

This course was developed as a part of the follwoing VLIR-UOS Cross-Cutting projects:

•Statistics: 2011-2016, 2017.

•Statistics: 2017.

Statistics for development: 2018-2022.



The >eR-Biostat initative Making R based education materials in statistics accessible for all

Basic concepts in statistical modeling using R: simple linear regression

Developed by

Legesse Kassa Debusho (UNISA, South Africa) and Ziv Shkedy (Hasselt University)

https://erbiostat.wixsite.com/erbiostat

AST UPDATED: 2022



ER-BioStat



GitHub https://github.com/eR-Biostat

Email: erbiostat@gmail.com





Contents

- Simple linear regression:
 - Introduction and model formulation.
 - Fitting a simple linear regression model using the lm() function in R.
 - Model diagnostic.
 - Model diagnostic in R.

https://erbiostat.wixsite.com/erbiostat

Recommended reading

Introductory Statistics for the Life and Biomedical Sciences First Edition

Julie Vu Preceptor in Statistics Harvard University

David Harrington
Professor of Biostatistics (Emeritus)
Harvard T.H. Chan School of Public Health
Dana-Farber Cancer Institute

This book can be purchased for \$0 on Leanpub by adjusting the price slider.

Purchasing includes access to a tablet-friendly version of this PDF where margins have been minimized.

The book is available for free online:

https://www.openintro.org/book/biostat/

Chapter 6: Simple linear regression

Recommended reading

Introductory Statistics for the Life and Biomedical Sciences First Edition

Julie Vu Preceptor in Statistics Harvard University

David Harrington

Professor of Biostatistics (Emeritus) Harvard T.H. Chan School of Public Health Dana-Farber Cancer Institute

This book can be purchased for \$0 on Leanpub by adjusting the price slider.

Purchasing includes access to a tablet-friendly version of this PDF where margins have been minimized.

- In this part of the course, we cover mainly Chapter 6.
- The examples that are used in the slides for illustration are not the same as the examples in the book.
- Use the R program to reproduce the examples.

Chapter 6: Simple linear regression



Part 1 Simple linear regression

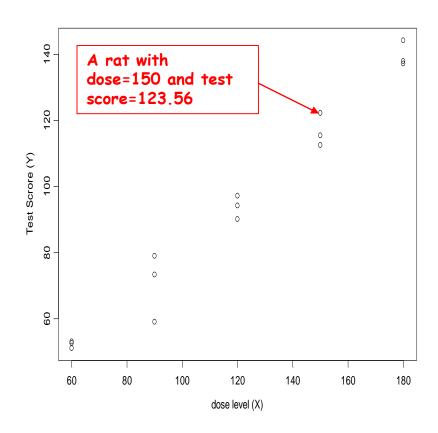


Introduction

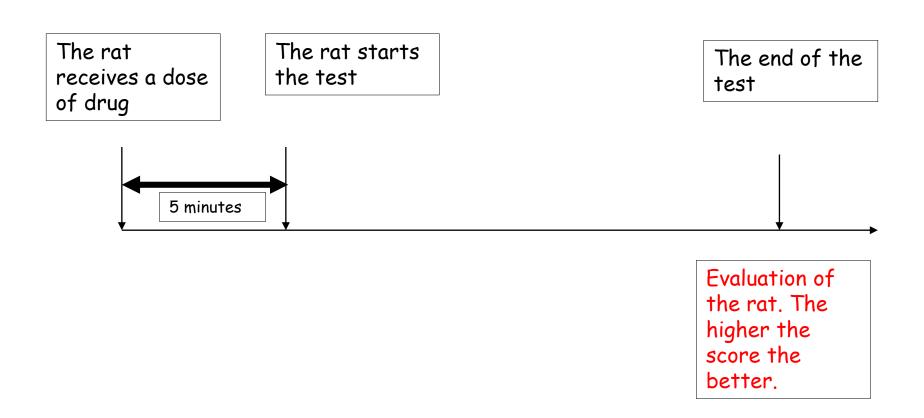
A Biopharmaceutical problem

- A group of 15 rats received a dose of a drug and then had to complete a test.
- It is assumed that the performance of the rat (=test score) depends on the dose level.

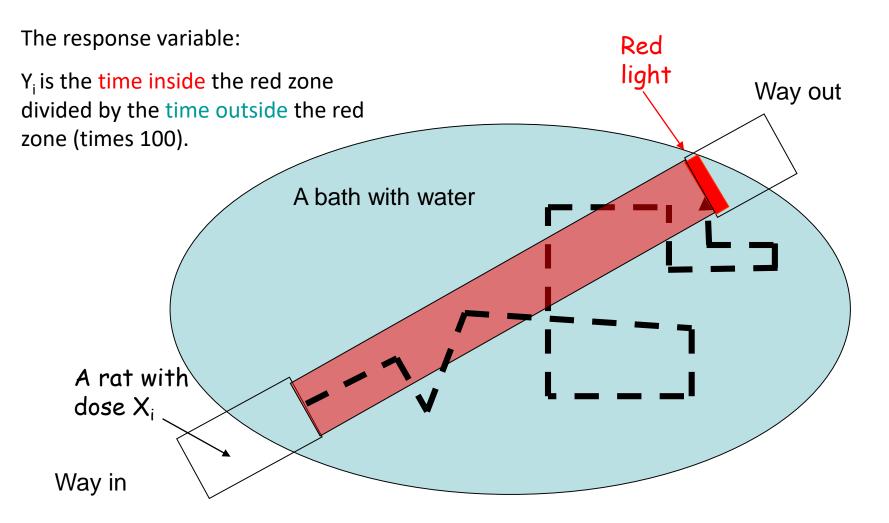
The data



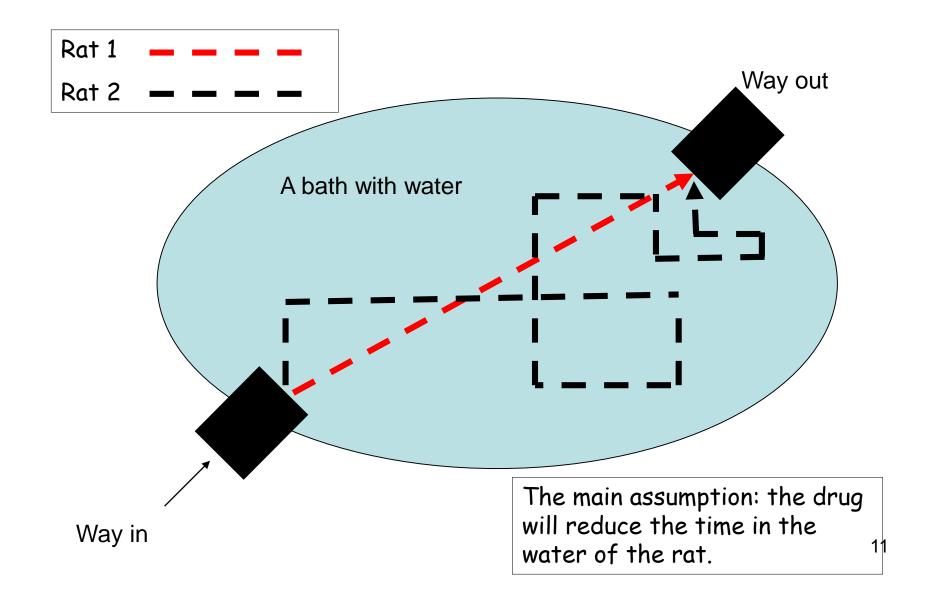
Description of the experiment



The evaluation of the rat



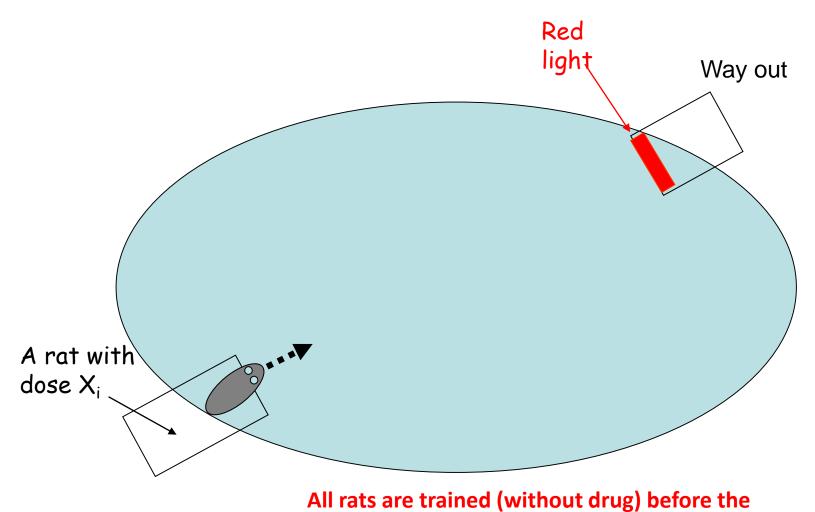
Description of the experiment



The evaluation of the eat



The evaluation of the rat



experiment to swim to the red light!!!

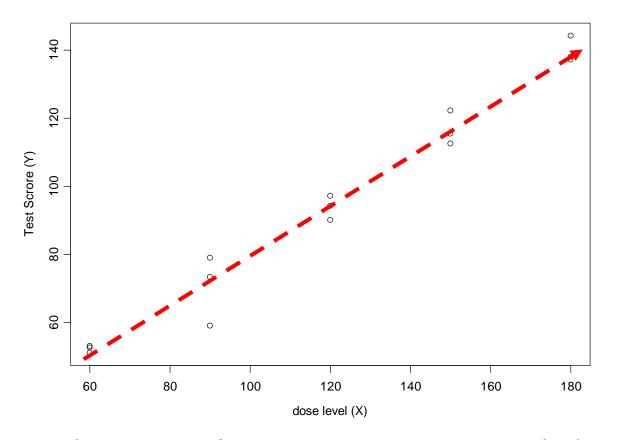
The scientific question

Does the performance of the rat depend on the dose level?

