

Getting to do statistics in R

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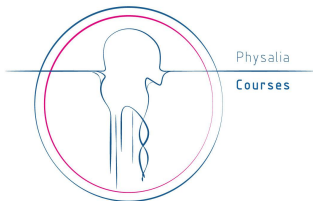
Leibniz Institute of Zoo and Wildlife Research

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**Leibniz Institute for Zoo
and Wildlife Research**

IN THE FORSCHUNGSVERBUND BERLIN E.V.



Getting started with R

- 1 Some basic tests
- 2 Principal Component Analysis
- 3 Linear Models
- 4 Generalised Linear Models
- 5 Other linear models

R provides many statistical tests out of the box

E.g. the usual correlation tests:

```
cor(x = iris$Sepal.Length, y = iris$Sepal.Width, method = "pearson")  
## [1] -0.1175698
```

R provides many statistical tests out of the box

E.g. the usual correlation tests:

```
cor(x = iris$Sepal.Length, y = iris$Sepal.Width, method = "pearson")  
## [1] -0.1175698
```

```
cor.test(x = iris$Sepal.Length, y = iris$Sepal.Width, method = "pearson")  
##  
## Pearson's product-moment correlation  
##  
## data: iris$Sepal.Length and iris$Sepal.Width  
## t = -1.4403, df = 148, p-value = 0.1519  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.27269325 0.04351158  
## sample estimates:  
## cor  
## -0.1175698
```

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E.g. the usual correlation tests:

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cor.test(x = iris$Sepal.Length, y = iris$Sepal.Width, method = "pearson")  
##  
## Pearson's product-moment correlation  
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## sample estimates:  
## cor  
## -0.1175698
```

Note: two other methods are available: “spearman” & “kendall”.

R provides many statistical tests out of the box

Many (not all) tests allow for the use of a formula-based syntax:

```
cor.test(formula = ~ Sepal.Length + Sepal.Width, data = iris)

##
## Pearson's product-moment correlation
##
## data: Sepal.Length and Sepal.Width
## t = -1.4403, df = 148, p-value = 0.1519
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.27269325 0.04351158
## sample estimates:
## cor
## -0.1175698
```

is synonymous to:

```
cor.test(x = iris$Sepal.Length, y = iris$Sepal.Width)

##
## Pearson's product-moment correlation
##
## data: iris$Sepal.Length and iris$Sepal.Width
## t = -1.4403, df = 148, p-value = 0.1519
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.27269325 0.04351158
## sample estimates:
## cor
## -0.1175698
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing two unpaired groups:

The *t*-test (parametric):

```
t.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
       y = iris$Sepal.Length[iris$Species == "setosa"])

##
## Welch Two Sample t-test
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Sepal.Length[iris$Species == "setosa"]
## t = 10.521, df = 86.538, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.7542926 1.1057074
## sample estimates:
## mean of x mean of y
##      5.936      5.006
```

R provides many statistical tests out of the box

E.g. test(s) for comparing two unpaired groups:

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```
t.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
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##
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## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Sepal.Length[iris$Species == "setosa"]
## t = 10.521, df = 86.538, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.7542926 1.1057074
## sample estimates:
## mean of x mean of y
##      5.936      5.006
```

The Mann-Whitney U test (non-parametric):

```
wilcox.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
            y = iris$Sepal.Length[iris$Species == "setosa"])

##
##  Wilcoxon rank sum test with continuity correction
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Sepal.Length[iris$Species == "setosa"]
## W = 2331.5, p-value = 8.346e-14
## alternative hypothesis: true location shift is not equal to 0
```


R provides many statistical tests out of the box

E.g. `test(s)` for comparing two paired groups:

The paired *t*-test (parametric):

```
t.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
       y = iris$Petal.Length[iris$Species == "versicolor"], paired = TRUE)

##
## Paired t-test
##
## data: iris$Sepal.Length[iris$Species == "versicolor"] and iris$Petal.Length[iris$Species == "versicolor"]
## t = 34.006, df = 49, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.576957 1.775043
## sample estimates:
## mean of the differences
##                1.676
```

R provides many statistical tests out of the box

E.g. test(s) for comparing two paired groups:

The paired *t*-test (parametric):

```
t.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
       y = iris$Petal.Length[iris$Species == "versicolor"], paired = TRUE)

##
## Paired t-test
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Petal.Length[iris$Species == "versicolor"]
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## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.576957 1.775043
## sample estimates:
## mean of the differences
##                1.676
```

The Wilcoxon-signed-rank test (non-parametric):

```
wilcox.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
            y = iris$Petal.Length[iris$Species == "versicolor"], paired = TRUE)

