Trinity College Dublin
Coláiste na Tríonóide, Baile Átha Cliath
The University of Dublin

UNIVERSITY OF CAMBRIDGE

Introduction to R, Github and Gitlab

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Outline:

- Why R? What can R do?
- Basic commands and operations
- Data analysis in R
- Github and Gitlab

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- Why R? What can R do?
- Basic commands and operations
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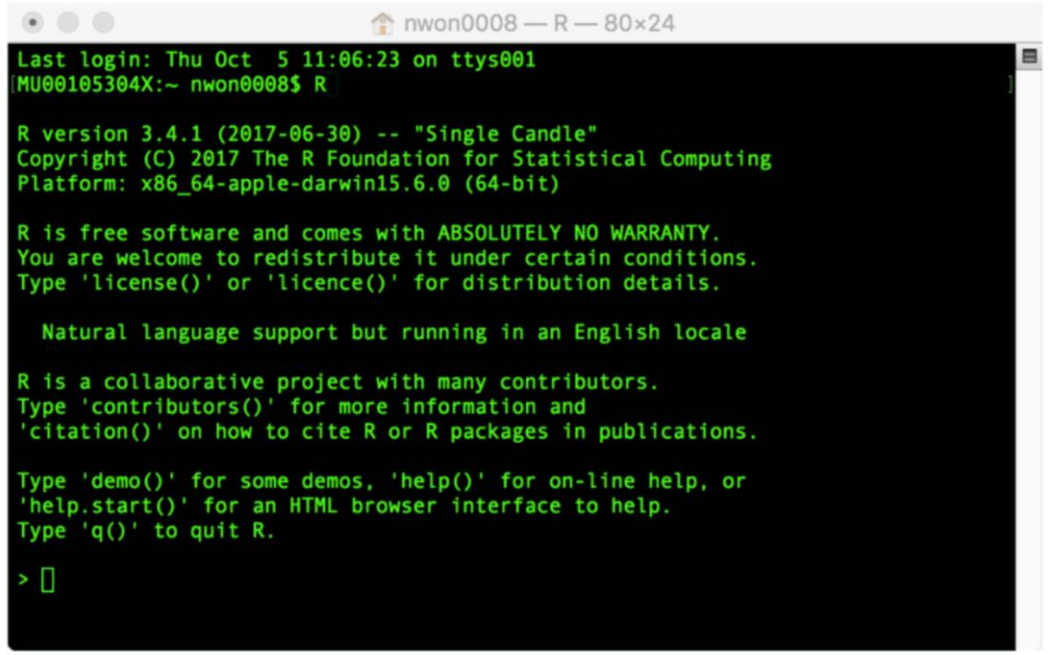
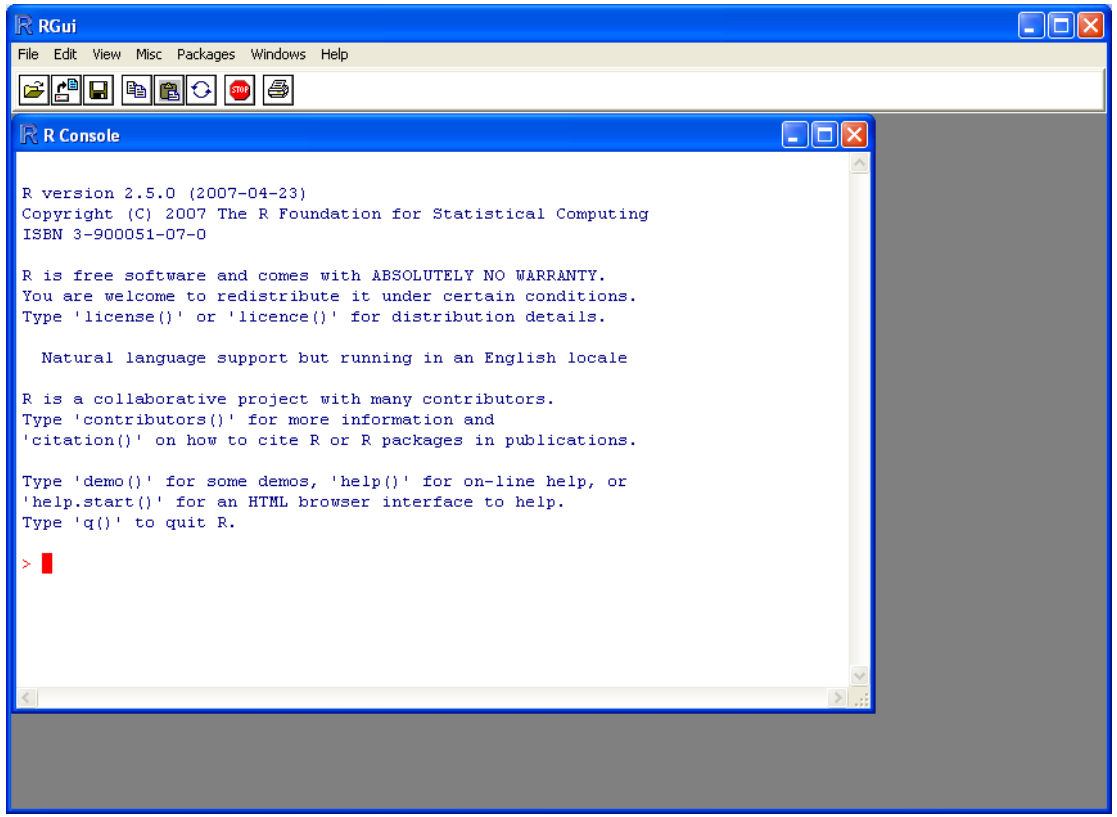
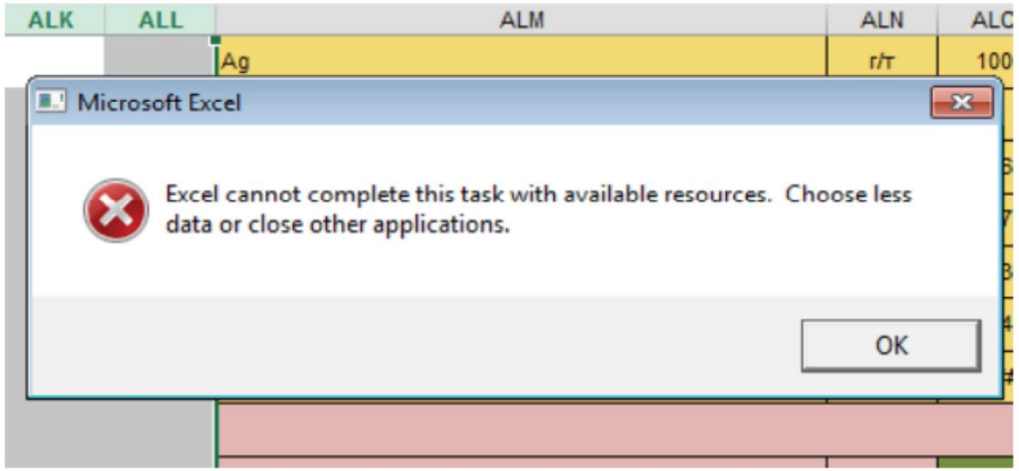
Why R? What can R do?