A good drug is expected to improve the rats' performance (swim directly to the red light)

The scientists expect that: the higher the dose the better the performance

The data

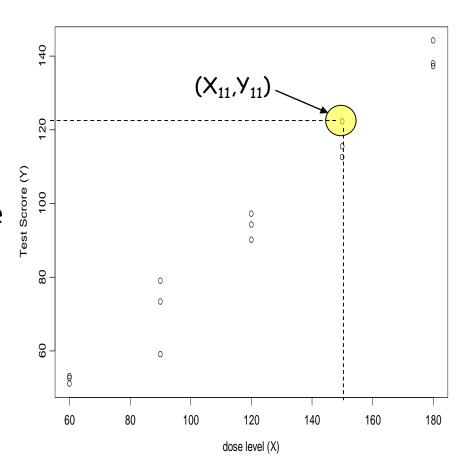


Upward trend: in general, test score increases with dose level

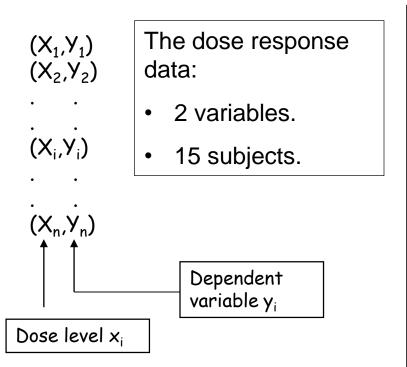
Regression terminology

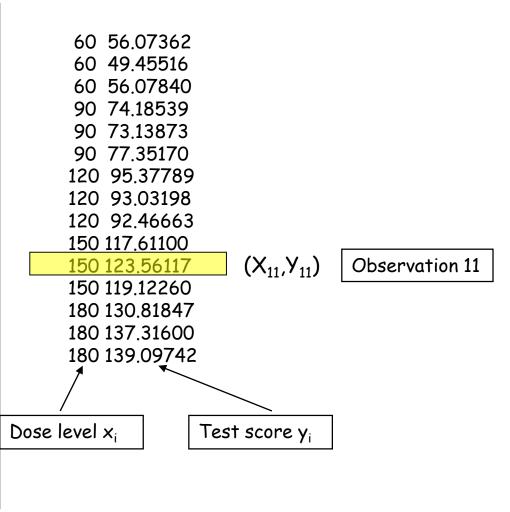
- The test score (Y_i) is the dependent variable. It depends on the dose level (X_i).
- The dose level is called the independent variable or the predictor.
- The observation unit:

$$(X_i, Y_i)$$
, $i=1,2,...,n$.



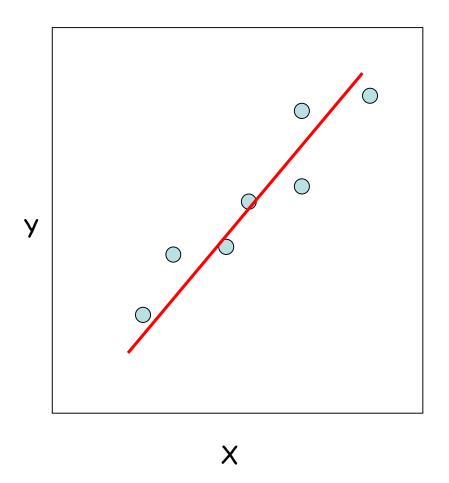
Data structure



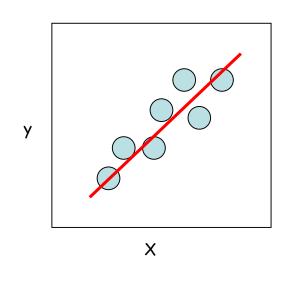


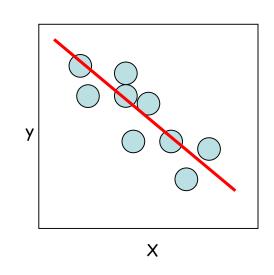
What is a **Simple** Linear Regression model?

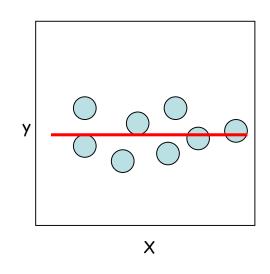
 A regression model is a statistical model which aims to describe the relationship between a predictor (the dose level) and a dependent variable (test score) with a straight line.



Properties of the simple linear regression model: trends





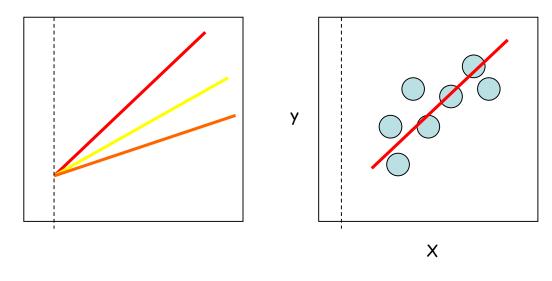


Upward trend

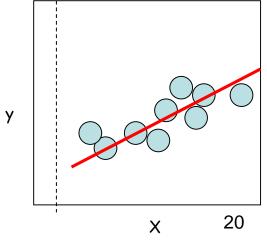
Downward trend

Y does not depend on X = no trend

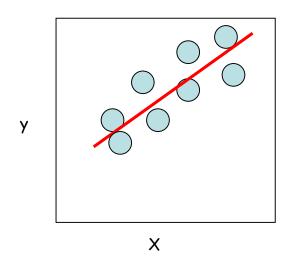
Parameters of the simple linear regression model: slope

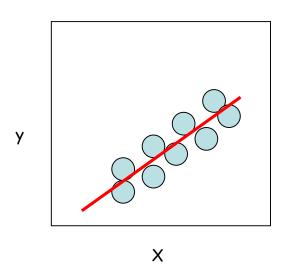


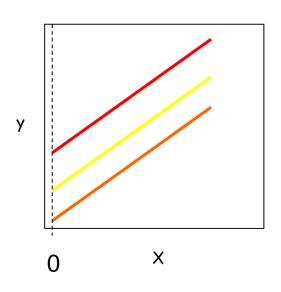
The slope is the change in the mean of Y for a unit change in X.



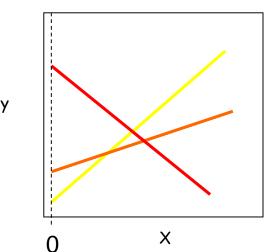
Parameters of the simple linear regression model: intercept





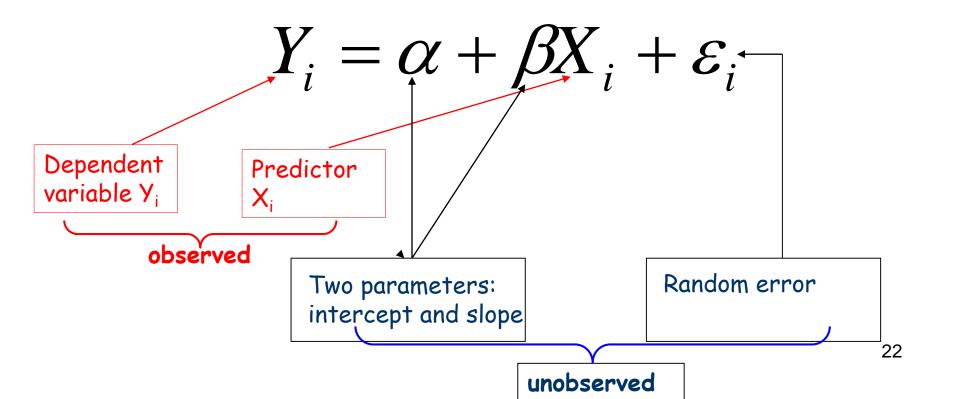


The intercept is the height of the regression line when X=0.



A Simple Linear Regression model: model formulation

• We assume that the relationship between the predictor and the response can be described with the model:



Estimation (I)

·a and b are the estimators for alpha and

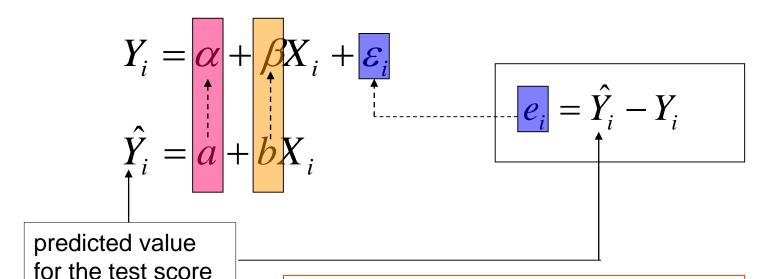
·e; (the residual) is the estimator for the

 We need to estimate the unobserved parameters of the model:

(the estimator for the

test score)

The estimator for the random error:

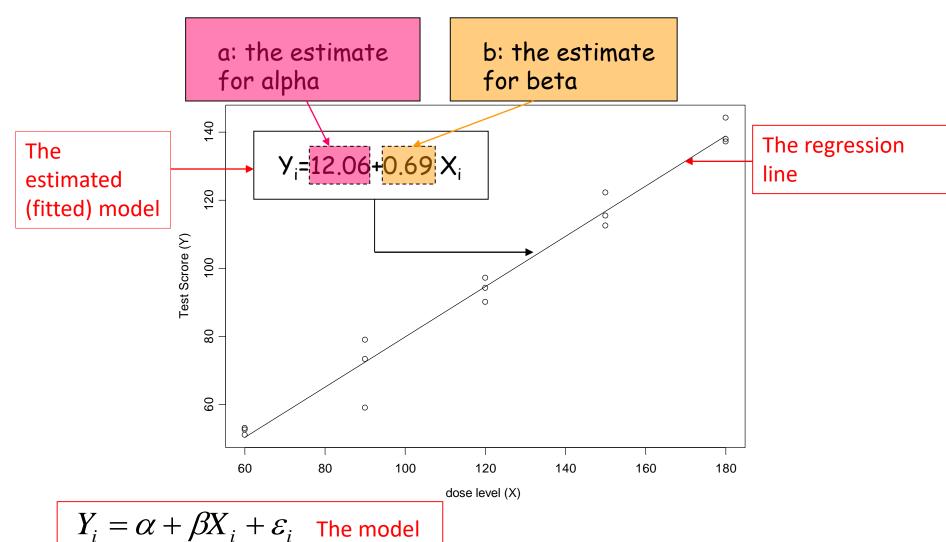


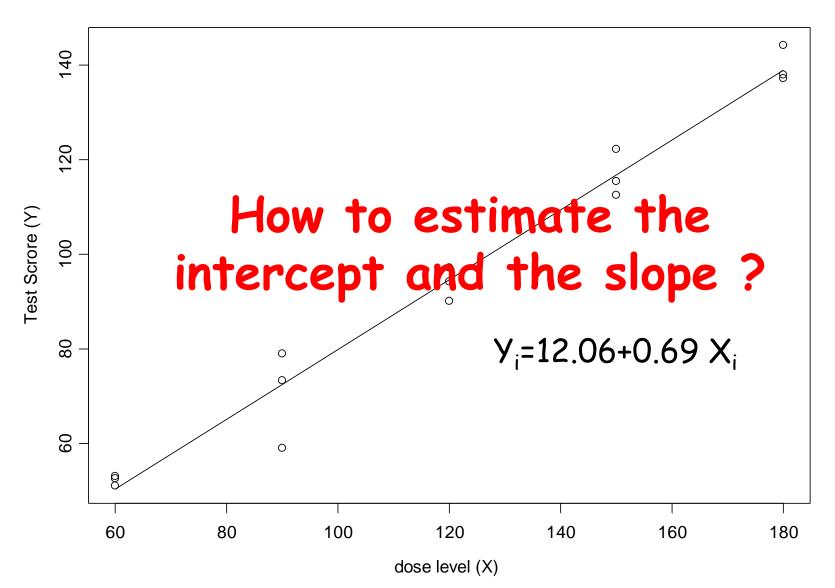
beta

random error

23

Regression model & the data



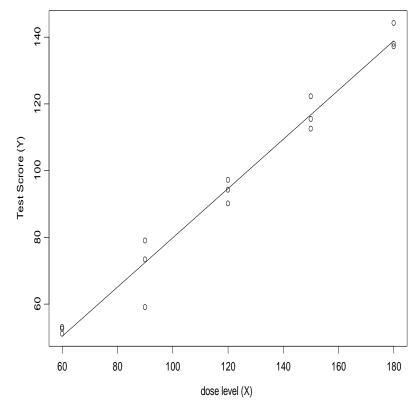


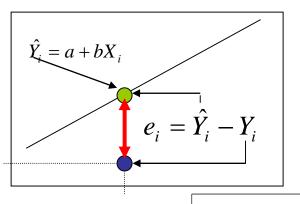
Regression model & the data

A EXAMPLE OF PERFECT FIT...

Test Scrore drug Concentration

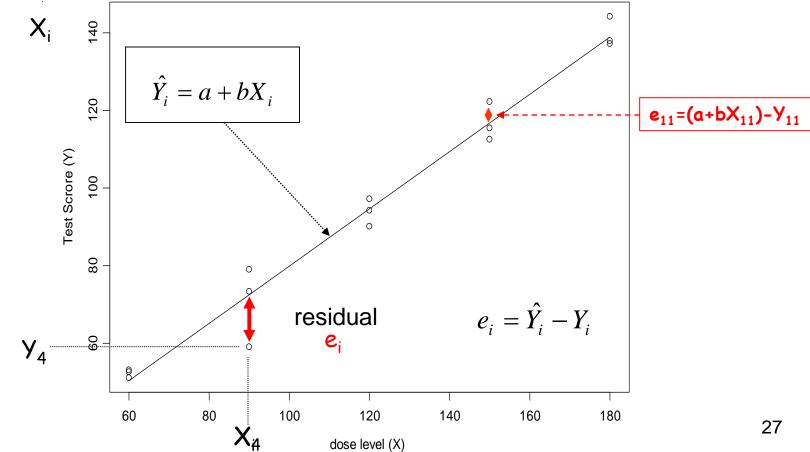
....BUT WE DO NOT EXPECT A PERFECT FIT...





The residuals

The difference between the observed response and the predicted response.



Estimation (II): The Least Squares Criterion

- How to estimate the intercept and slope?
- We want that the fitted model (the line which describes the relationship between Y and X) will be "close" to the data.
- The residual sum of squares = sum (residual)².
- The least squares criterion: choose intercept and slope which minimize the residual sum of squares

$$RSS = \sum_{i=1}^{n} (\hat{Y}_i - Y_i)^2$$

Parameter estimates

$$Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$
, $\varepsilon_i \sim N(0, \sigma^2)$

 $\bar{x} \& \bar{y}$

$$\hat{\beta}_{1} = \frac{\sum_{i=i}^{n} (x_{i} - \bar{x})(y_{i} - \bar{y})}{\sum_{i=1}^{n} (x_{i} - \bar{x})^{2}}$$

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$$

Unknown parameters in the model

OLS estimates for β_0 and β_1 (for a and b)

Parameter estimate for the variance

$$Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$
, $\varepsilon_i \sim N(0, \sigma^2)$

$$\hat{\sigma}^2 = \frac{1}{n-2} \sum_{i=1}^{n} r_i^2 = \frac{1}{n-2} \sum_{i=1}^{n} (y_i - (b_0 + b_1 x_i))^2$$

$$\hat{\beta}_0 \& \hat{\beta}_1$$

Inference

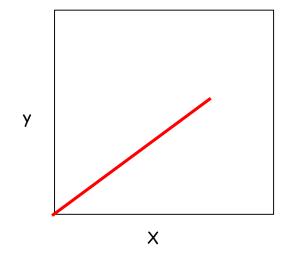
$$H_0: \beta_0 = 0$$
$$H_1: \beta_0 \neq 0$$

$$H_1: \beta_0 \neq 0$$

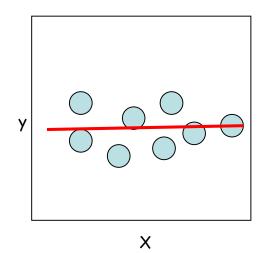
 $H_0: \beta_1 = 0$ $H_1: \beta_1 \neq 0$

$$H_1: \beta_1 \neq 0$$

Intercept equals to zero



Slope equals to zero



Test statistics

For the simple linear regression model:

$$Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i \qquad i = 1,...n$$

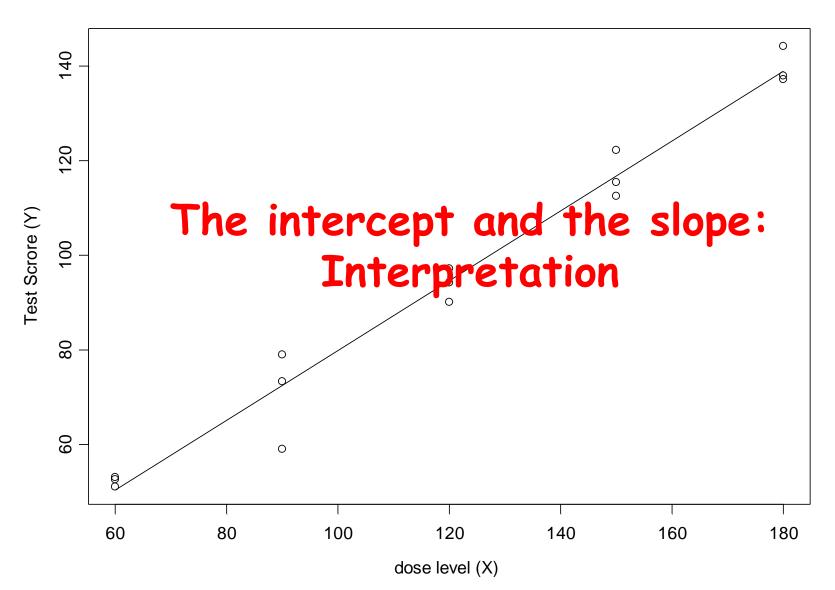
$$\varepsilon_i \sim N(0, \sigma^2)$$

Test statistic for β_1

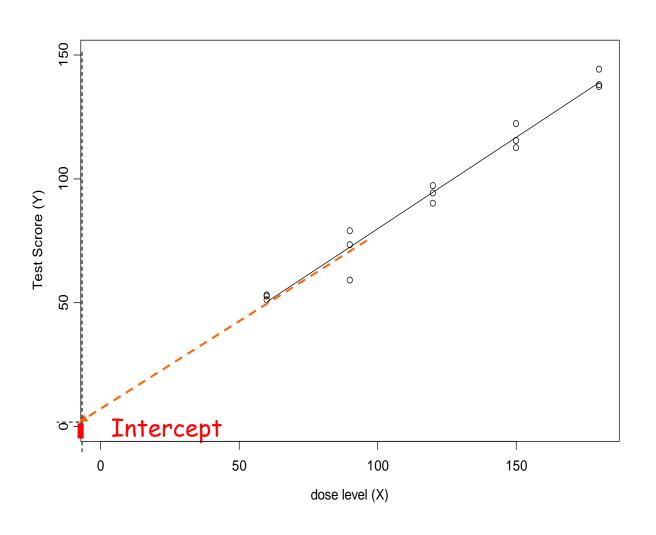
$$\frac{(\hat{\beta}_1 - \beta_1)}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2}} \sim t_{n-2}$$

Test statistic for β_0

$$\frac{(\hat{\beta}_0 - \beta_0)}{\hat{\sigma} \sqrt{\frac{1}{n} + \frac{\bar{x}}{\sum_{i=1}^{n} (x_i - \bar{x})^2}}} \sim t_{n-2}$$



Interpretation: the Intercept



The intercept is the predicted test score for dose level zero:

For X_i=0 we have:

Predicted test score=12.09+0.

