

# ST2304 - Statistical Modelling for Biologists/Biotechnologists

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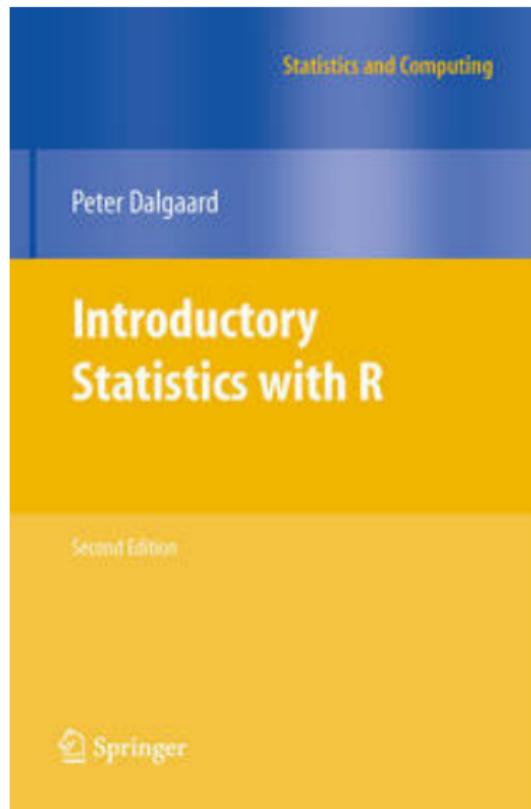
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# Administration Matters

- ▶ Reference Group
- ▶ Blackboard

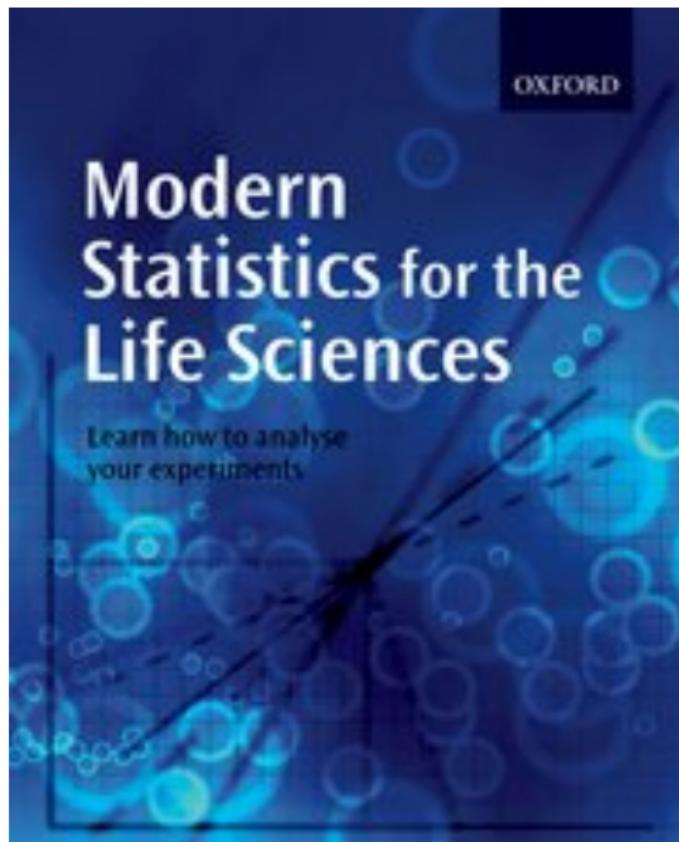
## Text Books

*Introductory statistics with R* by Peter Dalgaard



## Text Books

Grafen & Hails: Modern Statistics for the Life Sciences



## Previous Knowledge

What do you know?  
(so I don't assume too much!)