##
## Wilcoxon signed rank test with continuity correction
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Petal.Length[iris$Species == "versicolor"]
## V = 1275, p-value = 7.454e-10
## alternative hypothesis: true location shift is not equal to 0
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing two paired groups:

The paired *t*-test (parametric):

```
t.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
       y = iris$Petal.Length[iris$Species == "versicolor"], paired = TRUE)

##
## Paired t-test
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Petal.Length[iris$Species == "versicolor"]
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The Wilcoxon-signed-rank test (non-parametric):

```
wilcox.test(x = iris$Sepal.Length[iris$Species == "versicolor"],
            y = iris$Petal.Length[iris$Species == "versicolor"], paired = TRUE)

##
## Wilcoxon signed rank test with continuity correction
##
## data:  iris$Sepal.Length[iris$Species == "versicolor"] and iris$Petal.Length[iris$Species == "versicolor"]
## V = 1275, p-value = 7.454e-10
## alternative hypothesis: true location shift is not equal to 0
```

Note: if you forget to specify that the data are paired, it won't run the right test!

R provides many statistical tests out of the box

E.g. test(s) for comparing more than 2 unpaired groups:

The Kurskal-Wallis test (non-parametric):

```
kruskal.test(formula = Petal.Length ~ Species, data = iris)
##
##  Kruskal-Wallis rank sum test
##
## data:  Petal.Length by Species
## Kruskal-Wallis chi-squared = 130.41, df = 2, p-value < 2.2e-16
```

R provides many statistical tests out of the box

E.g. test(s) for comparing more than 2 unpaired groups:

The Kruskal-Wallis test (non-parametric):

```
kruskal.test(formula = Petal.Length ~ Species, data = iris)
##
##  Kruskal-Wallis rank sum test
##
## data:  Petal.Length by Species
## Kruskal-Wallis chi-squared = 130.41, df = 2, p-value < 2.2e-16
```

The “*test for equal means in a one-way layout*” (parametric):

```
oneway.test(formula = Petal.Length ~ Species, data = iris)
##
##  One-way analysis of means (not assuming equal variances)
##
## data:  Petal.Length and Species
## F = 1828.1, num df = 2.000, denom df = 78.073, p-value < 2.2e-16
```

R provides many statistical tests out of the box

E.g. test(s) for comparing more than 2 unpaired groups:

The Kurskal-Wallis test (non-parametric):

```
kruskal.test(formula = Petal.Length ~ Species, data = iris)
##
##  Kruskal-Wallis rank sum test
##
## data:  Petal.Length by Species
## Kruskal-Wallis chi-squared = 130.41, df = 2, p-value < 2.2e-16
```

The “*test for equal means in a one-way layout*” (parametric):

```
oneway.test(formula = Petal.Length ~ Species, data = iris)
##
##  One-way analysis of means (not assuming equal variances)
##
## data:  Petal.Length and Species
## F = 1828.1, num df = 2.000, denom df = 78.073, p-value < 2.2e-16
```

Note: linear models for a more sophisticated parametric alternative (see later).

R provides many statistical tests out of the box

E.g. `test(s)` for comparing more than 2 paired groups:

The Quade test (non-parametric):

```
quade.test(y = as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width"))))  
##  
## Quade test  
##  
## data: as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width")])  
## Quade F = 454.3, num df = 2, denom df = 298, p-value < 2.2e-16
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing more than 2 paired groups:

The Quade test (non-parametric):

```
quade.test(y = as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width"))))  
##  
## Quade test  
##  
## data: as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width")])  
## Quade F = 454.3, num df = 2, denom df = 298, p-value < 2.2e-16
```

The Friedman test (non-parametric):

```
friedman.test(y = as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width"))))  
##  
## Friedman rank sum test  
##  
## data: as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width")])  
## Friedman chi-squared = 300, df = 2, p-value < 2.2e-16
```


R provides many statistical tests out of the box

E.g. `test(s)` for comparing more than 2 paired groups:

The Quade test (non-parametric):

```
quade.test(y = as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width"))))
##
## Quade test
##
## data: as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width")])
## Quade F = 454.3, num df = 2, denom df = 298, p-value < 2.2e-16
```

The Friedman test (non-parametric):

```
friedman.test(y = as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width"))))
##
## Friedman rank sum test
##
## data: as.matrix(iris[, c("Petal.Length", "Sepal.Length", "Petal.Width")])
## Friedman chi-squared = 300, df = 2, p-value < 2.2e-16
```

Note: linear mixed-effects models for parametric alternative.

