' 'estimate' 'null.value'
'alternative' 'method' 'data.name' 'conf.int'

In [37]:

cor: 0.962865431402796

In [38]:

cor: 43.3872373820692

In [40]:

0.949052459311114 0.972985317378797

$$0.95 \leqslant CorrelationValue \leqslant 0.972$$

In [41]:

'two.sided'

In [62]:

4.67500390732856e-86

In [ ]:

In [44]:

```
Warning message in chisq.test(iris$Petal.Length, iri
s$Petal.Width):
“Chi-squared approximation may be incorrect”


        Pearson's Chi-squared test

data:  iris$Petal.Length and iris$Petal.Width
X-squared = 1144.1, df = 882, p-value = 5.143e-09
```

In [45]:

```
also installing the dependencies ‘xts’, ‘quadprog’



  There are binary versions available but the source
versions are later:
                     binary source needs_compilation
quadprog              1.5-5  1.5-7              TRUE
PerformanceAnalytics  1.5.2  1.5.3              TRUE


The downloaded binary packages are in
        /var/folders/hw/83xf1jxs0b58xft1b6ghk0280000
gn/T//RtmpY6bkoz/downloaded_packages

installing the source packages ‘quadprog’, ‘Performa
nceAnalytics’
```

In [37]:

```
Loading required package: xts
Loading required package: zoo

Attaching package: ‘zoo’

The following objects are masked from ‘package:base’
:

    as.Date, as.Date.numeric


Attaching package: ‘PerformanceAnalytics’

The following object is masked from ‘package:graphic
s’:

    legend
```

- is Petal.Width related to Petal.Length really?
- is the relation between the two variables strong enough to claim they are related?
- Can we use the Data from just 150 Observations to make a claim about all the population of ORchedia?

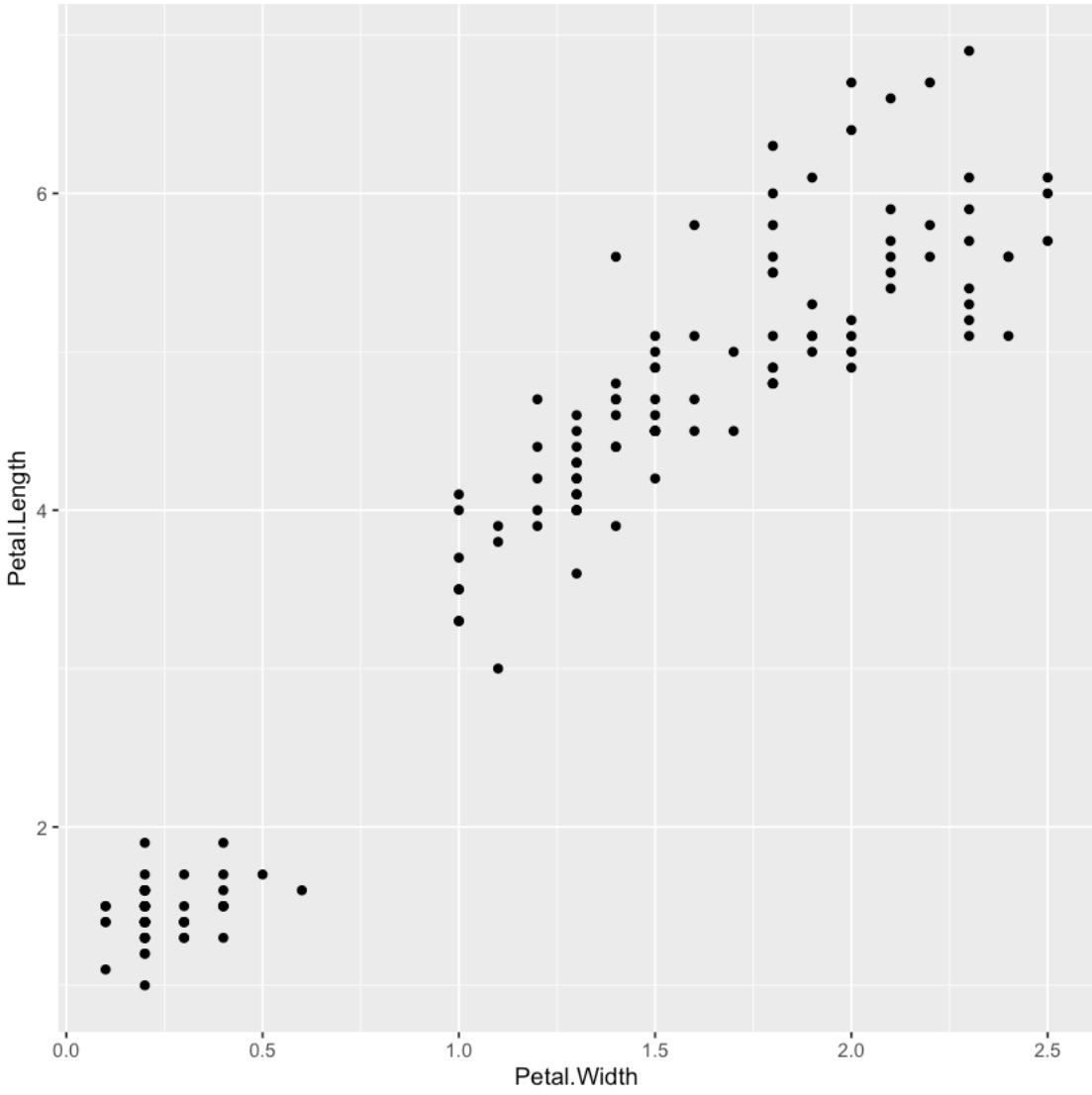
In [46]:

التخطيط البياني

In [47]:

In [ ]:

In [48]:



بناء النموذج*Buildthemodel*

In [49]:

In [50]:

In [51]:

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
eedom
Multiple R-squared:  0.9271,     Adjusted R-squared:
```

In [52]:

```
Attaching package: ‘dplyr’


The following object is masked from ‘package:GGally’
:

    nasa


The following objects are masked from ‘package:stats
’:

    filter, lag


The following objects are masked from ‘package:base’
:

    intersect, setdiff, setequal, union
```

In [53]:

```
'coefficients'  'residuals'  'effects'  'rank'  'fitted.values'  'assign'
'qr'  'df.residual'  'xlevels'  'call'  'terms'  'model'
```

In [54]:

```
'(Intercept)'  'Petal.Width'
```

In [55]:

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [56]:

In [57]:

A tibble: 1 × 11

r.squared	adj.r.squared	sigma	statistic	p.value	df	log
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dl
0.9271098	0.9266173	0.4782058	1882.452	4.675004e-86	2	-101.17

In [59]:

A tibble: 2 × 5

term	estimate	std.error	statistic	p.value
<chr>	<dbl>	<dbl>	<dbl>	<dbl>
(Intercept)	1.083558	0.07296696	14.84998	4.043318e-31
Petal.Width	2.229940	0.05139623	43.38724	4.675004e-86

In [60]:

2.88913185794091

In [61]:

A tibble: 1 × 3

var_e	var_y	R_squared
<dbl>	<dbl>	<dbl>
0.227146	3.116278	0.9271098

```
Residual standard error: 0.4782 on 148 degrees of freedom
Multiple R-squared:  0.9271,    Adjusted R-squared:  0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

In [21]:

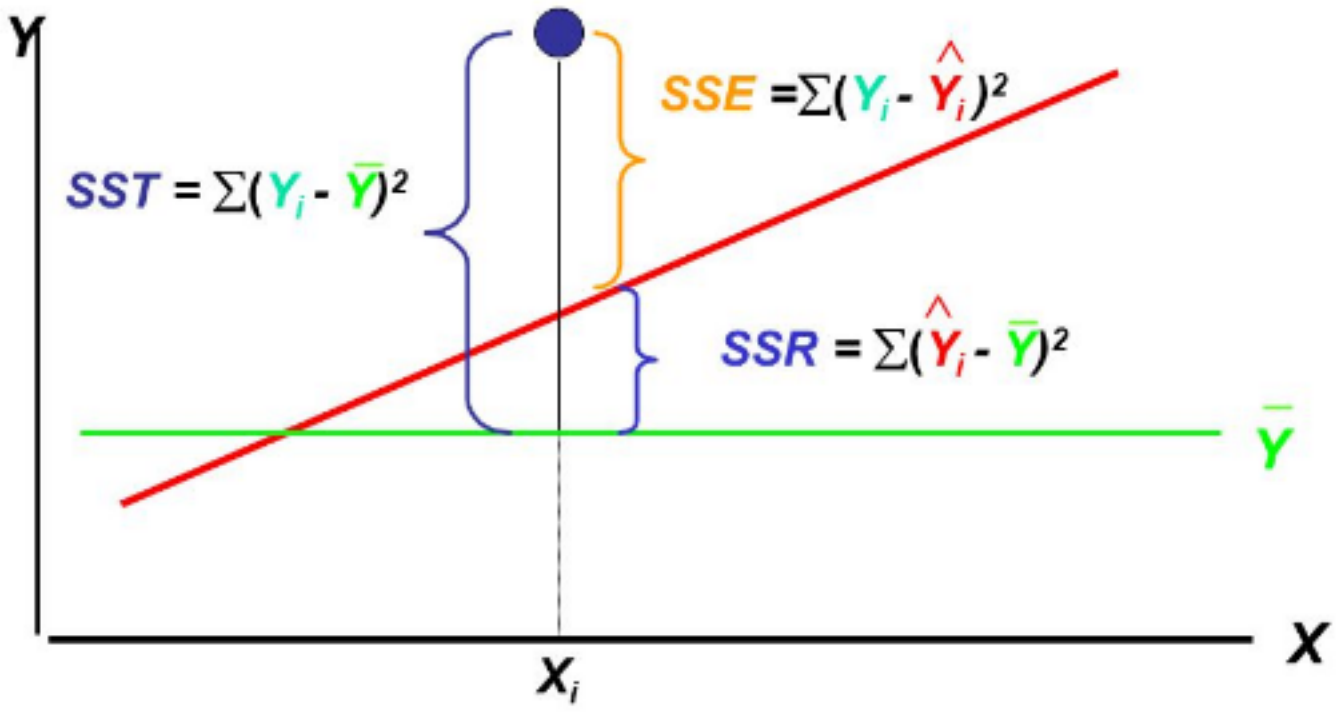
```
Error in eval(expr, envir, enclos): object 'r' not f
ound
Traceback:
```

In [18]:

'/Users/medamin/Projets/DataScience'

In [27]:

'/Users/medamin/Projets/DataScience'



In [22]:

177.389749986549

r$estimate^2

In [23]:

43.384046692607

It's also known as the residual standard deviation (RSD), and it can be defined as "

Fstatistics

F-value measures the significance of the OverALL model nad not just one variable. And this has more use when there is more than one explanatory variable.

- for one vriable. we have

$$F = t_v^2$$

$$F = \frac{\frac{R^2}{k-1}}{\frac{1-R^2}{n-k}}$$

$$F = \frac{MeanSquareModel}{MeanSquareError}$$

$$F = \frac{\frac{SSM}{Df_m.Model}}{\frac{SSE}{Df_e.Err}}$$

Type *Markdown* and LaTeX: α^2

In [21]:

1882.17832647462

In [22]:

1882.6921

In [ ]:

In [ ]:

In [23]:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [61]:

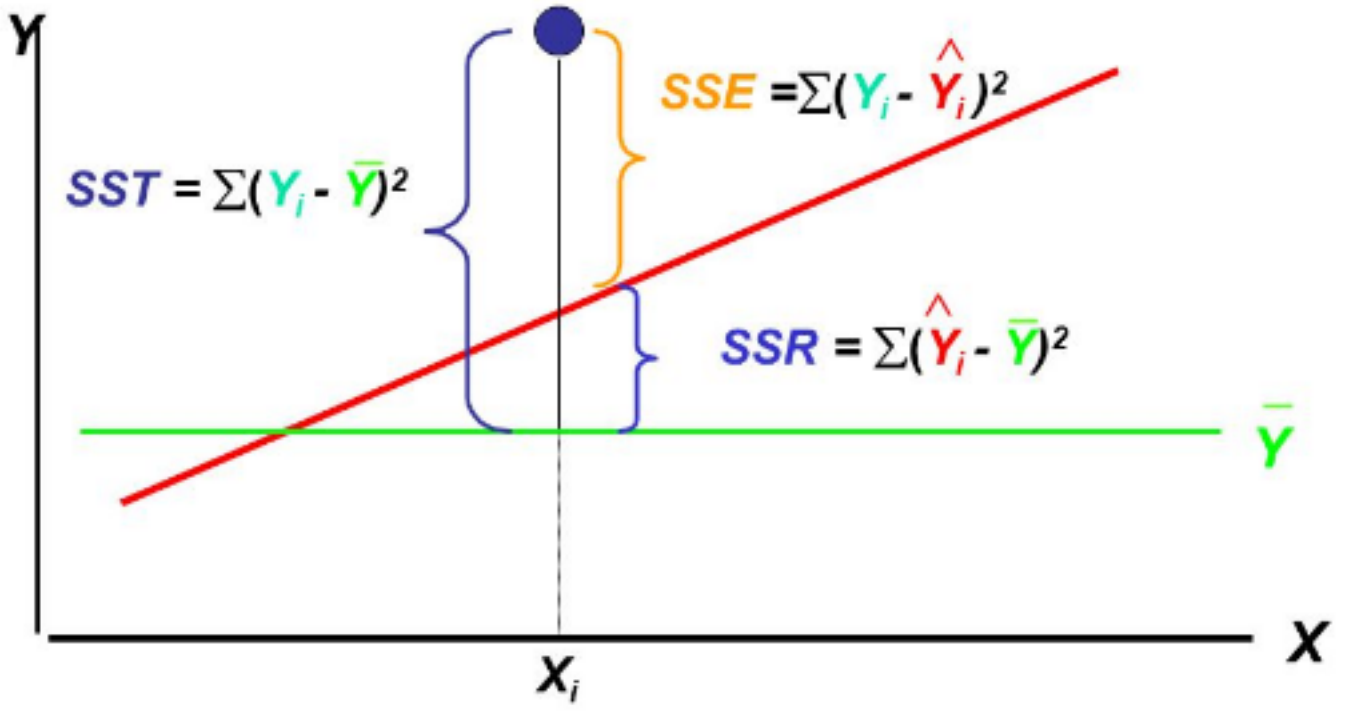
1882.45207643143

Multiple R-Squared:

Goodness Of Fit

This is percentage of variation in the response variable that is explained by the variation on the explanatory variable.

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST} = \frac{\sum(\hat{y} - \bar{y})^2}{\sum(y_i - \bar{y})^2}$$



$$0 \leqslant R^2 \leqslant 1$$

R^2 = Coefficient Of Determination

R^2 = describes proportion of variance in y that is predictable from x

R^2 = Y can not be predicted from x

Middle values indicate the extent y is predictable.

R^2 = is correlated to Correlation

For a simple linear regression; = $R^2 = r^2$

$$SST = \sum (y_i - \bar{y})^2$$

$$SSE = \sum (y_i - \hat{y})^2$$

$$SSR = \sum (\hat{y} - \bar{y})^2$$

In [43]:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

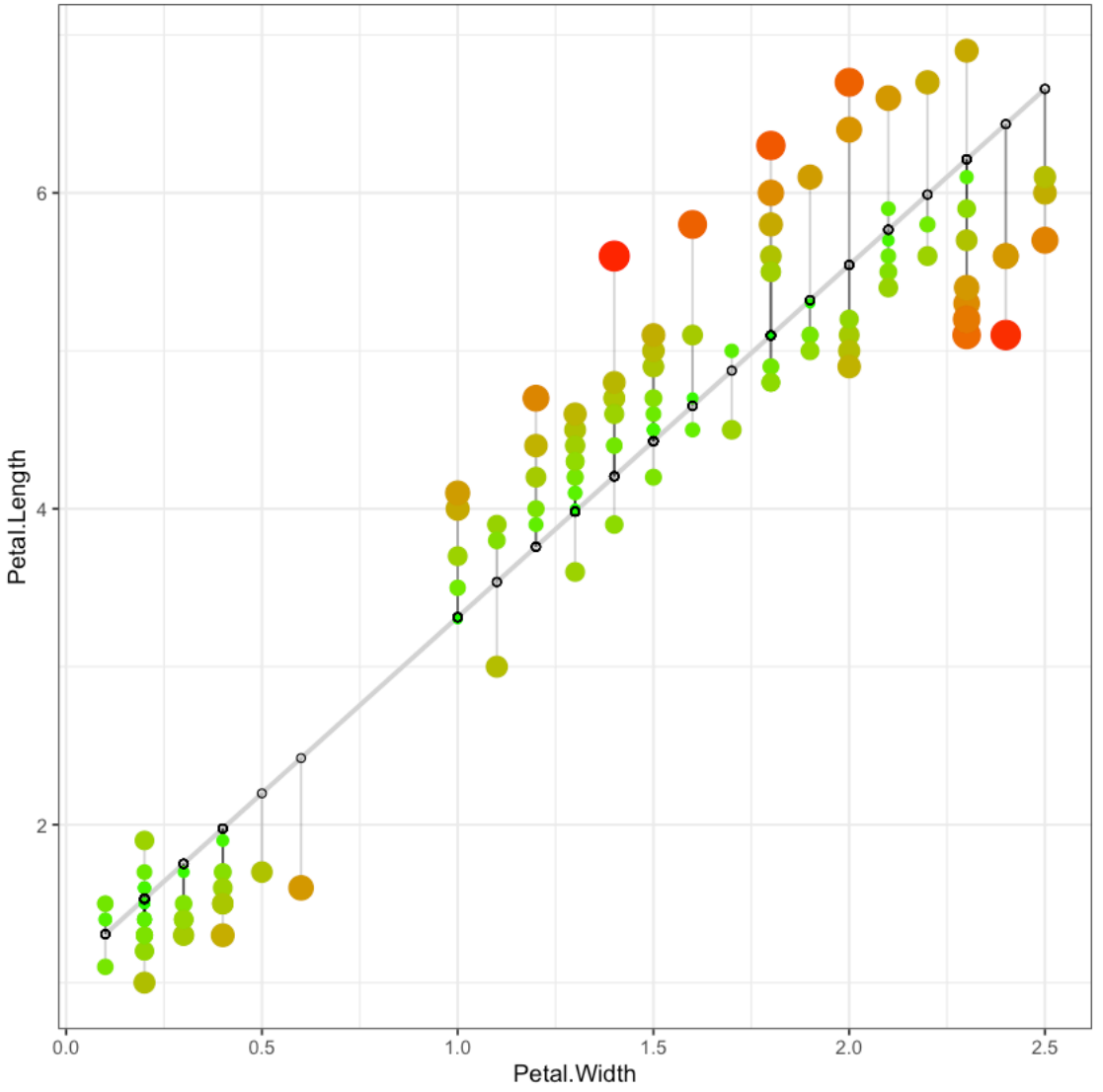
In [ ]:

Adjusted R-Square

$$\bar{R}^2 = 1 - \frac{\frac{SSE}{n-k}}{\frac{SST}{n-1}}$$

Residual Variation

In [30]:

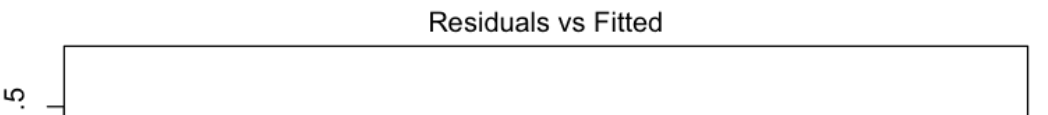


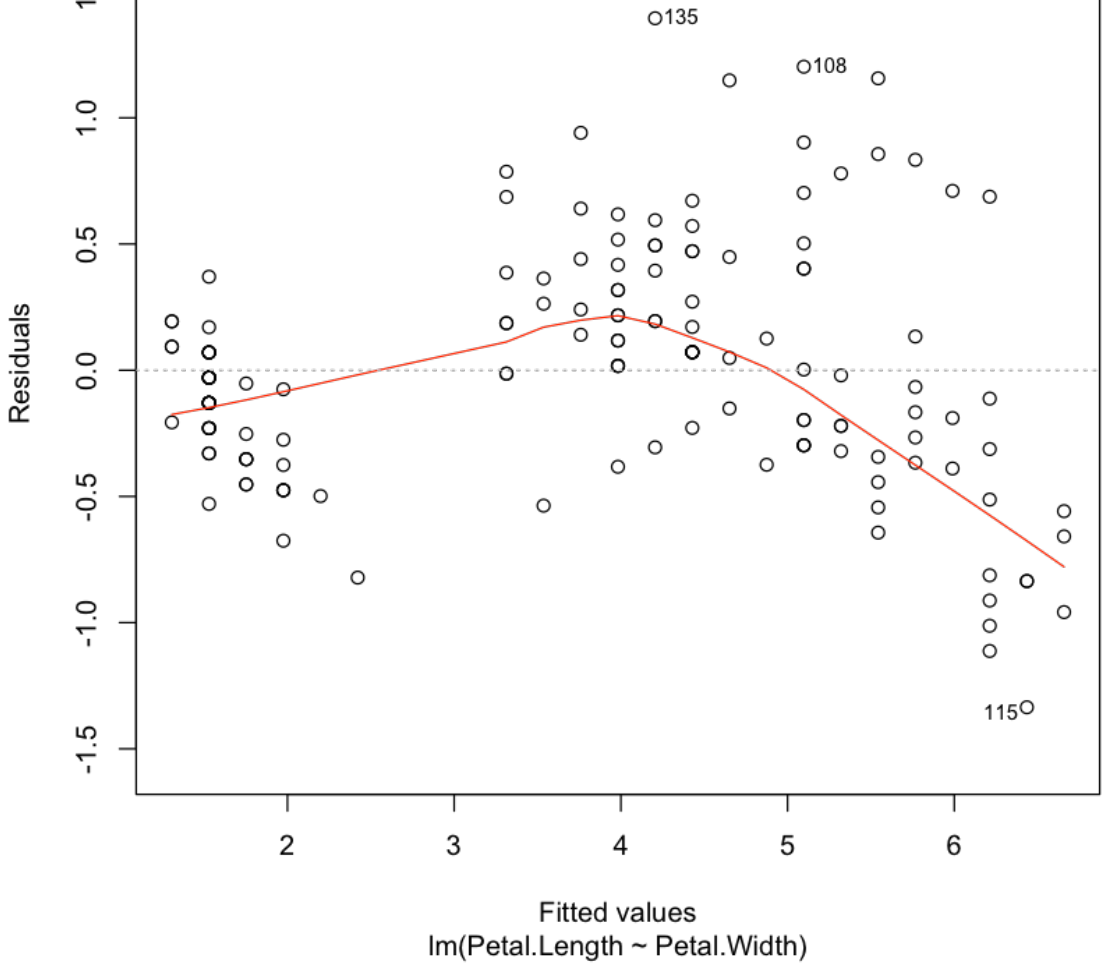
- Rsiduals.
  - Sum to Zero.
  - randomly distributed above and below Zero