# Mathematics

- ▶ logarithms/exponentials
- ▶ differentiation
- ▶ integration

# Probability

- ▶ Conditional Probability
- ▶ Expectation  $E(X)$
- ▶ Independence
- ▶ Probability distribution

# Statistics

- ▶ Averages
- ▶ Variance, standard deviation
- ▶ Covariance, correlation
- ▶ t-tests
- ▶ regression (fitting a straight line)

# Programming

- ▶ Languages
  - ▶ C, BASIC, Python, Java, Python
  - ▶ R
- ▶ Object Oriented Programming

# Why do we need statistical modelling?

Because the world is complex!

## Face width and Fitness

Men with wider faces are more aggressive

But does this affect their fitness?

- ▶ survival in the Winter War
- ▶ number of (legitimate) offspring

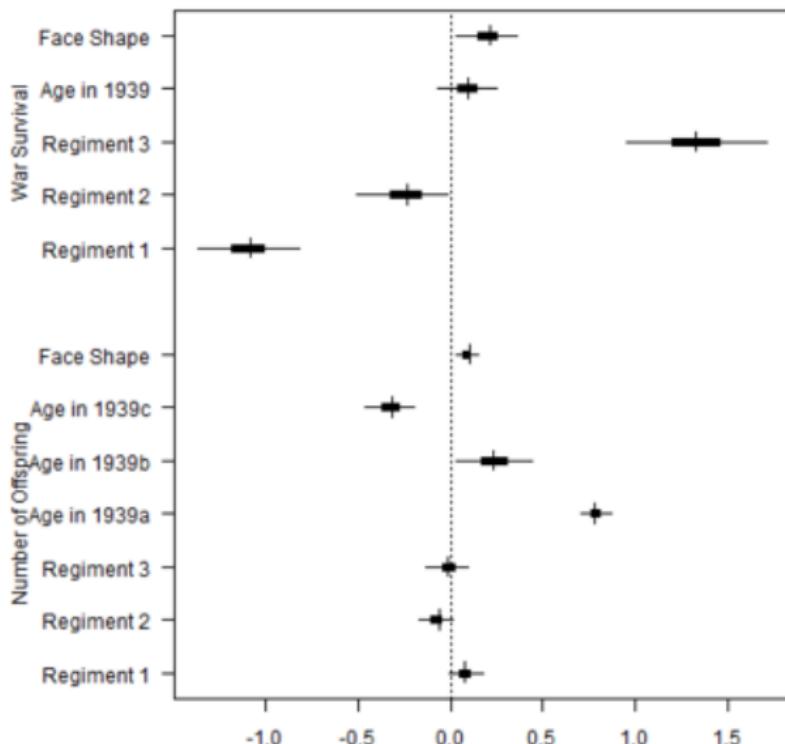
## Face width and Fitness

But other things affect fitness - regiment - rank - survival affects number of offspring