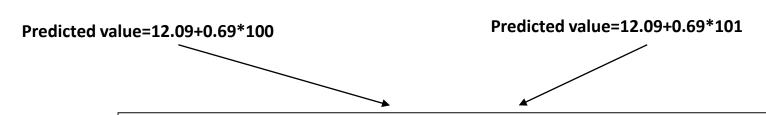
Interpretation: the slope

Suppose that we have two rats: the first received a dose of 100 and the second dose of 101.

WHAT IS THE DIFFERENCE BETWEEN THE PREDICTED VALUES OF THE TWO RATS?

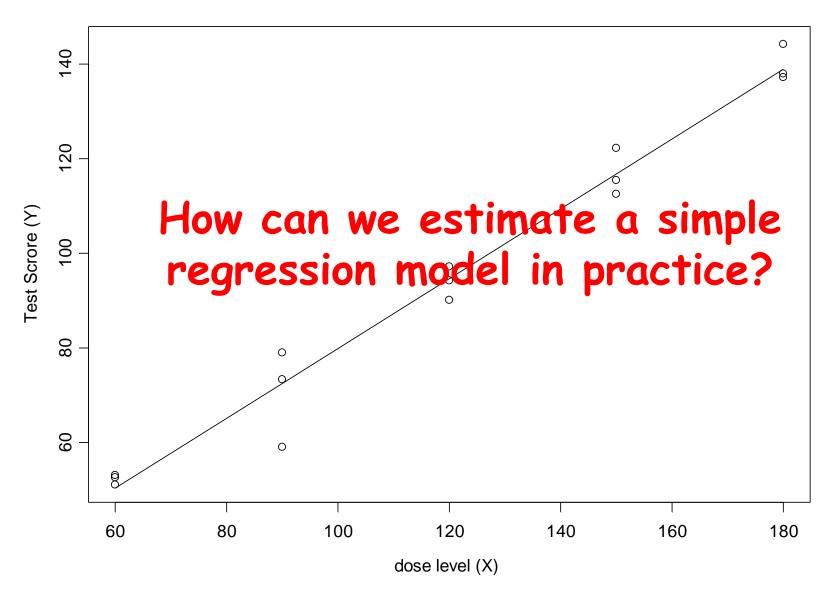
Dose level 100:

Dose level 101:



(12.09+0.69*101)-(12.09+0.69*100)=0.69

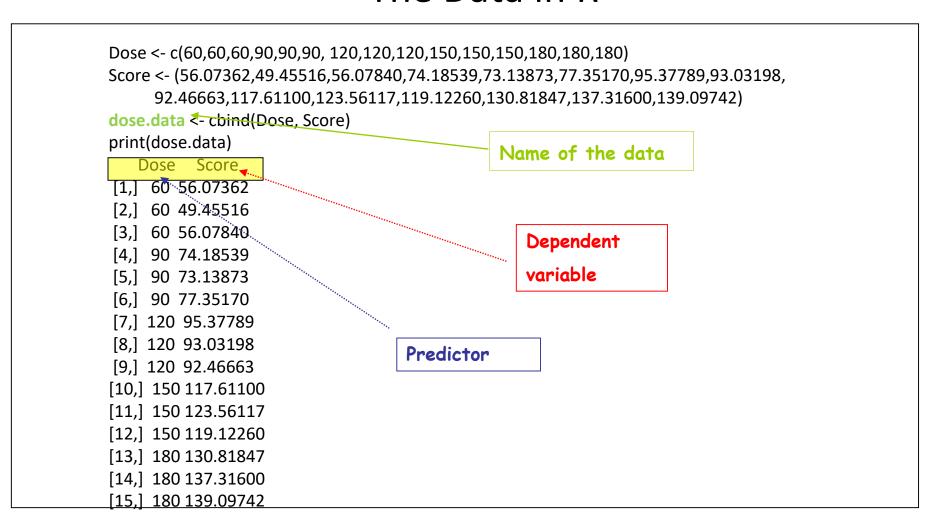
The difference is equal to 0.69 which is the value of the slope





Part 2 Fitting a simple linear regression in R using the Im() function

The Data in R



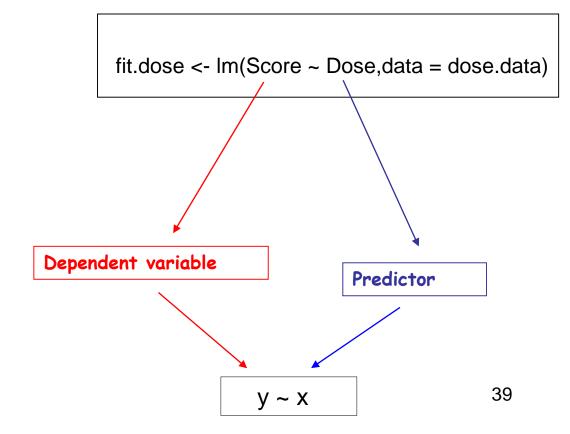
The function Im() in R

 Simple linear regression model can be fitted in R using the function lm().

The model statement:

Score ~ Dose

 Example of R script for function lm()



Fitting the model in R

```
Dose <- c(60,60,60,90,90,90, 120,120,120,150,150,150,180,180,180)
Score <- (56.07362,49.45516,56.07840,74.18539,73.13873,77.35170,95.37789,93.03198,
     92.46663,117.61100,123.56117,119.12260,130.81847,137.31600,139.09742)
dose.data <- cbind(Dose, Score)</pre>
print(dose.data)
   Dose Score
[1,] 60 56.07362
[2,] 60 49.45516
[3,] 60 56.07840
[4,] 90 74.18539
                                                         Dependent
[5,] 90 73.13873
[6,] 90 77.35170
                                                         variable
[7,] 120 95.37789
[8,] 120 93.03198
[9,] 120 92.46663
                                        Predictor
[10,] 150 117.61100
[11,] 150 123.56117
[12,] 150 119.12260
[13,] 180 130.81847
[14,] 180 137.31600
[15,] 180 139.09742
> fit.dose <- Im(Score ~ Dose) <-
                                                         Y_i = \alpha + \beta X_i + \varepsilon_i
```

> summary(fit.dose)

$$Im(y \sim x)$$

Output

ESTIMATION

INFERENCE

Coefficients:

Estimate

(Intercept) **12.06329**

Dose **0.69652**

Std. Error t value Pr(>|t|)

0.71389 4.445 0.000661 ***

0.02132 32.666 7.28e-14 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '' 1

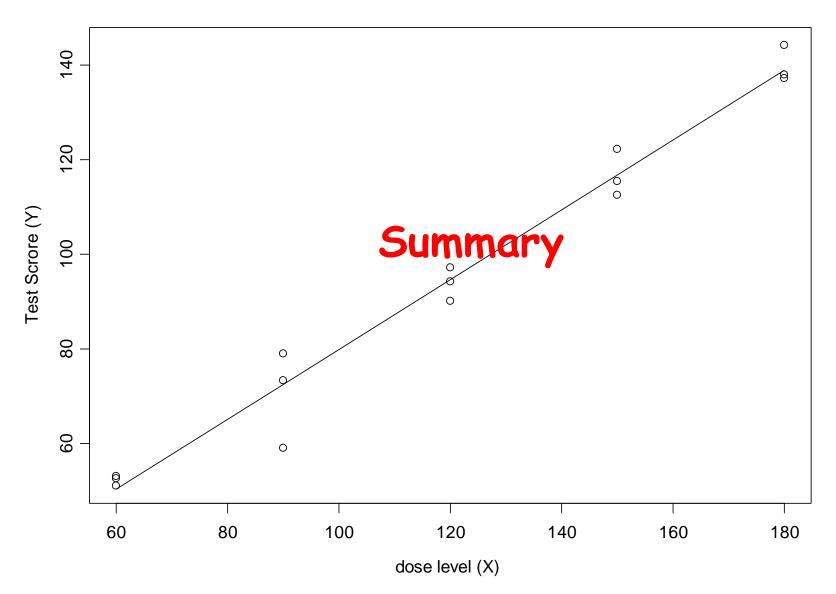
Residual standard error: 3.504 on 13 degrees of freedom

Multiple R-squared: 0.988, Adjusted R-squared: 0.987

F-statistic: 1067 on 1 and 13 DF, p-value: 7.279e-14

The intercept: what is the test score for dose=0

The slope: how much the response change for a unit change in the predictor



Technical details (Estimation)

A simple linear regression model has the form:

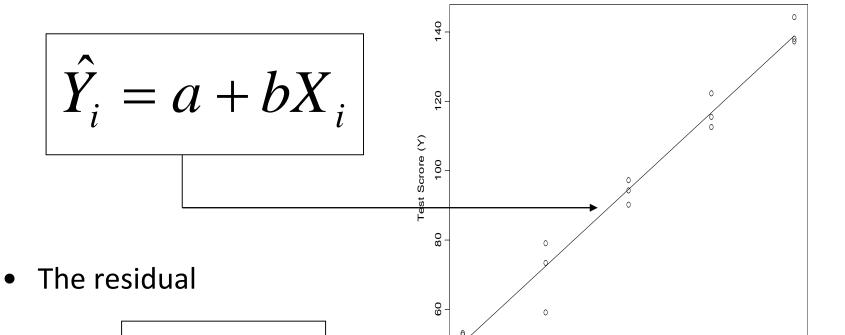
$$Y_i = \alpha + \beta X_i + \varepsilon_i$$

- α (β_0) and β (β_1) are the parameters in the model and \mathcal{E} is the random error.
- We can estimate α and β by minimizing the residual sum of squares

$$RSS = \sum_{i=1}^{n} (\alpha - \beta X_i - Y_i)^2$$

Technical details (Estimation)

The estimated model



dose level (X)

Technical Details (Estimation)

We assume that the relationship between Y_i and X_i can be described with a statistical model $Y_i = \alpha + \beta X_i + \varepsilon_i$

We assume that the random error \mathcal{E} is normally distributed.	$\varepsilon \sim N(0, \sigma^2)$
The mean of ${\mathcal E}$ is equal to zero	$E(\varepsilon_i) = 0$
The conditional mean of Y_i (given the value of X_i)	$E(Y_i \mid X_i) = \alpha + \beta X_i$
The estimator for the conditional mean of Y _i (the fitted model=the regression line)	$\hat{E}(Y_i \mid X_i) = a + bX_i = \hat{Y}_i$
The residual: the estimator for ${\cal E}$	$e_i = \hat{Y}_i - Y_i$
Least square criterion: choose a and b that minimize the residuals sum of squares	$RSS = \sum_{i=1}^{n} (\alpha - \beta X_i - Y_i)^2$ 45



Part 3 Model diagnostic

Simple regression model: assumptions

We consider the following linear regression model

$$Y_i = \alpha + \beta \times X_i + \varepsilon_i$$

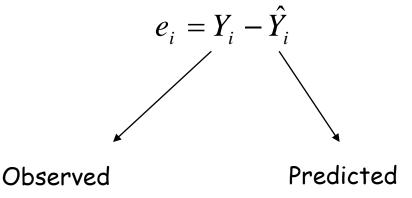
The random error is assumed to be normal distributed:

$$\varepsilon_i \sim N(0, \sigma^2)$$

We also assume that the variance is constant, i.e., $\varepsilon_1, \varepsilon_2,, \varepsilon_n$ are outcome of a normal distribution with mean zero and equal variances.

How to check the model assumptions? (1)

• The random error, ε_i , is unknown but we can estimate ε_i with the residuals



- The residuals can be used in order to check the model asaumptions.
- We focus on:
 - 1) the distribution of e_i
 - 2) the variability of e_i

How to check the model assumptions? (2)

 We assume that the mean of Y_i is linear with respect to X:

$$E(Y)_i = \alpha + \beta \times X_i$$

This is true only if

$$E(\varepsilon_i) = 0$$

 The residuals can be used in order to check the linearity assumption.

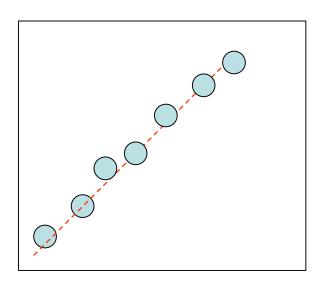
residuals O The residuals in this plot should distribute around zero and do not show any systematic pattern.

predictor

Assumption 1: The distribution of e_i

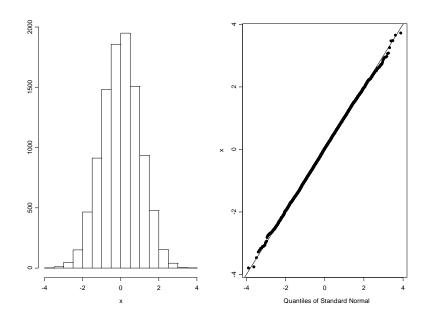
- The distribution of e_i is expected to be normal with mean zero and variance σ^2 .
- qq-normal plot (or normal probability plot) is a graphical tool that can be used in order to asses the normality assumption.

If the normalty
 assumption holds we
 expect qq-normal plot
 will be a srtight line.



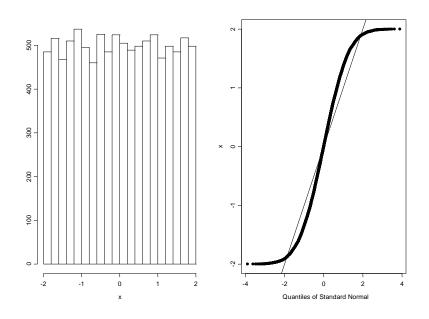
An example of qq-normal plot form N(0,1)

- Sample of 10000
 observations from N(0,1)
- The qqnormal plot is a stright line.
- If the random error ε_i is normal distributed, the qqnormal plot of the residuals should be a stright line.



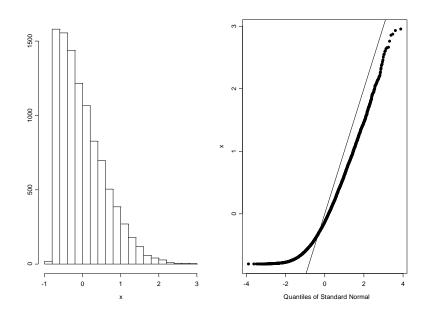
An example of qq-normal plot of a heavy tail distribution

- Sample of 10000
 observations from
 U(-2,2).
- S shape of the qqnormal plot.
- This is an example of a symatric distribution with more observations (relativly to the normal distribution) at the tails.



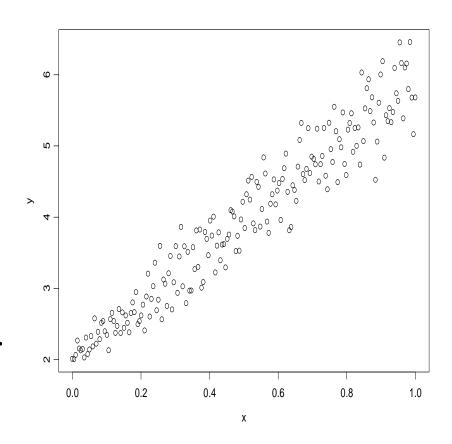
An example of qq-normal plot of a skwed distribution

- Sample of 10000
 observations from a skewed
 distribution.
- The distribution is skewed to the right and the points in the applot are not follow the stright line.



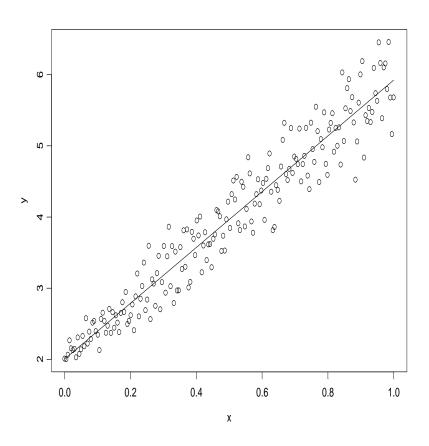
Assumption 2: Constant variance

- This is an example of a dataset in which the variance is not constant.
- The variance increases when the value of X increases.
- However, there is a linear relatioship between the predictor and the response.



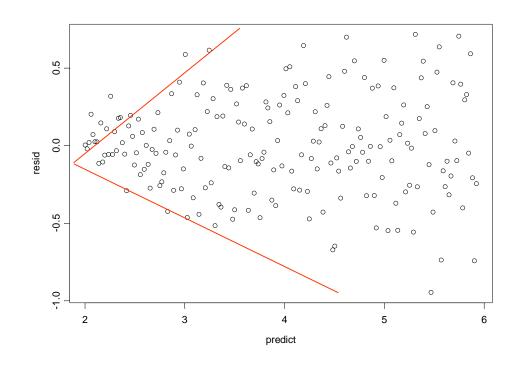
The data and the resrssion line

• The model seems to fit the data well, it captures the structure of the mean.

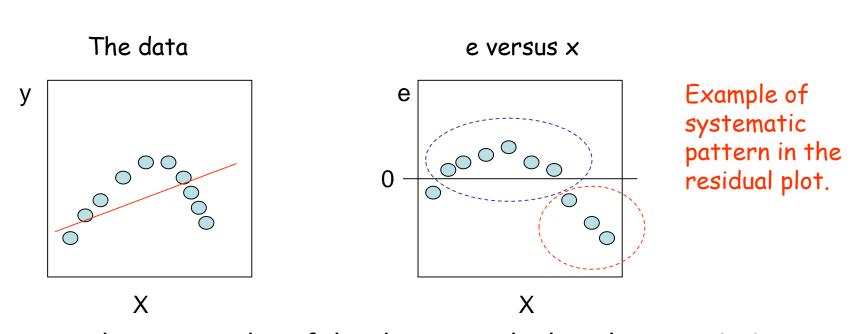


Residuals plot: residuals versus the predicted values

- A clear pattern.
- As the predicted values increase the variability among the residuals increase (a "megaphone" shape).

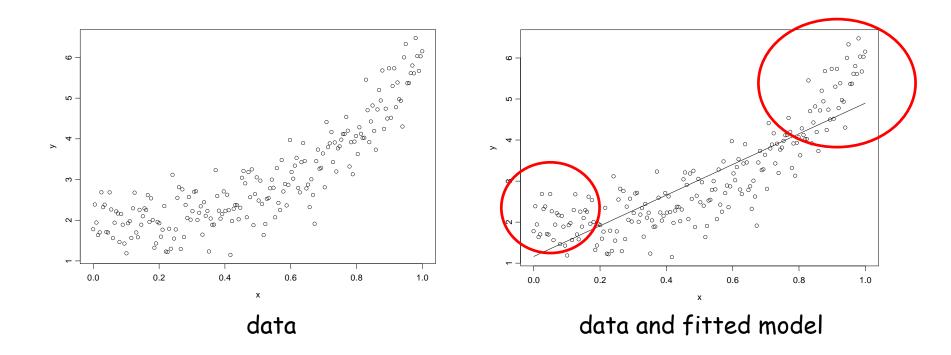


Assumption 3: Linearity



- The scatterplot of the data reveals that the association between the response and the predictor is not linear.
- The residuals plot (in the right) reveals a clear pattern among the residuals which depends on the value of X.

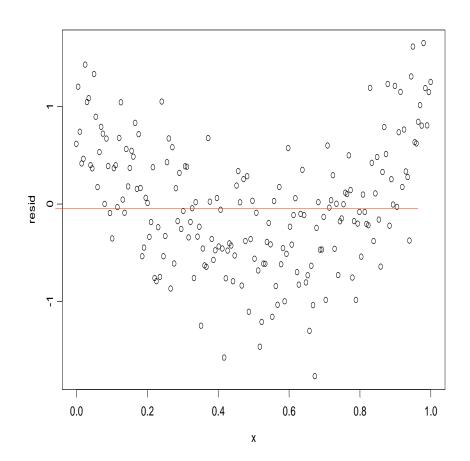
Systematic patterns



• The model underestimates the value of Y when the value of X is relatively small or large.

Linearity: residuals plot

- Clear systematic pattern among the residuals.
- The residuals are positive for small and large value of X and negative in the middle.
- This means that there is structure in the data that the linear regression model did not capture.



Bottom line about model diagnostic

- We let the residuals to tell us the story.
- Departure from model assumptions (constant variance, normality and linearity) can be investigated using qq-plot and residuals plots.



Part 4 Model diagnostic using R

Fitting the model in R

```
Dose <- c(60,60,60,90,90,90, 120,120,120,150,150,150,180,180,180)
Score <- (56.07362,49.45516,56.07840,74.18539,73.13873,77.35170,95.37789,93.03198,
     92.46663,117.61100,123.56117,119.12260,130.81847,137.31600,139.09742)
dose.data <- cbind(Dose, Score)
print(dose.data)
   Dose Score
[1,] 60 56.07362
[2,] 60 49.45516
[3,] 60 56.07840
[4,] 90 74.18539
[5,] 90 73.13873
[6,] 90 77.35170
[7,] 120 95.37789
[8,] 120 93.03198
[9,] 120 92.46663
                                                                 Y_i = \alpha + \beta X_i + \varepsilon_i
[10,] 150 117.61100
[11,] 150 123.56117
[12,] 150 119.12260
[13,] 180 130.81847
[14,] 180 137.31600
[15,] 180 139.09742
```

> fit.dose <- Im(Score ~ Dose)

The output

>summary(fit.dose)

Call:

Im(formula = Test_score ~ Dose_level, data = dose)

Residuals:

```
Min 1Q Median 3Q Max -6.619 -2.113 -0.121 2.221 7.020
```

INFERENCE

Coefficients:

```
Estimate Std. Error t value Pr(>|t|)
(Intercept) 12.06329 2.71389 4.445 0.000661 ***
Dose_level 0.69652 0.02132 32.666 7.28e-14 ***
```

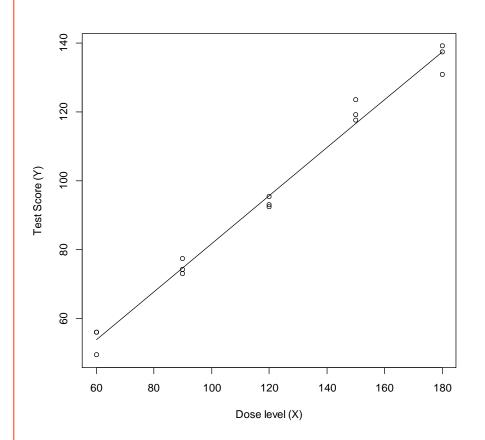
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ESTIMATION

Residual standard error: 3.504 on 13 degrees of freedom Multiple R-squared: 0.988, Adjusted R-squared: 0.987 F-statistic: 1067 on 1 and 13 DF, p-value: 7.279e-14

Data and predicted model

```
>plot(Dose,Score,
    ylab = "TestScore (Y)",
    xlab = "Doselevel (X)")
>x <- Dose
>y <- fit.dose$fit
>lines(x,y)
```



The output

ANOVA Table:

> aov(fit.dose)

```
Call:
    aov(formula = fit.dose)

Regression Sum of Squares

Terms:

Dose_level Residuals

Sum of Squares 13098.798 159.579

Deg. of Freedom 1 13
```

Residual standard error: 3.503618 Estimated effects may be unbalanced

Graphical output

```
> par(mfrow=c(2,2))
```

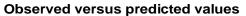
- > plot(fit.dose\$fit,xlab="Observed",
 ylab="Predicted", main = "Observed versus,
 predicted values")
- > abline(0,1)
- > hist(fit.dose\$resid,col=0,main="Histogram for
- + residuals")
- > qqnorm(fit.dose\$resid)

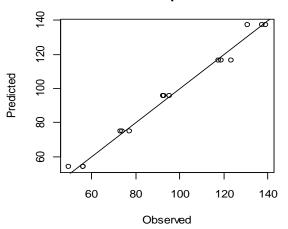
This statemnt produces the qqnormal plot (to check normality)

This statemnt produces the plot of the observed versus the predicted values (to check if the variance is constant)

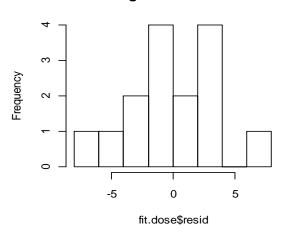
This statemnt produces the Histogram of residuals (to check normality)

Graphical output

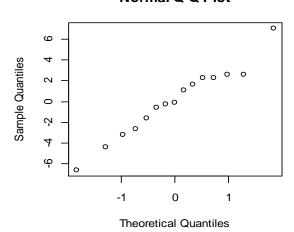




Histogram for residuals



Normal Q-Q Plot



Diagnostic plots

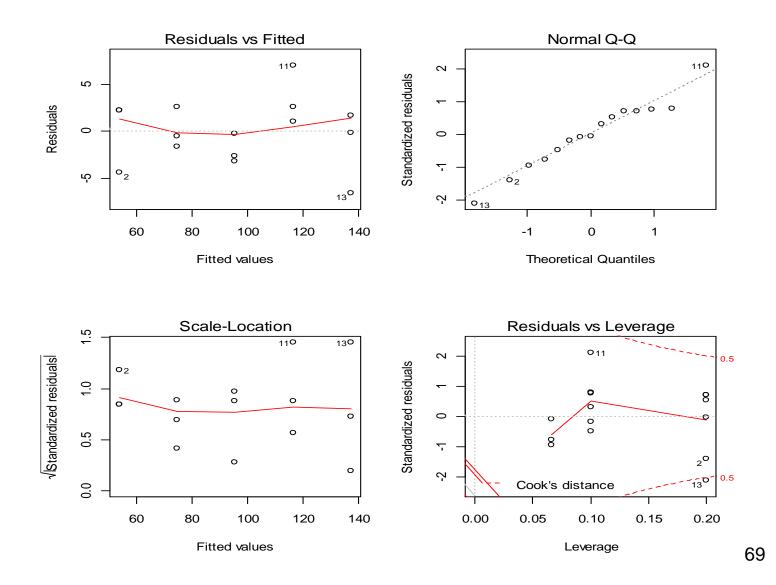
```
> par(mfrow = c(2,2))
```

> plot(fit.dose)

This statement produces the following figures:

- A plot of the residuals versus the predicted values (to check if the variance is constant).
- A qqnormal plot (to check normality).
- A scale-location plot (to check if the variance is constant),
- A plot of residuals versus leverage (to check if there are influential observations).

Diagnostic plots



Residual analyses

```
## Normality test ##
> shapiro.test(residuals(fit.dose))
##Constant variance test ##
> library(lmtest)
> bptest(fit.dose)
#Testing the Independence Assumption #
library(Imtest)
dwtest(fit.dose, alternative =
+ "two.sided")
```

```
Shapiro-Wilk normality test
```

data: residuals(fit.dose)
W = 0.9723, p-value = 0.8907

studentized Breusch-Pagan test

data: fit.dose BP = 1.0129, df = 1, p-value = 0.3142

Durbin-Watson test

data: fit.dose

DW = 2.0775, p-value = 0.8863

alternative hypothesis: true autocorrelation is not 0



Part 5

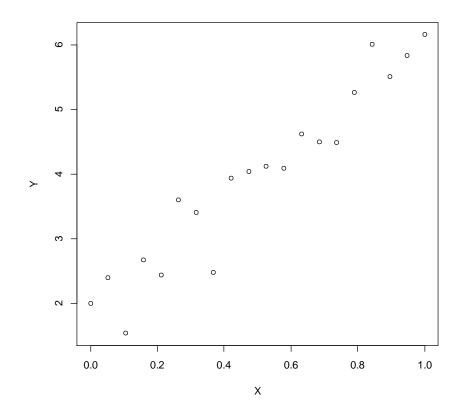
Four examples for model diagnostic

Four examples

- Example 1: all model asgsumptions hold.
- Example 2: the variance is not constant.
- Example 3: structure in the residuals.
- Example 4: the distribution of the residuals is not a Normal distribution.