R provides many statistical tests out of the box

E.g. `test(s)` for comparing variances between groups:

The F-test (parametric):

```
var.test(x = iris$Sepal.Length, y = iris$Petal.Length) ## max 2 groups, must be normally distributed
##
## F test to compare two variances
##
## data:  iris$Sepal.Length and iris$Petal.Length
## F = 0.22004, num df = 149, denom df = 149, p-value < 2.2e-16
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.1594015 0.3037352
## sample estimates:
## ratio of variances
##          0.2200361
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing variances between groups:

The F-test (parametric):

```
var.test(x = iris$Sepal.Length, y = iris$Petal.Length) ## max 2 groups, must be normally distributed
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## F test to compare two variances
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## data:  iris$Sepal.Length and iris$Petal.Length
## F = 0.22004, num df = 149, denom df = 149, p-value < 2.2e-16
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.1594015 0.3037352
## sample estimates:
## ratio of variances
##          0.2200361
```

The Bartlett test (parametric):

```
bartlett.test(formula = Sepal.Length ~ Species, data = iris)
##
## Bartlett test of homogeneity of variances
##
## data:  Sepal.Length by Species
## Bartlett's K-squared = 16.006, df = 2, p-value = 0.0003345
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing variances between groups (continues):

The Fligner test (non-parametric):

```
fligner.test(formula = Sepal.Length ~ Species, data = iris)
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  Sepal.Length by Species
## Fligner-Killeen:med chi-squared = 11.618, df = 2, p-value = 0.003
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing variances between groups (continues):

The Fligner test (non-parametric):

```
fligner.test(formula = Sepal.Length ~ Species, data = iris)
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  Sepal.Length by Species
## Fligner-Killeen:med chi-squared = 11.618, df = 2, p-value = 0.003
```

Note: also `ansari.test()` and `mood.test()` for rank-based two-sample test for a difference in scale parameters.

R provides many statistical tests out of the box

E.g. `test(s)` for comparing 2 distributions:

The Kolmogorov-Smirnov test (non-parametric):

```
ks.test(x = iris$Sepal.Length, y = iris$Petal.Length)
## Warning in ks.test(x = iris$Sepal.Length, y = iris$Petal.Length): p-value will be approximate in the presence of ties
##
## Two-sample Kolmogorov-Smirnov test
##
## data: iris$Sepal.Length and iris$Petal.Length
## D = 0.56, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

R provides many statistical tests out of the box

E.g. `test(s)` for comparing 2 distributions:

The Kolmogorov-Smirnov test (non-parametric):

```
ks.test(x = iris$Sepal.Length, y = iris$Petal.Length)
## Warning in ks.test(x = iris$Sepal.Length, y = iris$Petal.Length): p-value will be approximate in the presence of ties
##
## Two-sample Kolmogorov-Smirnov test
##
## data:  iris$Sepal.Length and iris$Petal.Length
## D = 0.56, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

The Shapiro-Wilk Normality test (non-parametric):

```
set.seed(2L)
shapiro.test(x = rnorm(100))
##
## Shapiro-Wilk normality test
##
## data:  rnorm(100)
## W = 0.97498, p-value = 0.05375
```

R provides many statistical tests out of the box

E.g. test(s) for comparing a binomial outcome to a probability (exact):

The exact binomial test:

```
binom.test(x = 8, n = 10, p = 0.5)
##
## Exact binomial test
##
## data: 8 and 10
## number of successes = 8, number of trials = 10, p-value = 0.1094
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.4439045 0.9747893
## sample estimates:
## probability of success
## 0.8
```


R provides many statistical tests out of the box

E.g. `test(s)` for comparing two independent proportions:

The “*test of equal proportions*”:

```
prop.test(x = cbind(success = c(8, 4), failure = c(2, 6)))
## Warning in prop.test(x = cbind(success = c(8, 4), failure = c(2, 6))): Chi-squared approximation may be incorrect
##
## 2-sample test for equality of proportions with continuity correction
##
## data:  cbind(success = c(8, 4), failure = c(2, 6))
## X-squared = 1.875, df = 1, p-value = 0.1709
## alternative hypothesis: two.sided
## 95 percent confidence interval:
## -0.0919928  0.8919928
## sample estimates:
## prop 1 prop 2
##    0.8    0.4
```

R provides many statistical tests out of the box

E.g. test(s) of independence:

The Fisher exact test:

```
fisher.test(WorldPhones, simulate.p.value = TRUE, B = 100) ## simulation needed as too large for exact test!  
##  
## Fisher's Exact Test for Count Data with simulated p-value (based on 100 replicates)  
##  
## data: WorldPhones  
## p-value = 0.009901  
## alternative hypothesis: two.sided
```

R provides many statistical tests out of the box

E.g. test(s) of independence:

The Fisher exact test:

```
fisher.test(WorldPhones, simulate.p.value = TRUE, B = 100) ## simulation needed as too large for exact test!  
##  
## Fisher's Exact Test for Count Data with simulated p-value (based on 100 replicates)  
##  
## data: WorldPhones  
## p-value = 0.009901  
## alternative hypothesis: two.sided
```

The Chi-squared test for independence:

```
chisq.test(WorldPhones)  
##  
## Pearson's Chi-squared test  
##  
## data: WorldPhones  
## X-squared = 2194.4, df = 36, p-value < 2.2e-16
```

R provides many statistical tests out of the box

E.g. test(s) of independence:

The Fisher exact test:

```
fisher.test(WorldPhones, simulate.p.value = TRUE, B = 100) ## simulation needed as too large for exact test!
##
## Fisher's Exact Test for Count Data with simulated p-value (based on 100 replicates)
##
## data: WorldPhones
## p-value = 0.009901
## alternative hypothesis: two.sided
```

The Chi-squared test for independence:

```
chisq.test(WorldPhones)
##
## Pearson's Chi-squared test
##
## data: WorldPhones
## X-squared = 2194.4, df = 36, p-value < 2.2e-16
```

Note: the McNemar test is also available when the same subjects are measured in two conditions (see `?mcnemar.test`).

Packages provide even more simple statistical tests!

Some examples:

- `coin` provides permutation implementations of many tests.
- `nsm3` provides tons of non-parametric tests.
- `PMCMR` provides post-hoc tests for non-parametric tests.
- `nortest` provides several tests for normality.

Note: this list is only a very small subset!!

A note before we continue

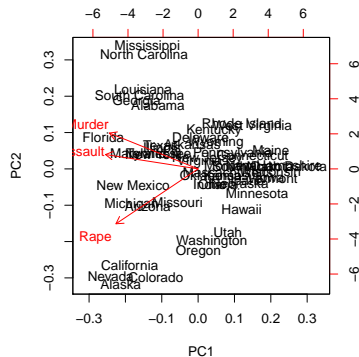
R primary goal is to perform statistical analyses. So among the many thousands of packages many focus on statistical tools and by no means I will try to cover or even summarise this diversity. I have chosen to only illustrate some of the tools I know and that I have used to show you how to do some statistics in **R**. Since time is limited, I will not for example illustrate any Bayesian methods, nor machine learning methods, although some good packages exist for that too!

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PCA without packages

```
pca_US <- prcomp(~ Murder + Assault + Rape, data = USArrests, scale. = TRUE)
biplot(x = pca_US)
```



PCA without packages

```
summary(pca_US)
```

```
## Importance of components:
```

```
##           PC1      PC2      PC3  
## Standard deviation    1.5358 0.6768 0.42822  
## Proportion of Variance 0.7862 0.1527 0.06112  
## Cumulative Proportion 0.7862 0.9389 1.00000
```

PCA without packages

```
summary(pca_US)

## Importance of components:
##              PC1      PC2      PC3
## Standard deviation  1.5358 0.6768 0.42822
## Proportion of Variance 0.7862 0.1527 0.06112
## Cumulative Proportion 0.7862 0.9389 1.00000
```

```
PC1 <- pca_US$x[, "PC1"]
mean(PC1)

## [1] -8.905095e-17

sd(PC1)

## [1] 1.535767
```

```
PC2 <- pca_US$x[, "PC2"]
mean(PC2)

## [1] -9.438739e-17

sd(PC2)

## [1] 0.6767949
```

PCA with ade4

```
library(ade4)

pca_US_ade4 <- dudi.pca(df = USArrests[, -3], scale = TRUE, scannf = FALSE)

summary(pca_US_ade4)

## Class: pca dudi
## Call: dudi.pca(df = USArrests[, -3], scale = TRUE, scannf = FALSE)
##
## Total inertia: 3
##
## Eigenvalues:
##      Ax1      Ax2      Ax3
## 2.3586 0.4581 0.1834
##
## Projected inertia (%):
##      Ax1      Ax2      Ax3
## 78.619 15.268 6.112
##
## Cumulative projected inertia (%):
##      Ax1  Ax1:2  Ax1:3
## 78.62  93.89 100.00
```

PCA with ade4

```
library(ade4)

pca_US_ade4 <- dudi.pca(df = USArrests[, -3], scale = TRUE, scannf = FALSE)

summary(pca_US_ade4)