We need a model to disentangle all these

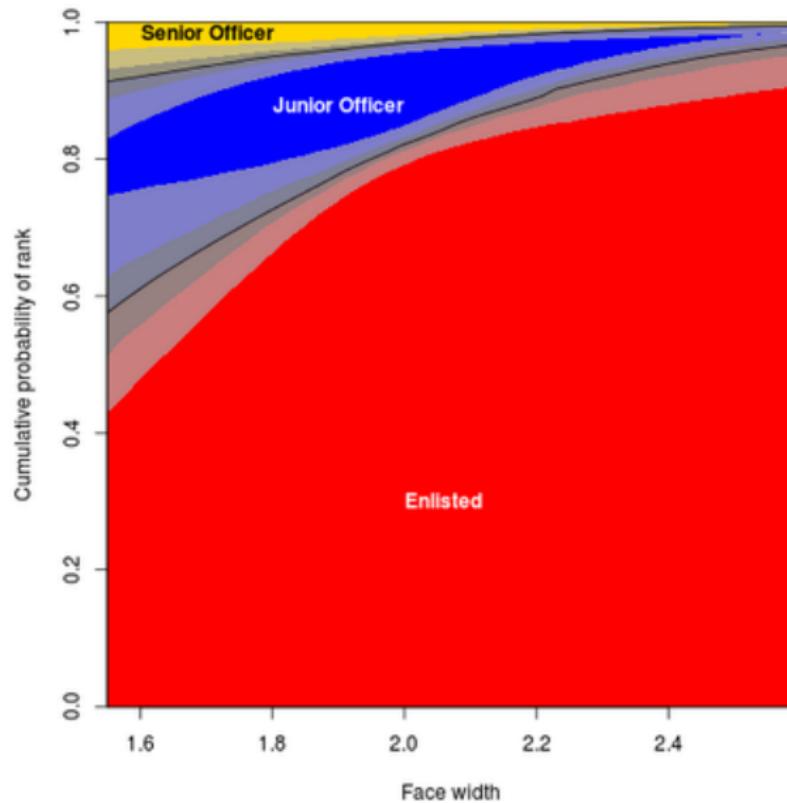
# Face width and Fitness

Men with wider faces had more offspring, and might have slightly lower survival



# Face width and Fitness

But thinner face -> higher rank



## Statistical Modelling: Brain size in birds

- ▶ What sort of question can we ask?
- ▶ What is likely to influence brain size?
  - ▶ actual brain size
  - ▶ what we measure

# Data Analysis

Different stages

Outline the full work flow

Modelling is only a part of this!

First, collect the data



Figure 5:

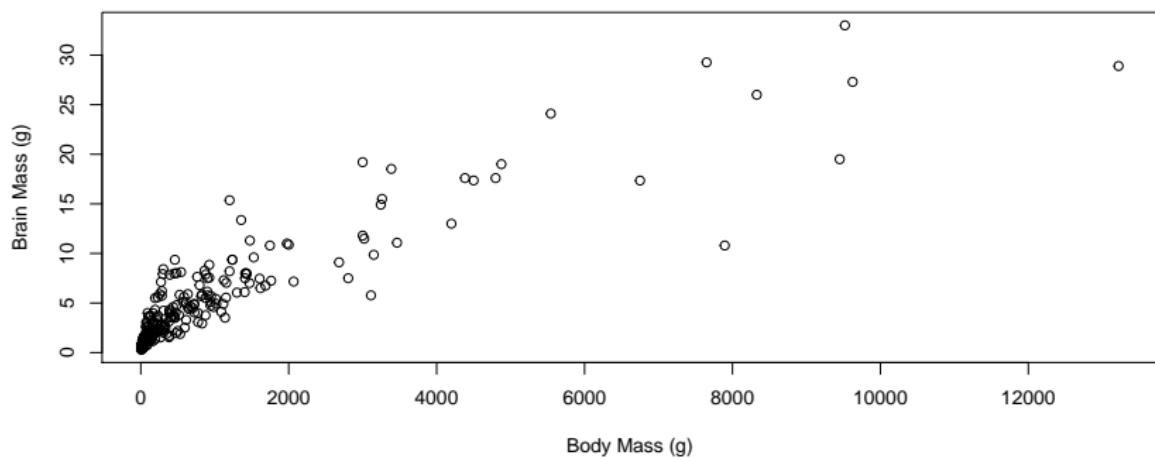
## Format the data

- ▶ Get it into the right format so you can use it
- ▶ For big problems, use a data base
- ▶ Store the data in a convenient format, e.g. .csv

```
BirdBrains <- read.csv("ece32961-sup-0001-TableS1.csv")
names(BirdBrains) <- gsub("Brain.*", "Brain", names(BirdBrains))
names(BirdBrains)[grep("resou", names(BirdBrains))] <- "Boo"
```