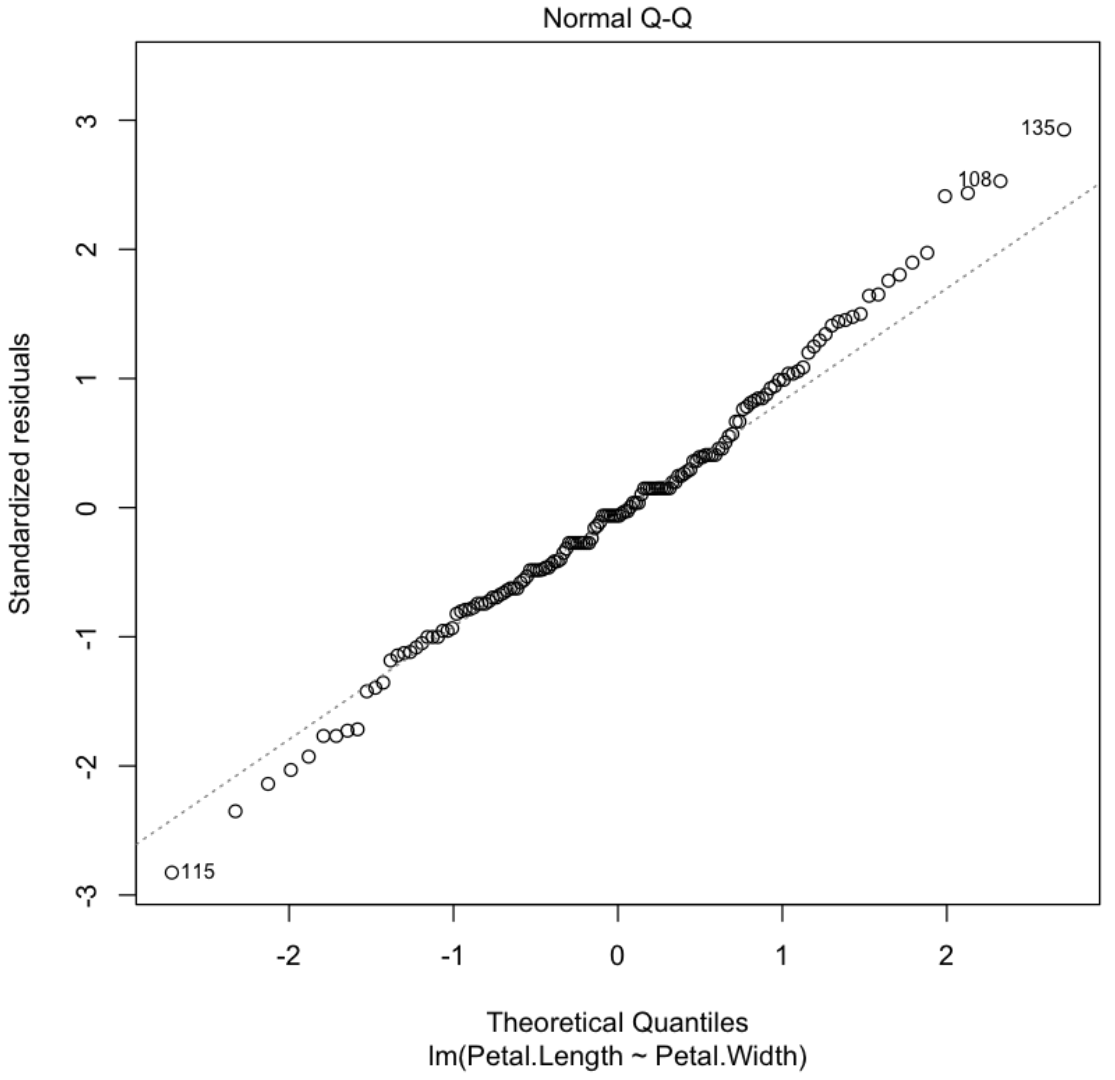
In [26]:

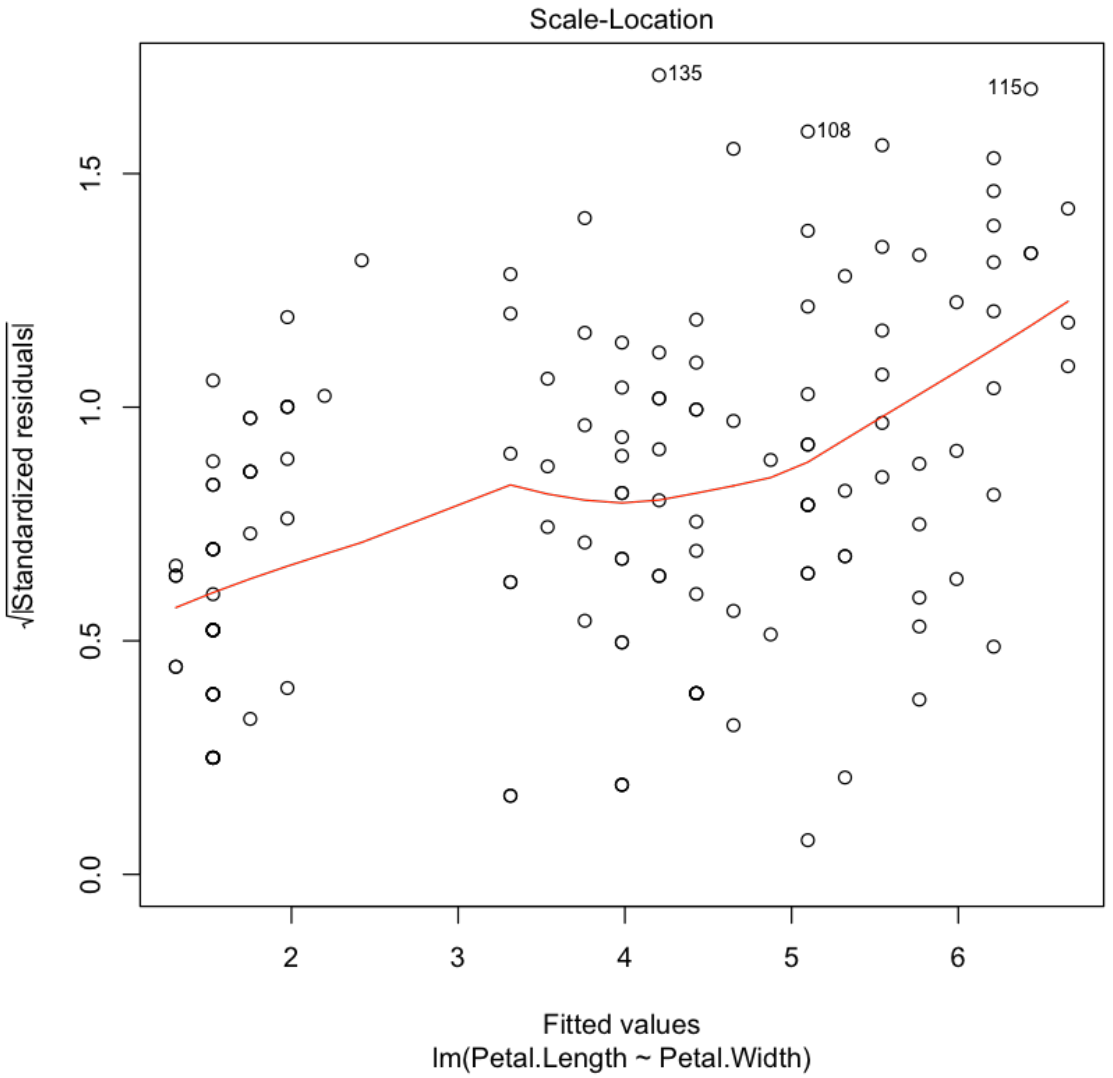
'coefficients' 'residuals' 'effects' 'rank' 'fitted.values' 'assign'
'qr' 'df.residual' 'xlevels' 'call' 'terms' 'model'

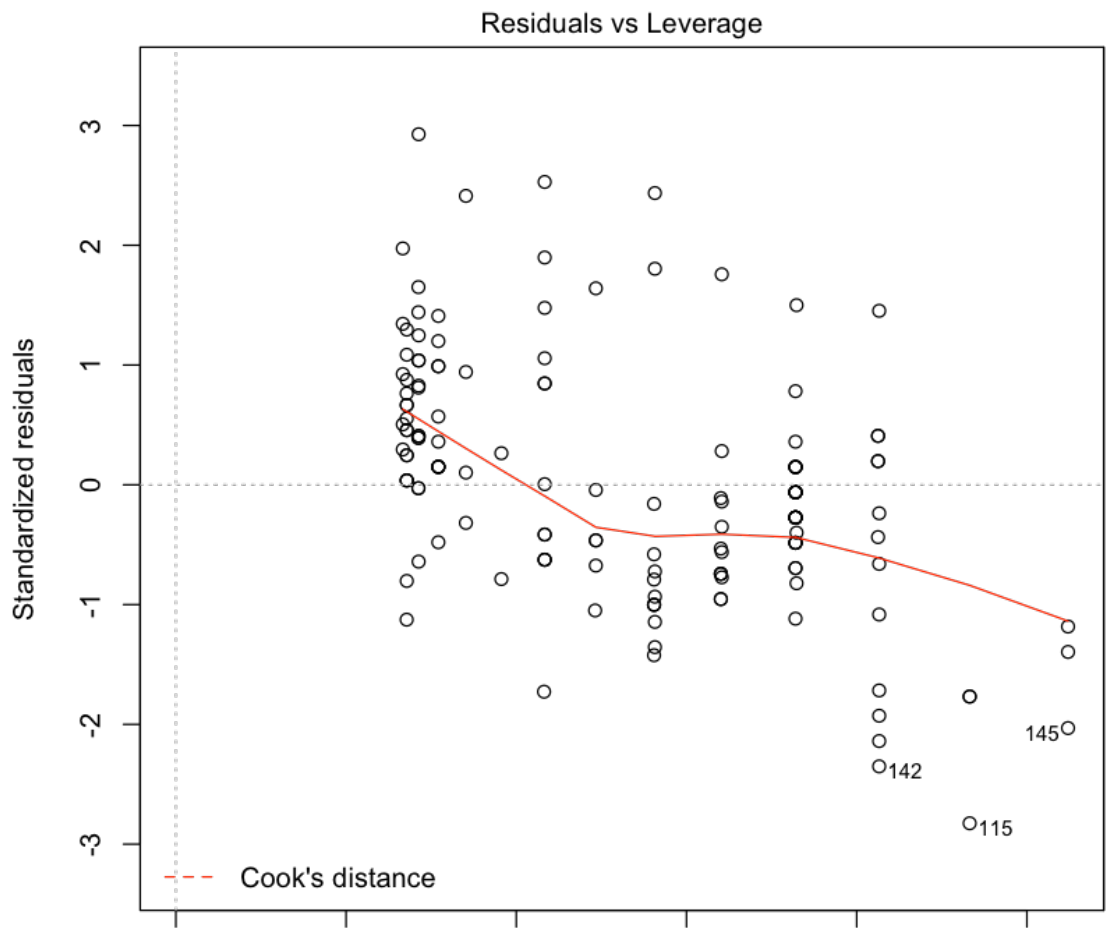
In [57]:

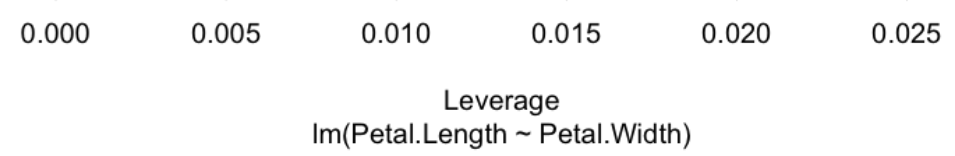



Residuals
Fitted values
lm(Petal.Length ~ Petal.Width)
135
108
115


Normal Q-Q
Standardized residuals
Theoretical Quantiles
lm(Petal.Length ~ Petal.Width)
135
108
115


Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
2
3
4
5
6
135
108
115
Fitted values
lm(Petal.Length ~ Petal.Width)


Residuals vs Leverage
Standardized residuals
3
2
1
0
-1
-2
-3
145
142
115
Cook's distance



In [32]:

```
Error in eval(expr, envir, enclos): object 'lmModel'
not found
Traceback:
```

In [ ]:

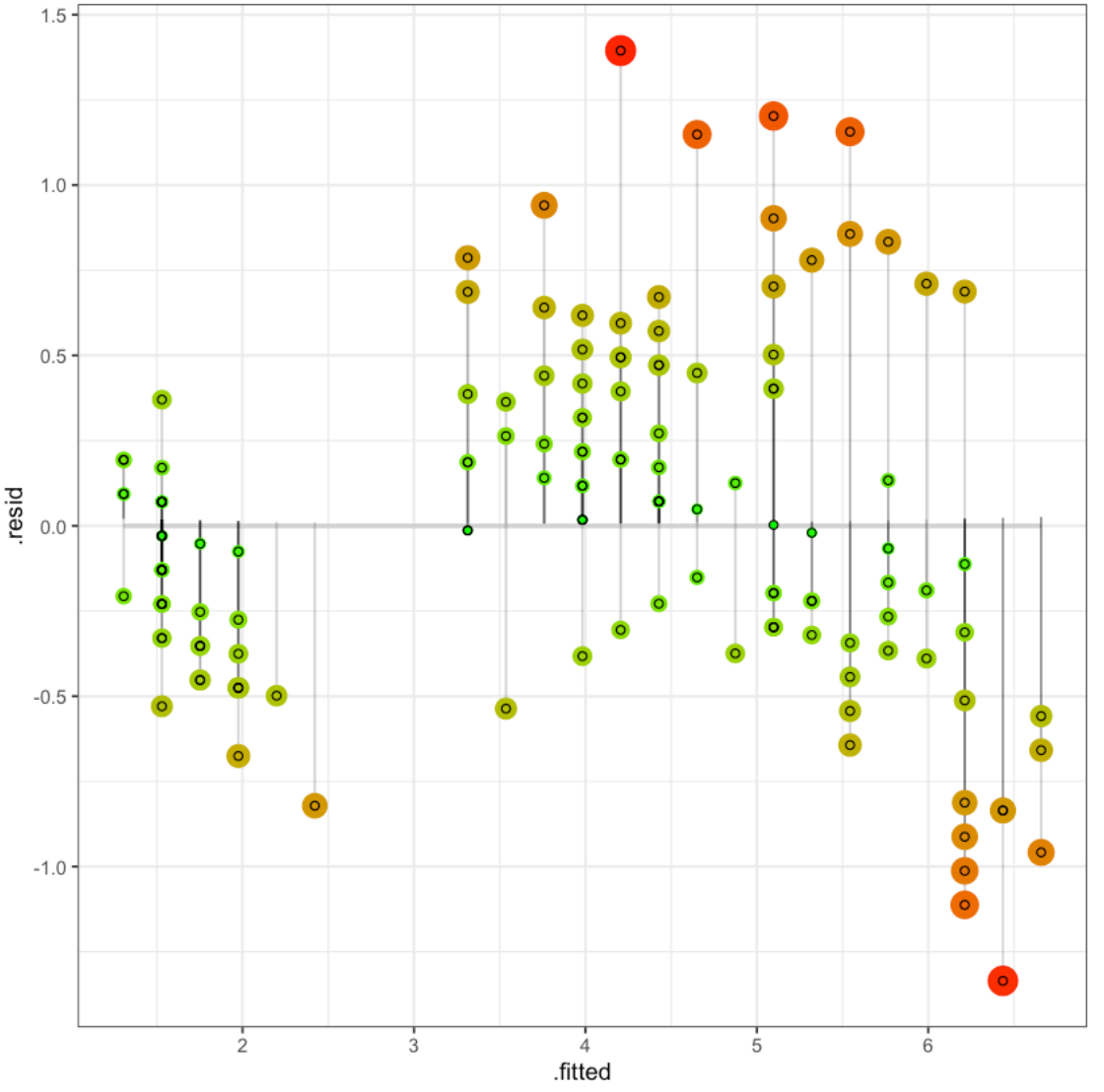
In [24]:

'Petal.Length' 'Petal.Width' '.fitted' '.se.fit' '.resid' '.hat'
'.sigma' '.cooksd' '.std.resid'

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [27]:



In [28]:

A anova: 2 × 5

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
	<int>	<dbl>	<dbl>	<dbl>	<dbl>
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [29]:

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
eedom
Multiple R-squared:  0.9271,     Adjusted R-squared:
```

In [83]:

0.4782

0.127248536455561

- Typically we have a regression model looks like this: $Y=\beta 0+\beta 1X+\epsilon$ where ϵ is an error term independent of X
- If $\beta 0$ and $\beta 1$ are known, we still cannot perfectly predict Y using X due to ϵ. Therefore, we use RSE as a judgement value of the Standard Deviation of ϵ
- RSE is s just an estimate of the Standard Deviation of ϵ. in other term how the prediction or response deviates from the regression line.

It's also known as the residual standard deviation (RSD), and it can be defined as

$$RSE = \sqrt{\frac{RSS}{n-2}} = \sqrt{\frac{\sum (y_i - \hat{y})}{n-2}}$$

. The smaller the RSE. =>. the model fits the data well

In [84]:

0.127248536455561

In [55]:

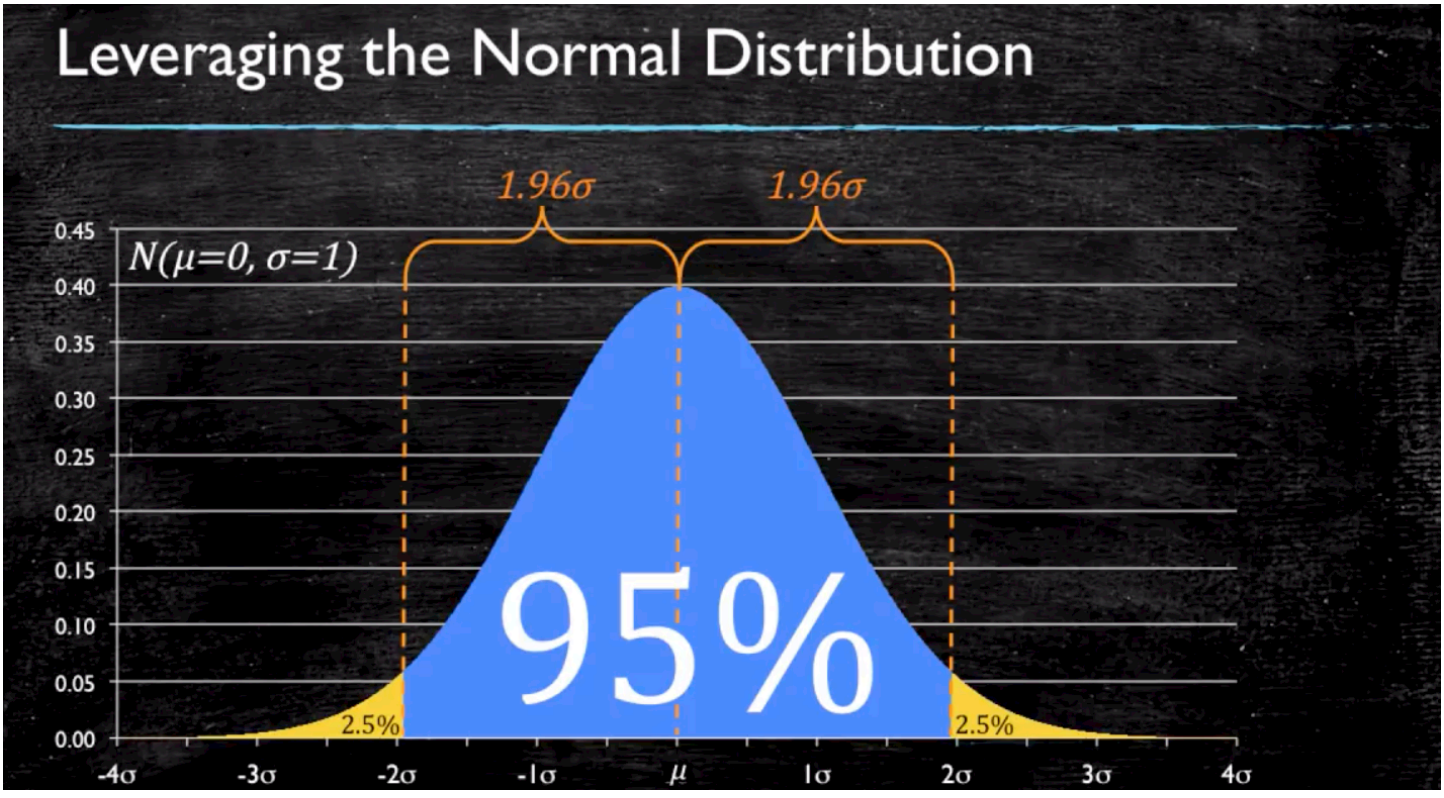
0.962865431402796

$$ln(\frac{p}{1-p}) = b_0 + b_i x$$

the model interpretentation

- Petal.Length= 1.08356 + 2.22994 x + e if Petal.Width increases by 1, Petal.Length will increase by 2.23.
  (is this enough to assess the correlation between the 2 variables) Of course NO.
- we have to recall that we fount this estimate based on a single sample. What's about the whole population. (with a single sample, we have to deal with incertainty)

. it's standard to work with 95% confidence intervals, which means we are 95% certain true values lies wihtin our interval.



In [109]:

```
        Pearson's product-moment correlation

data:  iris$Petal.Length and iris$Petal.Width
t = 43.387, df = 148, p-value < 2.2e-16
alternative hypothesis: true correlation is not equa
l to 0
95 percent confidence interval:
 0.9490525 0.9729853
sample estimates:
      cor
0.9628654
```

- we are 95% confident that my population mean is bigger than 0.95 and less than 0.973

In [ ]:

In [24]:

```
        One Sample t-test

data:  iris$Petal.Length
t = 26.073, df = 149, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 3.473185 4.042815
sample estimates:
mean of x
    3.758
```

In [ ]:

In [ ]:

In [111]:

3.758

In [112]:

0.238575993390587

In [113]:

3.51942400660941

In [ ]:

In [21]:

```
Start:  AIC=-219.33
Petal.Length ~ Petal.Width

             Df Sum of Sq    RSS     AIC
<none>                      33.84 -219.33
- Petal.Width  1    430.48 464.33  171.49


Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Coefficients:
(Intercept)  Petal.Width
      1.084        2.230
```

In [19]:

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species


1.30234800000309
```

In [115]:

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species
```

In [116]:

```
1.65521450617873
```

In [ ]:

In [ ]:

In [ ]:

In [ ]:

how to access. the model parameters.

In [118]:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
```

- Coefficient = 2.23 and the Std Error =0.051. This tell us about typpical variation of this coefficient.The Std Error gives kind of average Expected Error term from this particular sample value.
  (t statistice)Error_t= Estimate / Std_Error
- The higher the t-statistic the more significant the variable is. HIgher in magnitude Petal.Width -> t1= 2.2299/0.05514

P-Value

P-value< 5% P-value gives us an indication how extreme this coefficient if the Petal.Width coefficient equals to Zero. Here we've to Evoque The Null hypothesis where linear regression's coefficient are Zeros. We start at the hypothesis that there is no effect of Petal.width coeficient on the Petal.Length prediction model. briefly, P-value gives the probability of this coefficient occuring just due to random chance. In other term, it tells if the Petal.Width coefficient has no effect ont the Target variable Petal.Length.

At 5% we test wether this variable is significant or not. there’s minimal chance that this predictor is not meaningful for the regression.