- R is a language and environment for statistical computing and graphics;
- It is open source and free software package;
- Lots of resources, packages and support





R vs Excel



Ziemann et al. Genome Biology (2016) 17:177
DOI 10.1186/s13059-016-1044-7

Genome Biology

COMMENT Open Access

Gene name errors are widespread in the scientific literature

Mark Ziemann[1], Yotam Eren[1,2] and Assam El-Osta[1,3*]

Abstract

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

Keywords: Microsoft Excel, Gene symbol, Supplementary data

Abbreviations: GEO, Gene Expression Omnibus; JIF, journal impact factor

frequently reused. Our aim here is to raise awareness of the problem.

We downloaded and screened supplementary files from 18 journals published between 2005 and 2015 using a suite of shell scripts. Excel files (.xls and.xlsx suffixes) were converted to tabular separated files (tsv) with ssconvert (v1.12.9). Each sheet within the Excel file was converted to a separate tsv file. Each column of data in the tsv file was screened for the presence of gene symbols. If the first 20 rows of a column contained five or more gene symbols, then it was suspected to be a list of gene symbols, and then a regular expression (regex) search of the entire column was applied to identify gene symbol errors. Official gene symbols from Ensembl version 82, accessed November 2015, were obtained for

- Dragging and updating formula;
- Spreadsheets can get really big and confusing;
- Lack of quick way to get a summary of the data;
- …

R vs Excel

- Point-and-click software is not time efficient;
- Automating tasks will pay off within the time frame of a PhD and thereafter