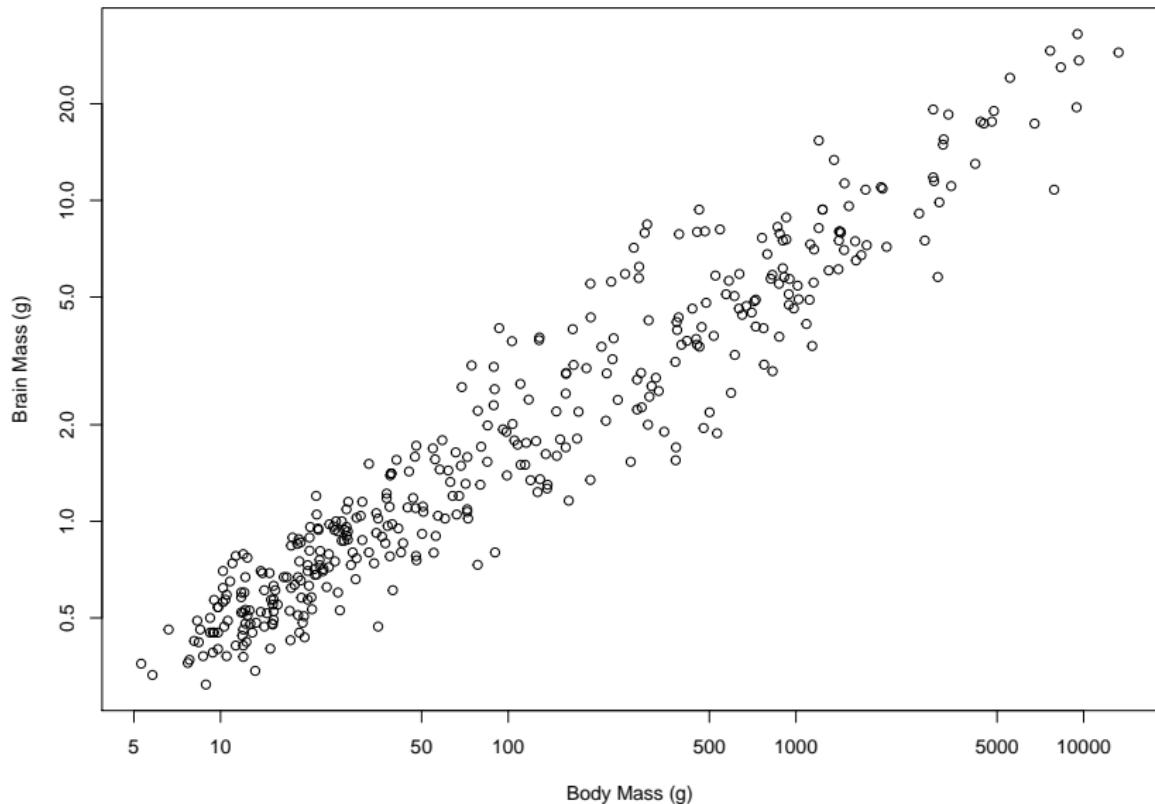
## Look at the data

- ▶ Plot, calculate some summaries
- ▶ Spot any possible problems
  - ▶ Typos etc.



# Look at the data

Nicer as a log-log plot?



## Start the modelling

- ▶ What are the questions you are asking?
- ▶ What are problems in the data that you need to worry about?
- ▶ Do we need additional data?

## Start the modelling

How does body size affect brain size in birds? - is it similar to mammals?

Does the relationship differ between different groups of bird?