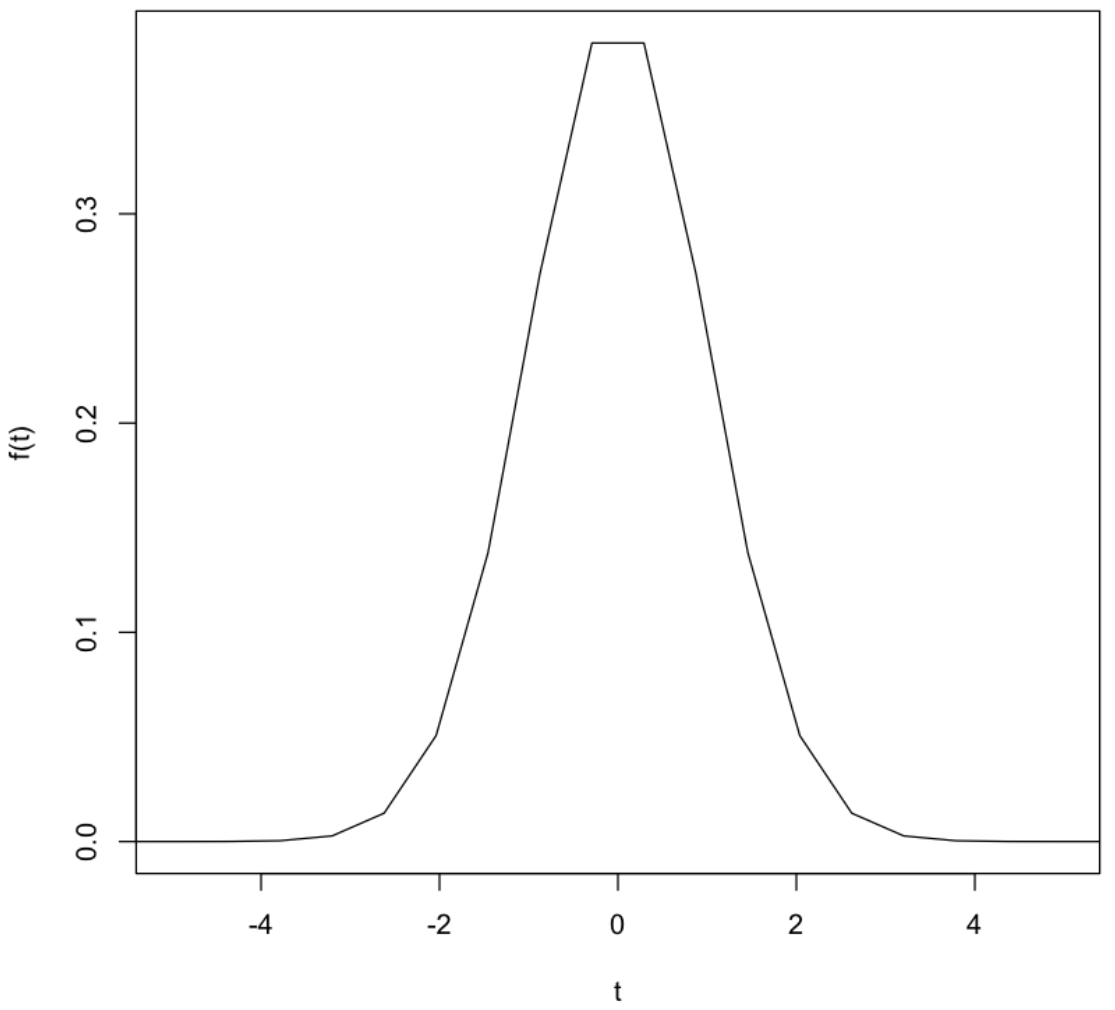
F statistic

The F-statistic is equal to 430.48/0.229 = 1882.452. The distribution is F(1, 148), and the probability of observing a value greater than or equal to 1882.452 is less than 0.001. There is strong evidence that \beta_1 is not equal to zero.

The r^2 term is equal to 0.577, indicating that 57.7% of the variability in the response is explained by the explanatory variable.

In [ ]:

In [119]:



In [121]:

	2.5 %	97.5 %
(Intercept)	0.9393664	1.227750
Petal.Width	2.1283752	2.331506

In [192]:

0.921379160712566

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris
)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.08356    0.07297   14.85   <2e-16 ***
Petal.Width  2.22994    0.05140   43.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 0.4782 on 148 degrees of fr
```

In [122]:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Petal.Width	1	430.48065	430.4806468	1882.452	4.675004e-86
Residuals	148	33.84475	0.2286808	NA	NA

In [67]:

```
        Welch Two Sample t-test

data:  iris$Sepal.Length and iris$Petal.Length
t = 13.098, df = 211.54, p-value < 2.2e-16
alternative hypothesis: true difference in means is
not equal to 0
95 percent confidence interval:
 1.771500 2.399166
sample estimates:
mean of x mean of y
 5.843333  3.758000
```

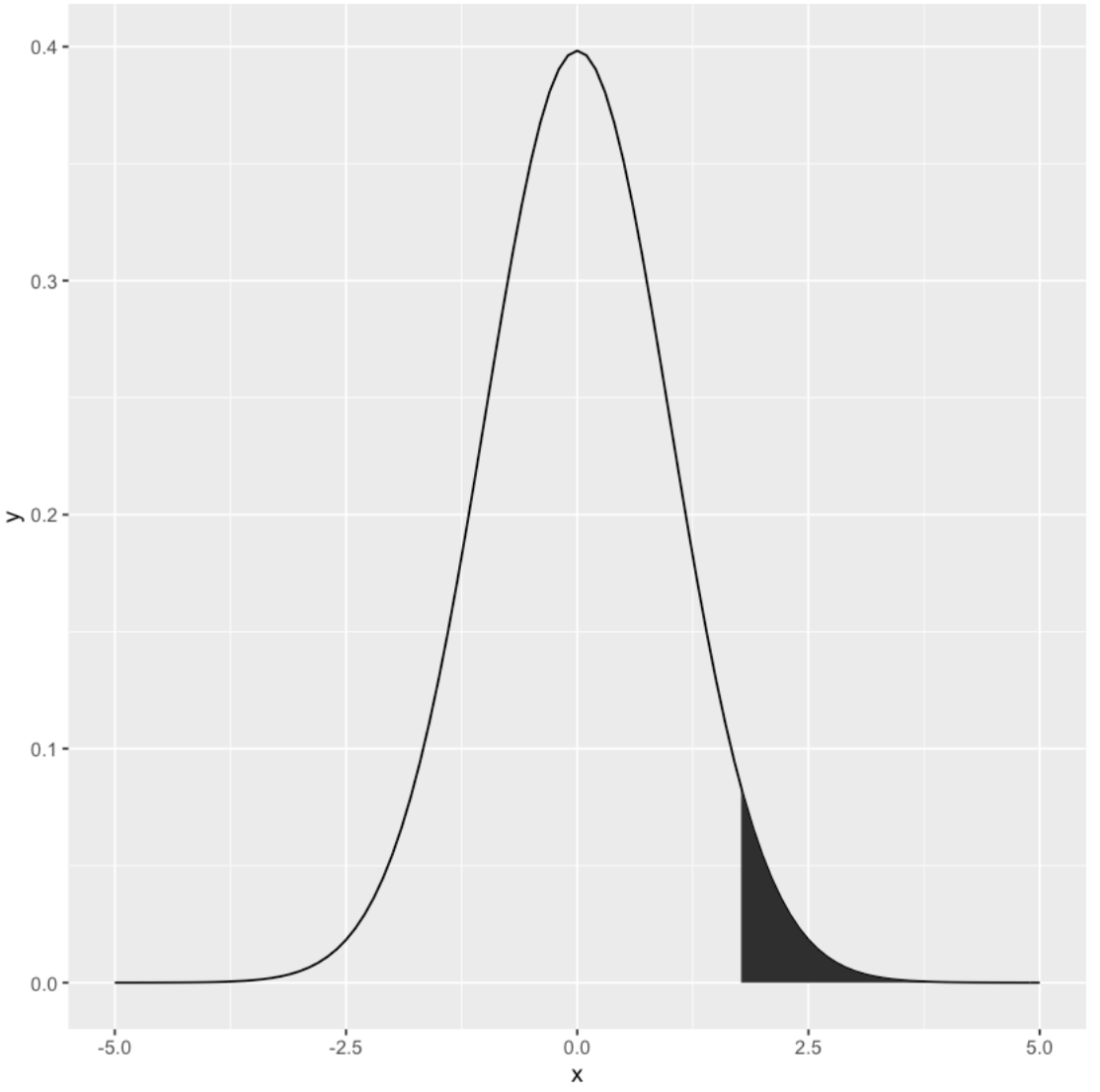
In [4]:

2.28134

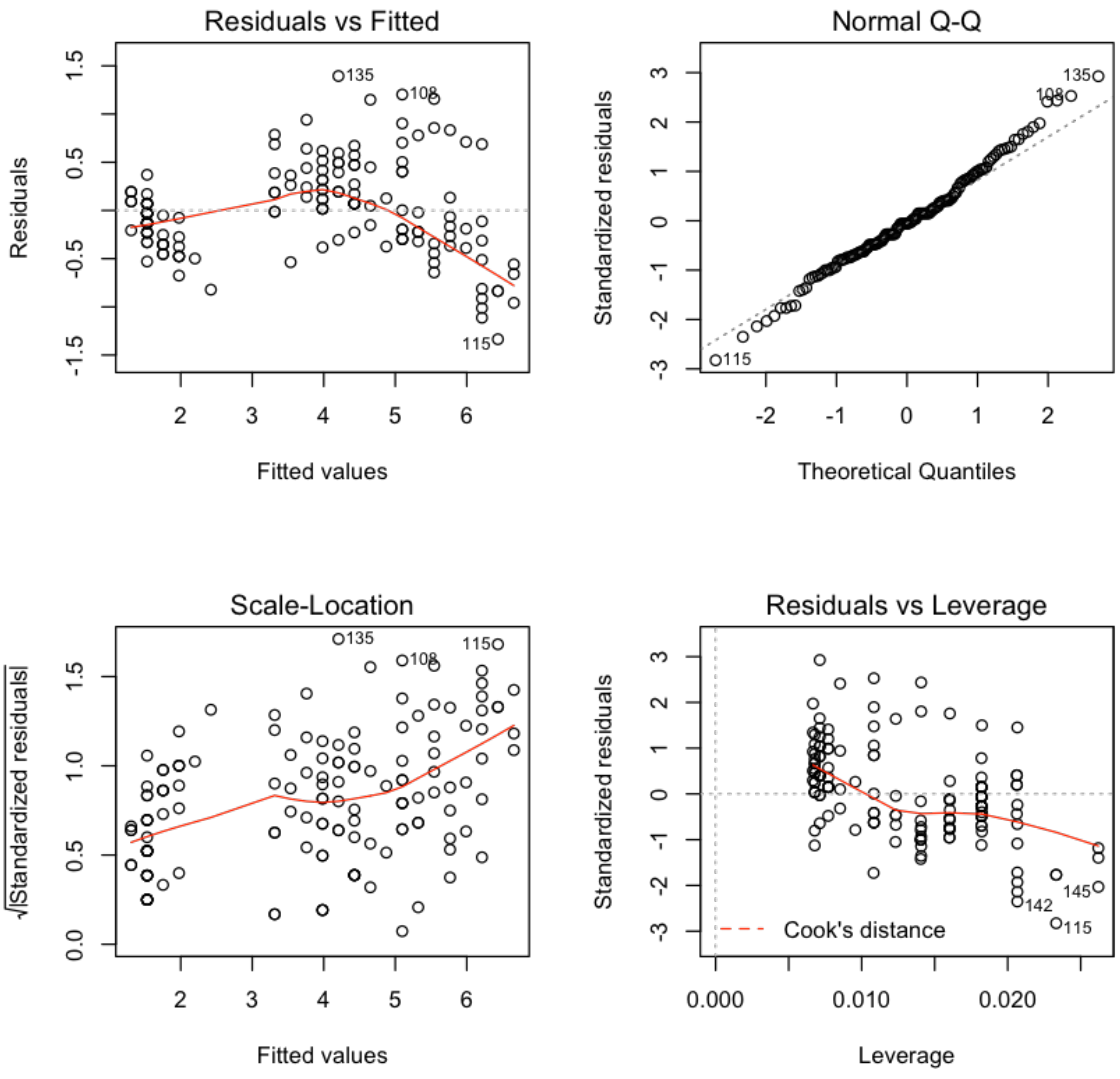
In [ ]:

In [ ]:

In [66]:



In [227]:



In [ ]:

In [ ]:

In [124]:

```
Error in eval(expr, envir, enclos): object 'Residual
' not found
Traceback:
```

In [127]:

In [128]:

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Resid
5.1	3.5	1.4	0.2	setosa	-0.12954
4.9	3.0	1.4	0.2	setosa	-0.12954
4.7	3.2	1.3	0.2	setosa	-0.22954
4.6	3.1	1.5	0.2	setosa	-0.02954
5.0	3.6	1.4	0.2	setosa	-0.12954
5.4	3.9	1.7	0.4	setosa	-0.27553

In [131]:

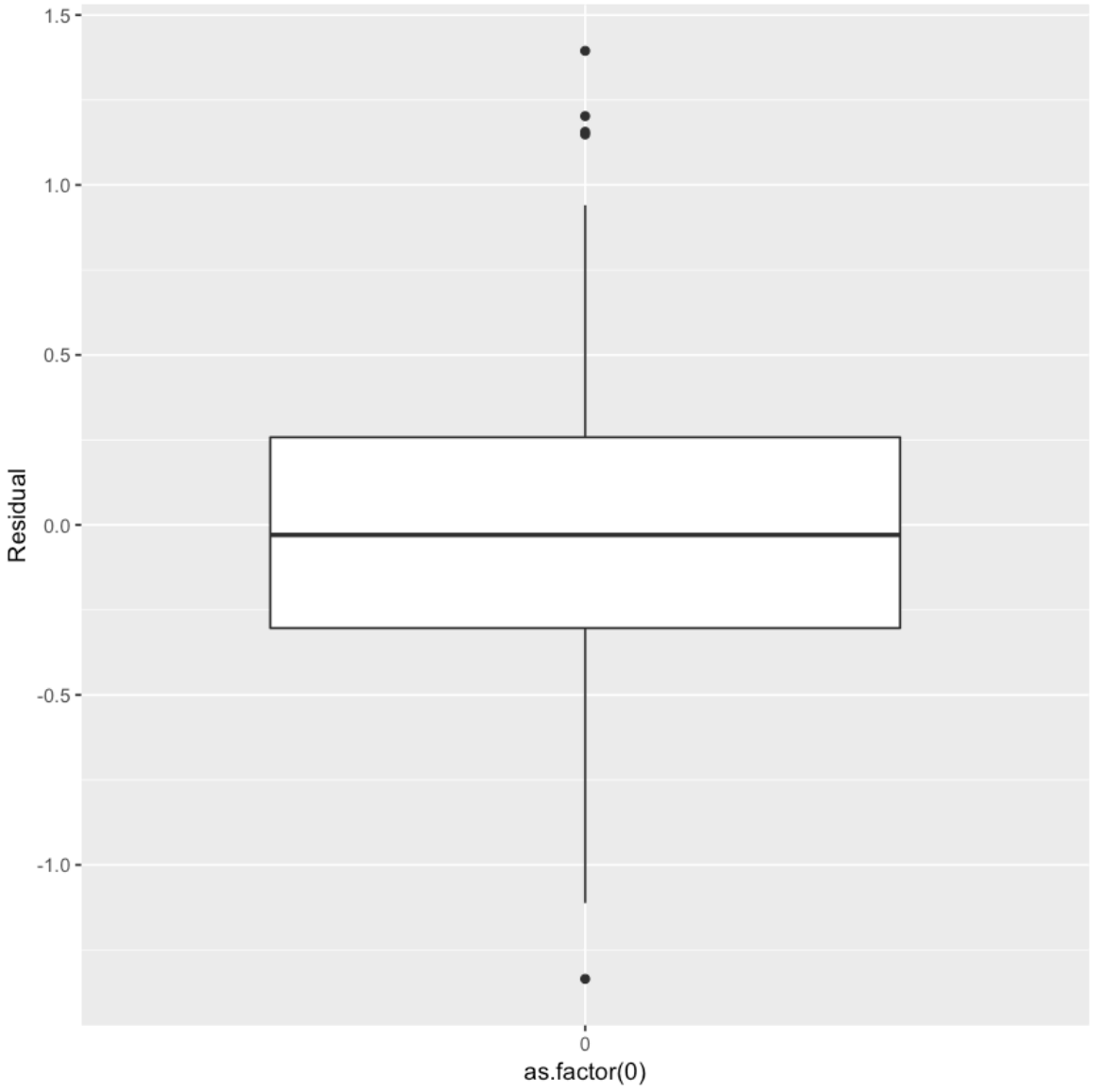
0.0389140929405684

In [133]:

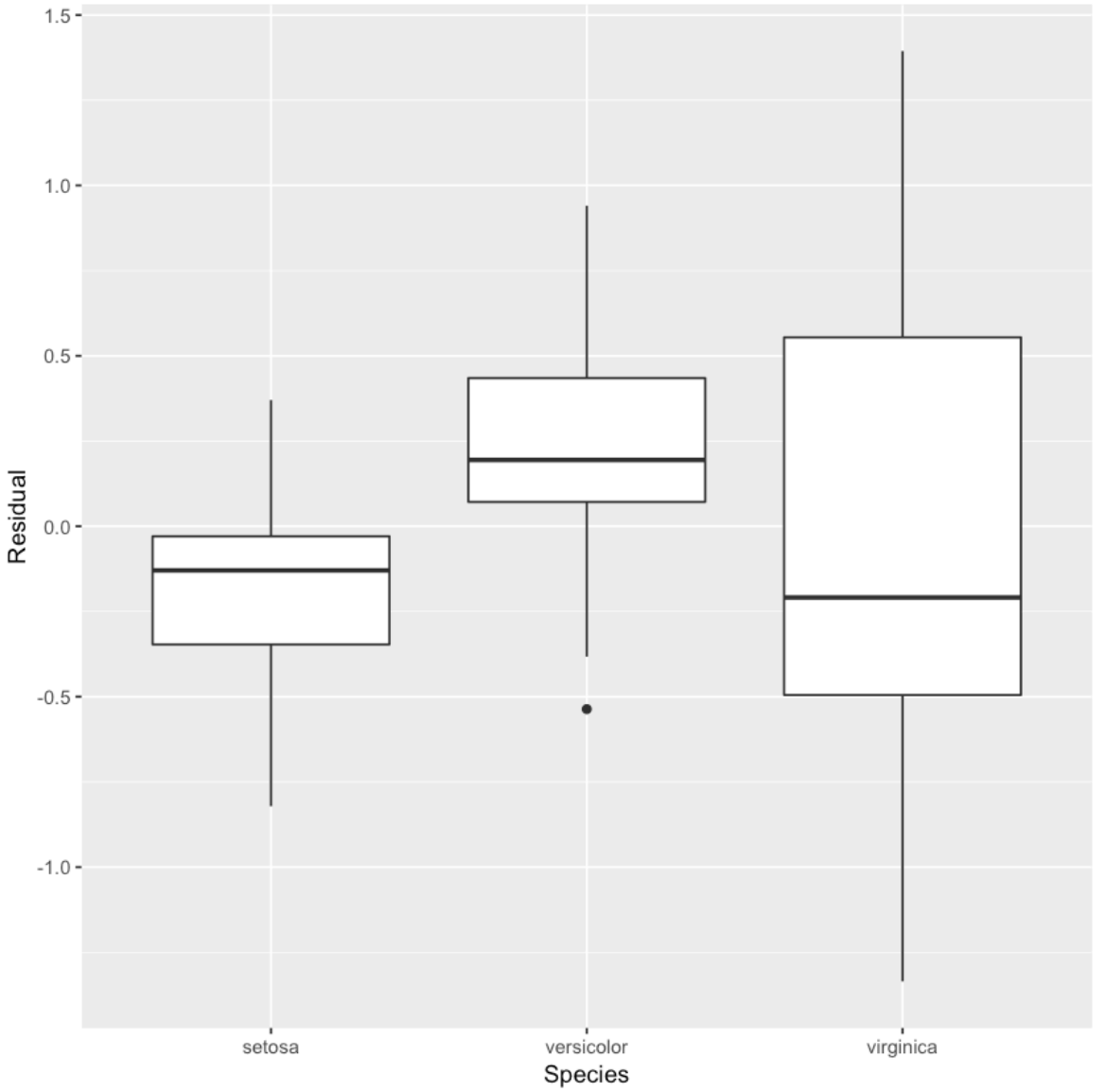
-0.0778281858811368 0.0778281858811369

In [ ]:

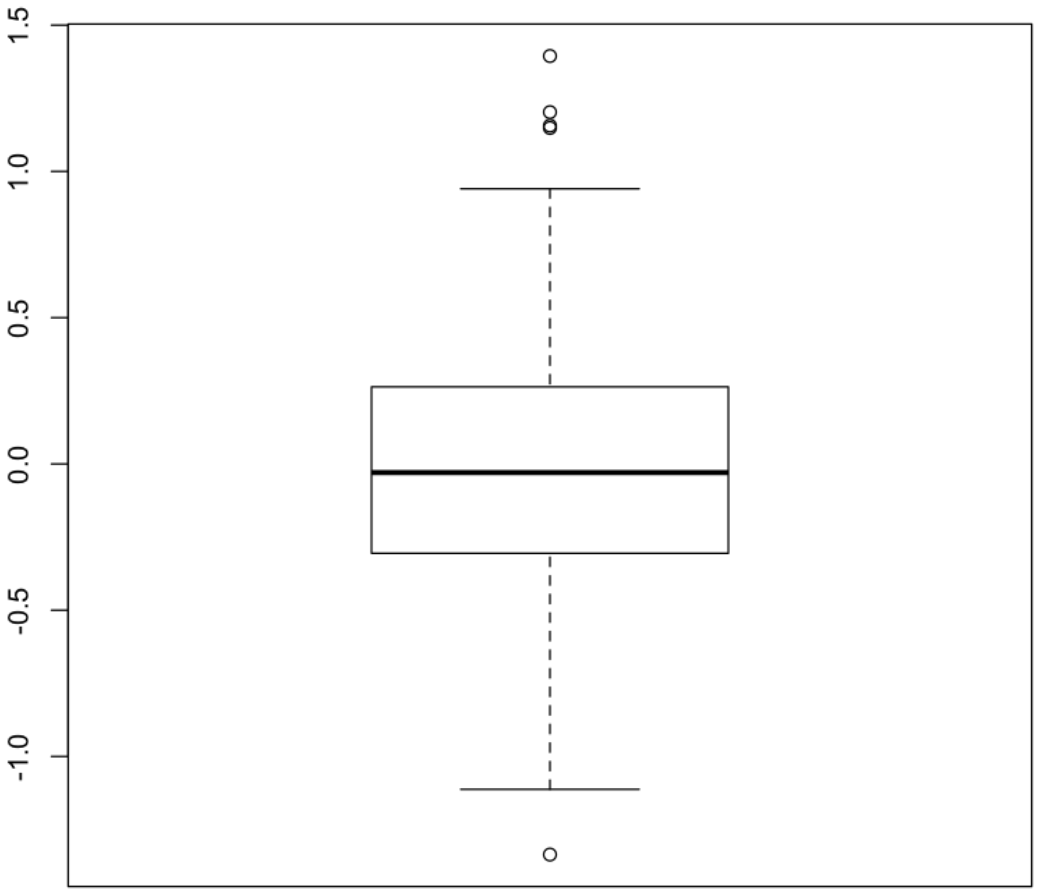
In [134]:



In [135]:


1.5
1.0
0.5
0.0
-0.5
-1.0
Residual
setosa
versicolor
virginica
Species

In [136]:



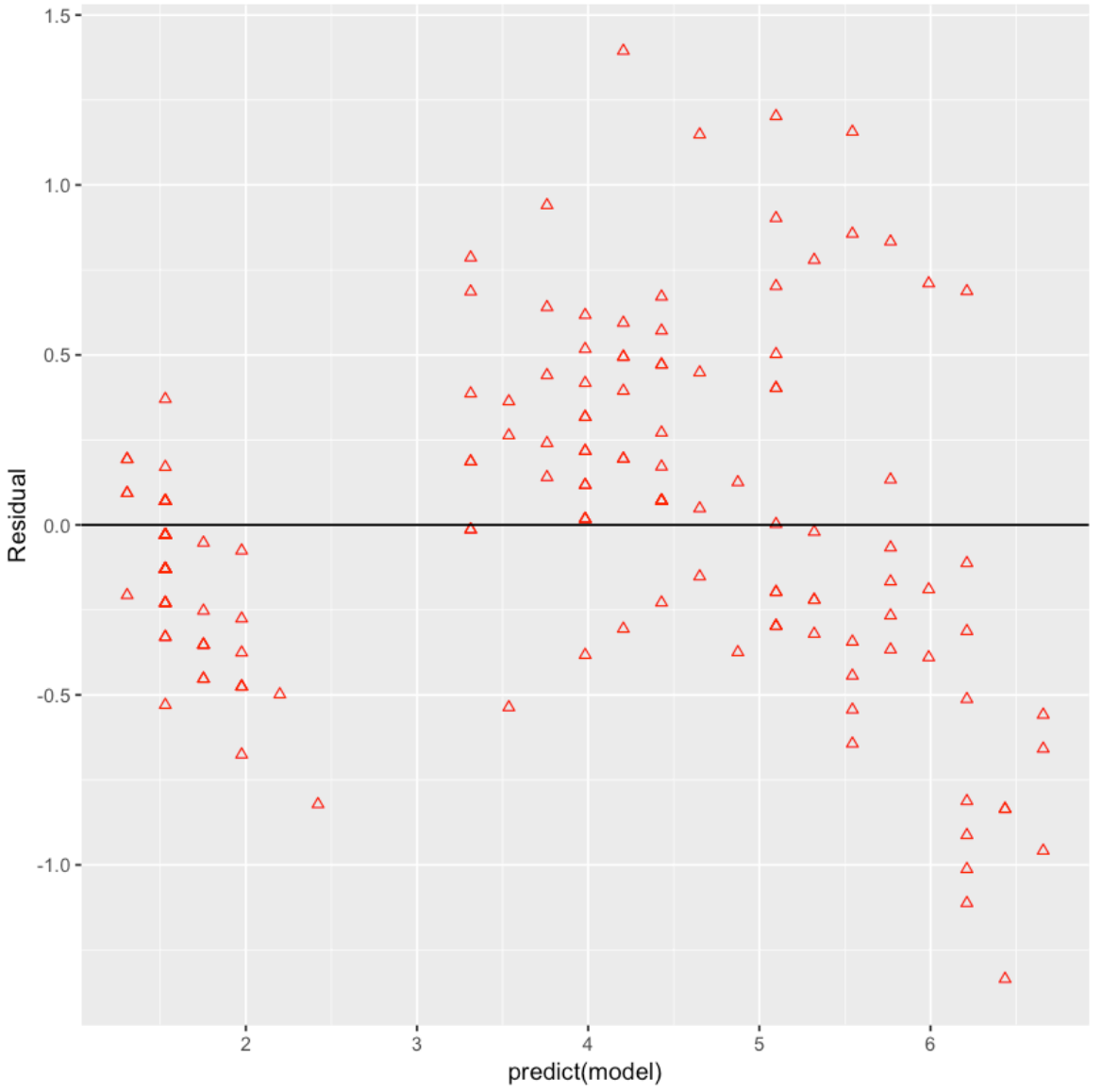