## Class: pca dudi
## Call: dudi.pca(df = USArrests[, -3], scale = TRUE, scannf = FALSE)
##
## Total inertia: 3
##
## Eigenvalues:
##      Ax1      Ax2      Ax3
## 2.3586 0.4581 0.1834
##
## Projected inertia (%):
##      Ax1      Ax2      Ax3
## 78.619 15.268 6.112
##
## Cumulative projected inertia (%):
##      Ax1  Ax1:2  Ax1:3
## 78.62  93.89 100.00
```

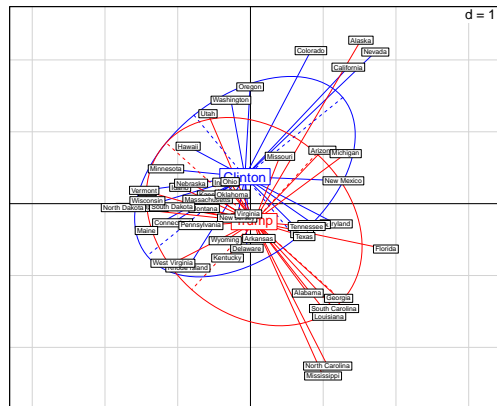
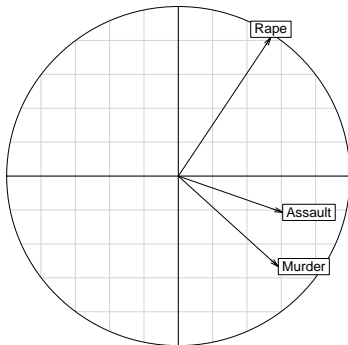
```
USArrests$Vote <- rep("Trump", times = 50)
Clinton_state <- c("California", "Colorado", "Connecticut", "Delaware", "Hawaii",
  "Illinois", "Maine", "Maryland", "Massachusetts", "Minnesota", "Nevada",
  "New Hampshire", "New Jersey", "New Mexico", "New York", "Oregon",
  "Rhode Island", "Vermont", "Virginia", "Washington")
USArrests[Clinton_state, "Vote"] <- "Clinton"
USArrests$Vote <- factor(USArrests$Vote)
```

PCA with ade4

```

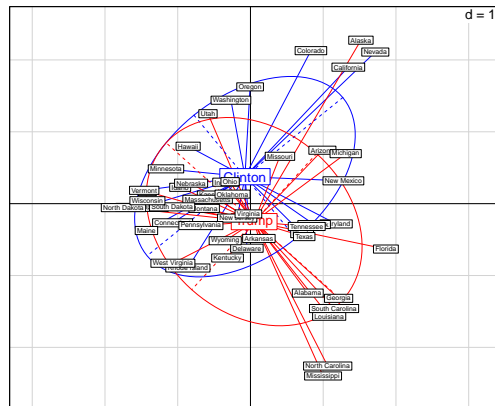
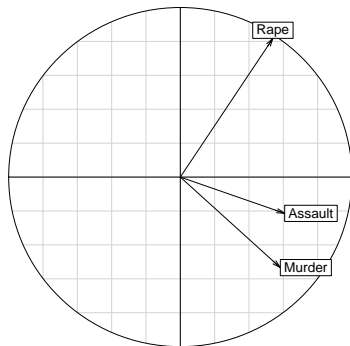
par(mfrow = c(1, 2))
s.corcircle(dfxy = pca_US_ade4$c1)
s.class(dfxy = pca_US_ade4$l1, fac = USArrests$Vote, col = c("blue", "red"))
s.label(dfxy = pca_US_ade4$l1, label = rownames(USArrests), add.plot = TRUE, clabel = 0.5)

```



PCA with ade4

```
par(mfrow = c(1, 2))
s.corcircle(dfxy = pca_US_ade4$c1)
s.class(dfxy = pca_US_ade4$l1, fac = USArrests$Vote, col = c("blue", "red"))
s.label(dfxy = pca_US_ade4$l1, label = rownames(USArrests), add.plot = TRUE, clabel = 0.5)
```



Note: using `co` & `li` instead of `c1` & `l1` would respect the relative contribution of each principal component according to the variance they capture.

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- 5 Other linear models

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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).

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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.

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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

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- classical linear models (t-test, correlation, linear regression, ANOVA, ANCOVA): LM
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- 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/courtio1/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

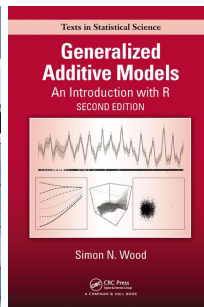
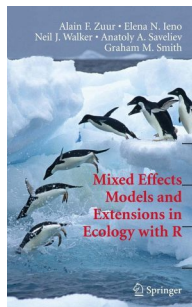
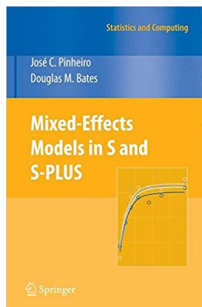
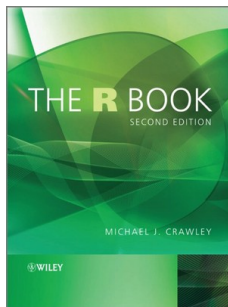
R is very rich in terms of capabilities to fit linear models due to an increasing number of dedicated packages!

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



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 headaches)

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 headaches)

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
```

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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:

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

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

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

The linear model: specifications

Matrix notation:

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

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

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

- Y = the vector of observations
- \hat{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)

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- 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

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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

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- 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!

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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
```

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##           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

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And thus the standard errors:

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

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

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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

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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
```

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## [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!

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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 performs 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
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## ---
## 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!

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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
```

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```

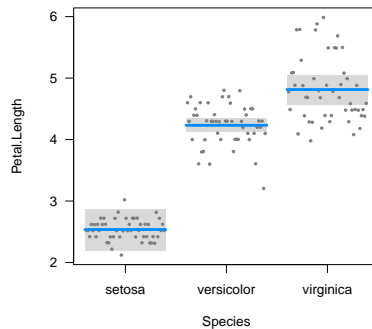
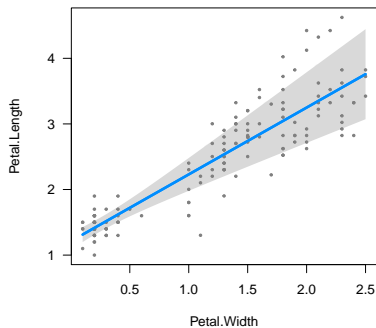
As expected, observations are equal to the fitted values + residuals:

```
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
```

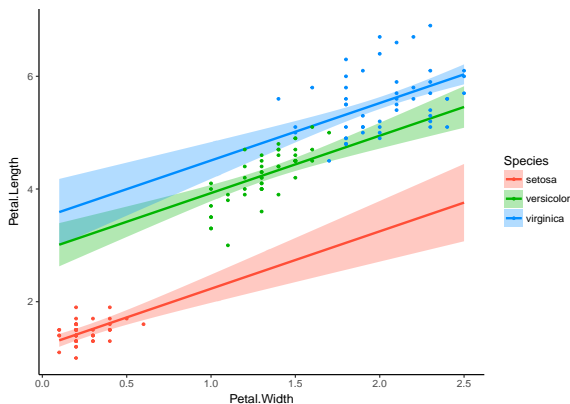
Plotting predictions: fast & dirty

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



Plotting predictions: fast & less dirty

```
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

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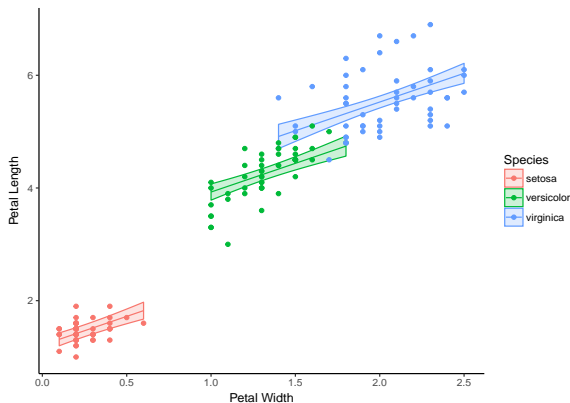
Then, it is easy:

```
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”

```
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()
```



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Assumptions behind linear models

Model structure:

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

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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.

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- thinking
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- 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)

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

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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.

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- change design matrix (change parameterization or drop redundant effects) \rightarrow argument `formula`
- change the experimental design
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Note: strong albeit imperfect collinearity is not great either; possible check correlation between estimates (\rightarrow `cov2cor(vcov(mod))`) and variance inflation factors (\rightarrow `vif(mod)`).

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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.

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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)

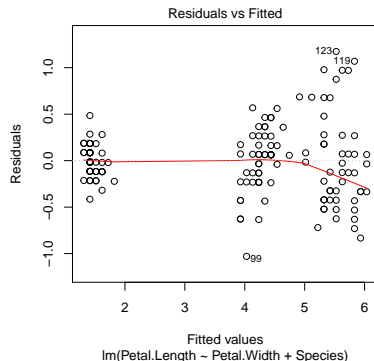
A lack of independence (serial autocorrelation) in the residuals can appear if there is a departure from linearity, if data have been sampled non-randomly (e.g. spatial or temporal series), or if there is an overarching structure (e.g. repeated measures within individuals, families, species, ...). Lack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

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Diagnostic by eye:

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



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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 0.054
## Alternative hypothesis: rho != 0
```

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

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Alternatives:

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

Assumptions: constant variance (homoscedasticity)

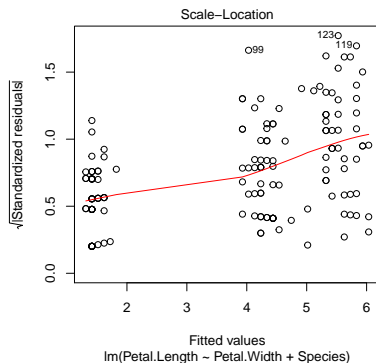
Heteros(c/k)edasticity can emerge when there is a mean - variance relationship, when there is non independence between observations, when reaction norm changes according to the treatment. It can create both false positives and false negative.

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Diagnostic by eye:

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



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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
```

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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:
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```

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Alternatives:

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

Assumptions: normality

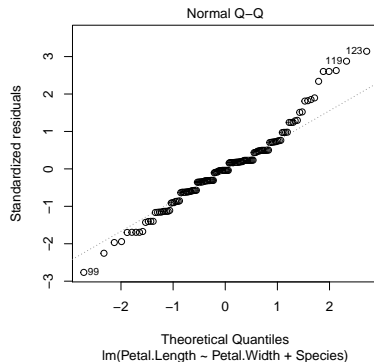
The distribution of residuals can be skewed, this is often caused by the presence of outliers, and/or when the process generating the data is very different from normal (e.g. Poisson, Binomial...).

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Diagnostic by eye:

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



Assumptions: normality

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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
```

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- taking outliers out (mindfully!)

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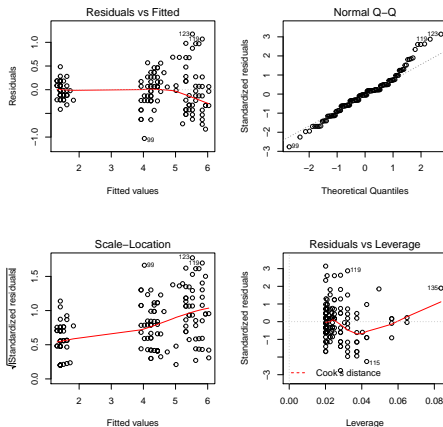
Alternatives:

- GLM (if stemming from the data generating process) → function `glm`

Assumptions: simple glimpse

You can check all assumptions about the errors at once:

```
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.Spccsvrs dfb.Spccsvrg  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  0.000000  0.000000    0.00000    0.000000  0.00000 1.000 0.00e+00 0.0000
```

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"

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- `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 overall ad hoc recipe to spot influential observation (not to be taken too seriously)

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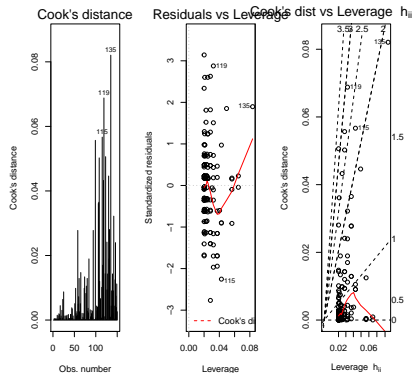
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Assumptions: outliers

There are also plotting possibilities:

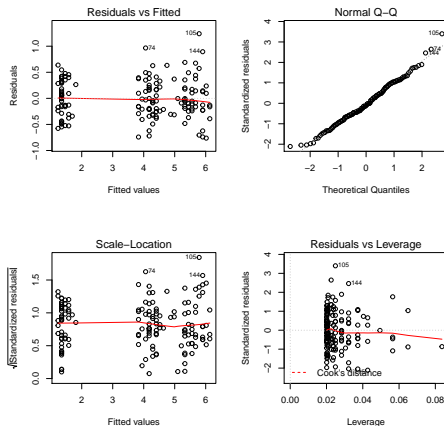
```
par(mfrow = c(1, 3))
plot(mod, which = 4:6)
```



Assumptions: simple glimpse at residuals

What would it look like if it was perfect?

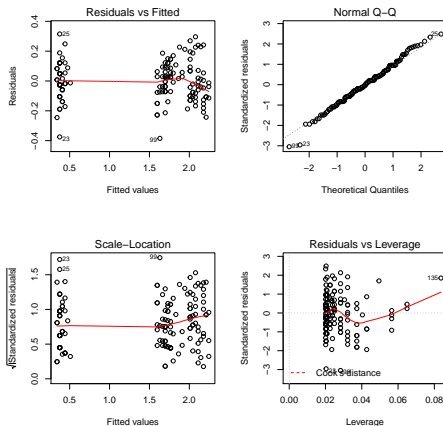
```
iris$Fake.Petal.Length <- simulate(object = mod)[, 1] ## redo it, it will change each time!
mod_perfect <- lm(Fake.Petal.Length ~ Petal.Width + Species, data = iris)
par(mfrow = c(2, 2))
plot(mod_perfect)
```



Assumptions: fixing iris

Fixing attempt:

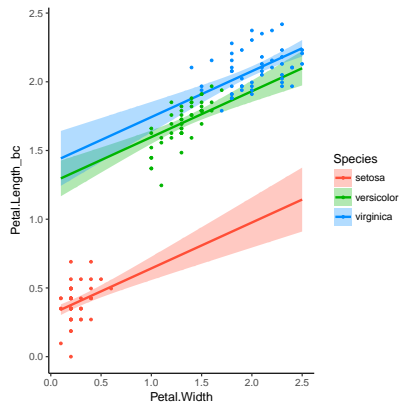
```
bc <- powerTransform(mod)
iris$Petal.Length_bc <- bcPower(iris$Petal.Length, lambda = bc$lambda)
mod_bc <- lm(Petal.Length_bc ~ Petal.Width + Species, data = iris)
par(mfrow = c(2, 2))
plot(mod_bc)
```



Assumptions: fixing iris

Plotting predictions:

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

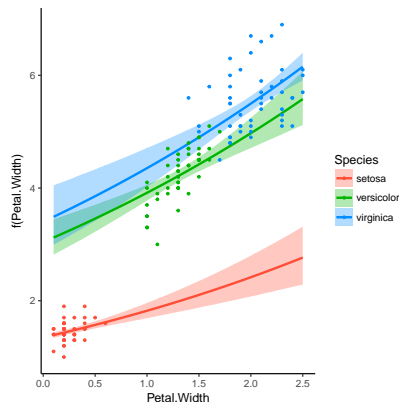


Note: that is not very useful because it is on the BoxCoxed scale!

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()
```



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Getting started with R

- 1 Some basic tests
- 2 Principal Component Analysis
- 3 Linear Models
- 4 Generalised Linear Models**
- 5 Other linear models

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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 binomial processes (counts)
- variances (positive continuous)

The generalised linear model: specifications

Definition:

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

with:

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

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

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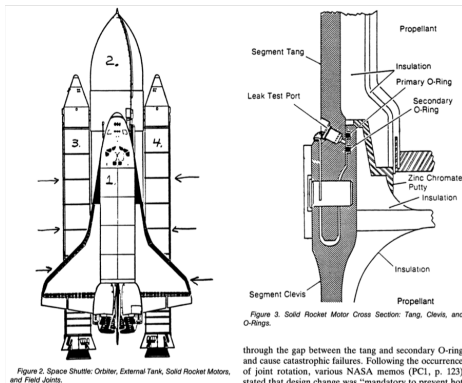
Notation:

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- 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



```
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:

```
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:

```
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)
```


The generalised linear model: specifications

In R notation:

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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

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```

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

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```

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:

```
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```
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"
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```
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.

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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(conft(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
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head(conft(mod_horsekick))

## Waiting for profiling to be done...
##           2.5 %   97.5 %
## (Intercept) -0.7566949 0.2298300
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## 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 recipe, it all depends on the link function used. . .

Interpreting estimates

There is no general recipe, 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!

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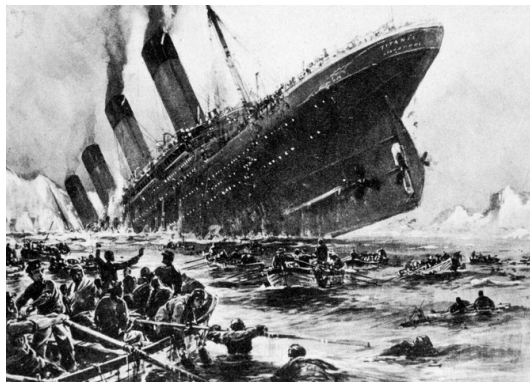
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The generalised linear model: challenge

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
```

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