## Fit the model

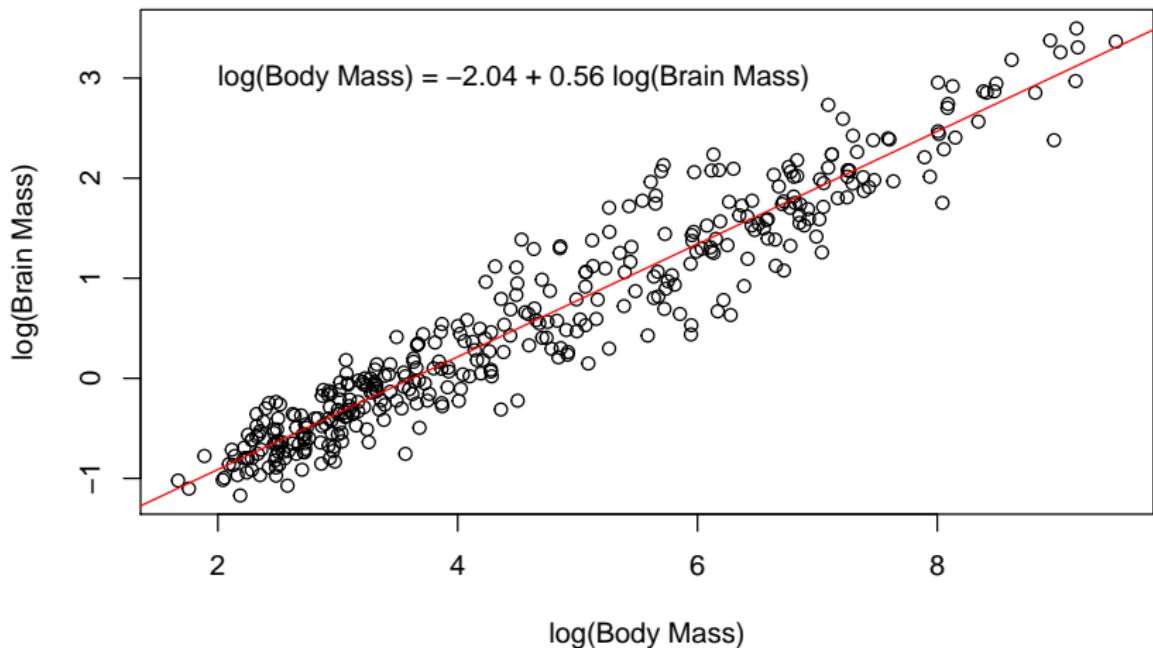
Get the computer to do it Look at the output

```
bird.mod <- lm(log(Brain) ~ log(Body), data=BirdBrains)
summary(bird.mod)
```

```
##
## Call:
## lm(formula = log(Brain) ~ log(Body), data = BirdBrains)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.87213 -0.20022 -0.01783  0.19395  0.94904
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.037838   0.043114 -47.27   <2e-16 ***
## log(Body)    0.563159   0.008625  65.29   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## The Fitted Model

```
par(mfrow=c(1,1), mar=c(4.1,4.1,1,1))
plot(log(BirdBrains$Body), log(BirdBrains$Brain), type="p")
abline(bird.mod, col=2)
text(2, 3, paste0("log(Body Mass) = ", round(coef(bird.mod)
```

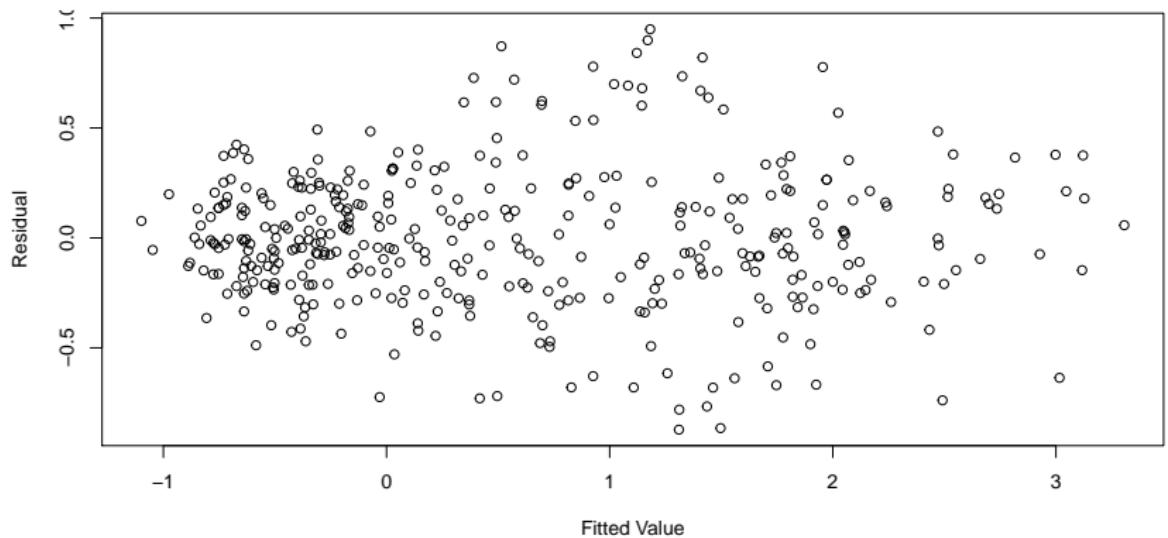


## Check the Model

- ▶ Does it fit well?
- ▶ Outliers?
- ▶ Assumptions OK? e.g. linearity
- ▶ Can you understand the results?

## Check the Model