```
# Get a summary report of the model
summary(model)
```

```
Call:
lm(formula = Petal.Length ~ Petal.Width, data = iris)

Residuals:
     Min       1Q   Median       3Q      Max
-1.33542 -0.30347 -0.02955  0.25776  1.39453
```

In [137]:

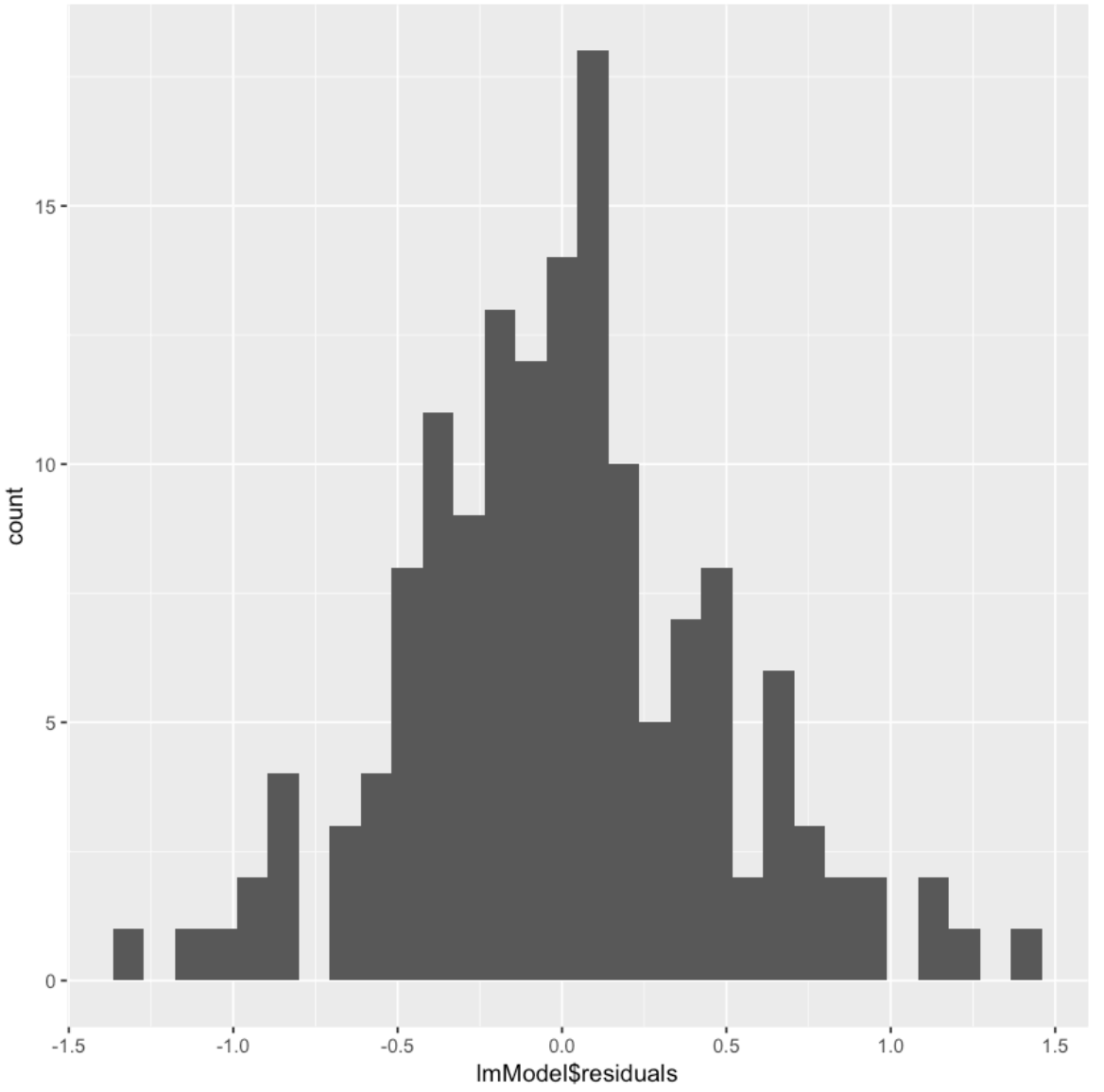
```
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max
.
-1.33542 -0.30347 -0.02955  0.00000  0.25776  1.3945
3
```

In [138]:



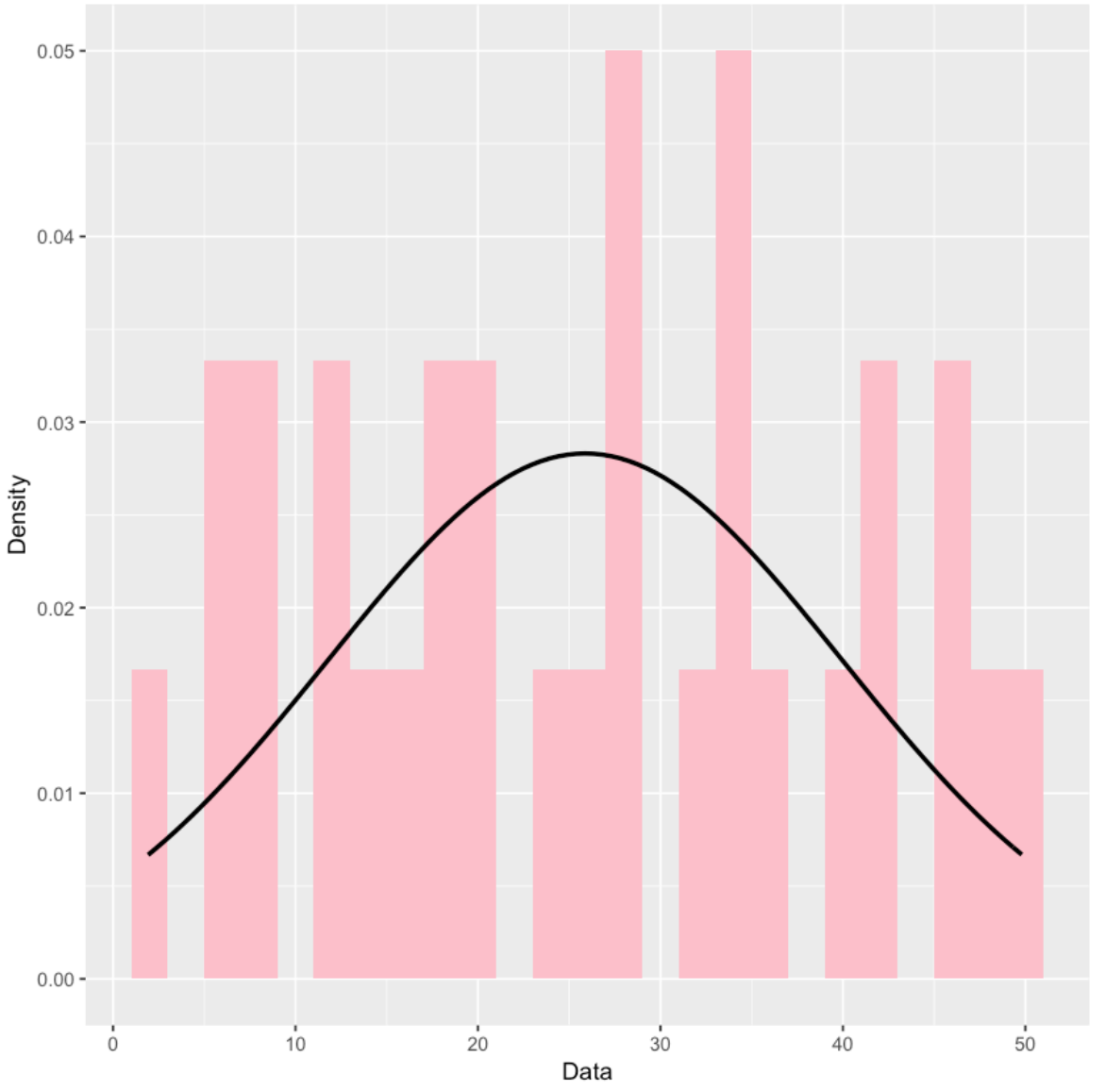
In [49]:

```
`stat_bin()` using `bins = 30`. Pick better value wi
th `binwidth`.
```



In [ ]:

In [145]:



In [152]:

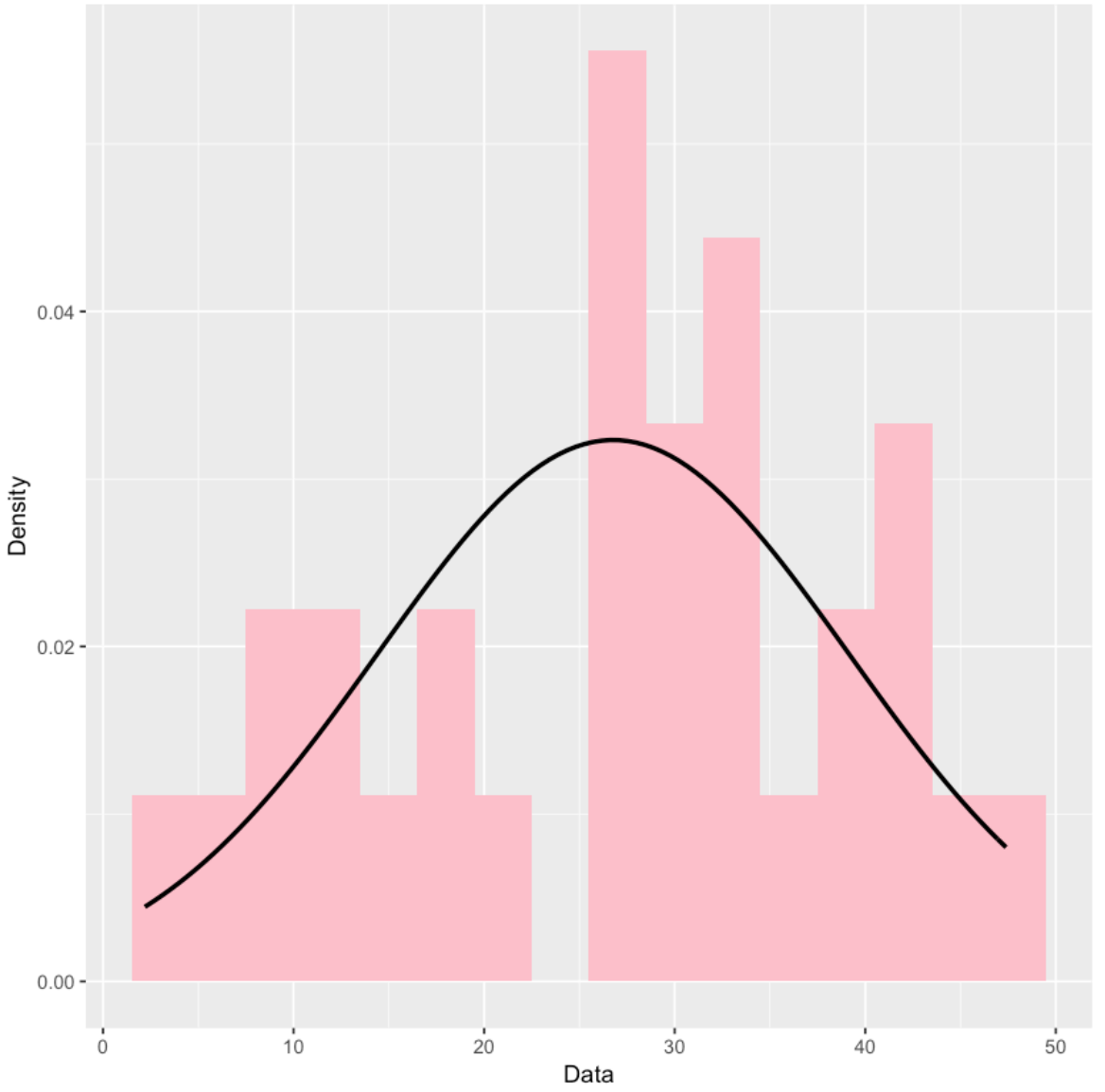
In [156]:

14.0930419142395

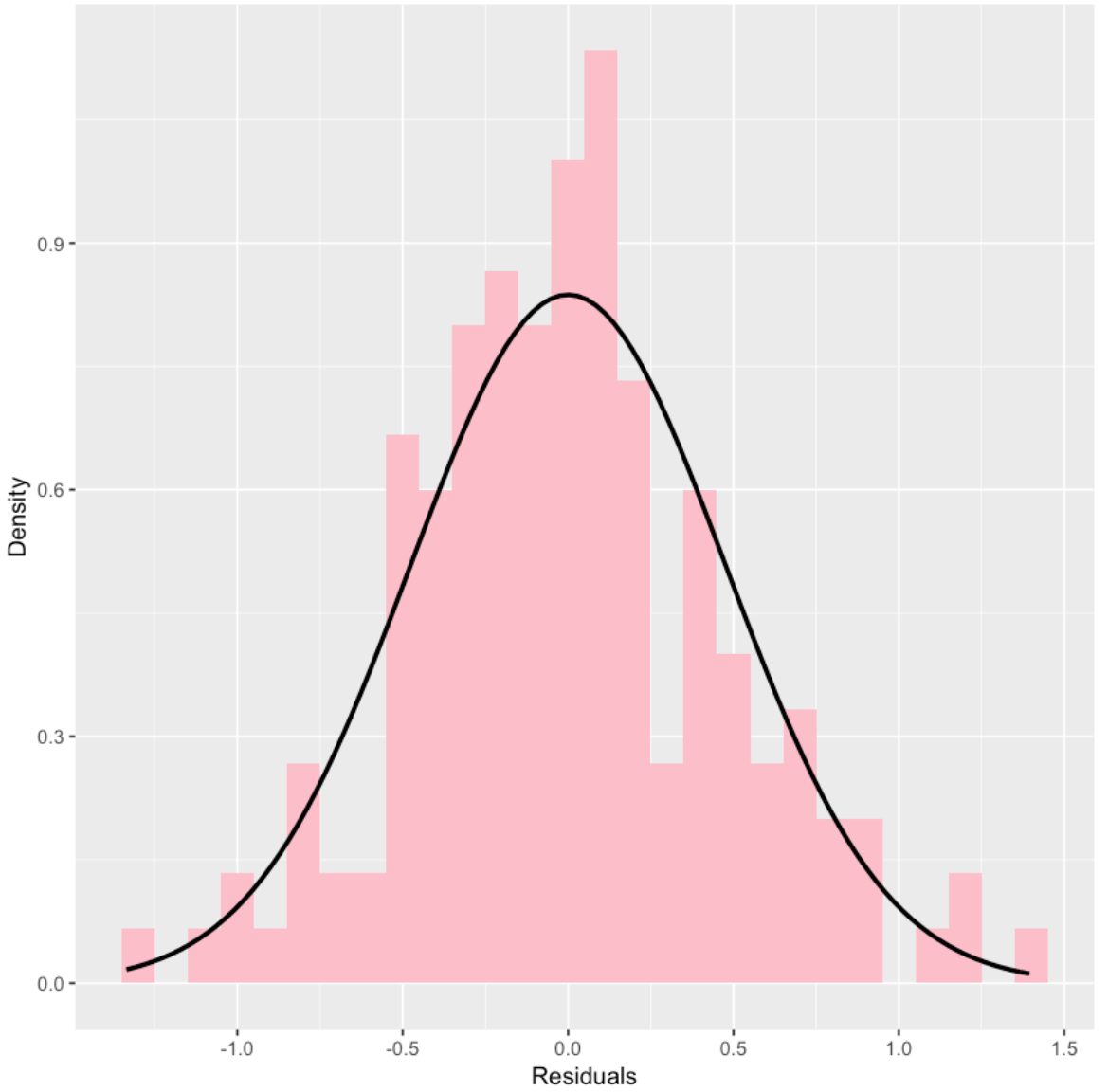
In [157]:

25.8732585030841

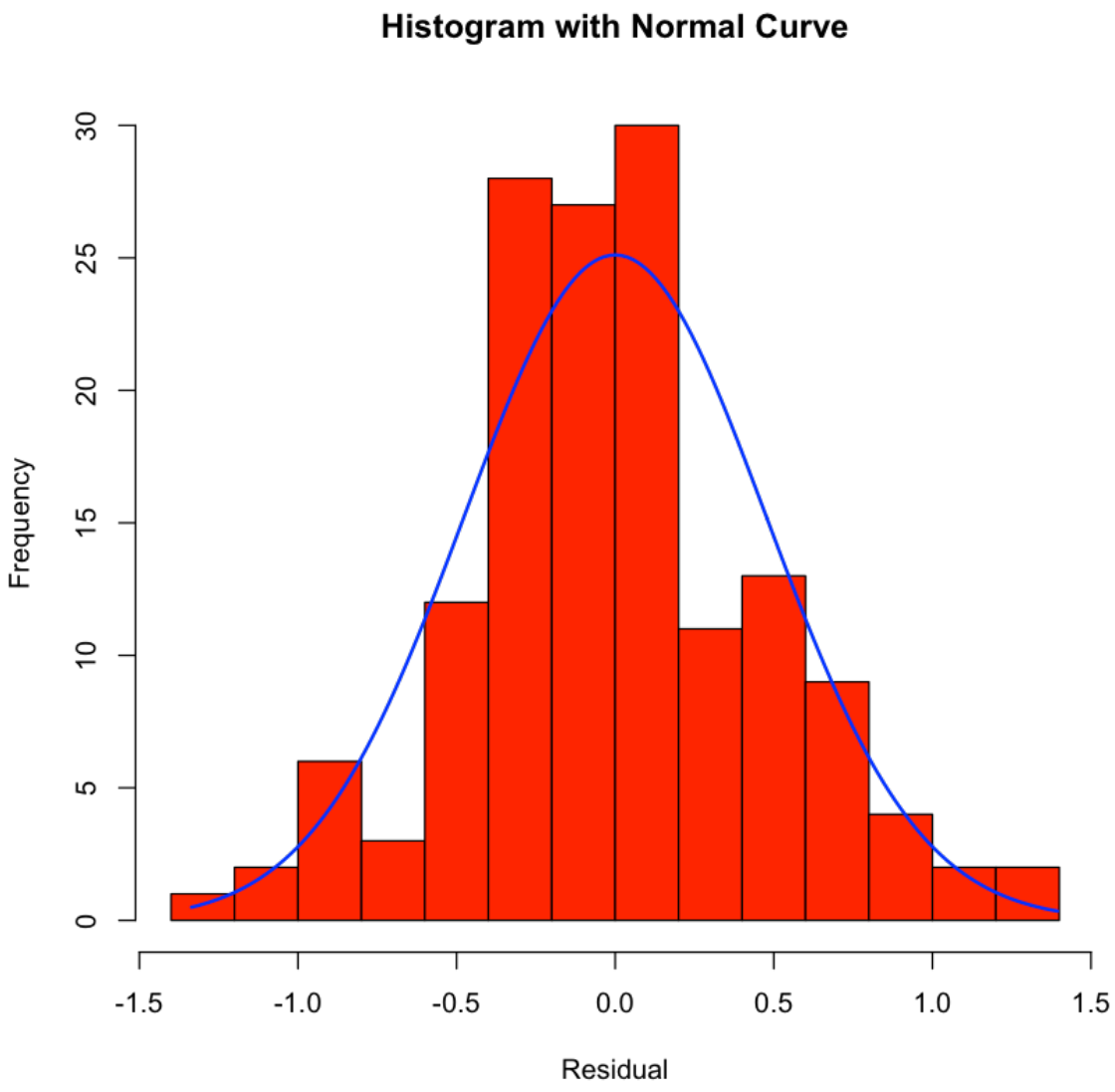
In [166]:



In [52]:



In [173]:



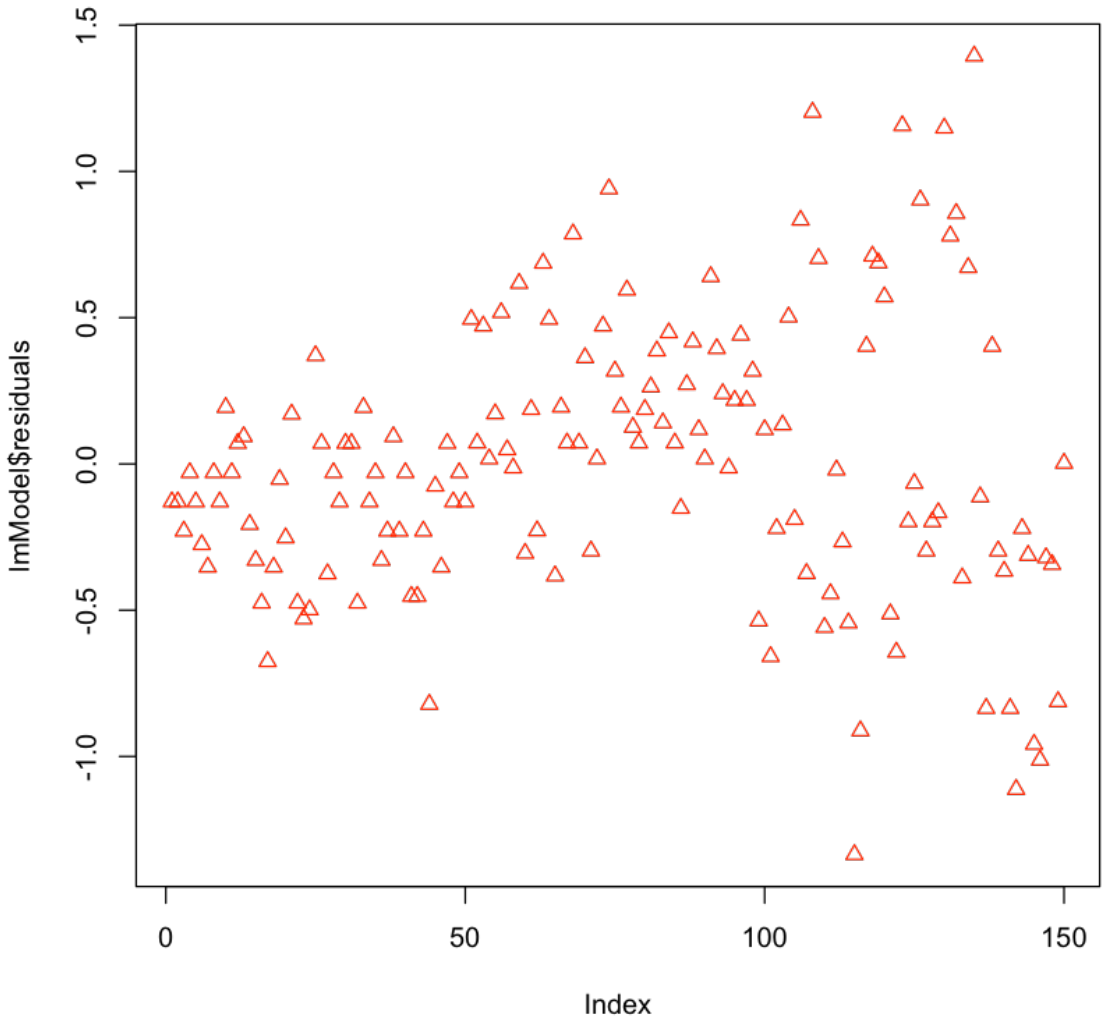
In [298]:

'Sepal.Length' 'Sepal.Width' 'Petal.Length' 'Petal.Width' 'Species'

How to interpret Residuals?

- Residuals follow roughtly normal distribution. We can do so by checking histogram od residuals. If the histogram of residuals looks normal then we have a valid model.

In [16]:



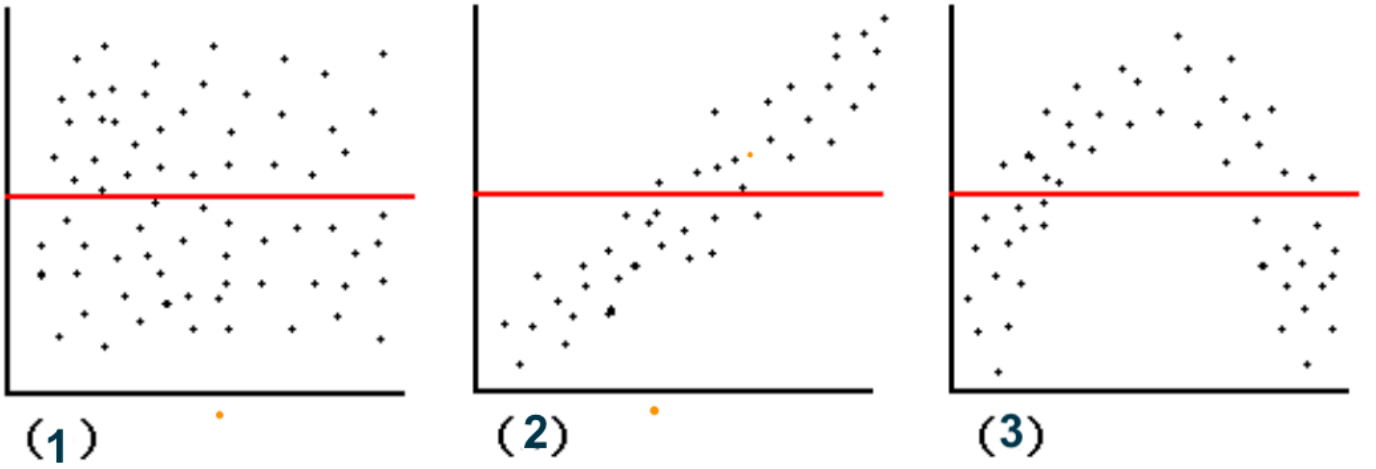
In [ ]:

In [ ]:

In [ ]:

- A very important point is that we need to check is that our residuals follow roughly normal distribution. We can do so by checking histogram of residuals. If the histogram of residuals looks normal then we have a valid model.

How to interpret Patterns in Residual Plots ?



Residual Plot (a)

- Residuals are randomly distributed around regression line
- Residuals follow normal distribution
- Residuals are Homoscedastic.
- Linear model is valid.

Residual Plot (b)

- Residuals are non randomly distributed around regression line
- Residuals increase as the predicted value increases, which could mean that we might be missing a variable or - two and some predictive pattern is being leaked as a residual.
- Residuals are Homoscedastic.
- Linear model is not valid (if it has intercept), check for explanatory variables which might explain the linear residual or the model has failed to account for intercept
- Or the plot does not belong to a linear model at all another option is that the model might be a model forced to pass through origin i.e a non intercept model

Residual Plot (c)

- Residuals are non randomly distributed around regression line
- Residuals are Homoscedastic
- Residuals have curve pattern to them. -Linear model is not valid. Curved residual pattern might mean that we may have to fit a polynomial of some order to explain the curved pattern of residuals.

In [ ]:

In [ ]:

In [ ]:

In [ ]:

In [ ]:

visualize The Model

In [75]:

(Intercept)
1.08355803285051
Petal.Width
2.22994049512186

In [ ]:

In [115]:

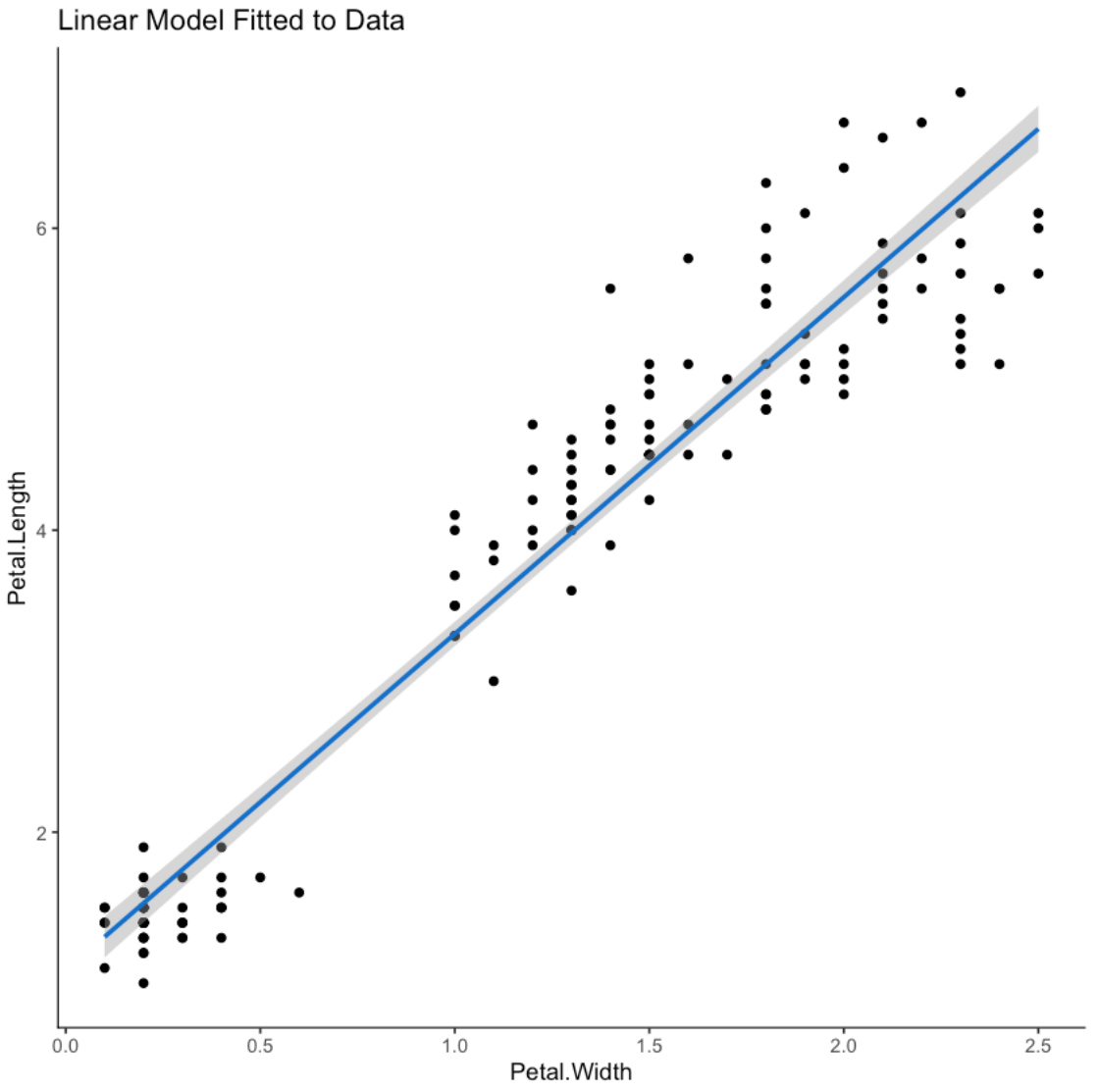
```
Error in geom_abline(intercept = model$coefficients[
1], slope = model$coefficients[2], : object 'model'
not found
Traceback:

1. geom_abline(intercept = model$coefficients[1], sl
ope = model$coefficients[2],
 .     color = "red", lwd = 2)
```

In [ ]:

In [114]:

```
Error in paste("y = ", round(model$coefficients[2],
2), "*x ", round(model$coefficients[1], : object 'mo
del' not found
Traceback:

1. paste("y = ", round(model$coefficients[2], 2), "*
x ", round(model$coefficients[1],
 .     2))
```

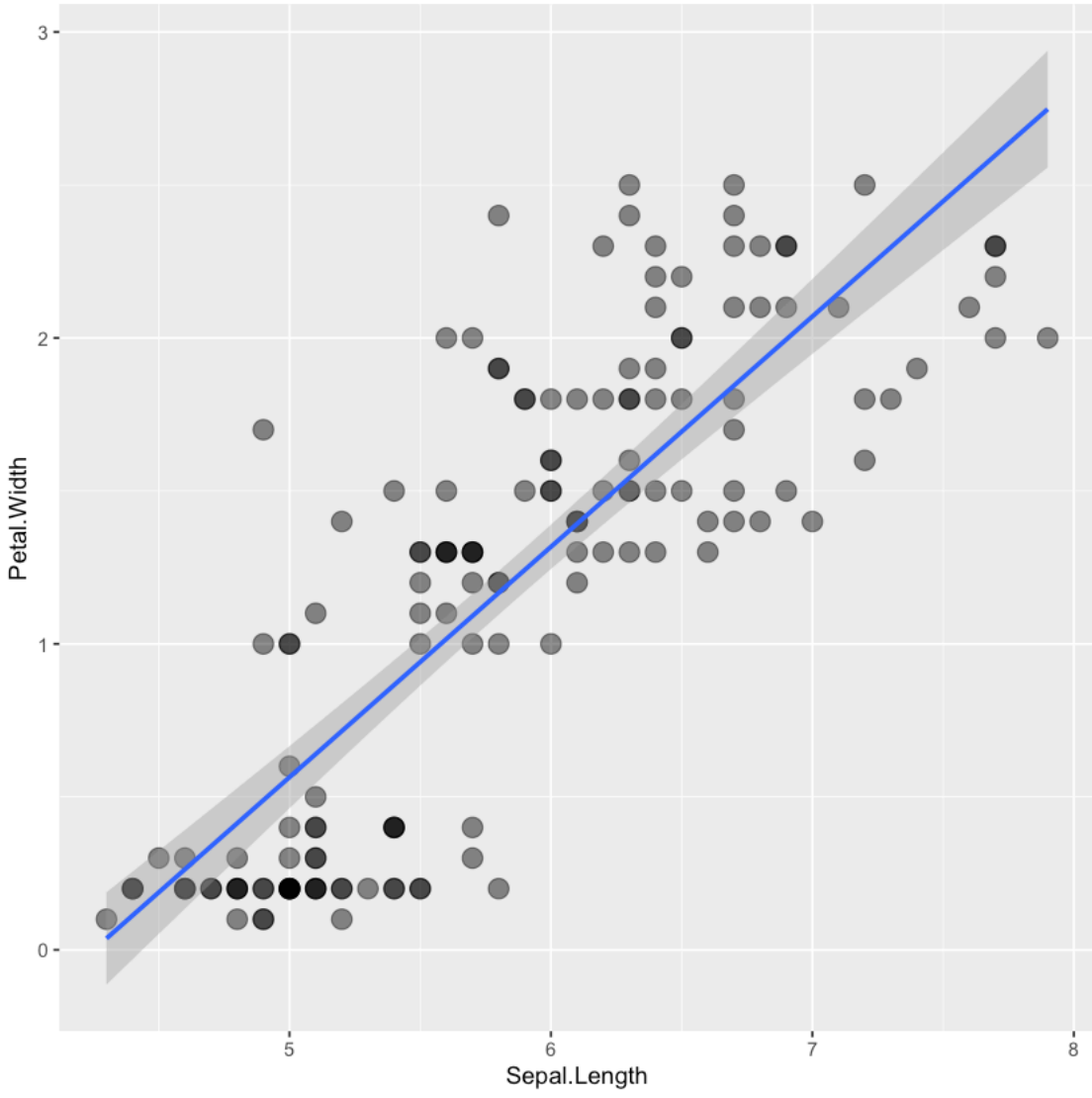
In [112]:



- The gray shading around the line represents a confidence interval of 0.95, the default for the stat_smooth() function, which smoothes data to make patterns easier to visualize. This 0.95 confidence interval is the probability that the true linear model for the girth and volume of all black cherry trees will lie within the confidence interval of the regression model fitted to our data. Even though this model fits our data quite well, there is still variability within our observations.

Another alternative for Sepal Length & Width

In [105]:



- here we can either test the ***model*** with a new dataframe using coeficients' model or throught the **predict** instruction

In [106]:

4.42846877553331 8.66535571626484 12.2332605084598

1
4.42846877553331
2
8.66535571626484
3
12.2332605084598

In [107]:

In [108]:

A tibble: 6 × 9

Petal.Length	Petal.Width	.fitted	.se.fit	.resid	.ha
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.3	0.2	1.529546	0.06451814	-0.22954613	0.0182026
1.5	0.2	1.529546	0.06451814	-0.02954613	0.0182026
1.4	0.2	1.529546	0.06451814	-0.12954613	0.0182026
1.7	0.4	1.975534	0.05667741	-0.27553423	0.0140472

In [109]:

1
1.52954613187489
2
1.52954613187489
3
1.52954613187489
4
1.52954613187489
5
1.52954613187489
6
1.97553423089926

In [110]:

```
```

-2.94556046220862e-15

In [111]:

```
```

A tibble: 1 × 1

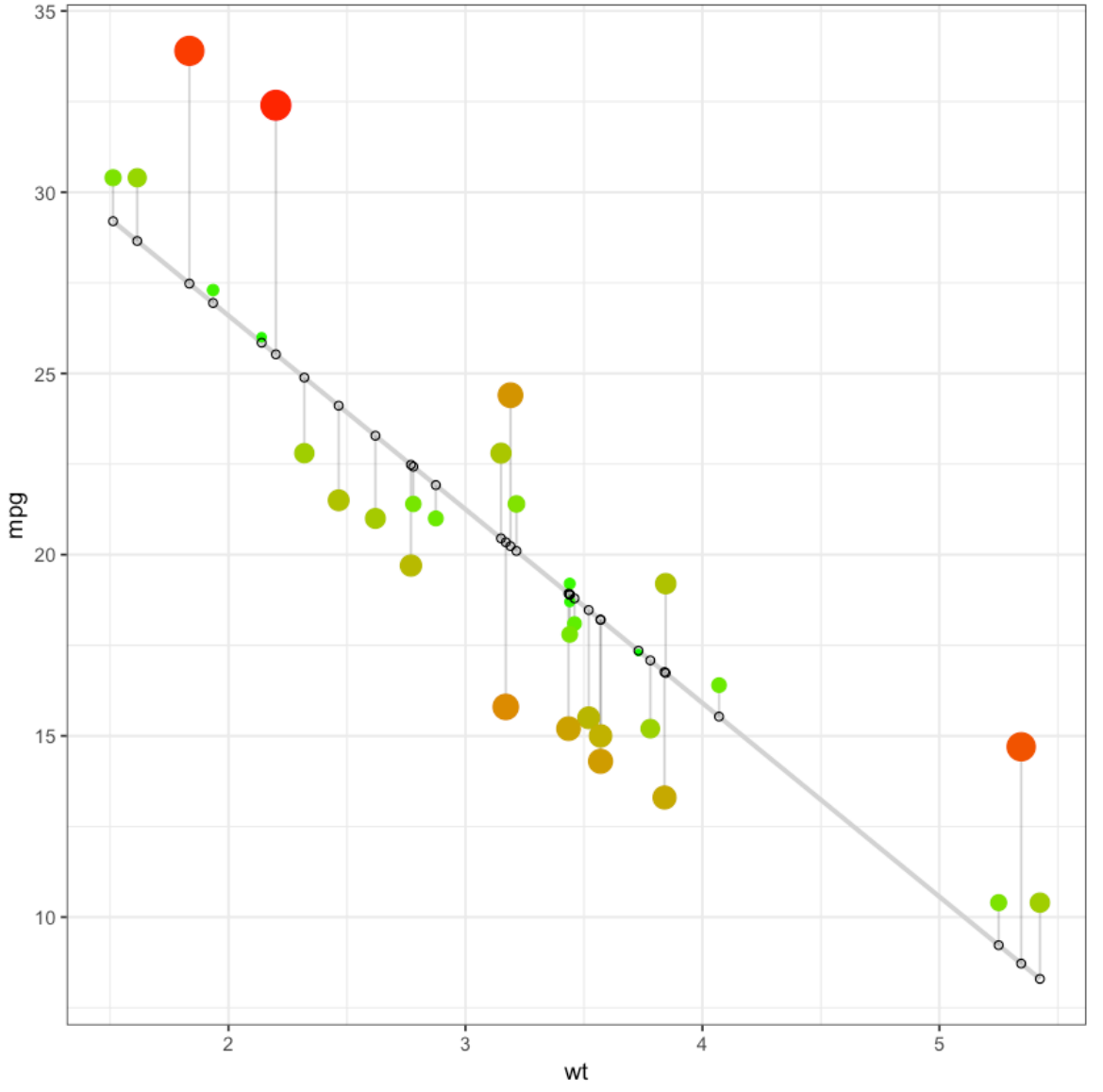
Sum
<dbl>
-2.94556e-15

In [ ]:

```
```

Residuals

In [75]:



In [76]:

```
Call:
lm(formula = mpg ~ wt, data = cars)

Residuals:
    Min      1Q  Median      3Q     Max
-4.5432 -2.3647 -0.1252  1.4096  6.8727

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  37.2851     1.8776  19.858  < 2e-16 ***
wt           -5.3445     0.5591  -9.559 1.29e-10 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

Residual standard error: 3.046 on 30 degrees of free
dom
Multiple R-squared:  0.7528,    Adjusted R-squared:
0.7446
```

In [77]:

```
'coefficients'  'residuals'  'effects'  'rank'  'fitted.values'  'assign'
'qr'  'df.residual'  'xlevels'  'call'  'terms'  'model'
```

In [ ]:

In [78]:

```
Don't know how to automatically pick scale for objec
t of type function. Defaulting to continuous.
ERROR while rich displaying an object: All columns i
n a tibble must be 1d or 2d objects:
* Column `y` is function
Traceback:
1. FUN(X[[i]], ...)
2. tryCatch(withCallingHandlers({
 .     rpr <- mime2repr[[mime]](obj)
 .     if (is.null(rpr))
 .         return(NULL)
 .     prepare_content(is.raw(rpr), rpr)
 . }, error = error_handler), error = outer_handler)
3. tryCatchList(expr, classes, parentenv, handlers)
4. tryCatchOne(expr, names, parentenv, handlers[[1L]
])
5. doTryCatch(return(expr), name, parentenv, handler
)
6. withCallingHandlers({
```

In [79]:

mpg	.fitted	.resid
21.0	23.28261	-2.2826106
21.0	21.91977	-0.9197704
22.8	24.88595	-2.0859521
21.4	20.10265	1.2973499
18.7	18.90014	-0.2001440
18.1	18.79325	-0.6932545

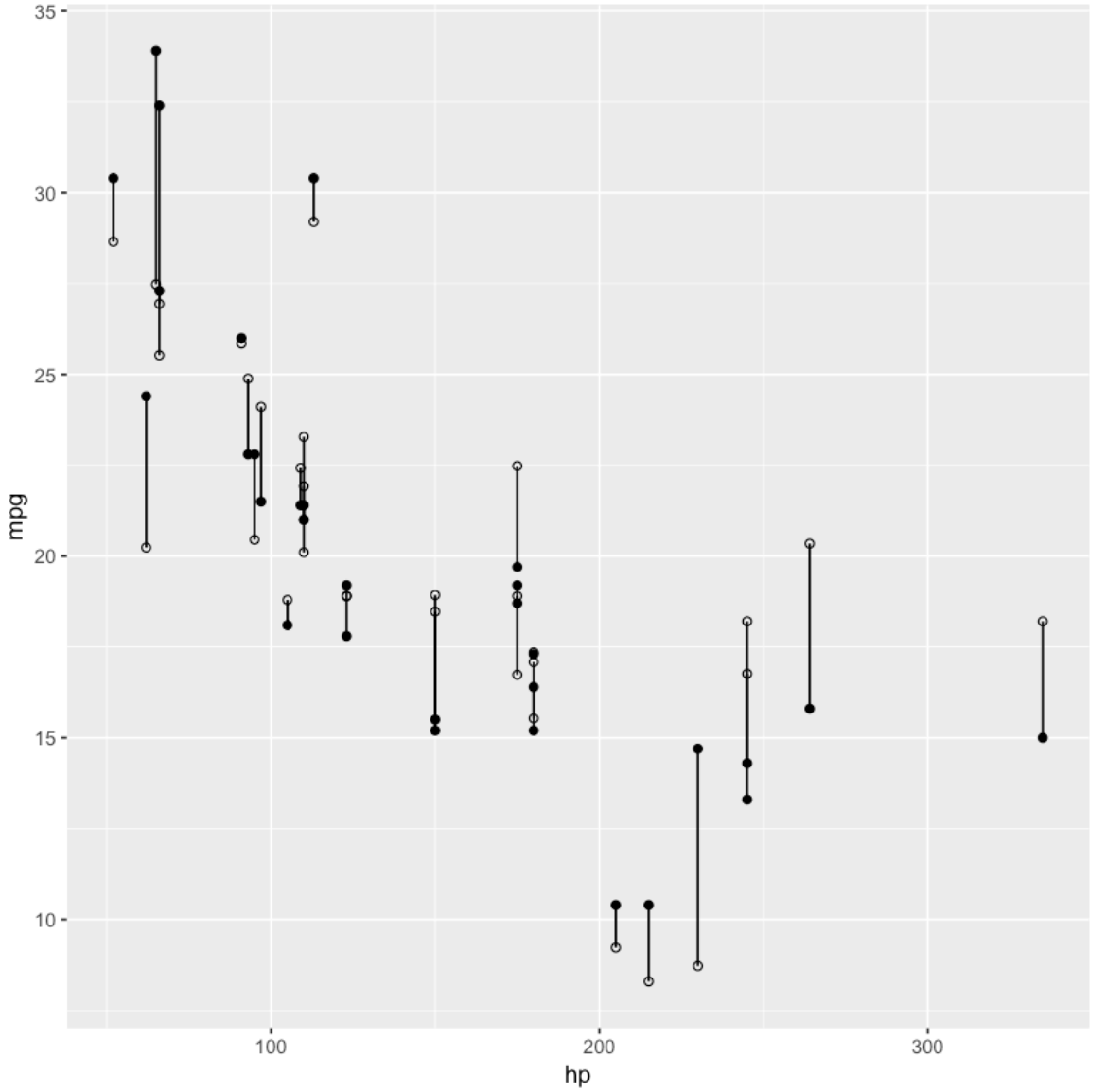
In [86]:

Mazda RX4
-2.28261064680868
Mazda RX4 Wag
-0.91977039576432
Datsun 710
-2.08595211862542
Hornet 4 Drive
1.29734993896137
Hornet Sportabout
-0.200143957176023
Valiant
-0.693254525721567

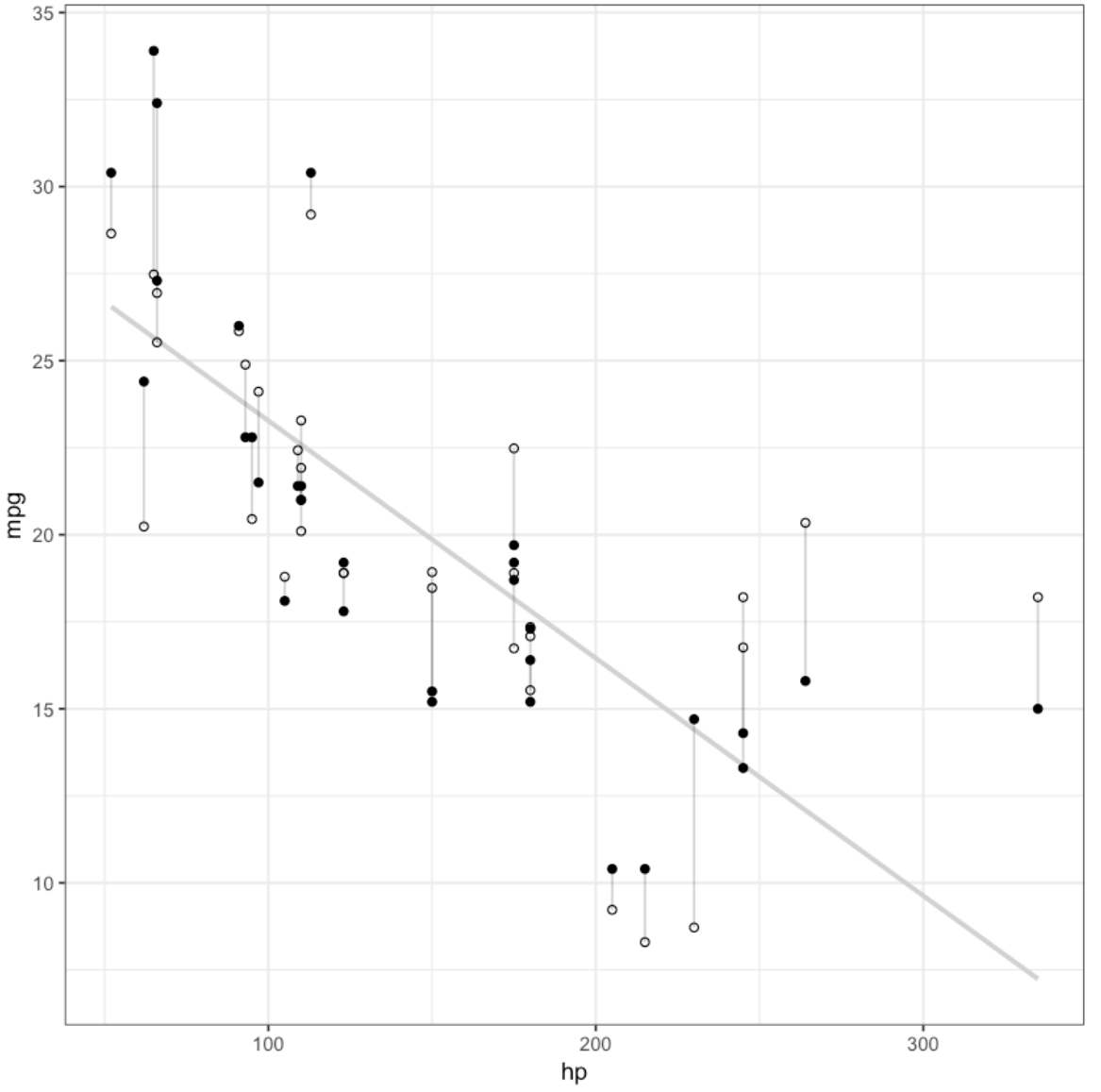
Mazda RX4
23.2826106468086
Mazda RX4 Wag
21.9197703957643
Datsun 710
24.8859521186254
Hornet 4 Drive
20.1026500610386
Hornet Sportabout
18.900143957176
Valiant
18.7932545257216

In [88]:

```
```



In [89]:



In [97]:

In [98]:

```
`NULL` must evaluate to column positions or names, n
ot a double vectorTraceback:

1. mtcars %>% gather(key = "iv", value = "x", -Sepal
.Width) %>%
 .     ggplot(aes(x = x, y = Sepal.Width))
2. withVisible(eval(quote(`_fseq`(`_lhs`)), env, env
))
3. eval(quote(`_fseq`(`_lhs`)), env, env)
4. eval(quote(`_fseq`(`_lhs`)), env, env)
5. `_fseq`(`_lhs`)
6. freduce(value, `_function_list`)
7. function_list[[i]](value)
8. gather(., key = "iv", value = "x", -Sepal.Width)
9. gather.data.frame(., key = "iv", value = "x", -Se
pal.Width)
10. unname(tidyselect::vars_select(names(data), !!!q
uos))
11. tidyselect::vars_select(names(data), !!!quos)
```

In [ ]:

In [69]:

'.rownames' 'mpg' 'wt' '.fitted' '.se.fit' '.resid' '.hat'
'.sigma' '.cooksd' '.std.resid'

In [70]:

.rownames	mpg	wt	.fitted	.se.fit	.resid	.hat	
Mazda RX4	21.0	2.620	23.28261	0.6335798	-2.2826106	0.04326896	3
Mazda RX4 Wag	21.0	2.875	21.91977	0.5714319	-0.9197704	0.03519677	3
Datsun 710	22.8	2.320	24.88595	0.7359177	-2.0859521	0.05837573	3
Hornet 4 Drive	21.4	3.215	20.10265	0.5384424	1.2973499	0.03125017	3
Hornet Sportabout	18.7	3.440	18.90014	0.5526562	-0.2001440	0.03292182	3
Valiant	18.1	3.460	18.79325	0.5552829	-0.6932545	0.03323551	3

In [71]:

```
Warning message:
“Unknown or uninitialised column: 'coef'.”

NULL
```

In [ ]:

In [ ]:

In [ ]:

In [ ]:

In [ ]:

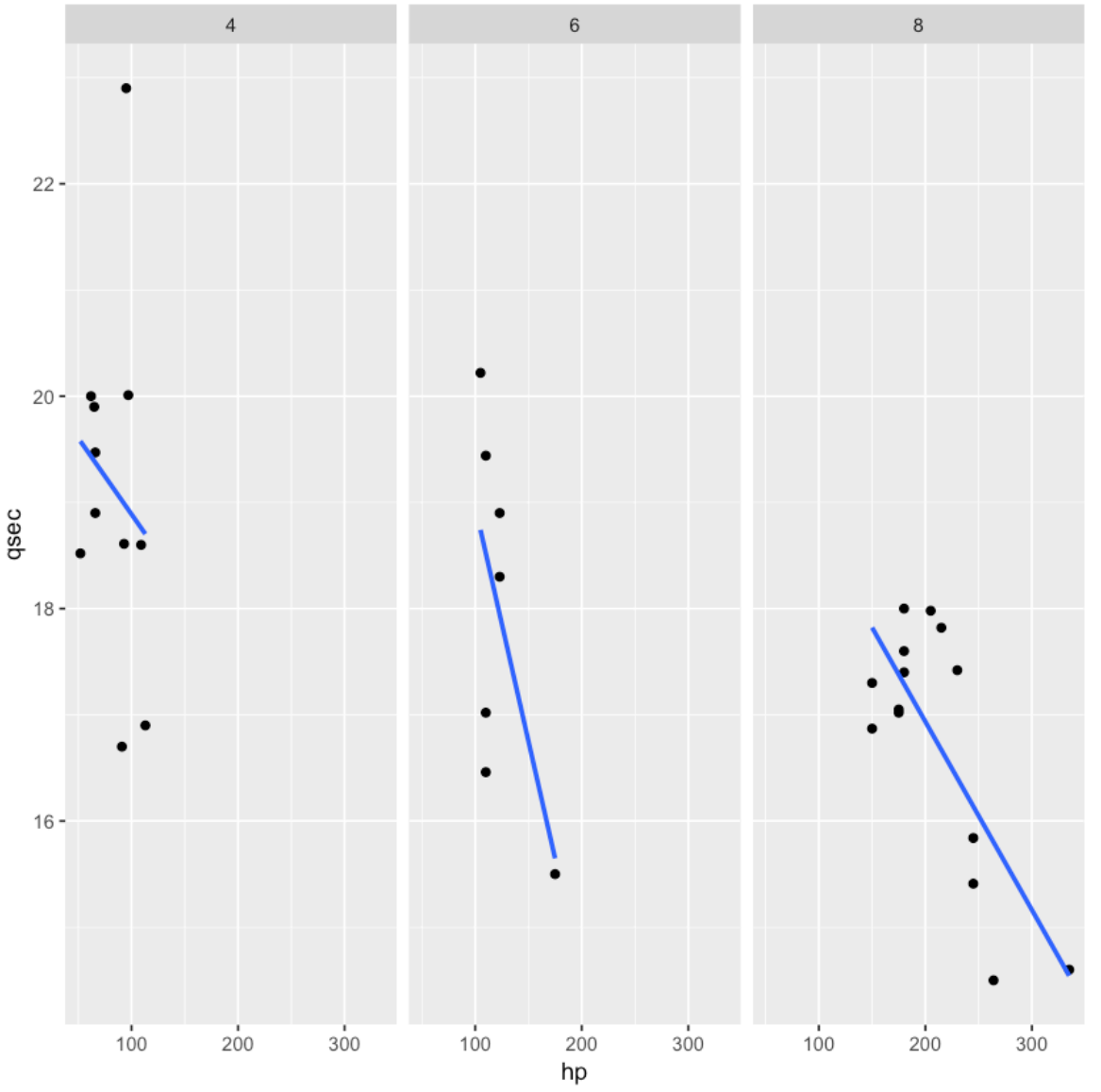
In [ ]:

In [ ]:

In [12]:

```
Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats
’:

    filter, lag

The following objects are masked from ‘package:base’
:

    intersect, setdiff, setequal, union
```

In [17]:



In [128]:

```
Warning message in x < as.matrix(cbind(1, Petal.Leng
th, Petal.Width)):
“longer object length is not a multiple of shorter o
bject length”
```

A matrix: 150 × 3 of type lgl

	Petal.Length	Petal.Width
TRUE	TRUE	FALSE
TRUE	TRUE	TRUE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
TRUE	TRUE	FALSE
FALSE	TRUE	FALSE
TRUE	TRUE	FALSE

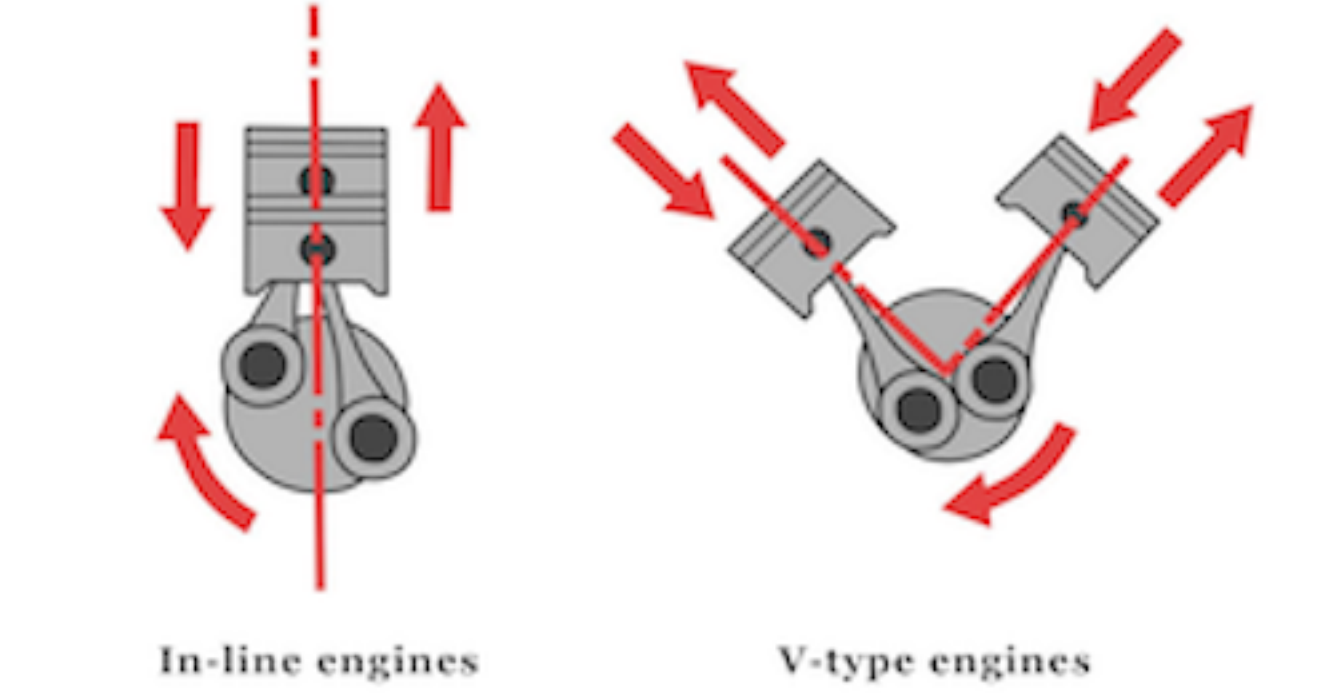
In [ ]:

In [ ]:

المسألة

We want to create a model that helps us to predict the probability of a vehicle having a V engine or a straight engine given a weight of 2100 lbs and engine displacement of 180 cubic inches.

نود انشاء نموذج قادر على التنبؤ باحتمال ان V او inline بناء على خاصيتي سعة المحرك disp و وون السيارة wt تكون خصائص محرك سيارة على شكل



First we fit the model:

We use the glm() function, include the variables in the usual way, and specify a binomial error distribution, as follows:

the Analysis Factor (https://www.theanalysisfactor.com)

In [ ]:

In [ ]:

In [53]:

In [54]:

```

Call:
glm(formula = vs ~ wt + disp, family = "binomial", d
ata = mtcars)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.67506  -0.28444  -0.08401   0.57281   2.08234

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.60859    2.43903   0.660    0.510
wt           1.62635    1.49068   1.091    0.275
disp        -0.03443    0.01536  -2.241    0.025 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’
0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to b
e 1)
```

Deviance

- We see from the estimates of the coefficients that weight influences vs positively, while displacement has a slightly negative effect
- We also see that the coefficient of weight is non-significant ($p > 0.05$), while the coefficient of displacement is significant
- the estimates (coefficients of the predictors weight and displacement) are now in units called logits
- Deviance is a measure of goodness of fit of a generalized linear model.

The null deviance shows how well the response variable is predicted by a model that includes only the intercept (grand mean) where as residual with inclusion of independent variables. Or rather its'a a measure of badness of fit.

```
– higher numbers indicate worse fit.
```

Above, you can see that addition of 2 (31-29 =2) independent variablesdecreased the deviance to 21.4 from 43.86, a significant reduction in deviance.The Residual Deviance has reduced by 22.46 with a loss of two degrees of freedom.

If your Null Deviance is really small, it means that the Null Model explains the data pretty well. Likewise with your Residual Deviance.

```
– The null deviance shows how well the response variable
is predicted by a model that includes only the intercept
(grand mean).
```

Fisher's Scoring

```
 – the Fisher's Scoring Algorithm needed six iterations t
o perform the fit. This doesn't really tell you a lot tha
t you need to know, other than the fact that the model di
d indeed converge, and had no trouble doing it.
```

Information Criteria

The Akaike Information Criterion (AIC) provides a method for assessing the quality of your model through comparison of related models. It's based on the Deviance, but penalizes you for making the model more complicated. Much like adjusted R-squared, it's intent is to prevent you from including irrelevant predictors.

In [ ]:

Remember, our goal here is to calculate a predicted probability of a V engine, for specific values of the predictors: a weight of 2100 lbs and engine displacement of 180 cubic inches.

To do that, we create a data frame called newdata, in which we include the desired values for our prediction.

In [63]:

Now we use the predict() function to calculate the predicted probability. We include the argument type="response" in order to get our prediction.

In [64]:

1: 0.840625522555481

The predicted probability is 0.24.

In [59]:

```
Updating HTML index of packages in '.Library'
Making 'packages.html' ... done
```

In [60]:

```
ResourceSelection 0.3-5          2019-07-22
```

In [61]:

```
        Hosmer and Lemeshow goodness of fit (GOF) te
st

data:  mtcars$vs, fitted(modelLM)
X-squared = 6.4717, df = 8, p-value = 0.5945
```

- Our model seems to fit well because we have no significance difference between the model and the observed Data since P-value is above 0.05.

In [62]:

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	car
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	

In [ ]:

In [ ]:

In [10]:

In [19]:

```
The following objects are masked from A (pos = 3):

    anxiety, numeracy, success

The following objects are masked from A (pos = 4):

    anxiety, numeracy, success
```

'numeracy' 'anxiety' 'success'

In [21]:

numeracy	anxiety	success
6.6	13.8	0
7.1	14.6	0
7.3	17.4	0
7.5	14.9	1
7.9	13.4	0
7.9	13.5	1

In [15]:

10.722

In [22]:

In [23]:

```
Call:
glm(formula = success ~ numeracy * anxiety, family =
binomial)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.85712  -0.33055   0.02531   0.34931   2.01048