R is more efficient

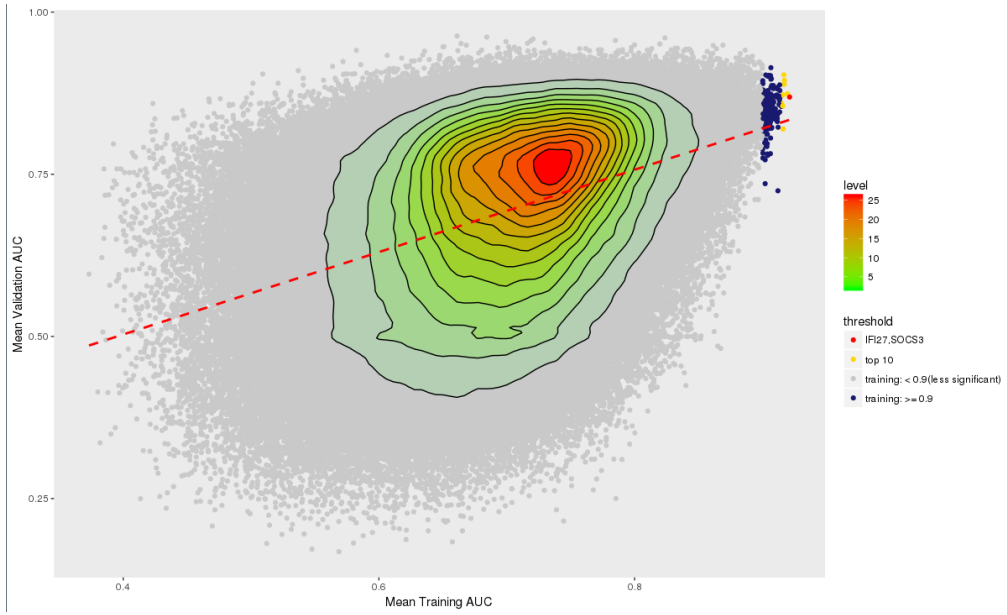
R vs Excel

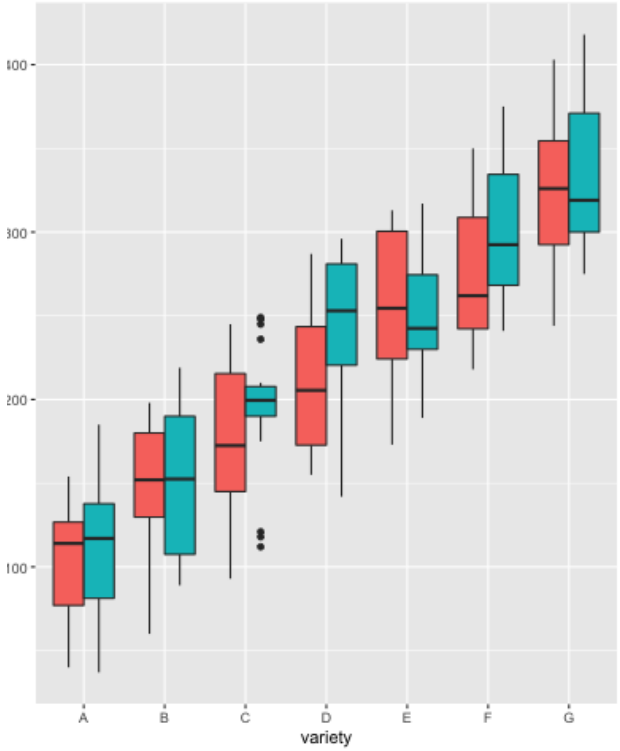
- **Reproducibility:** there is an increasing expectation that material, data and analysis details are provided alongside the research, this is easier when analyses are script based.