```
par(mar=c(4.1,4.1,0.1,1))
plot(fitted(bird.mod), resid(bird.mod), type="p", xlab="Fit
```



## Interpret the model

Back to biology!

The slope is 0.56, with a 95% confidence interval of 0.55 to 0.58.

This is less than it is for mammal, where the slope is 0.75 (95% confidence interval: 0.69 to 0.81

Part of the reason for this is variation between bird orders. If we correct for order, the slope is 0.66, 95% confidence interval: 0.64 to 0.68.

# A Quick Overview of R

A statistics programme

The language (S) designed for statistics

Object oriented

Interpreted language

## Basic Syntax: Assignment

```
x <- 2  
x
```

```
## [1] 2
```

```
(y <- 1:3)
```

```
## [1] 1 2 3
```

```
(z <- c(4.5,6.7,-3))
```

```
## [1] 4.5 6.7 -3.0
```

# A Calculator

```
x + y
```

```
## [1] 3 4 5
```

```
exp(z)
```

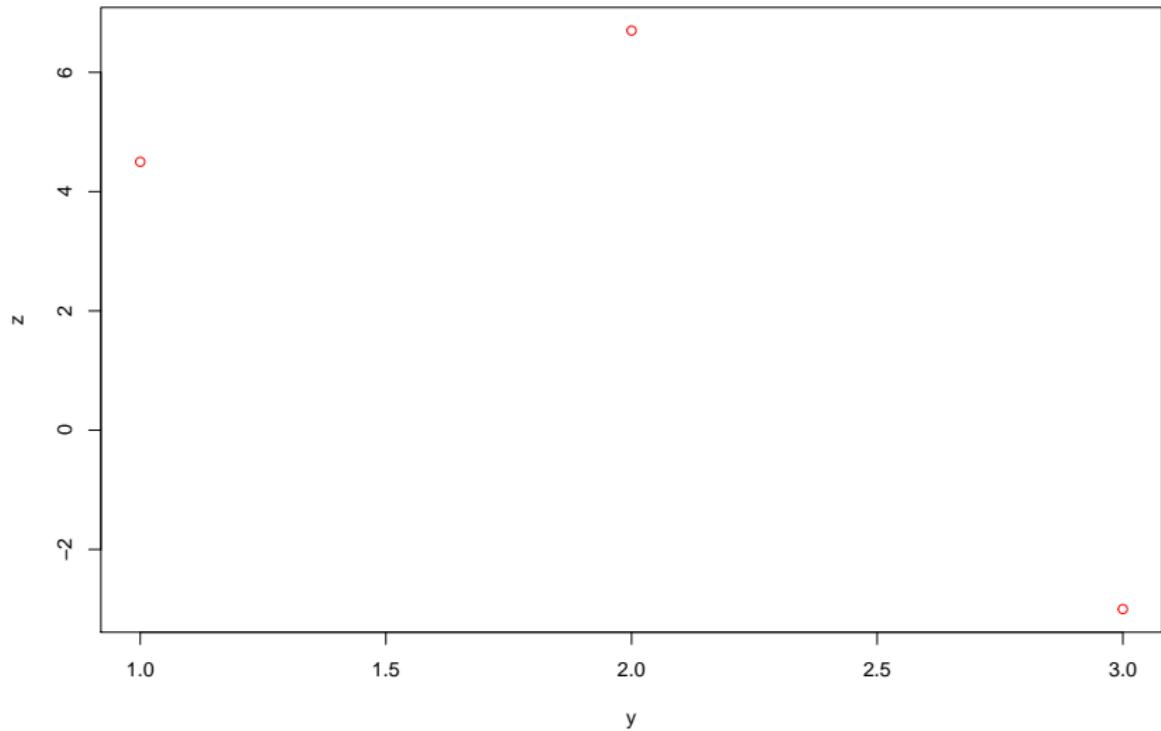
```
## [1] 90.01713130 812.40582517 0.04978707
```