Coefficients:
                 Estimate Std. Error z value Pr(>|z|
)
(Intercept)       0.87883   46.45256   0.019    0.98
5
numeracy          1.94556    4.78250   0.407    0.68
4
anxiety          -0.44580    3.25151  -0.137    0.89
1
numeracy:anxiety -0.09581    0.33322  -0.288    0.77
4
```

In [40]:

46

In [41]:

	Df	Deviance	Resid. Df	Resid. Dev
NULL	NA	NA	49	68.02920
numeracy	1	17.73804731	48	50.29115
anxiety	1	22.00552914	47	28.28562
numeracy:anxiety	1	0.08491994	46	28.20070

In [29]:

In [30]:

In [27]:

6.6 15.7

In [28]:

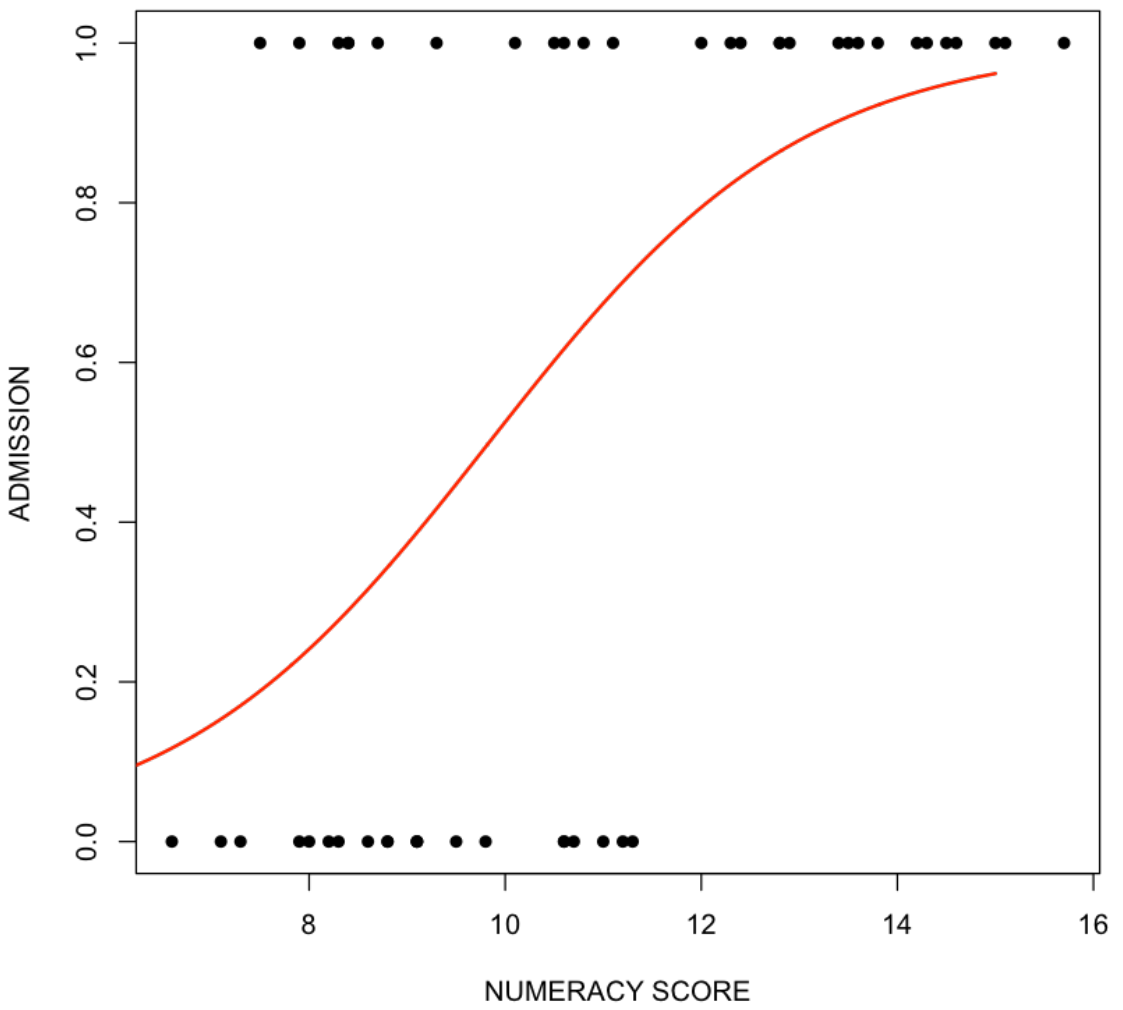
10.1 17.7

In [ ]:

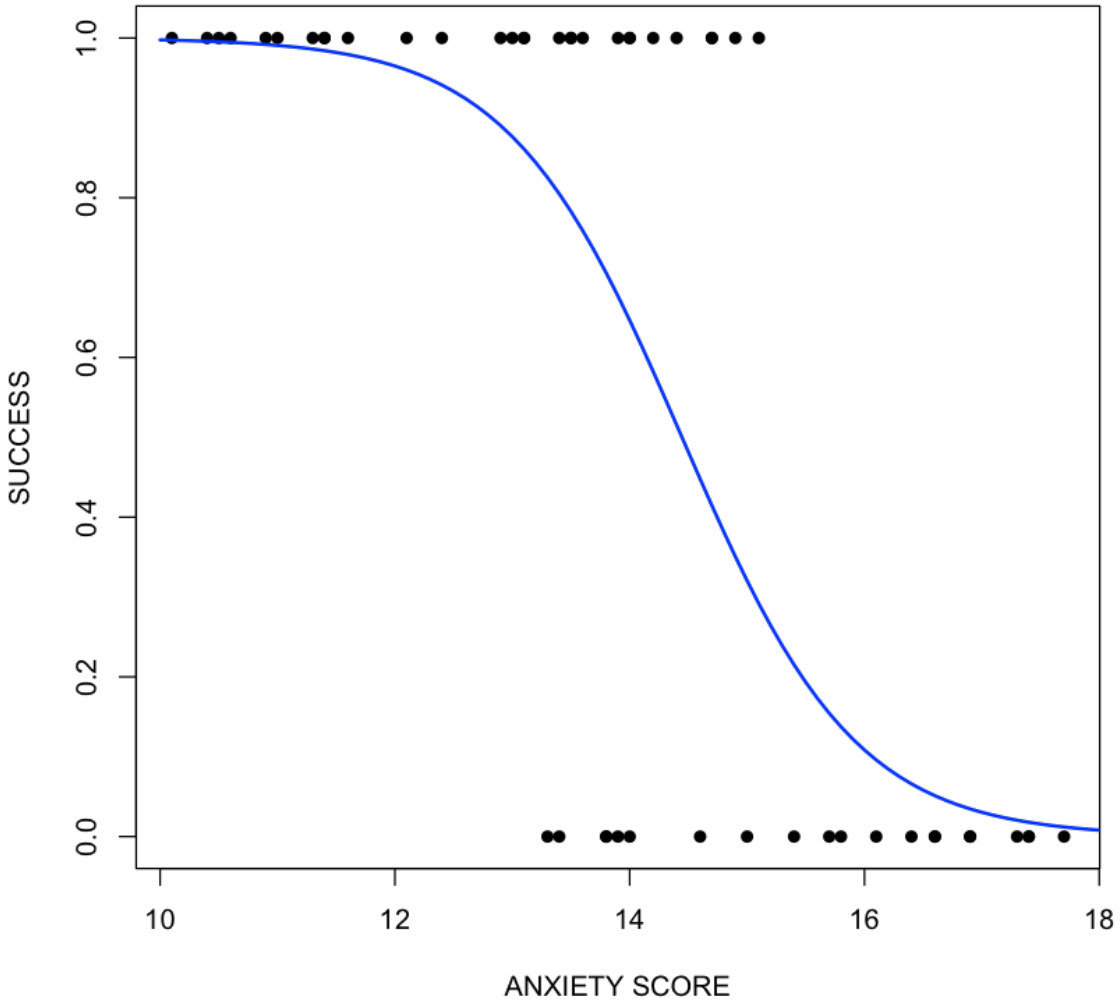
In [35]:

In [ ]:

In [36]:



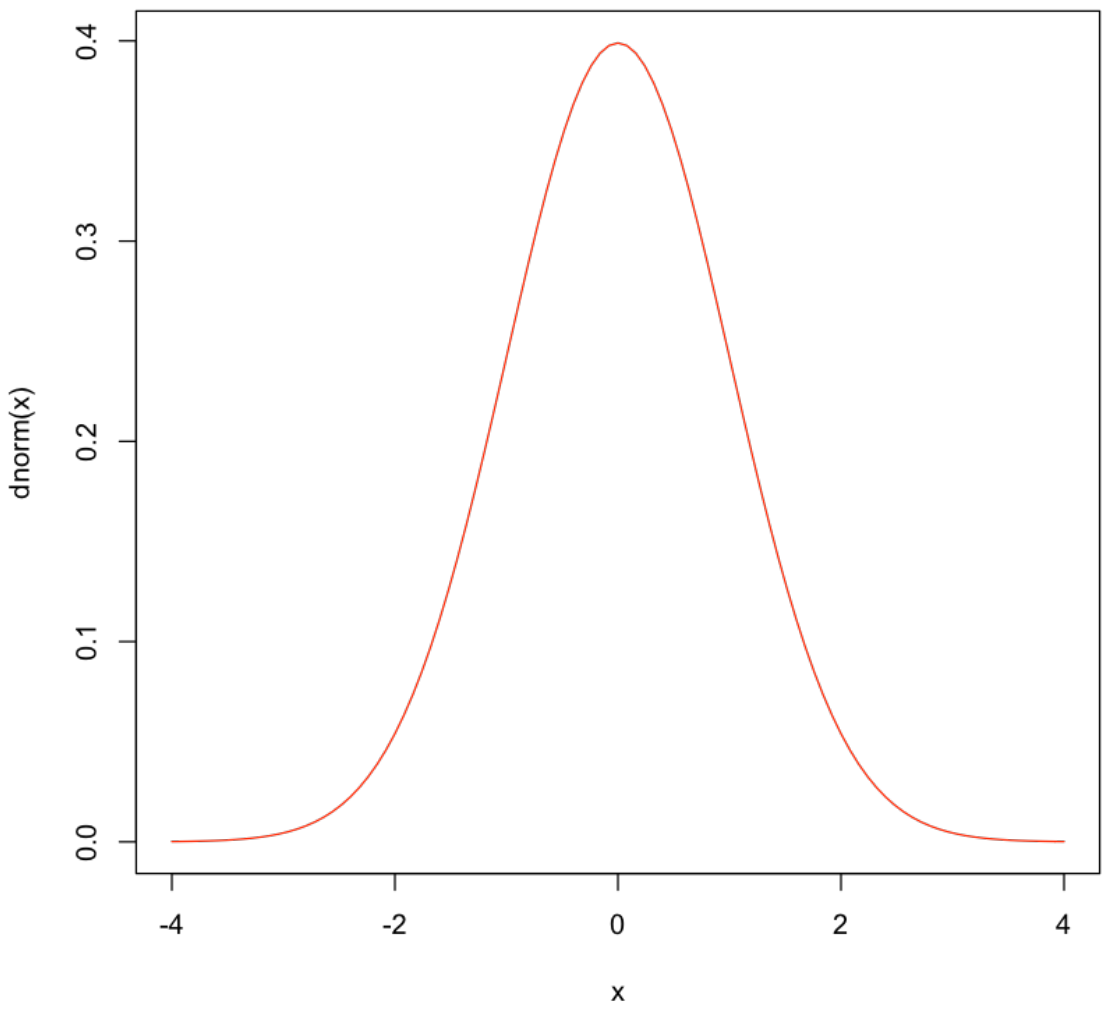
In [37]:



In [39]:

```
Error in ggplot(cars, aes(x = as.factor(0), y = spee
d)): could not find function "ggplot"
Traceback:
```

In [1]:



In [2]:

```
Error in ggplot(data.frame(x = c(-2, 4)), aes(x)): c
ould not find function "ggplot"
Traceback:
```

هذا هو الجدول.

In [151]:

```
    setosa versicolor  virginica
        50         50         50
```

In [152]:

12

In [153]:

In [154]:

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Resid
5.1	3.5	1.4	0.2	setosa	-0.12954
4.9	3.0	1.4	0.2	setosa	-0.12954
4.7	3.2	1.3	0.2	setosa	-0.22954
4.6	3.1	1.5	0.2	setosa	-0.02954
5.0	3.6	1.4	0.2	setosa	-0.12954
5.4	3.9	1.7	0.4	setosa	-0.27553

In [155]:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	
145	6.7	3.3	5.7	2.5	virginica	-0.9
146	6.7	3.0	5.2	2.3	virginica	-1.0
147	6.3	2.5	5.0	1.9	virginica	-0.3
148	6.5	3.0	5.2	2.0	virginica	-0.3
149	6.2	3.4	5.4	2.3	virginica	-0.8
150	5.9	3.0	5.1	1.8	virginica	0.0

In [156]:

```
'data.frame':   150 obs. of  6 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.
4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4
2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.
5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.
2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versic
olor",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Residual    : num  -0.1295 -0.1295 -0.2295 -0.029
5 -0.1295 ...
```

In [157]:

'setosa' 'versicolor' 'virginica'

In [158]:

In [160]:

150

In [161]:

```
The following objects are masked from iris (pos = 3)
:

    Petal.Length, Petal.Width, Sepal.Length, Sepal.W
idth, Species


Species
    setosa versicolor  virginica
        50         50         50
```

In [238]:

```
corrplot 0.84 loaded
```

In [241]:

```
Warning message in if (is.na(na.method)) stop("inval
id 'use' argument"):
“the condition has length > 1 and only the first ele
ment will be used”

Error in cor(Petal.Length, Petal.Width, Sepal.Length
, Sepal.Width): invalid 'use' argument
Traceback:

1. cor(Petal.Length, Petal.Width, Sepal.Length, Sepa
l.Width)
2. stop("invalid 'use' argument")
```

In [243]:

```
Error in cor(iris): 'x' must be numeric
Traceback:

1. cor(iris)
2. stop("'x' must be numeric")
```

In [249]:

```
2

102

1

1
```

In [255]:

```
-0.42844010433054
```

In [ ]:

In [ ]:

In [232]:

In [233]:

values	ind
8.120639	x1
10.550930	x1
7.493114	x1
14.785842	x1
10.988523	x1
7.538595	x1
11.462287	x1
12.214974	x1
11.727344	x1
9.083835	x1
14.535344	x1
11.169530	x1
8.136278	x1
3.355900	x1
13.374793	x1
9.865199	x1
9.951429	x1
12.831509	x1
12.463664	x1
11.781704	x1
12.756932	x1
12.346409	x1

10.223695	x1
4.031945	x1
11.859477	x1
9.831614	x1
9.532613	x1
5.587743	x1
8.565550	x1
11.253825	x1
⋮	⋮
18.48213	x3
24.02912	x3
19.35626	x3
19.46133	x3
19.69943	x3
22.13800	x3
19.77931	x3
19.88710	x3
17.95502	x3
19.02719	x3
20.18048	x3
18.23332	x3
21.59449	x3
15.44482	x3
20.91967	x3
15.39065	x3
19.09707	x3
18.41516	x3
18.04372	x3
19.82931	x3
14.25692	x3
23.52975	x3
15.00508	x3

18.60941 x3

16.65224 x3

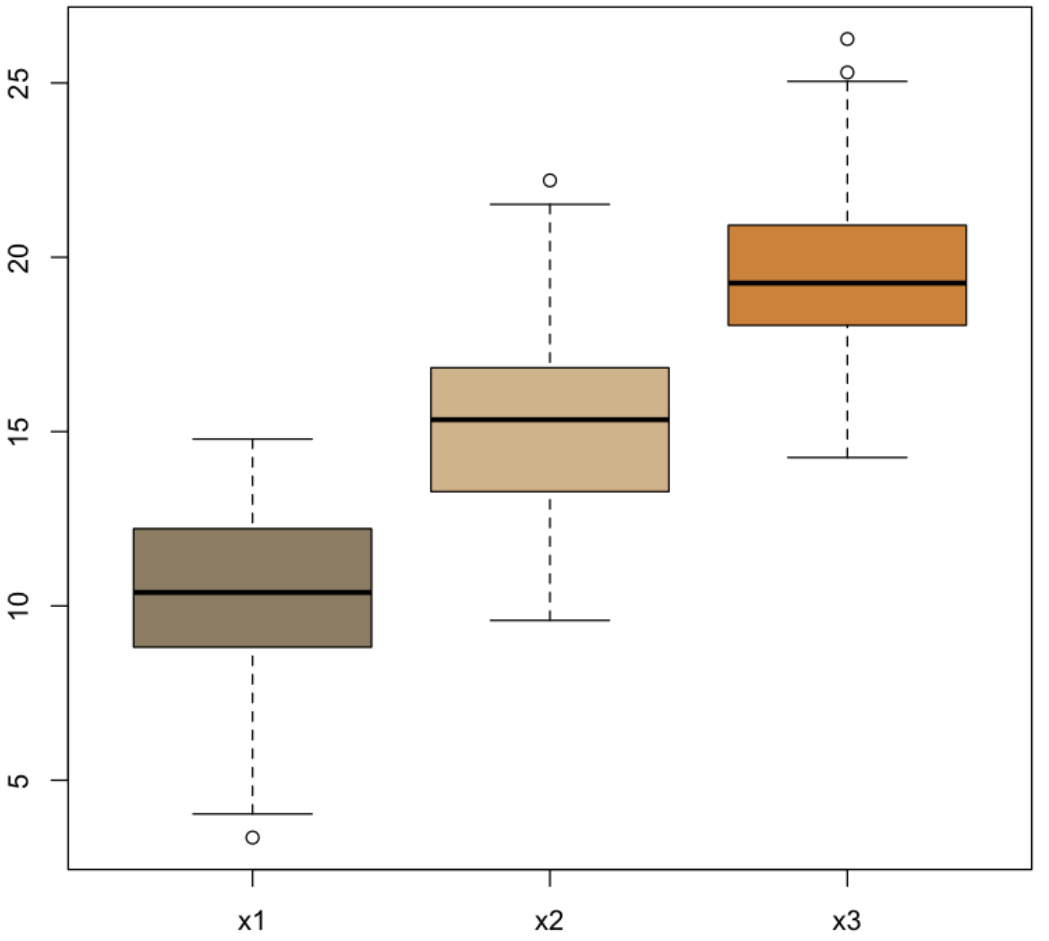
17.74754 x3

26.26150 x3

20.05219 x3

16.14110 x3

15.07818 x3



In [272]:

'x1' 'x2' 'x3'

In [271]:

```
Call:
   aov(formula = values ~ ind, data = datalong)

Terms:
                      ind Residuals
Sum of Squares  2141.158  1075.764
Deg. of Freedom        2       147

Residual standard error: 2.705203
Estimated effects may be unbalanced
```

In [ ]:

In [ ]:

In [ ]:

In [2]:

```
'data.frame':   32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22
.8 19.2 ...
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 .
..
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69
3.92 3.92 ...
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

In [ ]:

In [ ]:

In [ ]:

In [9]:

3

In [17]:

In [ ]:

In [78]:

```
Error in 1:n_groups: NA/NaN argument
Traceback:
```

In [23]:

```
21  21  22.8
```

In [100]:

In [ ]:

In [ ]:

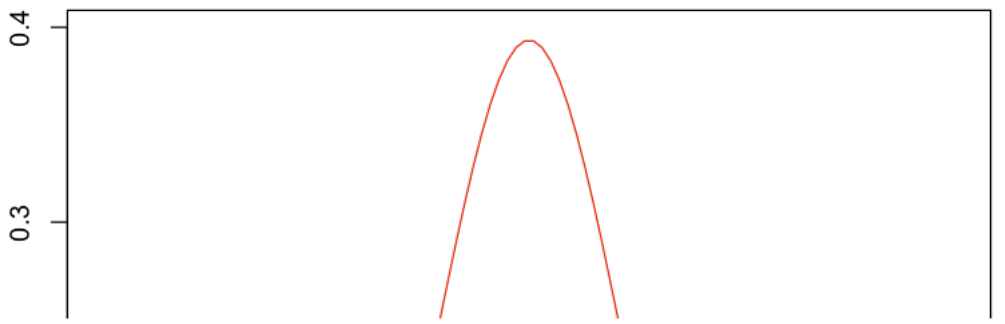
In [85]:

In [86]:

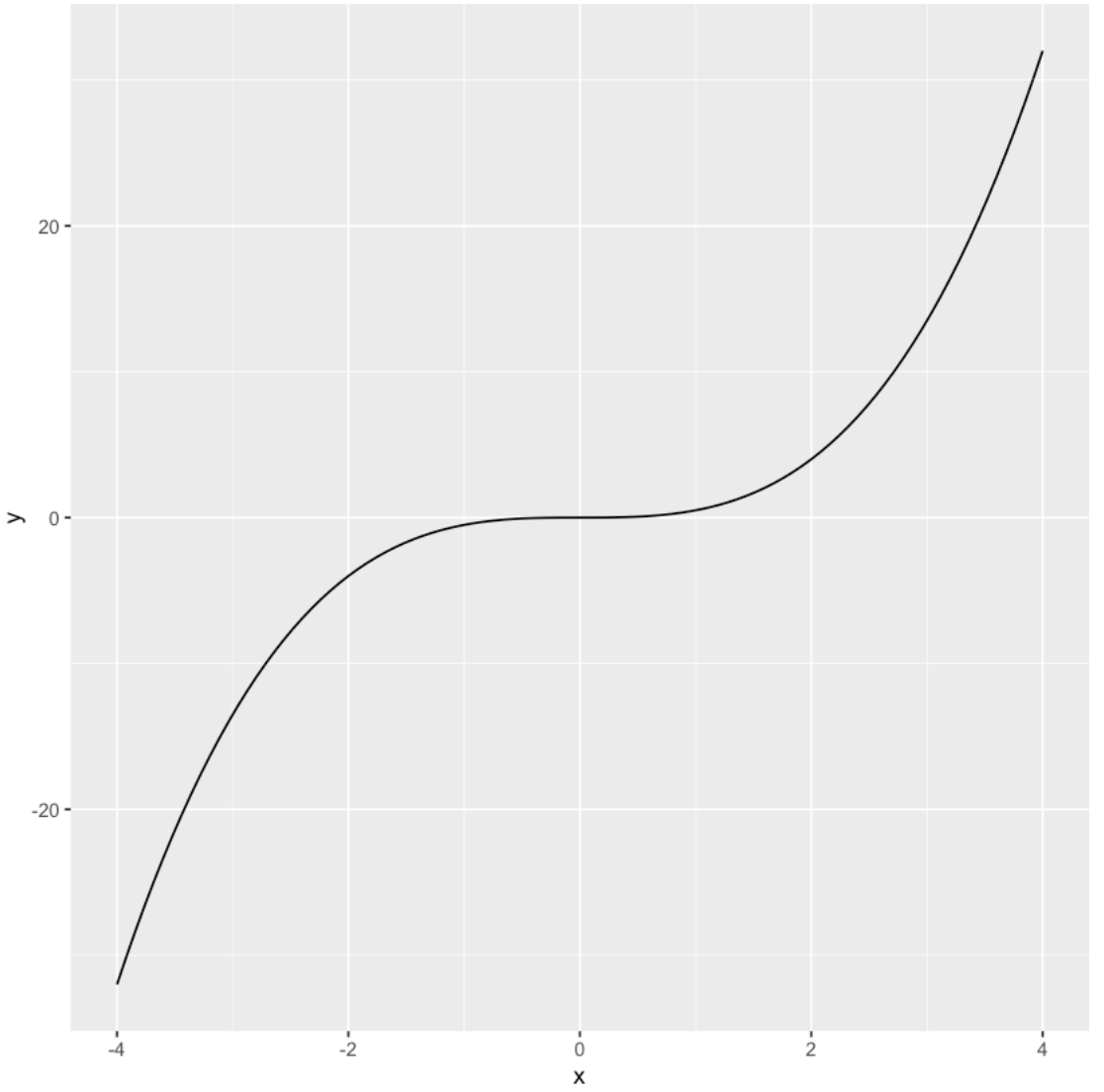
```
-4.38142823082222  3.12398526076645
```

In [77]:

```
Error in density.default(ts): argument 'x' must be n
umeric
Traceback:

1. lines(density(ts))
2. density(ts)
3. density.default(ts)
4. stop("argument 'x' must be numeric")
```

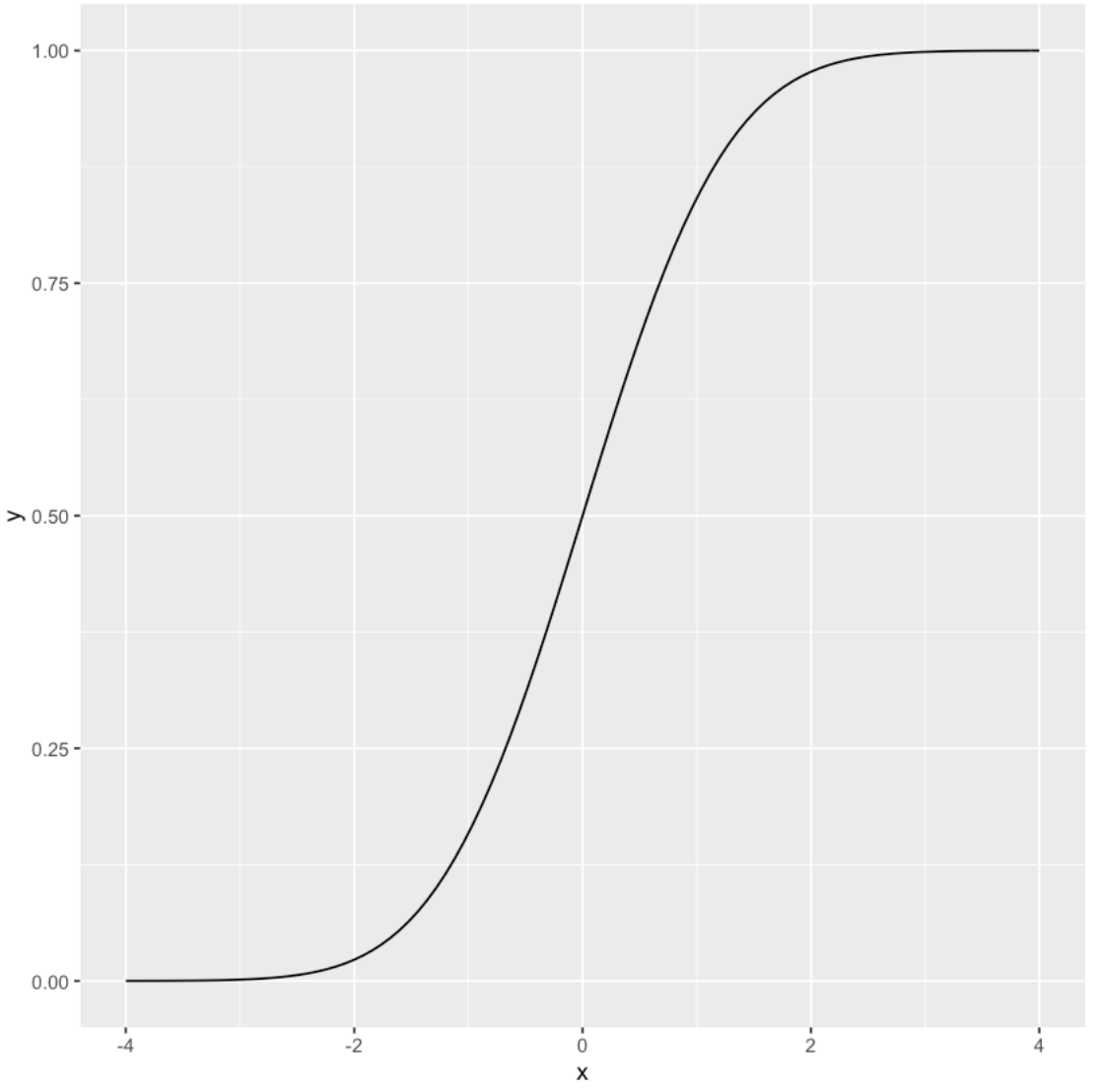


In [79]:

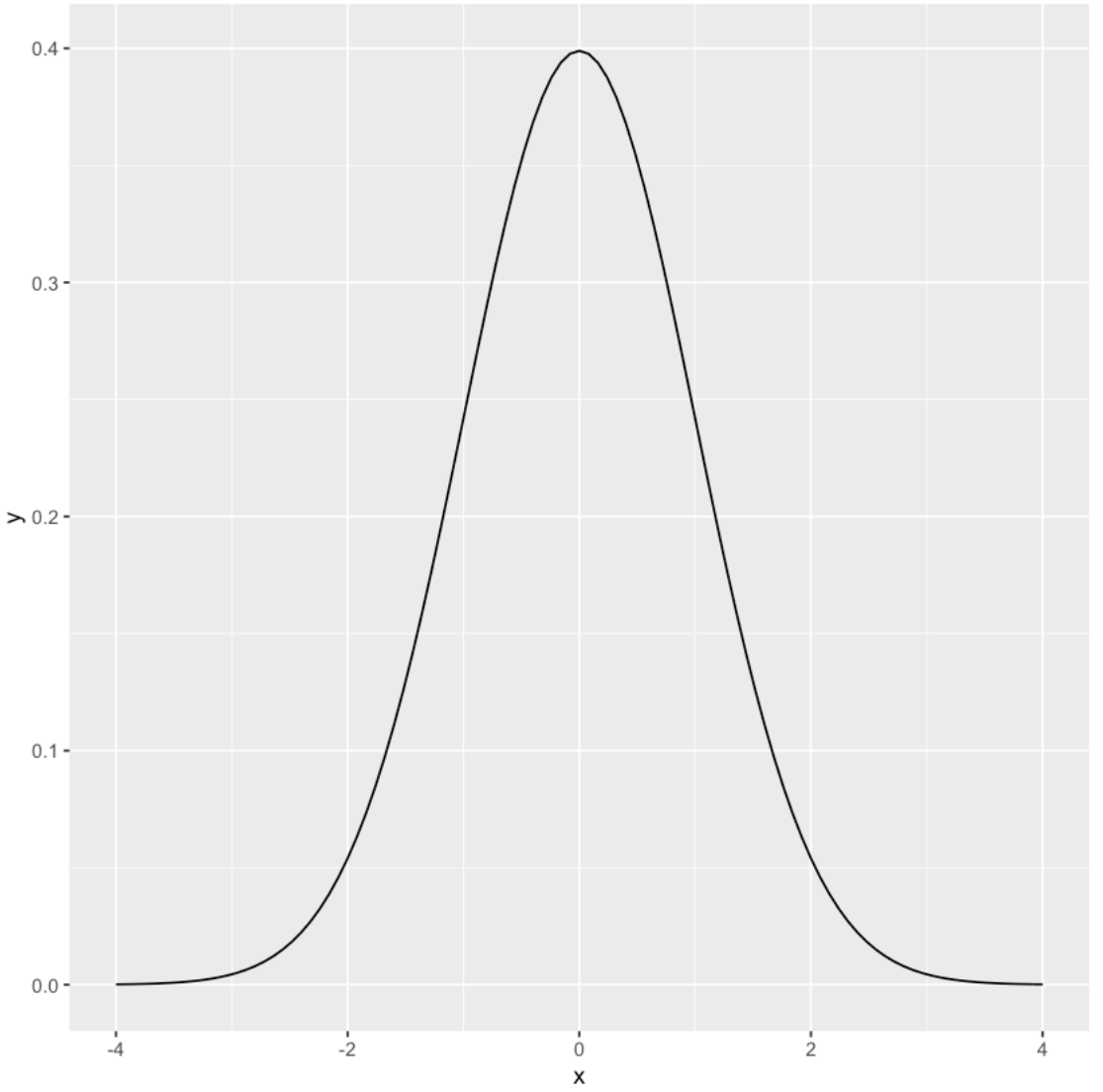


In [ ]:

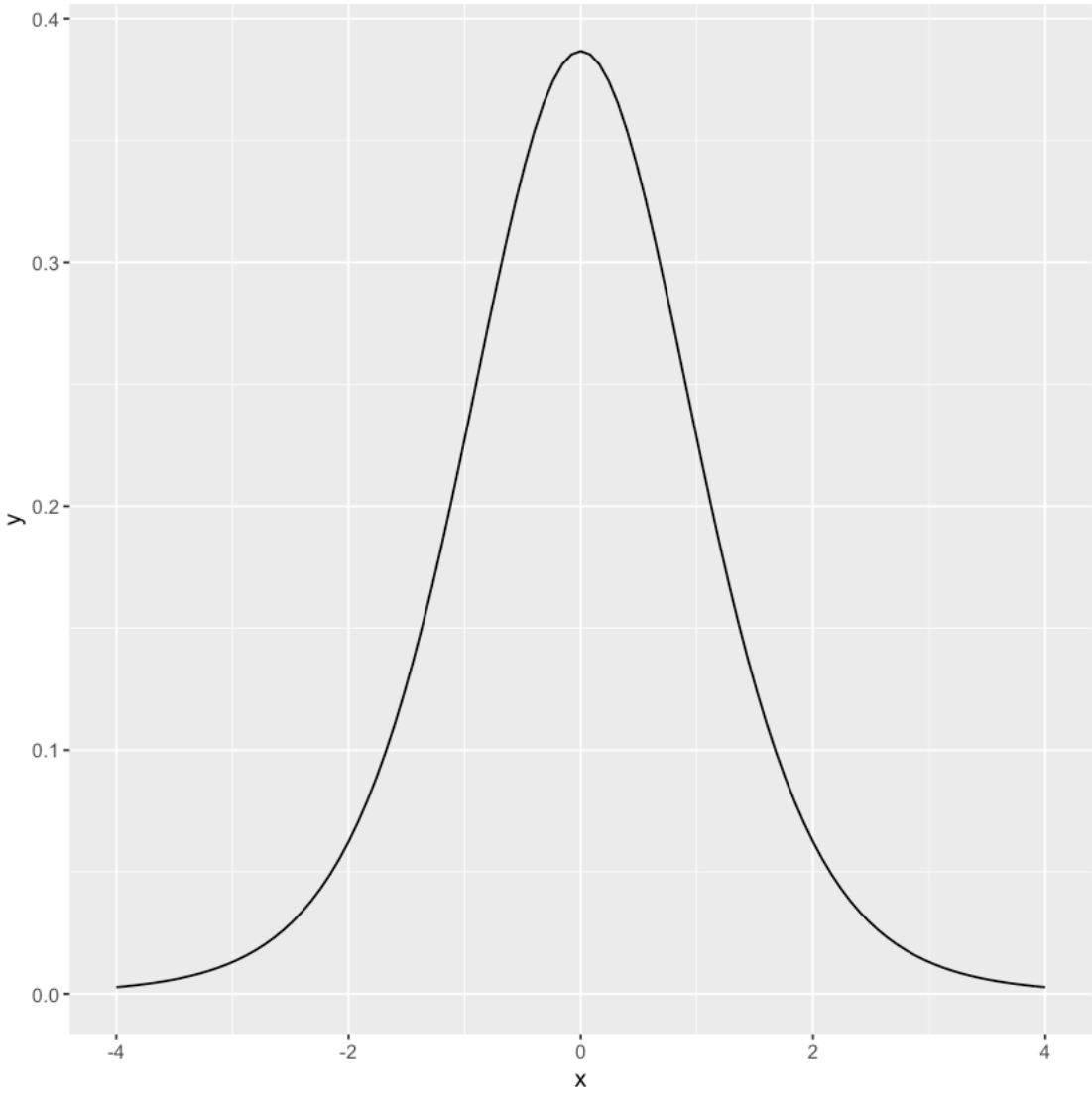
In [74]:



In [76]:



In [75]:



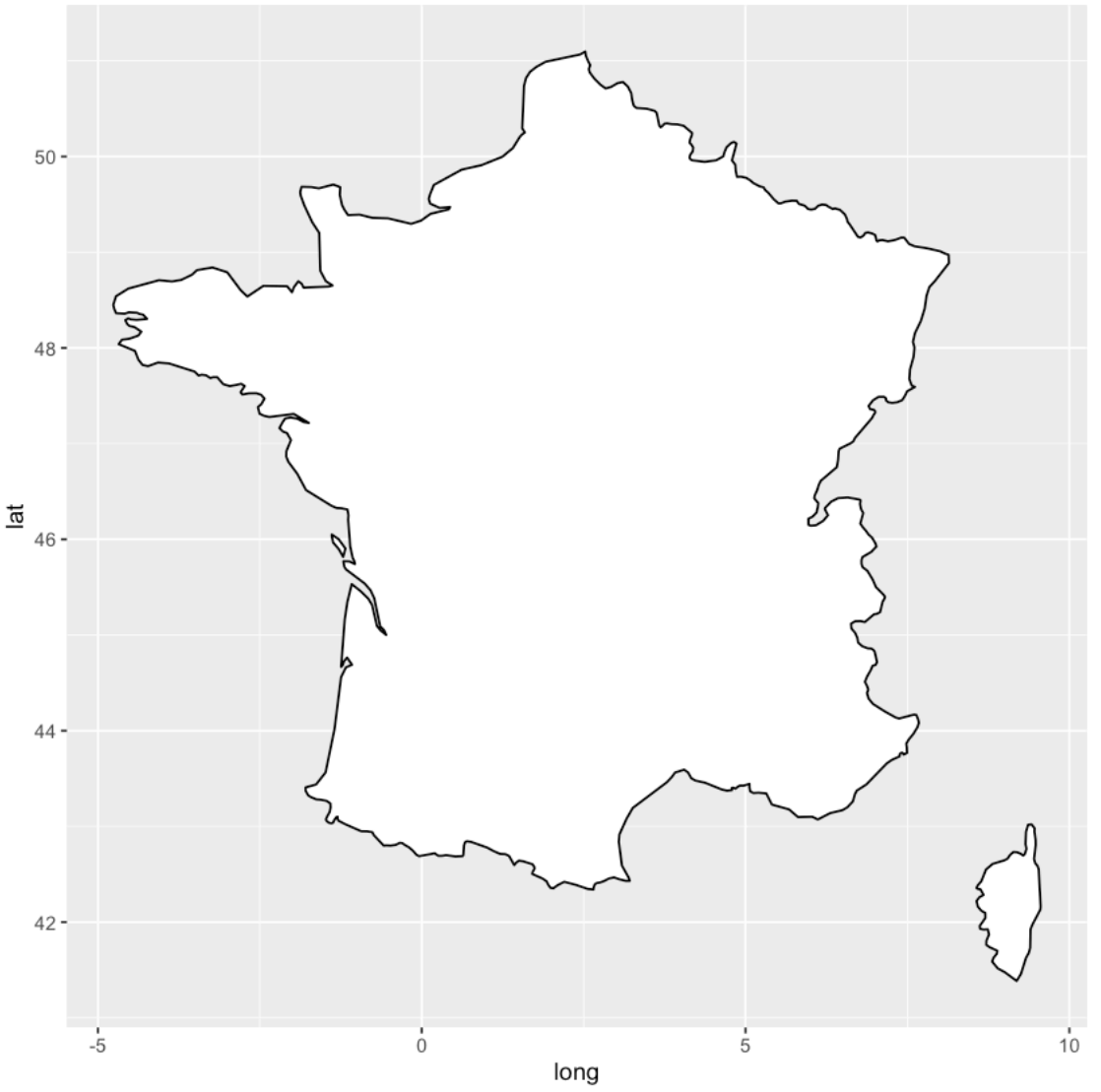
In [84]:

A data.frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<dbl>	<dbl>	<dbl>	<dbl>	<fct>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

In [92]:

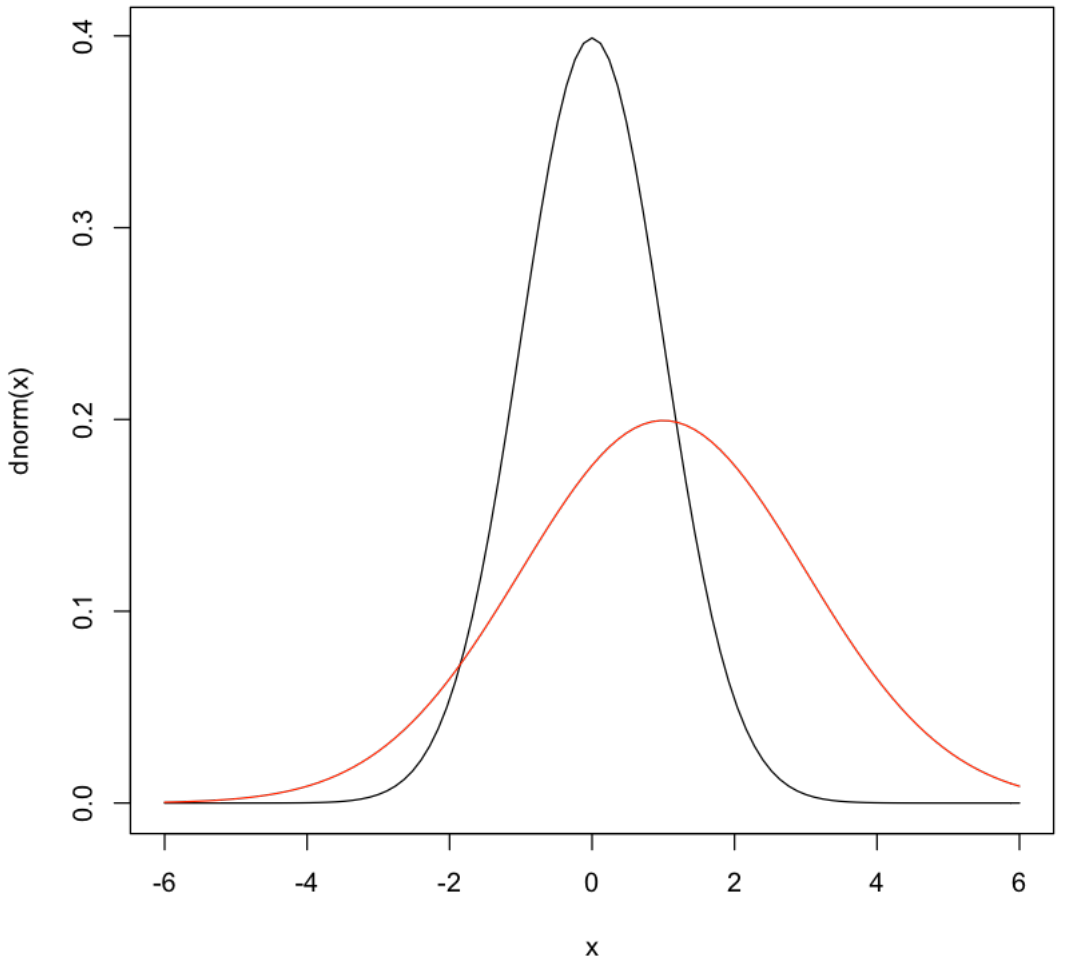
```
Loading required package: maps

Warning message:
“package ‘maps’ was built under R version 3.4.4”
```



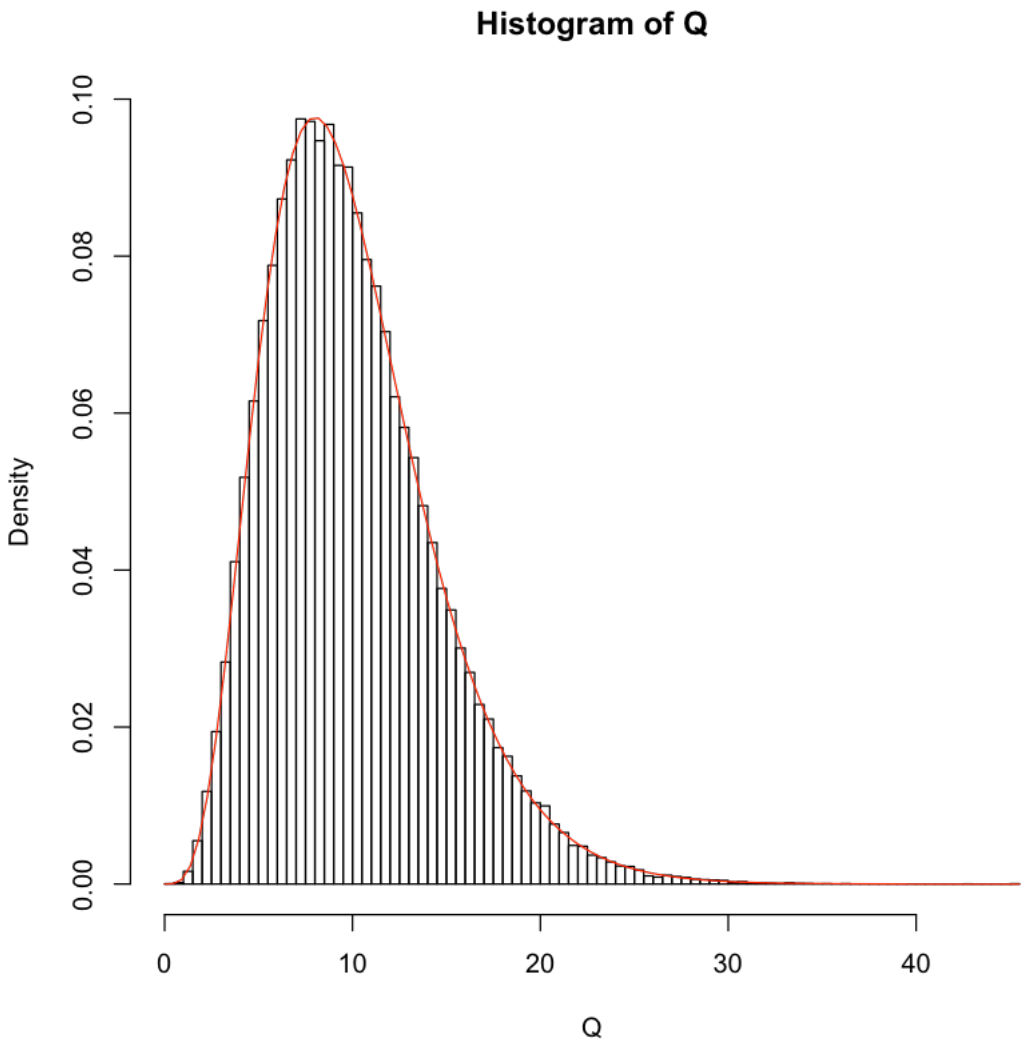
In [98]:

```
```

0.950528531966352



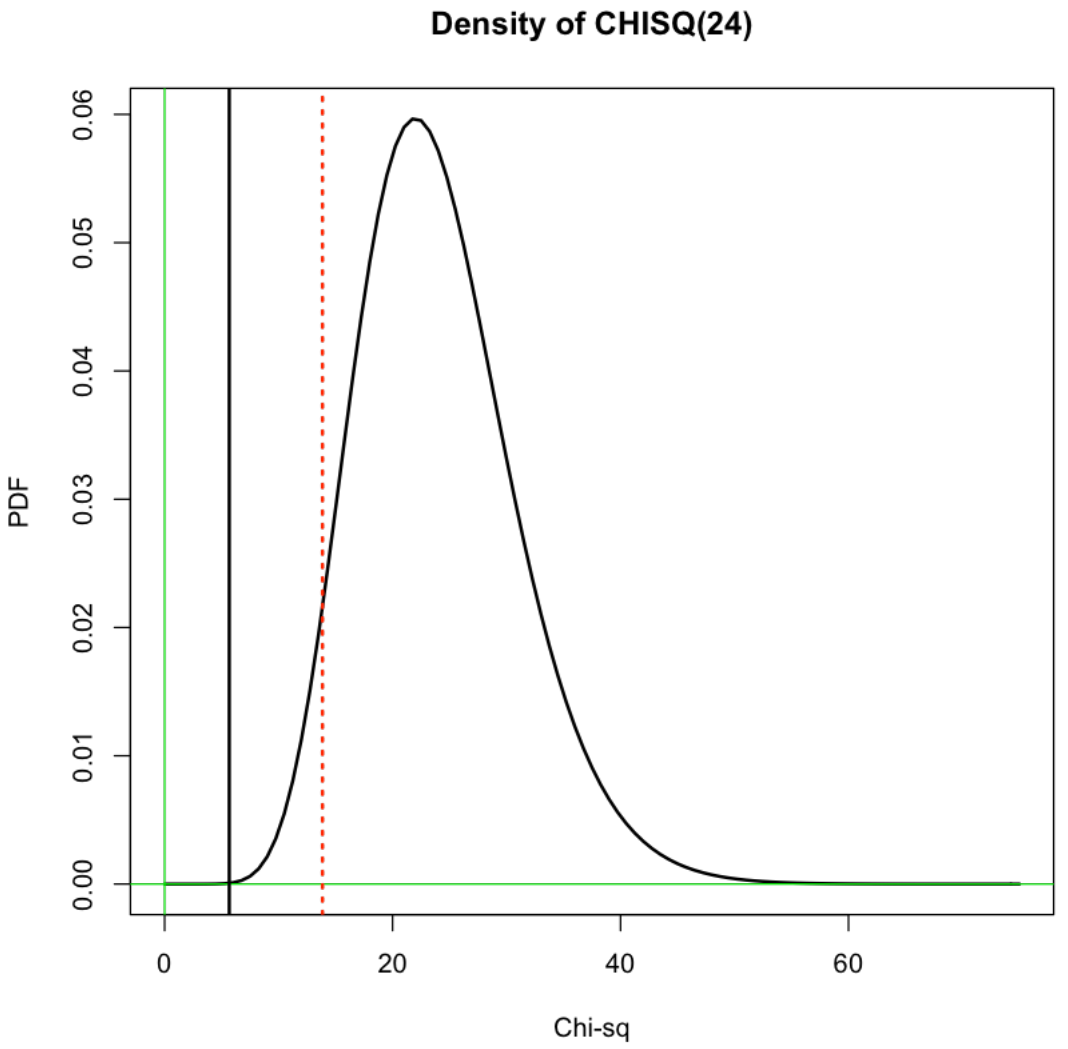
In [99]:



In [100]:

0.0162654403357515

In [104]:


Density of CHISQ(24)
PDF
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0
20
40
60
Chi-sq

In [ ]: