Getting to fit models in **R**

Alexandre Courtiol

Leibniz Institute of Zoo and Wildlife Research

June 2018

Leibniz Institute for Zoo and Wildlife Research
IN THE FORSCHUNGSVERBUND BERLIN E.V.

Physalia Courses

Getting started with **R**

What is a linear model?

A statistical model represents, often in considerably idealized form, the data-generating process (`https://en.wikipedia.org/wiki/Statistical_model`).

What is a linear model?

A statistical model represents, often in considerably idealized form, the data-generating process (`https://en.wikipedia.org/wiki/Statistical_model`).

In a linear model, the data-generating process is assumed to be a linear function: it is constructed from a set of terms by multiplying each term by a constant (a model parameter) and adding the results.

What is a linear model?

A statistical model represents, often in considerably idealized form, the data-generating process (`https://en.wikipedia.org/wiki/Statistical_model`).

In a linear model, the data-generating process is assumed to be a linear function: it is constructed from a set of terms by multiplying each term by a constant (a model parameter) and adding the results.

R allows to fit efficiently and easily all main kinds of linear models:

- classical linear models (t-test, correlation, linear regression, ANOVA, ANCOVA): LM
- generalized linear models (logistic regression, Poisson regression. . .): GLM
- linear mixed-effects models: LMM
- generalized linear mixed-effects models: GLMM
- general additive models & general additive mixed models: GAM & GAMM

What is a linear model?

A statistical model represents, often in considerably idealized form, the data-generating process (`https://en.wikipedia.org/wiki/Statistical_model`).

In a linear model, the data-generating process is assumed to be a linear function: it is constructed from a set of terms by multiplying each term by a constant (a model parameter) and adding the results.

R allows to fit efficiently and easily all main kinds of linear models:

- classical linear models (t-test, correlation, linear regression, ANOVA, ANCOVA): LM
- generalized linear models (logistic regression, Poisson regression. . .): GLM
- linear mixed-effects models: LMM
- generalized linear mixed-effects models: GLMM
- general additive models & general additive mixed models: GAM & GAMM

Note: I have a 100 hours course on the topic (`https://github.com/courtiol/LM2GLMM`) but it may be a bit terse without the bla bla. . .

Linear models in **R**

R is very rich in terms of capabilities to fit linear models due to an increasing number of dedicated packages!

For now, no other software seems to be remotely as good (prognostic: only `Julia` or `Python` may change that within a decade but I find it unlikely).

Linear models in **R**

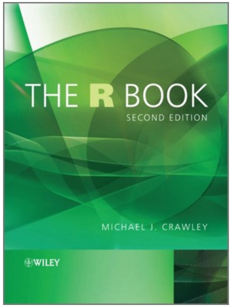
R is very rich in terms of capabilities to fit linear models due to an increasing number of dedicated packages!

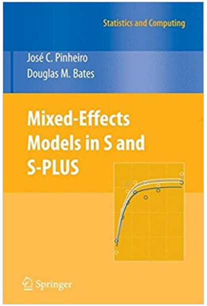
For now, no other software seems to be remotely as good (prognostic: only `Julia` or `Python` may change that within a decade but I find it unlikely).

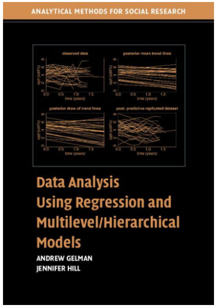
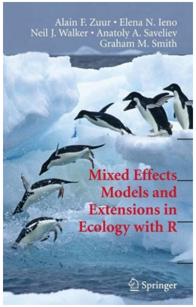
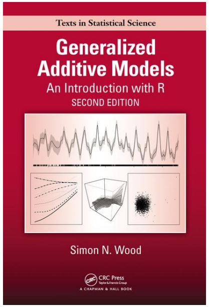
Models	Packages for fitting	Helper packages
LM	none; `spaMM`	`car`; `lmtest`; `visreg`
GLM	none; `spaMM`	`car`; `DHARMa`; `visreg`
LMM	`lme4`; `spaMM`; `glmmTMB`	`DHARMa`; `pbkrtest`
GLMM	`lme4`; `spaMM`; `glmmTMB`	`DHARMa`; `pbkrtest`
GAM	`mgcv`	`visreg`
GAMM	`mgcv`	

Note: those are my personal favorite ones, but they are plenty more out there.

Good books dealing with linear models in **R**






ANALYTICAL METHODS FOR SOCIAL RESEARCH
Data Analysis Using Regression and Multilevel/Hierarchical Models
ANDREW GELMAN
JENNIFER HILL

Alain F. Zuur • Elena N. Ieno
Neil J. Walker • Anatoly A. Saveliev
Graham M. Smith
Mixed Effects Models and Extensions in Ecology with R
Springer


Note: it is also useful to look at books not focussed on **R**!

Preparing data for (G)LM(M) & GA(M)

To maximize the chances of success prepare your data as follow:

- one row = one observation (if repeated measures, use several rows!)
- qualitative variables of class `factor` (check the levels, drop unused ones, set the reference properly)
- no `NA` (models can somewhat deal with them but it is a major source of headackes)

Preparing data for (G)LM(M) & GA(M)

To maximize the chances of success prepare your data as follow:

- one row = one observation (if repeated measures, use several rows!)
- qualitative variables of class `factor` (check the levels, drop unused ones, set the reference properly)
- no `NA` (models can somewhat deal with them but it is a major source of headackes)

Example of a good dataset:

```
head(iris)

##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 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

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","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

any(is.na(iris))

## [1] FALSE
```

Getting started with **R**

Getting started with **R**

The linear model: specifications

Simple notation:

$$y_i = \hat{\beta}_0 + \hat{\beta}_1 \times x_{1,i} + \hat{\beta}_2 \times x_{2,i} + \cdots + \hat{\beta}_p \times x_{p,i} + \varepsilon_i$$

The linear model: specifications

Simple notation:

$$y_i = \hat{\beta}_0 + \hat{\beta}_1 \times x_{1,i} + \hat{\beta}_2 \times x_{2,i} + \cdots + \hat{\beta}_p \times x_{p,i} + \varepsilon_i$$

$$y_i = \hat{y}_i + \varepsilon_i$$

The linear model: specifications

Simple notation:

$$y_i = \hat{\beta}_0 + \hat{\beta}_1 \times x_{1,i} + \hat{\beta}_2 \times x_{2,i} + \cdots + \hat{\beta}_p \times x_{p,i} + \varepsilon_i$$

$$y_i = \hat{y}_i + \varepsilon_i$$

- y_i = the observations to explain / response variable / dependent variable
- $\hat{y}_i$ = the fitted values
- $x_{j,i}$ = constants derived from the predictors / explanatory variables / independent variables
- $\hat{\beta}_j$ = the (model parameter / regression coefficient) estimates
- ε_i = the residuals (i.e. the estimates for the error which is Gaussian with constant variance)

The linear model: specifications

Matrix notation:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \dots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_{1,1} & x_{1,2} & \dots & x_{1,p} \\ 1 & x_{2,1} & x_{2,2} & \dots & x_{2,p} \\ 1 & x_{3,1} & x_{3,2} & \dots & x_{3,p} \\ \dots & \dots & \dots & \dots & \dots \\ 1 & x_{n,1} & x_{n,2} & \dots & x_{n,p} \end{bmatrix} \begin{bmatrix} \hat{\beta}_0 \\ \hat{\beta}_1 \\ \hat{\beta}_2 \\ \dots \\ \hat{\beta}_p \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \dots \\ \varepsilon_n \end{bmatrix}$$

The linear model: specifications

Matrix notation:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \dots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_{1,1} & x_{1,2} & \dots & x_{1,p} \\ 1 & x_{2,1} & x_{2,2} & \dots & x_{2,p} \\ 1 & x_{3,1} & x_{3,2} & \dots & x_{3,p} \\ \dots & \dots & \dots & \dots & \dots \\ 1 & x_{n,1} & x_{n,2} & \dots & x_{n,p} \end{bmatrix} \begin{bmatrix} \hat{\beta}_0 \\ \hat{\beta}_1 \\ \hat{\beta}_2 \\ \dots \\ \hat{\beta}_p \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \dots \\ \varepsilon_n \end{bmatrix}$$

$Y = X\widehat{\beta} + \varepsilon = \widehat{Y} + \varepsilon$

$\varepsilon = Y - \widehat{Y}$

The linear model: specifications

Matrix notation:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \dots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_{1,1} & x_{1,2} & \dots & x_{1,p} \\ 1 & x_{2,1} & x_{2,2} & \dots & x_{2,p} \\ 1 & x_{3,1} & x_{3,2} & \dots & x_{3,p} \\ \dots & \dots & \dots & \dots & \dots \\ 1 & x_{n,1} & x_{n,2} & \dots & x_{n,p} \end{bmatrix} \begin{bmatrix} \hat{\beta}_0 \\ \hat{\beta}_1 \\ \hat{\beta}_2 \\ \dots \\ \hat{\beta}_p \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \dots \\ \varepsilon_n \end{bmatrix}$$

$$Y = X\widehat{\beta} + \varepsilon = \widehat{Y} + \varepsilon$$

$$\varepsilon = Y - \widehat{Y}$$

- Y = the vector of observations
- Y = the vector of fitted values
- X = a matrix called the design matrix (or the model matrix)
- ε = the vector of residuals

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~ Petal.Width, data = iris)
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~ Petal.Width, data = iris)
```