Example 1: the data

- The sample size is equal to 20.
- The observation unit (x_i,y_i),
 i=1,...,20.
- The relatioship between X and Y seems to be linear.



Formulation of the model

We consider a linear regression model of the form

$$Y_i = \alpha + \beta \times X_i + \varepsilon_i$$

It is further assumed that the random error is normal distributed with mean 0 and constant variance σ^2 .

$$\varepsilon_i \sim N(0, \sigma^2)$$

The model in R:

fit.example1 <- lm(y ~ x, data = example1)
summary(fit.example1)
aov(fit.example1)</pre>

```
Call:
aov(formula = fit.example1)
```

Terms:

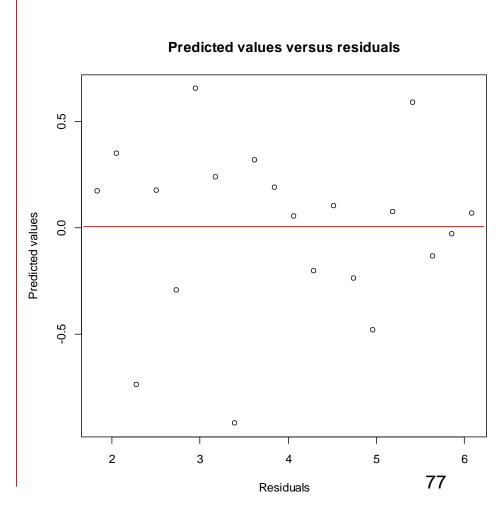
x Residuals
Sum of Squares 33.38747 2.99696
Deg. of Freedom 1 18

Residual standard error: 0.4080414 Estimated effects may be unbalanced

```
Call:
Im(formula = y \sim x, data = example 1)
Residuals:
         1Q Median 3Q
  Min
                             Max
-0.91702 -0.21027 0.07406 0.20531 0.65608
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.8260 0.1759 10.38 4.99e-09 ***
          Χ
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.408 on 18 degrees of freedom
Multiple R-squared: 0.9176, Adjusted R-squared: 0.9131
F-statistic: 200.5 on 1 and 18 DF, p-value: 3.364e-11
```

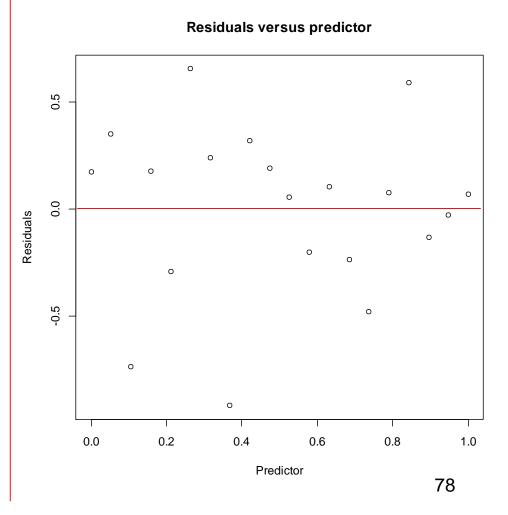
Constant variance: residuals versus predicted values

 We focus in this plot on the variabilty, if it constant we do not expect to patterns in this plot.



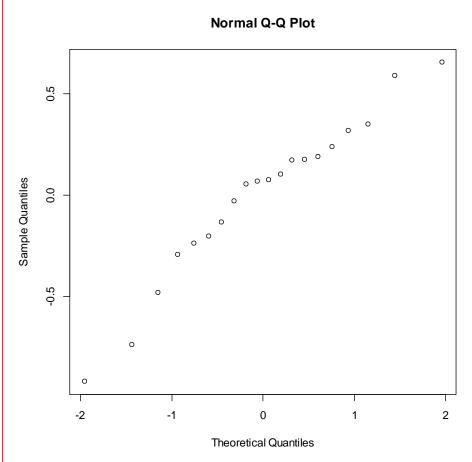
Linearity: residuals versus the predictor

 If the linear model is a "good model" (this means that the assumption that the mean of Y is linear with respect to X) we do not expect to patterns in this plot.

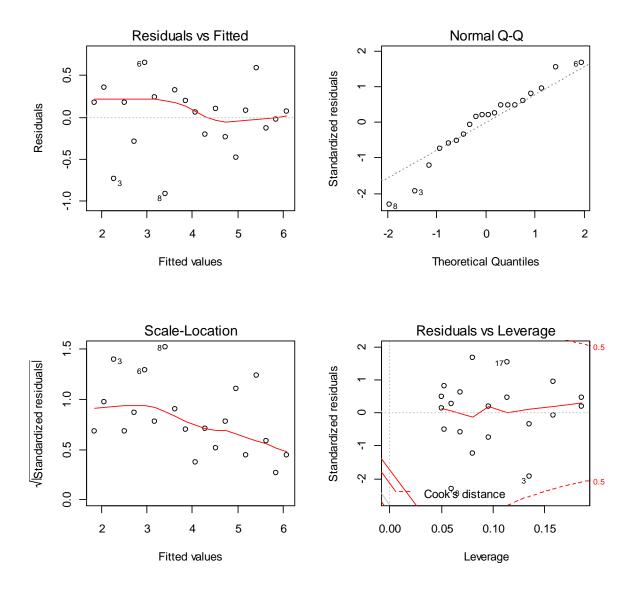


Normality: qqpolt for the residuals

 If the random error is normal distributed the points in the qqnormal plot should follow a stright line pattern.



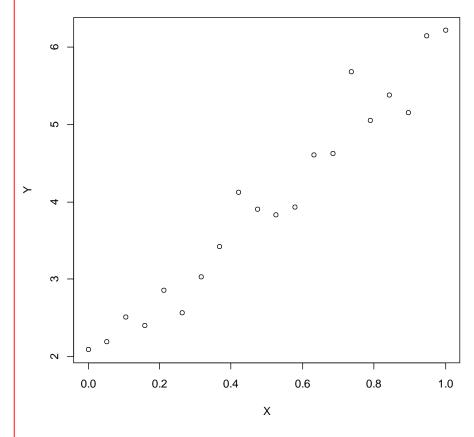
Diagnostic plots



Example 2: the data

- Sample size is 20.
- The relatioship seems to be linear. So the regression model should fit the data.
- Model in R:

```
#### Scatter plot of the data ####
plot(y ~ x, data = example2, ylab = "Y", xlab = "X")
#### Fitting the model ####
fit.example2 <- lm(y ~ x, data = example2)
summary(fit.example2)
aov(fit.example2)</pre>
```



```
> aov(fit.example2)
Call:
 aov(formula = fit.example2)
Terms:
            x Residuals
Sum of Squares 32.28117 1.64056
Deg. of Freedom
                         18
Residual standard error: 0.3018981
Estimated effects may be unbalanced
```

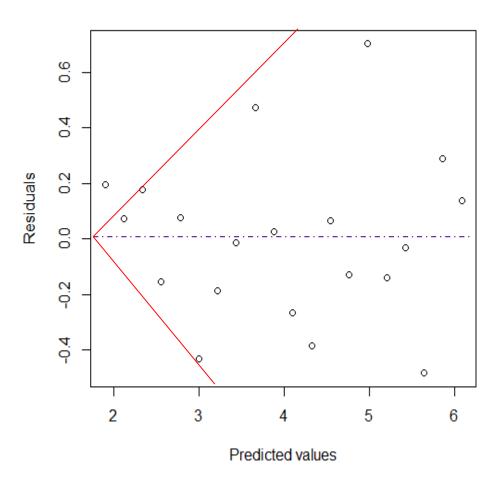
> summary(fit.example2)

```
Call:
Im(formula = y \sim x, data = example 2)
Residuals:
                        30
  Min
         1Q Median
                             Max
-0.48422 -0.16228 0.00692 0.14724 0.70333
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.8938  0.1301  14.55  2.13e-11 ***
          Χ
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.3019 on 18 degrees of freedom
Multiple R-squared: 0.9516, Adjusted R-squared: 0.9489
F-statistic: 354.2 on 1 and 18 DF, p-value: 2.745e-13
```

Constant variability

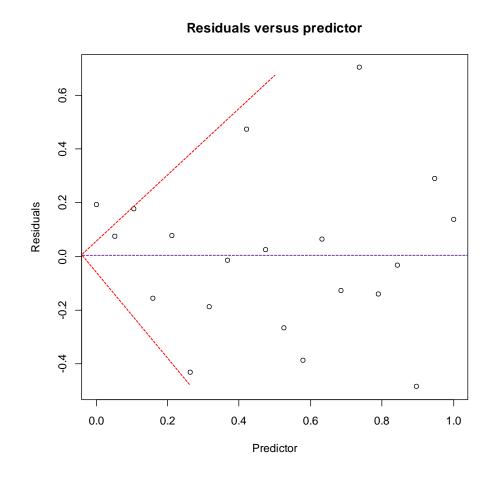
- A "megaphon" shape.
- The variability is not constant.
- The variability increase as the predicted values increase.

Predicted values versus residuals



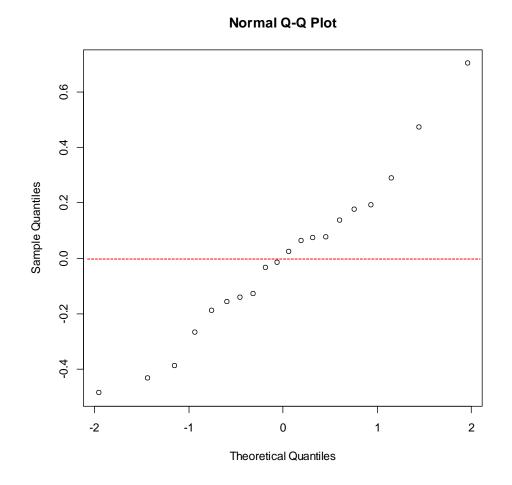
Linearity and constant variability: residuals versus the predictor

- Residuals distributed around zero.
- This means that the linear regression model captures the main pattern in the data.
- BUT it is clear that the variability is not constant.

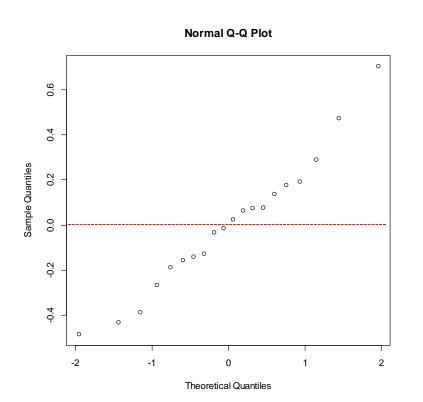


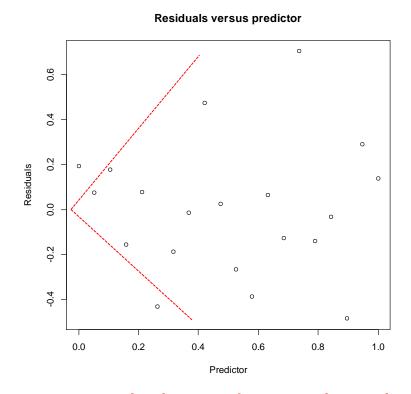
A qq-normal plot

 No pattern is detected so we conclude that the random error is normal distributed.



Do not use only one residuals plot for model diagnostic

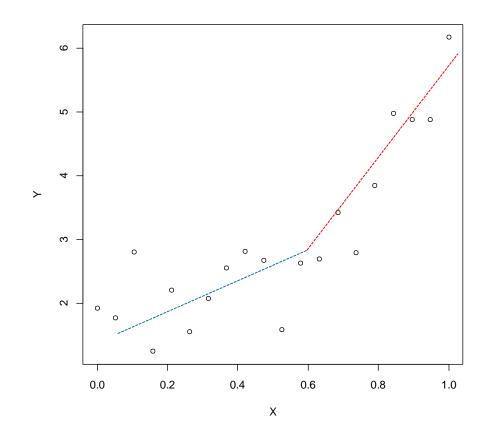




Another example in which the ganormal plot indicate that the random error is normal distributed and the the plot with the residuals versus the predictor indicates on non constant variance.

Example 3: the data

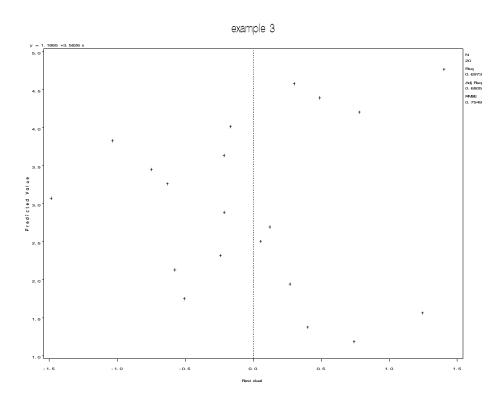
- Sample size is 20.
- The relatioship seems to be linear BUT NOT A STRIGHT LINE.
- This means that a simple linear regression model will not be able to capture all structure of the data.



```
> aov(fit.example3)
Call:
 aov(formula = fit.example3)
Terms:
            x Residuals
Sum of Squares 23.63339 10.25865
Deg. of Freedom
                          18
Residual standard error: 0.7549339
Estimated effects may be unbalanced
```

Constant variability

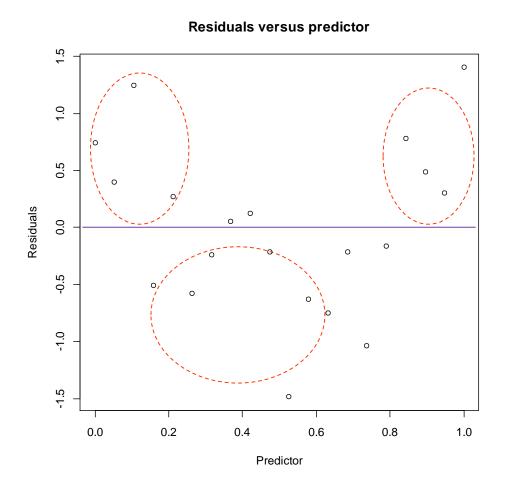
 The residuals plot do not reavel any pattern which indicates that the variance is not constant.



```
> summary(fit.example3)
Call:
Im(formula = y \sim x, data = example 3)
Residuals:
  Min
         10 Median 30 Max
-1.48495 -0.52386 -0.05503 0.42272 1.40292
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.1865  0.3254  3.647  0.00185 **
       Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.7549 on 18 degrees of freedom
Multiple R-squared: 0.6973, Adjusted R-squared: 0.6805
F-statistic: 41.47 on 1 and 18 DF, p-value: 4.64e-06
```

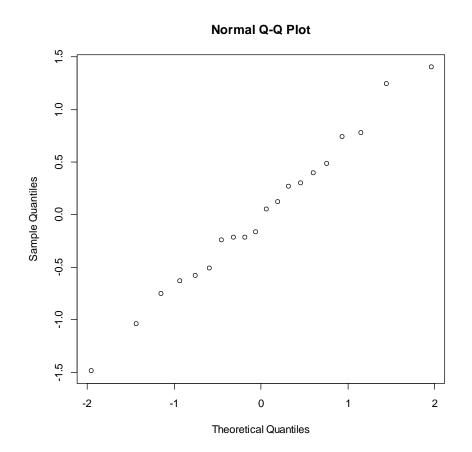
Linearity

- Pattern in the residual plot.
- We observed groups with positive and negative residuals.
- This means that the model does not capture all structure in the data.



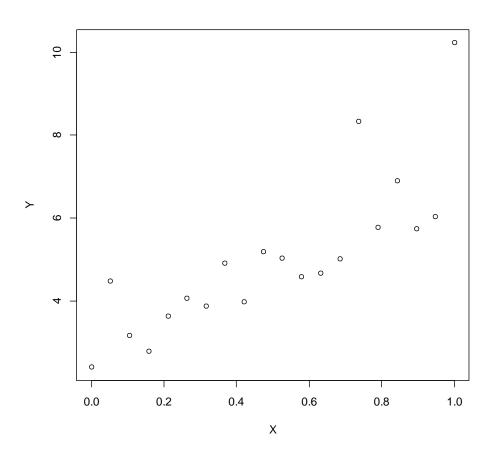
Normality

- A pattern of a sgtight line in the qqnormal plot.
- This indicate that the residuals follow a normal distribution.



Example 4: the data

 This is an example in which the three residuals plots reveal the same problem of the model which is not related to linearity and constant variability.



Example 4

External data: example4.txt

```
> aov(fit.example4)
```

```
Call: aov(formula = fit.example4)
```

Terms:

x Residuals
Sum of Squares 42.91607 22.07751
Deg. of Freedom 1 18

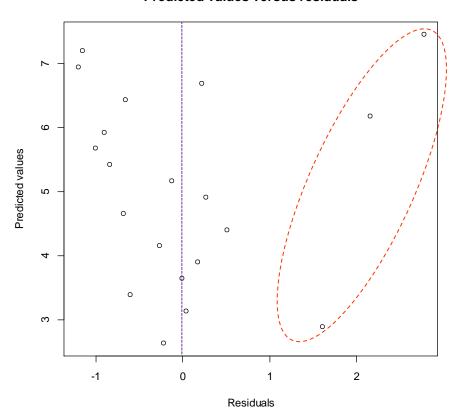
Residual standard error: 1.107487 Estimated effects may be unbalanced

```
> summary(fit.example4)
Call:
Im(formula = y \sim x, data = example 4)
Residuals:
  Min
        10 Median 30 Max
-1.2074 -0.7238 -0.1791 0.2265 2.7738
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.6287 0.4773 5.507 3.14e-05 ***
       Χ
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 1.107 on 18 degrees of freedom
Multiple R-squared: 0.6603, Adjusted R-squared: 0.6414
F-statistic: 34.99 on 1 and 18 DF, p-value: 1.341e-05
```

Residuals versus predicted values

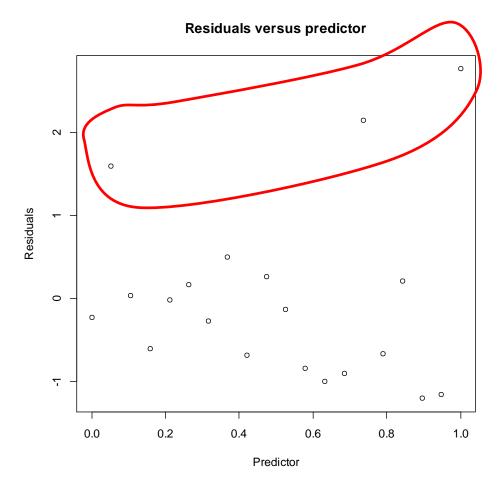
Three positive outliers.

Predicted values versus residuals



Residuals versus the predictor

 There are more negative residuals than positive residuals and three positive outliers.



Normality

- The pattern in the qqnormal plot indicates on departure from normality.
- Mind the three outliers.