```
z/y # = z[1]/y[1] z[2]/y[2] z[3]/y[3]
```

```
## [1] 4.50 3.35 -1.00
```

# Simple Plotting

```
plot(y, z, col=2)
```



## Functions & Objects

`exp(z)` & `plot(y, z)` are functions

`y` & `z` is an *arguments*: they are given to the function, which does something with them

The function returns an object: - `exp()` returns a vector - `plot()` returns `NULL` (i.e. nothing: the plot is a side-effect)

# Statistical Models

`lm()` is a more complicated function

We give it '`log(Brain) ~ log(Body)`' and `BirdBrains` as arguments

```
bird.mod <- lm(log(Brain) ~ log(Body), data=BirdBrains)
```

It returns something horrid

## A big object

```
str(bird.mod)
```

```
## List of 12
## $ coefficients : Named num [1:2] -2.038 0.563
##   ..- attr(*, "names")= chr [1:2] "(Intercept)" "log(Bod...
## $ residuals     : Named num [1:384] 0.2133 0.0616 0.1794 ...
##   ..- attr(*, "names")= chr [1:384] "1" "2" "3" "4" ...
## $ effects       : Named num [1:384] -11.196 -20.705 0.1608 ...
##   ..- attr(*, "names")= chr [1:384] "(Intercept)" "log(I...
## $ rank          : int 2
## $ fitted.values: Named num [1:384] 1.81 1 3.13 2.68 2.2...
##   ..- attr(*, "names")= chr [1:384] "1" "2" "3" "4" ...
## $ assign         : int [1:2] 0 1
## $ qr            :List of 5
##   ..$ qr      : num [1:384, 1:2] -19.596 0.051 0.051 0.051 ...
##   ... ..- attr(*, "dimnames")=List of 2
##   ... ... .$. : chr [1:384] "1" "2" "3" "4" ...
##   ... ... .$. : chr [1:2] "(Intercept)" "log(Body)"
```

## The power of objects

We usually don't need to know what is in an object: there are functions to get us what we want

```
coef(bird.mod)
```

```
## (Intercept) log(Body)
## -2.0378376 0.5631593
```

```
summary(bird.mod)$coefficients
```

	Estimate	Std. Error	t value	Pr(> t )
## (Intercept)	-2.0378376	0.043113631	-47.26667	1.110796e-11
## log(Body)	0.5631593	0.008625092	65.29314	2.544019e-22

## Data Types

Our basic data can be of different types, e.g. integer, real number, text, factor, logical