```
formula(mod)  ## the formula
## Petal.Length ~ Petal.Width
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~ Petal.Width, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width
## 1          1.4         0.2
## 2          1.4         0.2
## 3          1.3         0.2
## 4          1.5         0.2
## 5          1.4         0.2
## 6          1.7         0.4
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~ Petal.Width, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width
## 1          1.4         0.2
## 2          1.4         0.2
## 3          1.3         0.2
## 4          1.5         0.2
## 5          1.4         0.2
## 6          1.7         0.4
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~ Petal.Width, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width
## 1          1.4         0.2
## 2          1.4         0.2
## 3          1.3         0.2
## 4          1.5         0.2
## 5          1.4         0.2
## 6          1.7         0.4
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Petal.Width
## 1           1         0.2
## 2           1         0.2
## 3           1         0.2
## 4           1         0.2
## 5           1         0.2
## 6           1         0.4
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  Species, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Species
## 1          1.4  setosa
## 2          1.4  setosa
## 3          1.3  setosa
## 4          1.5  setosa
## 5          1.4  setosa
## 6          1.7  setosa
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Speciesversicolor Speciesvirginica
## 1           1                 0                0
## 2           1                 0                0
## 3           1                 0                0
## 4           1                 0                0
## 5           1                 0                0
## 6           1                 0                0
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width + Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width Species
## 1          1.4         0.2  setosa
## 2          1.4         0.2  setosa
## 3          1.3         0.2  setosa
## 4          1.5         0.2  setosa
## 5          1.4         0.2  setosa
## 6          1.7         0.4  setosa
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Petal.Width Speciesversicolor Speciesvirginica
## 1           1         0.2                 0                0
## 2           1         0.2                 0                0
## 3           1         0.2                 0                0
## 4           1         0.2                 0                0
## 5           1         0.2                 0                0
## 6           1         0.4                 0                0
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  Petal.Width + Species + Petal.Width:Species, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width + Species + Petal.Width:Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width Species
## 1          1.4         0.2  setosa
## 2          1.4         0.2  setosa
## 3          1.3         0.2  setosa
## 4          1.5         0.2  setosa
## 5          1.4         0.2  setosa
## 6          1.7         0.4  setosa
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Petal.Width Speciesversicolor Speciesvirginica Petal.Width:Speciesversicolor Petal.Width:Speciesvirginica
## 1           1         0.2                 0                0                             0                            0
## 2           1         0.2                 0                0                             0                            0
## 3           1         0.2                 0                0                             0                            0
## 4           1         0.2                 0                0                             0                            0
## 5           1         0.2                 0                0                             0                            0
## 6           1         0.4                 0                0                             0                            0
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  Petal.Width*Species, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width * Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width Species
## 1          1.4         0.2  setosa
## 2          1.4         0.2  setosa
## 3          1.3         0.2  setosa
## 4          1.5         0.2  setosa
## 5          1.4         0.2  setosa
## 6          1.7         0.4  setosa
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Petal.Width Speciesversicolor Speciesvirginica Petal.Width:Speciesversicolor Petal.Width:Speciesvirginica
## 1           1         0.2                 0                0                             0                            0
## 2           1         0.2                 0                0                             0                            0
## 3           1         0.2                 0                0                             0                            0
## 4           1         0.2                 0                0                             0                            0
## 5           1         0.2                 0                0                             0                            0
## 6           1         0.4                 0                0                             0                            0
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  Petal.Width/Species, data = iris)  ## dangerous
```

```
formula(mod)  ## the formula

## Petal.Length ~ Petal.Width/Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length Petal.Width Species
## 1          1.4         0.2  setosa
## 2          1.4         0.2  setosa
## 3          1.3         0.2  setosa
## 4          1.5         0.2  setosa
## 5          1.4         0.2  setosa
## 6          1.7         0.4  setosa
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Petal.Width Petal.Width:Speciesversicolor Petal.Width:Speciesvirginica
## 1           1         0.2                             0                            0
## 2           1         0.2                             0                            0
## 3           1         0.2                             0                            0
## 4           1         0.2                             0                            0
## 5           1         0.2                             0                            0
## 6           1         0.4                             0                            0
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  1, data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ 1
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

##   Petal.Length
## 1          1.4
## 2          1.4
## 3          1.3
## 4          1.5
## 5          1.4
## 6          1.7
```

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept)
## 1           1
## 2           1
## 3           1
## 4           1
## 5           1
## 6           1
```

The linear model: specifications

R formula notation:

```
mod <- lm(Petal.Length ~  ., data = iris)
```

```
formula(mod)  ## the formula

## Petal.Length ~ Sepal.Length + Sepal.Width + Petal.Width + Species
```

```
head(model_frame <- model.frame(mod))  ## the data used for the fit

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

```
head(model.response(model_frame))  ## the response variable

##   1   2   3   4   5   6
## 1.4 1.4 1.3 1.5 1.4 1.7
```

```
head(model.matrix(mod))  ## the model matrix

##   (Intercept) Sepal.Length Sepal.Width Petal.Width Speciesversicolor Speciesvirginica
## 1           1          5.1         3.5         0.2                 0                0
## 2           1          4.9         3.0         0.2                 0                0
## 3           1          4.7         3.2         0.2                 0                0
## 4           1          4.6         3.1         0.2                 0                0
## 5           1          5.0         3.6         0.2                 0                0
## 6           1          5.4         3.9         0.4                 0                0
```

The linear model: understanding the design matrix

It is most important to understand the design matrix because the interpretation of the parameters depend on it!

The design matrix depends on:

- your formula
- your data
- the contrasts (for qualitative variables)

The linear model: understanding the design matrix

It is most important to understand the design matrix because the interpretation of the parameters depend on it!

The design matrix depends on:

- your formula
- your data
- the contrasts (for qualitative variables)

By default, each category is compared to the first one:

```
mod <- lm(Petal.Length ~  Species, data = iris)
model.matrix(mod)[c(1, 51, 101), ]
```

```
##     (Intercept) Speciesversicolor Speciesvirginica
## 1             1                 0                0
## 51            1                 1                0
## 101           1                 0                1
```

The linear model: understanding the design matrix

It is most important to understand the design matrix because the interpretation of the parameters depend on it!

The design matrix depends on:

- your formula
- your data
- the contrasts (for qualitative variables)

By default, each category is compared to the first one:

```
mod <- lm(Petal.Length ~  Species, data = iris)
model.matrix(mod)[c(1, 51, 101), ]
```

```
##     (Intercept) Speciesversicolor Speciesvirginica
## 1             1                 0                0
## 51            1                 1                0
## 101           1                 0                1
```

But other several alternative exist; e.g.:

```
mod2 <- lm(Petal.Length ~  Species, data = iris, contrasts = list(Species = "contr.sum"))
model.matrix(mod2)[c(1, 51, 101), ]
```

```
##     (Intercept) Species1 Species2
## 1             1        1        0
## 51            1        0        1
## 101           1       -1       -1
```

The linear model: understanding the design matrix

It is most important to understand the design matrix because the interpretation of the parameters depend on it!

The design matrix depends on:

- your formula
- your data
- the contrasts (for qualitative variables)

By default, each category is compared to the first one:

```
mod <- lm(Petal.Length ~  Species, data = iris)
model.matrix(mod)[c(1, 51, 101), ]
```

```
##     (Intercept) Speciesversicolor Speciesvirginica
## 1             1                 0                0
## 51            1                 1                0
## 101           1                 0                1
```

But other several alternative exist; e.g.:

```
mod2 <- lm(Petal.Length ~  Species, data = iris, contrasts = list(Species = "contr.sum"))
model.matrix(mod2)[c(1, 51, 101), ]
```

```
##     (Intercept) Species1 Species2
## 1             1        1        0
## 51            1        0        1
## 101           1       -1       -1
```

Note 1: default contrats (`"contr.treatment"`) are easy to interpret!

The linear model: understanding the design matrix

It is most important to understand the design matrix because the interpretation of the parameters depend on it!

The design matrix depends on:

- your formula
- your data
- the contrasts (for qualitative variables)

By default, each category is compared to the first one:

```
mod <- lm(Petal.Length ~  Species, data = iris)
model.matrix(mod)[c(1, 51, 101), ]
```

```
##     (Intercept) Speciesversicolor Speciesvirginica
## 1             1                 0                0
## 51            1                 1                0
## 101           1                 0                1
```

But other several alternative exist; e.g.:

```
mod2 <- lm(Petal.Length ~  Species, data = iris, contrasts = list(Species = "contr.sum"))
model.matrix(mod2)[c(1, 51, 101), ]
```

```
##     (Intercept) Species1 Species2
## 1             1        1        0
## 51            1        0        1
## 101           1       -1       -1
```

Note 1: default contrats (`"contr.treatment"`) are easy to interpret!

Note 2: contrasts do not alter predicted values and thus likelihood, AIC...

The linear model: understanding the design matrix

Challenge: find out whether these different representations of gender are equivalent or not?

- `"boy"` vs `"girl"`
- `"male"` vs `"female"`
- 0 vs 1
- 1 vs 2
- `TRUE` vs `FALSE`

Note: no need to fit a model, use the function `model.matrix()` with a formula!

Getting started with R

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

Simply printing the object provides you with the parameter estimates:

```
mod
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width + Species, data = iris)
##
## Coefficients:
##       (Intercept)        Petal.Width  Speciesversicolor   Speciesvirginica
##             1.211              1.019              1.698              2.277
```

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

Simply printing the object provides you with the parameter estimates:

```
mod
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width + Species, data = iris)
##
## Coefficients:
##       (Intercept)        Petal.Width  Speciesversicolor   Speciesvirginica
##             1.211              1.019              1.698              2.277
```

If you need to work with them, use the specific extractor instead:

```
coefficients(mod) ## or coef(mod)
```

```
##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##          1.211397          1.018712          1.697791          2.276693
```

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

You can also easily extract the covariance matrix of the estimates:

```
vcov(mod)
```

```
##                    (Intercept)  Petal.Width Speciesversicolor Speciesvirginica
## (Intercept)        0.004256508 -0.005701674       0.003303912      0.007295083
## Petal.Width       -0.005701674  0.023177537      -0.025031740     -0.041256016
## Speciesversicolor  0.003303912 -0.025031740       0.032742072      0.047410394
## Speciesvirginica   0.007295083 -0.041256016       0.047410394      0.079143501
```

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

You can also easily extract the covariance matrix of the estimates:

```
vcov(mod)

##                    (Intercept)  Petal.Width Speciesversicolor Speciesvirginica
## (Intercept)        0.004256508 -0.005701674       0.003303912      0.007295083
## Petal.Width       -0.005701674  0.023177537      -0.025031740     -0.041256016
## Speciesversicolor  0.003303912 -0.025031740       0.032742072      0.047410394
## Speciesvirginica   0.007295083 -0.041256016       0.047410394      0.079143501
```

And thus the standard errors:

```
sqrt(diag(vcov(mod)))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##        0.06524192        0.15224171        0.18094771        0.28132455
```

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

You can also easily extract the covariance matrix of the estimates:

```
vcov(mod)

##                    (Intercept)  Petal.Width Speciesversicolor Speciesvirginica
## (Intercept)        0.004256508 -0.005701674       0.003303912      0.007295083
## Petal.Width       -0.005701674  0.023177537      -0.025031740     -0.041256016
## Speciesversicolor  0.003303912 -0.025031740       0.032742072      0.047410394
## Speciesvirginica   0.007295083 -0.041256016       0.047410394      0.079143501
```

And thus the standard errors:

```
sqrt(diag(vcov(mod)))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##        0.06524192        0.15224171        0.18094771        0.28132455
```

You can also get confidence intervals:

```
confint(mod)

##                       2.5 %   97.5 %
## (Intercept)       1.0824564 1.340338
## Petal.Width       0.7178294 1.319594
## Speciesversicolor 1.3401762 2.055407
## Speciesvirginica  1.7206988 2.832688
```

Parameter estimates

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
```

You can also easily extract the covariance matrix of the estimates:

```
vcov(mod)
```

```
##                    (Intercept)  Petal.Width Speciesversicolor Speciesvirginica
## (Intercept)         0.004256508 -0.005701674       0.003303912      0.007295083
## Petal.Width        -0.005701674  0.023177537      -0.025031740     -0.041256016
## Speciesversicolor   0.003303912 -0.025031740       0.032742072      0.047410394
## Speciesvirginica    0.007295083 -0.041256016       0.047410394      0.079143501
```

And thus the standard errors:

```
sqrt(diag(vcov(mod)))
```

```
##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##        0.06524192        0.15224171        0.18094771        0.28132455
```

You can also get confidence intervals:

```
confint(mod)
```

```
##                       2.5 %   97.5 %
## (Intercept)       1.0824564 1.340338
## Petal.Width       0.7178294 1.319594
## Speciesversicolor 1.3401762 2.055407
## Speciesvirginica  1.7206988 2.832688
```

Note: that reveals that there are much more information in the object `mod` than it is being printed!

The model object

The fitted model object is in fact a big list of class `"lm"`:

```
class(mod)
## [1] "lm"
typeof(mod)
## [1] "list"
names(mod)
##  [1] "coefficients"  "residuals"     "effects"       "rank"          "fitted.values" "assign"        "qr"
##  [8] "df.residual"   "contrasts"     "xlevels"       "call"          "terms"         "model"
```

So you can extract information from it; e.g.:

```
mod$df.residual
## [1] 146
```

but it is safer to use extractors if they are available!

Example of other outputs

There are quite a few extractors out there:

```
logLik(mod)

## 'log Lik.' -64.7851 (df=5)

AIC(mod)

## [1] 139.5702
```

Example of other outputs

There are quite a few extractors out there:

```
logLik(mod)

## 'log Lik.' -64.7851 (df=5)

AIC(mod)

## [1] 139.5702
```

Here is how you can get the list of S3 methods for the class `"lm"`:

```
methods(class = "lm")

##  [1] add1           alias          anova          case.names     coerce         confint        cooks.distance
##  [8] deviance       dfbeta         dfbetas        drop1          dummy.coef     effects        extractAIC
## [15] family         formula        hatvalues      influence      initialize     kappa          labels
## [22] logLik         model.frame    model.matrix   nobs           plot           predict        print
## [29] proj           qr             residuals      rstandard      rstudent       show           simulate
## [36] slotsFromS3    summary        variable.names vcov
## see '?methods' for accessing help and source code
```

Note: the list will change depending on the packages that are attached to the **R** session!

Getting started with **R**

Testing coefficients

For LM, simply use `summary()`:

```
summary(mod)
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width + Species, data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.02977 -0.22241 -0.01514  0.18180  1.17449
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        1.21140    0.06524  18.568  < 2e-16 ***
## Petal.Width        1.01871    0.15224   6.691 4.41e-10 ***
## Speciesversicolor  1.69779    0.18095   9.383  < 2e-16 ***
## Speciesvirginica   2.27669    0.28132   8.093 2.08e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3777 on 146 degrees of freedom
## Multiple R-squared:  0.9551,Adjusted R-squared:  0.9542
## F-statistic:  1036 on 3 and 146 DF,  p-value: < 2.2e-16
```

Testing predictors

Don't use the default `anova()` function which perform type-I analysis-of-variance:

```
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Petal.Length
##               Df Sum Sq Mean Sq  F value    Pr(>F)
## Petal.Width    1 430.48  430.48 3016.792 < 2.2e-16 ***
## Species        2  13.01    6.51   45.591 4.137e-16 ***
## Residuals    146  20.83    0.14
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Instead use the better function `Anova()` from the package `car` which perfroms type-II analysis-of-variance:

```
library(car)
Anova(mod)
```

```
## Anova Table (Type II tests)
##
## Response: Petal.Length
##               Sum Sq  Df F value    Pr(>F)
## Petal.Width   6.3892   1  44.775 4.409e-10 ***
## Species      13.0113   2  45.591 4.137e-16 ***
## Residuals    20.8334 146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Testing predictors

Don't use the default `anova()` function which perform type-I analysis-of-variance:

```
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Petal.Length
##              Df Sum Sq Mean Sq  F value    Pr(>F)
## Petal.Width   1 430.48  430.48 3016.792 < 2.2e-16 ***
## Species       2  13.01    6.51   45.591 4.137e-16 ***
## Residuals   146  20.83    0.14
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Instead use the better function `Anova()` from the package `car` which perfroms type-II analysis-of-variance:

```
library(car)
Anova(mod)
```

```
## Anova Table (Type II tests)
##
## Response: Petal.Length
##              Sum Sq  Df F value    Pr(>F)
## Petal.Width  6.3892   1  44.775 4.409e-10 ***
## Species     13.0113   2  45.591 4.137e-16 ***
## Residuals   20.8334 146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note: p-values are the same no matter the order of the predictors in the formula for type-II (but not for type-I!).

Testing the overall model

Before looking at significance for estimates or predictor, always start by checking that your model fits the data better than a null model:

```
mod <- lm(Petal.Length ~  Petal.Width + Species, data = iris)
mod_null <-  lm(Petal.Length ~  1, data = iris)
anova(mod, mod_null)
```

```
## Analysis of Variance Table
##
## Model 1: Petal.Length ~ Petal.Width + Species
## Model 2: Petal.Length ~ 1
##   Res.Df    RSS Df Sum of Sq    F    Pr(>F)
## 1    146  20.83
## 2    149 464.33 -3   -443.49 1036 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note 1: this was also given at the bottom of the summary table!

Note 2: here using `anova()` is perfectly fine!

Getting started with **R**

Fitted values

You can easily obtain the prediction for your observation (i.e. fitted values):

```
fitted(mod)[1:39]
```

```
##        1        2        3        4        5        6        7        8        9       10       11       12       13
## 1.415139 1.415139 1.415139 1.415139 1.415139 1.618882 1.517010 1.415139 1.415139 1.313268 1.415139 1.415139 1.313268
##       14       15       16       17       18       19       20       21       22       23       24       25       26
## 1.313268 1.415139 1.618882 1.618882 1.517010 1.517010 1.517010 1.415139 1.618882 1.415139 1.720753 1.415139 1.415139
##       27       28       29       30       31       32       33       34       35       36       37       38       39
## 1.618882 1.415139 1.415139 1.415139 1.415139 1.618882 1.313268 1.415139 1.415139 1.415139 1.415139 1.313268 1.415139
```

Fitted values

You can easily obtain the prediction for your observation (i.e. fitted values):

```
fitted(mod)[1:39]
```

```
##        1        2        3        4        5        6        7        8        9       10       11       12       13
## 1.415139 1.415139 1.415139 1.415139 1.415139 1.618882 1.517010 1.415139 1.415139 1.313268 1.415139 1.415139 1.313268
##       14       15       16       17       18       19       20       21       22       23       24       25       26
## 1.313268 1.415139 1.618882 1.618882 1.517010 1.517010 1.517010 1.415139 1.618882 1.415139 1.720753 1.415139 1.415139
##       27       28       29       30       31       32       33       34       35       36       37       38       39
## 1.618882 1.415139 1.415139 1.415139 1.415139 1.618882 1.313268 1.415139 1.415139 1.415139 1.415139 1.313268 1.415139
```

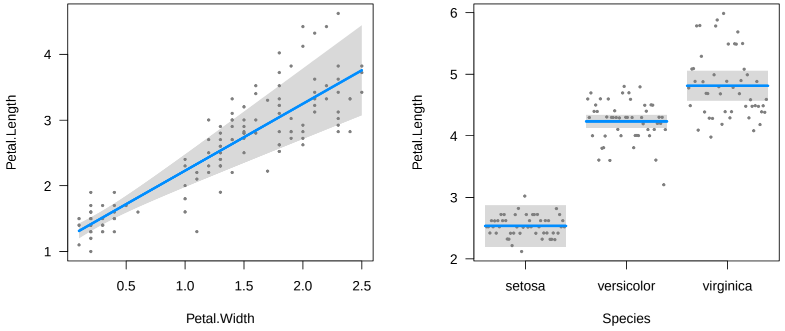
As expected, observations are equal to the fitted values + residuals:

```
head(cbind("response" = model.response(model.frame(mod)),
           "fitted" = fitted(mod),
           "resid" = residuals(mod),
           "fitted + resid" = fitted(mod) + residuals(mod)))
```

```
##   response   fitted       resid fitted + resid
## 1      1.4 1.415139 -0.01513927            1.4
## 2      1.4 1.415139 -0.01513927            1.4
## 3      1.3 1.415139 -0.11513927            1.3
## 4      1.5 1.415139  0.08486073            1.5
## 5      1.4 1.415139 -0.01513927            1.4
## 6      1.7 1.618882  0.08111841            1.7
```

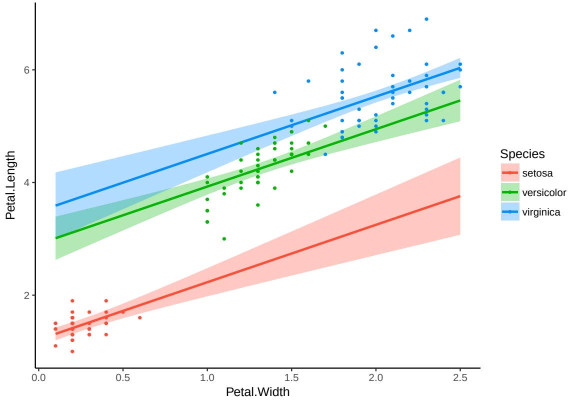
Plotting predictions: fast & dirty

```r
library(visreg)
par(mfrow = c(1, 2))
visreg(mod)
```



Plotting predictions: fast & less dirty

```r
library(visreg)
library(ggplot2)
visreg(fit = mod, xvar = "Petal.Width", by = "Species", overlay = TRUE, gg = TRUE) +
  theme_classic()
```



Note: if you have different quantitative predictors you can specify the value for the non focal predictor using the argument "cond".

Prediction by "hand"

The most difficult step is to create the data frame defining the predictor values:

```
library(dplyr)
data_for_predictions <- iris %>%
                            group_by(Species) %>%
                            do(data.frame(Petal.Width = seq(min(.$Petal.Width), max(.$Petal.Width), length.out = 30))) %>%
                            data.frame()
```

```
head(data_for_predictions)

##   Species Petal.Width
## 1  setosa   0.1000000
## 2  setosa   0.1172414
## 3  setosa   0.1344828
## 4  setosa   0.1517241
## 5  setosa   0.1689655
## 6  setosa   0.1862069
```

```
tail(data_for_predictions)

##      Species Petal.Width
## 85 virginica    2.310345
## 86 virginica    2.348276
## 87 virginica    2.386207
## 88 virginica    2.424138
## 89 virginica    2.462069
## 90 virginica    2.500000
```

Prediction by “hand”

The most difficult step is to create the data frame defining the predictor values:

```
library(dplyr)
data_for_predictions <- iris %>%
                            group_by(Species) %>%
                            do(data.frame(Petal.Width = seq(min(.$Petal.Width), max(.$Petal.Width), length.out = 30))) %>%
                            data.frame()
```

```
head(data_for_predictions)

##   Species Petal.Width
## 1  setosa   0.1000000
## 2  setosa   0.1172414
## 3  setosa   0.1344828
## 4  setosa   0.1517241
## 5  setosa   0.1689655
## 6  setosa   0.1862069
```

```
tail(data_for_predictions)

##      Species Petal.Width
## 85 virginica    2.310345
## 86 virginica    2.348276
## 87 virginica    2.386207
## 88 virginica    2.424138
## 89 virginica    2.462069
## 90 virginica    2.500000
```

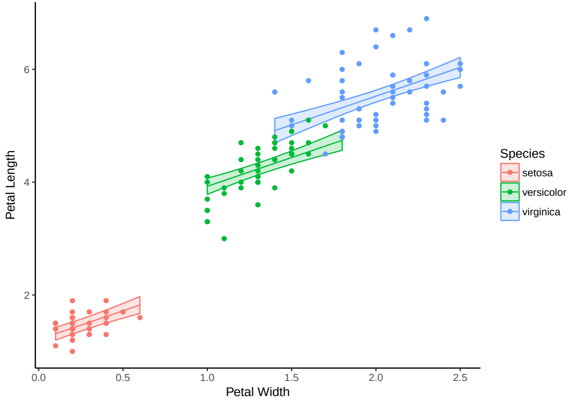
Then, it is easy:

```
pred_mod <- predict(object = mod, newdata = data_for_predictions, interval = "confidence") ## prediction intervals are also possible!
head(pred_mod)

##        fit      lwr      upr
## 1 1.313268 1.198914 1.427622
## 2 1.330832 1.218369 1.443296
## 3 1.348396 1.237613 1.459180
## 4 1.365960 1.256636 1.475284
## 5 1.383524 1.275430 1.491618
## 6 1.401088 1.293986 1.508190
```

Prediction by “hand”