```
(txt <- c("thing", "stuff", "thing")) # text
```

```
## [1] "thing" "stuff" "thing"
```

```
(f <- factor(c("thing", "stuff", "thing"))) # factor
```

```
## [1] thing stuff thing
```

```
## Levels: stuff thing
```

```
(lg <- c(TRUE, FALSE)) # logical
```

```
## [1] TRUE FALSE
```

## Using data types: indices

```
(a1 <- -5:5)
```

```
## [1] -5 -4 -3 -2 -1  0  1  2  3  4  5
```

```
a1[1]
```

```
## [1] -5
```

```
a1[c(3,5,6)]
```

```
## [1] -3 -1  0
```

## Using data types: subsetting

```
(logical.a1 <- a1 > 0)
```

```
## [1] FALSE FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE
```

```
(logical.a2 <- a1%/%2==0)
```

```
## [1] FALSE TRUE FALSE TRUE FALSE TRUE FALSE TRUE FALSE TRUE FA
```

```
a1[logical.a1]
```

```
## [1] 1 2 3 4 5
```

```
a1[logical.a1 & logical.a2]
```

```
## [1] 2 4
```

## Running an analysis

R has functions to read in data

```
MammalBrains <- read.table("mammals.dat", header = TRUE)
```

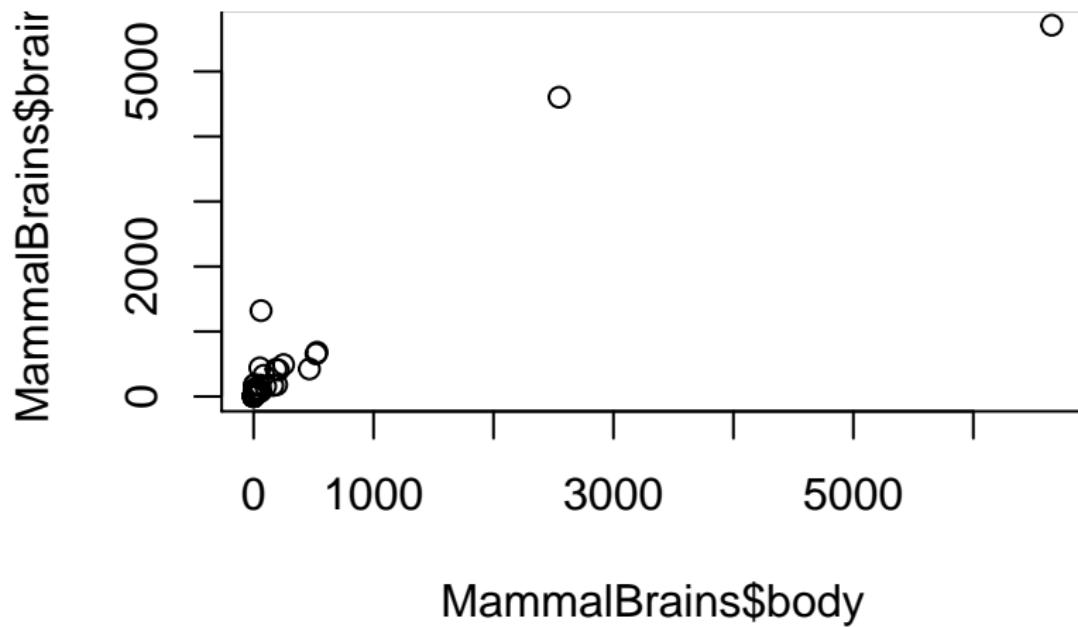
and write it out

```
write.csv(MammalBrains, "mammals.csv")
save(MammalBrains, x, file="mammals.RData")
```

## Saving plots

We can save plots in files: pdf, png, jpg, etc etc

```
par(mar=c(4.1,4.1,0,0))  
plot(MammalBrains$body, MammalBrains$brain)
```



```
png("MammalBrains.png")
```

# Functions

We can write our own functions....

```
HelloWorld <- function(str) {  
  if(!is.character((str)))  
    stop("str should be a character string you idiot")  
  cat(paste0("Hello World, ", str, "\n"))  
}
```

```
HelloWorld("Orpheus")
```

```
## Hello World, Orpheus!
```

## Packages

Packages put together a lot of functions (and objects etc.)

A lot of these are on CRAN

```
library(sp)
data(meuse)
coordinates(meuse) <- c("x", "y")
par(mar=c(2,2,1,1))
plot(meuse)
```



## Getting and Using R

You can download R from CRAN: <http://www.r-project.org/>

A lot of people use RStudio: <http://rstudio.org/>

## Finally

If you want to start using R now:

[https://www.math.ntnu.no/emner/TMA4268/2018v/1Intro/  
Rbeginner.html](https://www.math.ntnu.no/emner/TMA4268/2018v/1Intro/Rbeginner.html)