```r
data_for_plot <- cbind(pred_mod, data_for_predictions)
ggplot(data = data_for_plot, mapping = aes(x = Petal.Width, y = fit, colour = Species)) +
  geom_line() +
  geom_ribbon(mapping = aes(ymin = lwr, ymax = upr, fill = Species), alpha = 0.2) +
  geom_point(data = iris, mapping = aes(y = Petal.Length, x = Petal.Width, colour = Species)) +
  labs(x = "Petal Width", y = "Petal Length") +
  theme_classic()
```



Getting started with **R**

Assumptions behind linear models

Model structure:

- linearity
- lack of perfect multicollinearity (design matrix of full rank)
- predictor variables have fixed values

Assumptions behind linear models

Model structure:

- linearity
- lack of perfect multicollinearity (design matrix of full rank)
- predictor variables have fixed values

Errors:

- independence (no serial autocorrelation)
- constant variance (homoscedasticity)
- normality

Assumptions: linearity

Departure from linearity can originate from a multitude of reasons and can create all kinds of problems.

Assumptions: linearity

Departure from linearity can originate from a multitude of reasons and can create all kinds of problems.

Diagnostics:

- thinking
- other assumptions violated

Assumptions: linearity

Departure from linearity can originate from a multitude of reasons and can create all kinds of problems.

Diagnostics:

- thinking
- other assumptions violated

Solutions:

- different model structure → change the formula
- transform one or several predictors (e.g. polynomials) → function `poly()`
- transform the response (e.g. log and power transformation) → function `powerTransform()` in car (see later)

Assumptions: linearity

Departure from linearity can originate from a multitude of reasons and can create all kinds of problems.

Diagnostics:

- thinking
- other assumptions violated

Solutions:

- different model structure → change the formula
- transform one or several predictors (e.g. polynomials) → function `poly()`
- transform the response (e.g. log and power transformation) → function `powerTransform()` in `car` (see later)

Alternatives:

- non-linear models → function `nls` or dedicated package (e.g. `nlme`)
- general additive models → package `mgcv`

Assumptions: linearity

Departure from linearity can originate from a multitude of reasons and can create all kinds of problems.

Diagnostics:

- thinking
- other assumptions violated

Solutions:

- different model structure $\rightarrow$ change the formula
- transform one or several predictors (e.g. polynomials) $\rightarrow$ function `poly()`
- transform the response (e.g. log and power transformation) $\rightarrow$ function `powerTransform()` in `car` (see later)

Alternatives:

- non-linear models $\rightarrow$ function `nls` or dedicated package (e.g. `nlme`)
- general additive models $\rightarrow$ package `mgcv`

Quiz: can you express the following models as LM?

- $y_i = \hat{\alpha} + \varepsilon_i$
- $y_i = x_i^{\hat{\beta}} + \varepsilon_i$
- $y_i = \hat{\alpha} + \hat{\beta}_1 x_i + \hat{\beta}_2 x_i^2 + \hat{\beta}_3 x_i^3 + \varepsilon_i$

Assumptions: lack of perfect multicollinearity

The number of parameters to be estimated must be equal to the rank of the design matrix.

Caused by having less data than parameters or when there is linear dependence between the column vectors of the design matrix. In such case, some parameters cannot be computed.

Assumptions: lack of perfect multicollinearity

The number of parameters to be estimated must be equal to the rank of the design matrix.

Caused by having less data than parameters or when there is linear dependence between the column vectors of the design matrix. In such case, some parameters cannot be computed.

Diagnostics:

- plot the predictors against each other $\rightarrow$ function `pairs()`
- `findLinearCombos` from the package `caret`

Assumptions: lack of perfect multicollinearity

The number of parameters to be estimated must be equal to the rank of the design matrix.

Caused by having less data than parameters or when there is linear dependence between the column vectors of the design matrix. In such case, some parameters cannot be computed.

Diagnostics:

- plot the predictors against each other $\rightarrow$ function `pairs()`
- `findLinearCombos` from the package `caret`

Solutions:

- change design matrix (change parameterization or drop redundant effects) $\rightarrow$ argument `formula`
- change the experimental design
- collect more data

Assumptions: lack of perfect multicollinearity

The number of parameters to be estimated must be equal to the rank of the design matrix.

Caused by having less data than parameters or when there is linear dependence between the column vectors of the design matrix. In such case, some parameters cannot be computed.

Diagnostics:

- plot the predictors against each other $\rightarrow$ function `pairs()`
- `findLinearCombos` from the package `caret`

Solutions:

- change design matrix (change parameterization or drop redundant effects) $\rightarrow$ argument `formula`
- change the experimental design
- collect more data

Alternatives:

- none

Assumptions: lack of perfect multicollinearity

The number of parameters to be estimated must be equal to the rank of the design matrix.

Caused by having less data than parameters or when there is linear dependence between the column vectors of the design matrix. In such case, some parameters cannot be computed.

Diagnostics:

- plot the predictors against each other → function `pairs()`
- `findLinearCombos` from the package `caret`

Solutions:

- change design matrix (change parameterization or drop redundant effects) → argument `formula`
- change the experimental design
- collect more data

Alternatives:

- none

Note: strong albeit imperfect collinearity is not great either; possible check correlation between estimates (→ `cov2cor(vcov(mod))`) and variance inflation factors (→ `vif(mod)`).

Assumptions: predictor variables have fixed values

The dependent variable are represented by fixed values.

The presence of measurement errors is the main cause of violation. Violation can trigger both estimates and tests to be biased.

Assumptions: predictor variables have fixed values

The dependent variable are represented by fixed values.

The presence of measurement errors is the main cause of violation. Violation can trigger both estimates and tests to be biased.

Diagnostics:

- thinking & replication

Assumptions: predictor variables have fixed values

The dependent variable are represented by fixed values.

The presence of measurement errors is the main cause of violation. Violation can trigger both estimates and tests to be biased.

Diagnostics:

- thinking & replication

Solutions:

- often ignored in practice
- better measurements

Assumptions: predictor variables have fixed values

The dependent variable are represented by fixed values.

The presence of measurement errors is the main cause of violation. Violation can trigger both estimates and tests to be biased.

Diagnostics:

- thinking & replication

Solutions:

- often ignored in practice
- better measurements

Alternatives:

- multipurpose numerical approaches → function `optim()` or dedicated packages (e.g. `nloptr`, `rjags`, `nimble`, `rstan`)
- errors-in-variables models → not much directly but any procedure allowing for latent variables can handle that; packages (e.g. `sem`, `lavaan`, `OpenMX`)
- reduced major axis regression → dedicated packages (e.g. `lmodel2`)

Assumptions: independence (no serial autocorrelation)

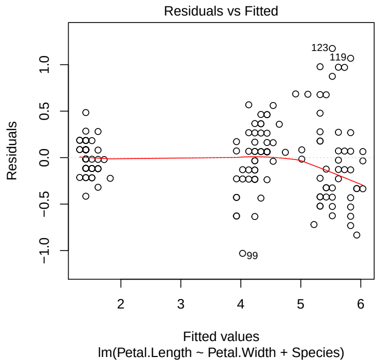
A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack of independence increases the risk of false positive (sometimes a lot).

Assumptions: independence (no serial autocorrelation)

A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack of independence increases the risk of false positive (sometimes a lot).

Diagnostic by eye:

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



Assumptions: independence (no serial autocorrelation)

A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack of independence increases the risk of false positive (sometimes a lot).

Diagnostic by Durbin-Watson test:

```
durbinWatsonTest(mod) ## from package car (DW varies between 0 & 4, 2 is best, you wish for non-significant p-value)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1       0.1313867      1.734855    0.08
##  Alternative hypothesis: rho != 0
```

Note: the alternative from the package `lmtest` offer to rank the residuals according to a variable.

Assumptions: independence (no serial autocorrelation)

A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack of independence increases the risk of false positive (sometimes a lot).

Diagnostic by Durbin-Watson test:

```
durbinWatsonTest(mod) ## from package car (DW varies between 0 & 4, 2 is best, you wish for non-significant p-value)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1       0.1313867      1.734855    0.08
##  Alternative hypothesis: rho != 0
```

Note: the alternative from the package `lmtest` offer to rank the residuals according to a variable.

Solutions:

- transformation or different model structure (see linearity)
- aggregation or sub-sampling

Assumptions: independence (no serial autocorrelation)

A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack of independence increases the risk of false positive (sometimes a lot).

Diagnostic by Durbin-Watson test:

```
durbinWatsonTest(mod) ## from package car (DW varies between 0 & 4, 2 is best, you wish for non-significant p-value)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1       0.1313867      1.734855    0.08
##  Alternative hypothesis: rho != 0
```

Note: the alternative from the package `lmtest` offer to rank the residuals according to a variable.

Solutions:

- transformation or different model structure (see linearity)
- aggregation or sub-sampling

Alternatives:

- general additive models (GAM and GAMM) $\rightarrow$ dedicated package `mgcv`
- mixed models (LMM and GLMM) $\rightarrow$ dedicated packages (e.g. `spaMM`, `lme4`)

Assumptions: constant variance (homoscedasticity)

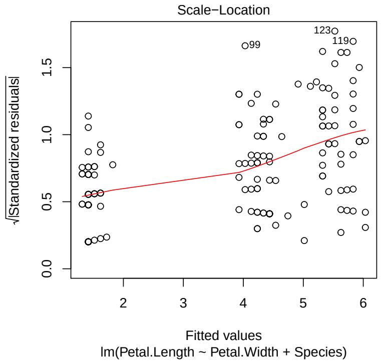
Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes acording to the treatement. It can create both false positives and false negative.

Assumptions: constant variance (homoscedasticity)

Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes acording to the treatement. It can create both false positives and false negative.

Diagnostic by eye:

```
plot(mod, which = 3)
```



Assumptions: constant variance (homoscedasticity)

Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes acording to the treatement. It can create both false positives and false negative.

Diagnostic by Breusch-Pagan test:

```
library(lmtest)
bptest(mod)  ## BP = df is best, you wish for non-significant p-value
```

```
##
##  studentized Breusch-Pagan test
##
## data:  mod
## BP = 28.571, df = 3, p-value = 2.755e-06
```

Assumptions: constant variance (homoscedasticity)

Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes acording to the treatement. It can create both false positives and false negative.

Diagnostic by Breusch-Pagan test:

```
library(lmtest)
bptest(mod)  ## BP = df is best, you wish for non-significant p-value
```

```
##
##  studentized Breusch-Pagan test
##
## data:  mod
## BP = 28.571, df = 3, p-value = 2.755e-06
```

Solutions: modeling the heteroscedasticity

```
library(spaMM)
mod_heter_spaMM <- fitme(Petal.Length ~  Petal.Width + Species,
                         resid.model = ~ Species,
                         data = iris)
AIC(mod)
```

```
## [1] 139.5702
```

```
print(AIC(mod_heter_spaMM)) ## much better fit!
```

```
##        marginal AIC:
##             87.84896
```

Assumptions: constant variance (homoscedasticity)

Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes acording to the treatement. It can create both false positives and false negative.

Diagnostic by Breusch-Pagan test:

```
library(lmtest)
bptest(mod)  ## BP = df is best, you wish for non-significant p-value
```

```
##
##  studentized Breusch-Pagan test
##
## data:  mod
## BP = 28.571, df = 3, p-value = 2.755e-06
```

Solutions: modeling the heteroscedasticity

```
library(spaMM)
mod_heter_spaMM <- fitme(Petal.Length ~  Petal.Width + Species,
                         resid.model = ~ Species,
                         data = iris)
AIC(mod)
```

```
## [1] 139.5702
```

```
print(AIC(mod_heter_spaMM)) ## much better fit!
```

```
##        marginal AIC:
##            87.84896
```

Alternatives:

- GLM (if stemming from an expected relationship between mean and variance) → function `glm`

Assumptions: normality

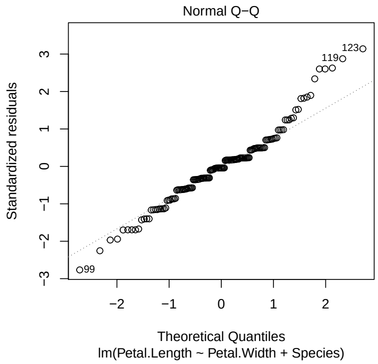
The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

Assumptions: normality

The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

Diagnostic by eye:

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



Assumptions: normality

The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

Diagnostic by test (many test are possible):

```
shapiro.test(mod$residuals)  ## stat = 1 when normal, you wish for non-significant p-value
```

```
##
##  Shapiro-Wilk normality test
##
## data:  mod$residuals
## W = 0.96925, p-value = 0.001924
```

Assumptions: normality

The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

Diagnostic by test (many test are possible):

```
shapiro.test(mod$residuals)  ## stat = 1 when normal, you wish for non-significant p-value
##
##  Shapiro-Wilk normality test
##
## data:  mod$residuals
## W = 0.96925, p-value = 0.001924
```

Solutions:

- transformation or different model structure (see linearity)
- taking outliers out (mindfully!)

Assumptions: normality

The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

Diagnostic by test (many test are possible):

```
shapiro.test(mod$residuals)  ## stat = 1 when normal, you wish for non-significant p-value
##
##  Shapiro-Wilk normality test
##
## data:  mod$residuals
## W = 0.96925, p-value = 0.001924
```

Solutions:

- transformation or different model structure (see linearity)
- taking outliers out (mindfully!)

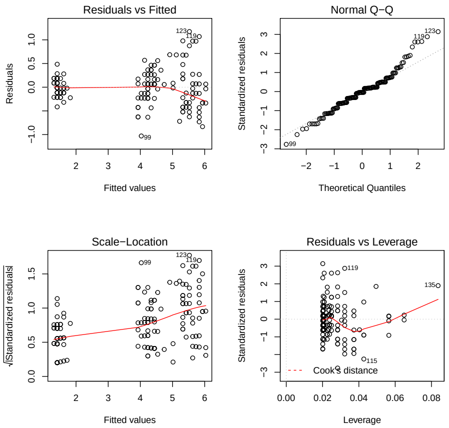
Alternatives:

- GLM (if stemming from the data generating process) $\rightarrow$ function `glm`

Assumptions: simple glimpse

You can check all assumptions about the erros at once:

```r
par(mfrow = c(2, 2))
plot(mod)
```



Assumptions: outliers

There is a powerful function in **R**:

```
influence.measures(mod)
```

```
## Influence measures of
##   lm(formula = Petal.Length ~ Petal.Width + Species, data = iris) :
##
##         dfb.1_  dfb.Pt.W dfb.Spcsvrs dfb.Spcsvrg    dffit cov.r   cook.d    hat inf
## 1   -0.005155  0.000756     0.00102    0.000367 -0.00582 1.049 8.51e-06 0.0203
## 2   -0.005155  0.000756     0.00102    0.000367 -0.00582 1.049 8.51e-06 0.0203
## 3   -0.039218  0.005750     0.00773    0.002791 -0.04424 1.046 4.92e-04 0.0203
## 4    0.028900 -0.004237    -0.00569   -0.002056  0.03260 1.048 2.67e-04 0.0203
## 5   -0.005155  0.000756     0.00102    0.000367 -0.00582 1.049 8.51e-06 0.0203
## 6    0.017579  0.013609    -0.02152   -0.018998  0.03386 1.052 2.89e-04 0.0239
## 7   -0.032568 -0.006861     0.01940    0.015075 -0.04511 1.047 5.12e-04 0.0205
## 8    0.028900 -0.004237    -0.00569   -0.002056  0.03260 1.048 2.67e-04 0.0203
## 9   -0.005155  0.000756     0.00102    0.000367 -0.00582 1.049 8.51e-06 0.0203
## 10   0.075521 -0.029709     0.00591    0.015059  0.07734 1.045 1.50e-03 0.0235
## 11   0.028900 -0.004237    -0.00569   -0.002056  0.03260 1.048 2.67e-04 0.0203
## 12   0.062998 -0.009237    -0.01241   -0.004483  0.07106 1.042 1.27e-03 0.0203
## 13   0.035054 -0.013790     0.00275    0.006990  0.03590 1.051 3.24e-04 0.0235
## 14  -0.086276  0.033940    -0.00676   -0.017203 -0.08835 1.043 1.96e-03 0.0235
## 15  -0.073339  0.010753     0.01445    0.005218 -0.08273 1.040 1.72e-03 0.0203
## 16  -0.025768 -0.019948     0.03155    0.027847 -0.04964 1.050 6.20e-04 0.0239
## 17  -0.069267 -0.053624     0.08480    0.074856 -0.13343 1.032 4.46e-03 0.0239
## 18  -0.032568 -0.006861     0.01940    0.015075 -0.04511 1.047 5.12e-04 0.0205
## 19   0.050956  0.010735    -0.03035   -0.023587  0.07058 1.042 1.25e-03 0.0205
## 20  -0.004733 -0.000997     0.00282    0.002191 -0.00656 1.049 1.08e-05 0.0205
## 21   0.097189 -0.014250    -0.01914   -0.006916  0.10963 1.033 3.01e-03 0.0203
## 22  -0.025768 -0.019948     0.03155    0.027847 -0.04964 1.050 6.20e-04 0.0239
## 23  -0.141957  0.020814     0.02796    0.010101 -0.16013 1.014 6.40e-03 0.0203
## 24  -0.003221 -0.005781     0.00761    0.007085 -0.00986 1.060 2.45e-05 0.0305
## 25   0.166055 -0.024347    -0.03271   -0.011816  0.18732 1.002 8.73e-03 0.0203
## 26   0.062998 -0.009237    -0.01241   -0.004483  0.07106 1.042 1.27e-03 0.0203
## 27   0.004091  0.003167     0.00501    0.004421  0.00788 1.053 1.56e-05 0.0239
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` → extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` → extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` → extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` → extent to which the estimate for `virginica` changes if a given observation is dropped

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

```
abbreviate(stats:::variable.names.lm(mod))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##            "(In)"            "Pt.W"         "Spcsvrs"          "Spcsvrg"
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` → extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` → extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` → extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` → extent to which the estimate for `virginica` changes if a given observation is dropped
- `dffit` → extent to which the predicted y-values changes if a given observation is dropped (scaled by the standard deviation of the fit at the point)

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

```
abbreviate(stats:::variable.names.lm(mod))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##            "(In)"            "Pt.W"         "Spcsvrs"         "Spcsvrg"
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` $\rightarrow$ extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` $\rightarrow$ extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` $\rightarrow$ extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` $\rightarrow$ extent to which the estimate for `virginica` changes if a given observation is dropped
- `dffit` $\rightarrow$ extent to which the predicted y-values changes if a given observation is dropped (scaled by the standard deviation of the fit at the point)
- `cov.r` $\rightarrow$ extent to which the covariance matrix of parameter estimates changes if a given observation is dropped

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

```
abbreviate(stats:::variable.names.lm(mod))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##            "(In)"            "Pt.W"         "Spcsvrs"          "Spcsvrg"
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` → extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` → extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` → extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` → extent to which the estimate for `virginica` changes if a given observation is dropped
- `dffit` → extent to which the predicted y-values changes if a given observation is dropped (scaled by the standard deviation of the fit at the point)
- `cov.r` → extent to which the covariance matrix of parameter estimates changes if a given observation is dropped
- `cook.d` → F statistics comparing simultaneously the changes in all estimates when the observation is dropped or not

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

```
abbreviate(stats:::variable.names.lm(mod))

##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##            "(In)"            "Pt.W"         "Spcsvrs"         "Spcsvrg"
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` $\rightarrow$ extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` $\rightarrow$ extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` $\rightarrow$ extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` $\rightarrow$ extent to which the estimate for `virginica` changes if a given observation is dropped
- `dffit` $\rightarrow$ extent to which the predicted y-values changes if a given observation is dropped (scaled by the standard deviation of the fit at the point)
- `cov.r` $\rightarrow$ extent to which the covariance matrix of parameter estimates changes if a given observation is dropped
- `cook.d` $\rightarrow$ F statistics comparing simultaneously the changes in all estimates when the observation is dropped or not
- `hat` $\rightarrow$ diagonal element of the hat matrix (the hat values); extent to which an observation is unusual in terms of X values (leverage)

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

```
abbreviate(stats:::variable.names.lm(mod))
```

```
##       (Intercept)       Petal.Width Speciesversicolor  Speciesvirginica
##            "(In)"            "Pt.W"         "Spcsvrs"          "Spcsvrg"
```

Assumptions: outliers

Interpretation of the output from `influence.measures(mod)`:

- `dfb.1_` → extent to which the intercept changes if a given observation is dropped
- `dfb.Pt.W` → extent to which the slope for `Petal.Width` changes if a given observation is dropped
- `dfb.Spcsvrs` → extent to which the estimate for `versicolor` changes if a given observation is dropped
- `dfb.Spcsvrg` → extent to which the estimate for `virginica` changes if a given observation is dropped
- `dffit` → extent to which the predicted y-values changes if a given observation is dropped (scaled by the standard deviation of the fit at the point)
- `cov.r` → extent to which the covariance matrix of parameter estimates changes if a given observation is dropped
- `cook.d` → *F* statistics comparing simultaneously the changes in all estimates when the observation is dropped or not
- `hat` → diagonal element of the hat matrix (the hat values); extent to which an observation is unusual in terms of X values (leverage)
- `inf` → some overal add hoc receipe to spot influential observation (not to be taken too seriously)

Note: for the df-betas, the name would change for another model as they use the abbreviated name of the estimates:

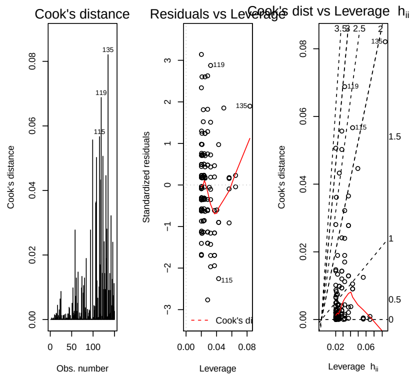
```
abbreviate(stats:::variable.names.lm(mod))

##        (Intercept)        Petal.Width Speciesversicolor  Speciesvirginica
##             "(In)"             "Pt.W"         "Spcsvrs"          "Spcsvrg"
```

Assumptions: outliers

There are also plotting possibilitites:

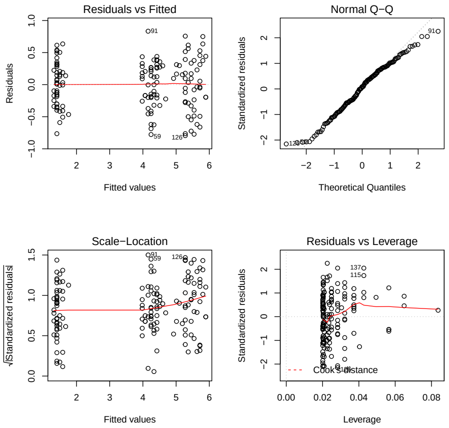
```r
par(mfrow = c(1, 3))
plot(mod, which = 4:6)
```



Assumptions: simple glimpse at residuals

What would it look like if it was perfect?

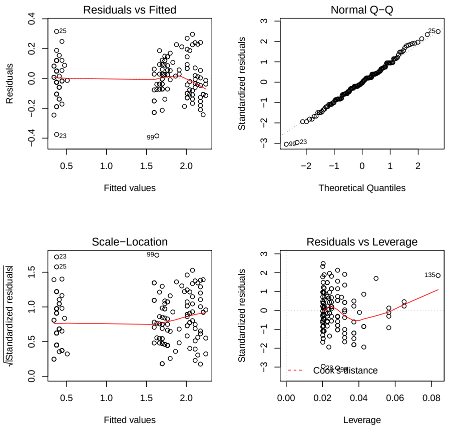
```r
iris$Fake.Petal.Length <- simulate(object = mod)[, 1]  ## redo it, it will change each time!
mod_perfect <- lm(Fake.Petal.Length ~  Petal.Width + Species, data = iris)
par(mfrow = c(2, 2))
plot(mod_perfect)
```



Assumptions: fixing iris

Fixing attempt:

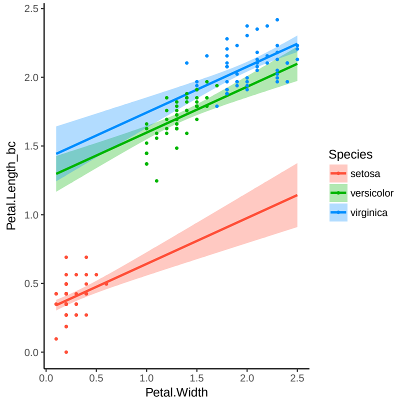
```
bc <- powerTransform(mod)
iris$Petal.Length_bc <- bcPower(iris$Petal.Length, lambda = bc$lambda)
mod_bc <- lm(Petal.Length_bc ~ Petal.Width + Species, data = iris)
par(mfrow = c(2, 2))
plot(mod_bc)
```



Assumptions: fixing iris

Plotting predictions:

```
visreg(fit = mod_bc, xvar = "Petal.Width", by = "Species", overlay = TRUE, gg = TRUE) +
  theme_classic()
```

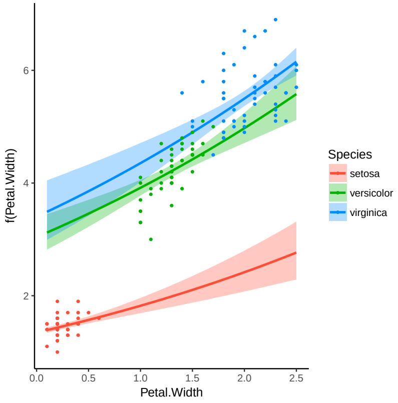


Note: that is not very useful because it is on the BoxCoxed scale!

Assumptions: fixing iris

Plotting predictions:

```
visreg(fit = mod_bc, xvar = "Petal.Width", by = "Species", overlay = TRUE, gg = TRUE,
       trans = function(x) bcnPowerInverse(x, lambda = bc$lambda, gamma = 0), partial = TRUE) +
  theme_classic()
```



Note: that is not very useful because it is on the BoxCoxed scale!

Getting started with **R**

Getting started with **R**

The generalised linear model: what for?

GLM are used for fitting data generating processes for which a relationship between mean and variance is expected.

The generalised linear model: what for?

GLM are used for fitting data generating processes for which a relationship between mean and variance is expected.

That includes the analysis of:

- binary events (probabilities)
- binomial events (probabilities)
- Poisson processes (counts)
- negative binomail processes (counts)
- variances (positive continuous)

The generalised linear model: specifications

Definition:

$$\mathrm{Y} = g^{-1}(\widehat{\eta}) + \varepsilon = g^{-1}(\mathrm{X}\widehat{\beta}) + \varepsilon$$

with:

- $\hat{\eta}_i = \hat{\beta}_0 + \hat{\beta}_1 \times x_{1,i} + \hat{\beta}_2 \times x_{2,i} + \cdots + \hat{\beta}_p \times x_{p,i}$
- $\mathrm{E(Y)} = \mu = g^{-1}(\eta)$
- $\mathrm{Var(Y)} = \phi \mathrm{V}(\mu)$

Notation:

- η the linear predictor
- g the link function (g^{-1} is sometimes called the mean function)
- V the variance function
- ϕ is the dispersion parameter

The generalised linear model: specifications

Definition:

$$Y = g^{-1}(\widehat{\eta}) + \varepsilon = g^{-1}(X\widehat{\beta}) + \varepsilon$$

with:

- $\hat{\eta}_i = \hat{\beta}_0 + \hat{\beta}_1 \times x_{1,i} + \hat{\beta}_2 \times x_{2,i} + \cdots + \hat{\beta}_p \times x_{p,i}$
- $E(Y) = \mu = g^{-1}(\eta)$
- $\text{Var}(Y) = \phi V(\mu)$

Notation:

- η the linear predictor
- g the link function (g^{-1} is sometimes called the mean function)
- V the variance function
- ϕ is the dispersion parameter

This is identical to the LM if:

- $\mu = g^{-1}(\eta) = \eta$, thus if g is the identity function
- $\phi = \sigma^2$, thus if the dispersion parameter equals the error variance
- $V(\mu) = 1$, thus if the variance function is constant

The generalised linear model: the Challenger dataset

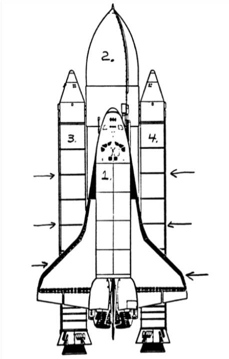


Figure 2. Space Shuttle: Orbiter, External Tank, Solid Rocket Motors, and Field Joints.

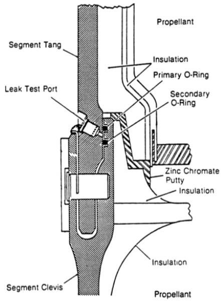


Figure 3. Solid Rocket Motor Cross Section: Tang, Clevis, and O-Rings.

through the gap between the tang and secondary O-ring and cause catastrophic failures. Following the occurrence of joint rotation, various NASA memos (PC1, p. 123) stated that design change was "mandatory to prevent hot

```
head(Challenger, n = 3L)
```

```
##   oring_tot oring_dt temp psi flight
## 1         6        0   66  50      1
## 2         6        1   70  50      2
## 3         6        0   69  50      3
```

Note: we will study both the probability that one oring fails (binary event) or that at least one oring fails (binomial event) as a function of the temperature.

The generalised linear model: the VonBort dataset

```
head(VonBort, n = 3L)

##   deaths year corps fisher
## 1      0 1875     G     no
## 2      0 1875     I     no
## 3      0 1875    II    yes
```

Note: we will compare the number of deaths caused by horse (or mule) kicks between the 14 corps of the Prussian army.

The generalised linear model: specifications

In **R** notation:

```r
Challenger$issue <- Challenger$oring_dt > 0

mod_challenger_binar <- glm(issue ~ temp, family = binomial(link = "logit"), data = Challenger)
```

The generalised linear model: specifications

In **R** notation:

```r
Challenger$issue <- Challenger$oring_dt > 0

mod_challenger_binar <- glm(issue ~ temp, family = binomial(link = "logit"), data = Challenger)
```

```r
Challenger$oring_ok <- Challenger$oring_tot - Challenger$oring_dt

mod_challenger_binom <- glm(cbind(oring_dt, oring_ok) ~ temp, family = binomial(link = "logit"), data = Challenger)
```

The generalised linear model: specifications

In **R** notation:

```
Challenger$issue <- Challenger$oring_dt > 0

mod_challenger_binar <- glm(issue ~ temp, family = binomial(link = "logit"), data = Challenger)
```

```
Challenger$oring_ok <- Challenger$oring_tot - Challenger$oring_dt

mod_challenger_binom <- glm(cbind(oring_dt, oring_ok) ~ temp, family = binomial(link = "logit"), data = Challenger)
```

```
mod_horsekick <- glm(deaths ~ corps, family = poisson(link = "log"), data = VonBort)
```

The generalised linear model: specifications

The `family` object contains all kinds of useful information required for the fitting procedure:

```
names(binomial(link = "logit"))
```

```
##  [1] "family"     "link"       "linkfun"    "linkinv"    "variance"   "dev.resids" "aic"        "mu.eta"
##  [9] "initialize" "validmu"    "valideta"   "simulate"
```

The generalised linear model: specifications

The `family` object contains all kinds of useful information required for the fitting procedure:

```
names(binomial(link = "logit"))

##  [1] "family"     "link"       "linkfun"    "linkinv"    "variance"   "dev.resids" "aic"        "mu.eta"
##  [9] "initialize" "validmu"    "valideta"   "simulate"
```

The link function:

```
probs <- seq(0.1, 0.9, by = 0.1)
logits <- binomial(link = "logit")$linkfun(mu = probs)
logits

## [1] -2.1972246 -1.3862944 -0.8472979 -0.4054651  0.0000000  0.4054651  0.8472979  1.3862944  2.1972246
```

The generalised linear model: specifications

The `family` object contains all kinds of useful information required for the fitting procedure:

```
names(binomial(link = "logit"))
## [1] "family"     "link"       "linkfun"    "linkinv"    "variance"   "dev.resids" "aic"        "mu.eta"
## [9] "initialize" "validmu"    "valideta"   "simulate"
```

The link function:

```
probs <- seq(0.1, 0.9, by = 0.1)
logits <- binomial(link = "logit")$linkfun(mu = probs)
logits
## [1] -2.1972246 -1.3862944 -0.8472979 -0.4054651  0.0000000  0.4054651  0.8472979  1.3862944  2.1972246
```

The inverse link function:

```
binomial(link = "logit")$linkinv(eta = logits)
## [1] 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
```

The generalised linear model: specifications

The `family` object contains all kinds of useful information required for the fitting procedure:

```
names(binomial(link = "logit"))

##  [1] "family"     "link"       "linkfun"    "linkinv"    "variance"   "dev.resids" "aic"        "mu.eta"
##  [9] "initialize" "validmu"    "valideta"   "simulate"
```

The link function:

```
probs <- seq(0.1, 0.9, by = 0.1)
logits <- binomial(link = "logit")$linkfun(mu = probs)
logits

## [1] -2.1972246 -1.3862944 -0.8472979 -0.4054651  0.0000000  0.4054651  0.8472979  1.3862944  2.1972246
```

The inverse link function:

```
binomial(link = "logit")$linkinv(eta = logits)

## [1] 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
```

The variance function:

```
binomial(link = "logit")$variance(mu = probs)

## [1] 0.09 0.16 0.21 0.24 0.25 0.24 0.21 0.16 0.09
```

The generalised linear model: specifications

The `family` object contains all kinds of useful information required for the fitting procedure:

```
names(binomial(link = "logit"))

##  [1] "family"     "link"       "linkfun"    "linkinv"    "variance"   "dev.resids" "aic"        "mu.eta"
##  [9] "initialize" "validmu"    "valideta"   "simulate"
```

The link function:

```
probs <- seq(0.1, 0.9, by = 0.1)
logits <- binomial(link = "logit")$linkfun(mu = probs)
logits

## [1] -2.1972246 -1.3862944 -0.8472979 -0.4054651  0.0000000  0.4054651  0.8472979  1.3862944  2.1972246
```

The inverse link function:

```
binomial(link = "logit")$linkinv(eta = logits)

## [1] 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
```

The variance function:

```
binomial(link = "logit")$variance(mu = probs)

## [1] 0.09 0.16 0.21 0.24 0.25 0.24 0.21 0.16 0.09
```

Note: you can use these functions to better understand GLM or when you need them to process some outputs.

Getting started with **R**

The outputs are similar to those from `lm` fits!

```
mod_challenger_binar
```

```
##
## Call:  glm(formula = issue ~ temp, family = binomial(link = "logit"),
##     data = Challenger)
##
## Coefficients:
## (Intercept)         temp
##     23.7750      -0.3667
##
## Degrees of Freedom: 22 Total (i.e. Null);  21 Residual
## Null Deviance:     26.4
## Residual Deviance: 14.43  AIC: 18.43
```

```
confint(mod_challenger_binar)
```

```
## Waiting for profiling to be done...
##                  2.5 %     97.5 %
## (Intercept)  7.2430347 58.1947978
## temp        -0.8772585 -0.1217173
```

The outputs are similar to those from `lm` fits!

```
mod_challenger_binom
```

```
##
## Call:  glm(formula = cbind(oring_dt, oring_ok) ~ temp, family = binomial(link = "logit"),
##     data = Challenger)
##
## Coefficients:
## (Intercept)         temp
##      8.8169      -0.1795
##
## Degrees of Freedom: 22 Total (i.e. Null);  21 Residual
## Null Deviance:     20.71
## Residual Deviance: 9.527  AIC: 24.87
```

```
confint(mod_challenger_binom)
```

```
## Waiting for profiling to be done...
##                   2.5 %      97.5 %
## (Intercept)  1.9549041 16.49138135
## temp        -0.3073739 -0.07257416
```

The outputs are similar to those from `lm` fits!

```
mod_horsekick
```

```
##
## Call:  glm(formula = deaths ~ corps, family = poisson(link = "log"),
##     data = VonBort)
##
## Coefficients:
## (Intercept)       corpsI      corpsII     corpsIII      corpsIV       corpsV      corpsVI     corpsVII    corpsVIII
##  -2.231e-01    4.072e-09   -2.877e-01   -2.877e-01   -6.931e-01   -3.747e-01    6.062e-02   -2.877e-01   -8.267e-01
##     corpsIX       corpsX      corpsXI     corpsXIV      corpsXV
##  -2.076e-01   -6.454e-02    4.463e-01    4.055e-01   -6.931e-01
##
## Degrees of Freedom: 279 Total (i.e. Null);  266 Residual
## Null Deviance:      323.2
## Residual Deviance: 297.1    AIC: 630.2
```

```
head(confint(mod_horsekick))
```

```
## Waiting for profiling to be done...
##                  2.5 %    97.5 %
## (Intercept) -0.7566949 0.2298300
## corpsI      -0.6999361 0.6999361
## corpsII     -1.0585453 0.4561131
## corpsIII    -1.0585453 0.4561131
## corpsIV     -1.5958865 0.1280845
## corpsV      -1.1704167 0.3841036
```

The outputs are similar to those from `lm` fits!

```
mod_horsekick

##
## Call:  glm(formula = deaths ~ corps, family = poisson(link = "log"),
##     data = VonBort)
##
## Coefficients:
## (Intercept)       corpsI      corpsII     corpsIII      corpsIV       corpsV      corpsVI     corpsVII    corpsVIII
##  -2.231e-01    4.072e-09   -2.877e-01   -2.877e-01   -6.931e-01   -3.747e-01    6.062e-02   -2.877e-01   -8.267e-01
##     corpsIX       corpsX      corpsXI     corpsXIV      corpsXV
##  -2.076e-01   -6.454e-02    4.463e-01    4.055e-01   -6.931e-01
##
## Degrees of Freedom: 279 Total (i.e. Null);  266 Residual
## Null Deviance:     323.2
## Residual Deviance: 297.1  AIC: 630.2

head(confint(mod_horsekick))

## Waiting for profiling to be done...
##                  2.5 %    97.5 %
## (Intercept) -0.7566949 0.2298300
## corpsI      -0.6999361 0.6999361
## corpsII     -1.0585453 0.4561131
## corpsIII    -1.0585453 0.4561131
## corpsIV     -1.5958865 0.1280845
## corpsV      -1.1704167 0.3841036
```

Note: but the interpretation of the parameters is very different since they are expressed on the scale of the linear predictor!!

Interpreting estimates

There is no general receipe, it all depends on the link function used. . .

Interpreting estimates

There is no general receipe, it all depends on the link function used. . .

- For logistic regressions (`link = "logit"`; not for all binomial models), use odd-ratios:

```
exp(coef(mod_challenger_binar)["temp"])
```

```
##      temp
## 0.6930169
```

```
1/exp(coef(mod_challenger_binar)["temp"])
```

```
##     temp
## 1.442966
```

Every decrease by one degree increases the odd of failure for at least one oring by 1.4 time!

```
exp(coef(mod_challenger_binom)["temp"])
```

```
##      temp
## 0.8356945
```

```
1/exp(coef(mod_challenger_binom)["temp"])
```

```
##    temp
## 1.19661
```

Every decrease by one degree increases the odd of failure for exactly one oring by 1.2 time!

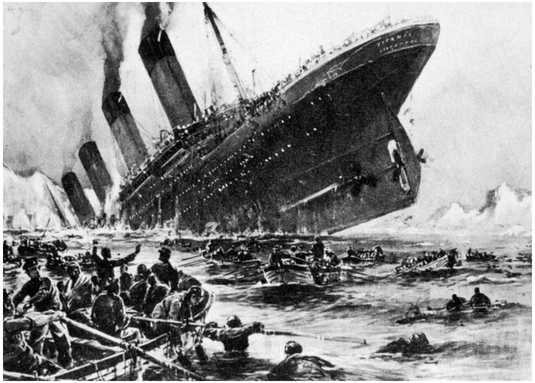
Getting started with **R**

Getting started with **R**

Getting started with **R**

The generalised linear model: challenge

Try to understand what influenced survival (i.e. access to lifeboats) during the Titanic disaster.



```
head(TitanicSurvival)
```

```
##                                 survived    sex     age passengerClass
## Allen, Miss. Elisabeth Walton        yes female 29.0000            1st
## Allison, Master. Hudson Trevor       yes   male  0.9167            1st
## Allison, Miss. Helen Loraine          no female  2.0000            1st
## Allison, Mr. Hudson Joshua Crei       no   male 30.0000            1st
## Allison, Mrs. Hudson J C (Bessi       no female 25.0000            1st
## Anderson, Mr. Harry                  yes   male 48.0000            1st
```

Getting started with **R**

Getting started with **R**

Getting started with **R**

Getting started with **R**

Getting started with **R**

Getting started with **R**

Getting started with **R**

Getting started with **R**