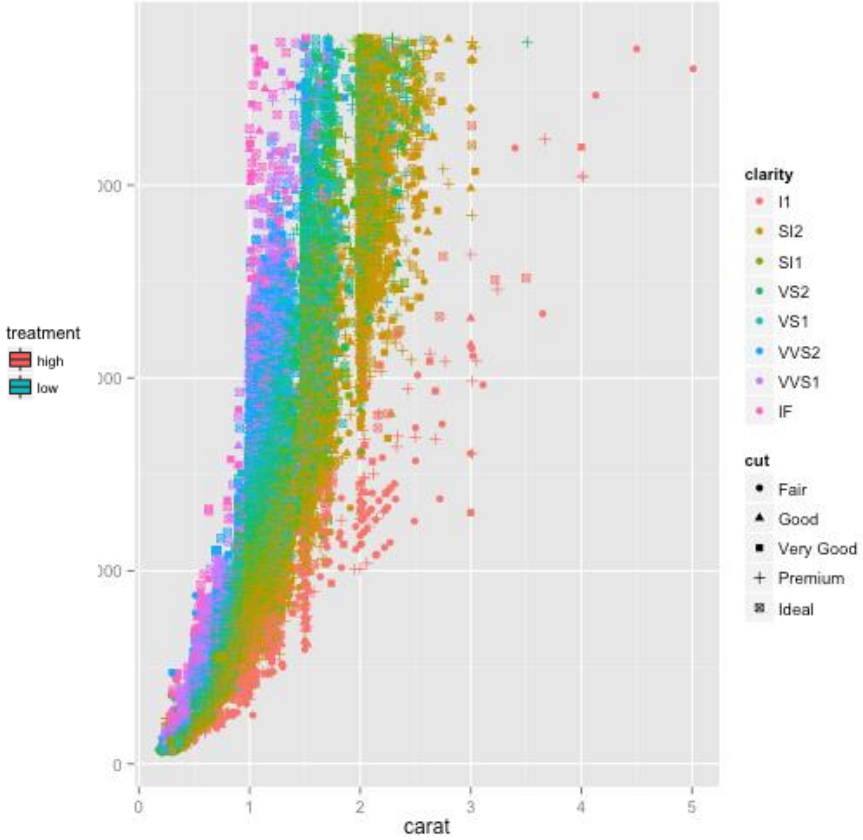
Flexibility:

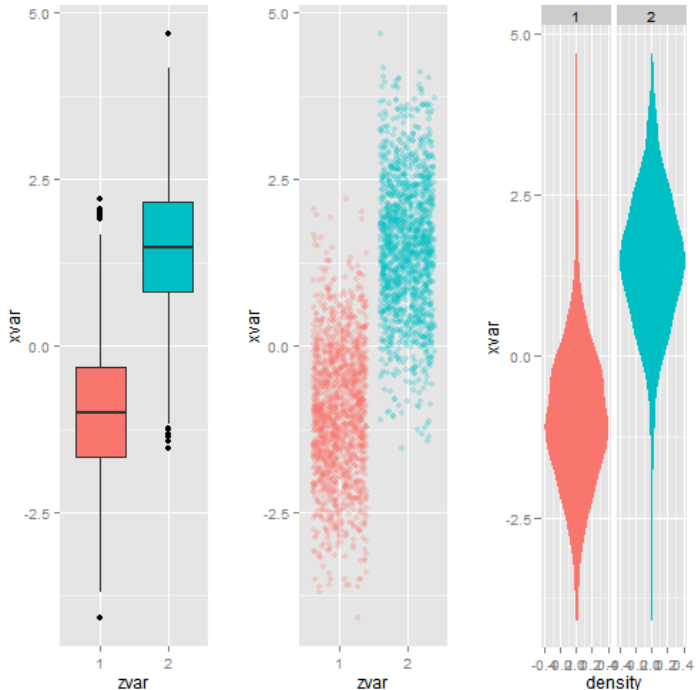
- Read different file formats;
- Compute analysis;
- Generate graphs and plots;
- Summary of your data;
- R works on vector, matrix and dataframe;
- Generate reports;

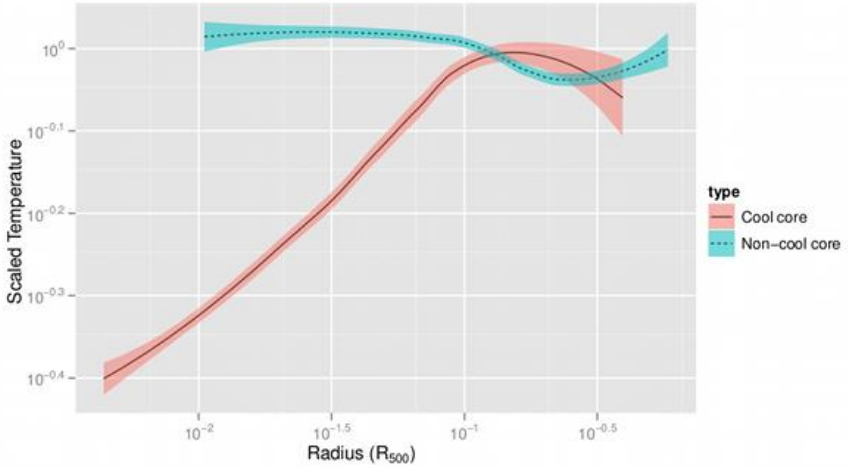
Why R? What can R do?

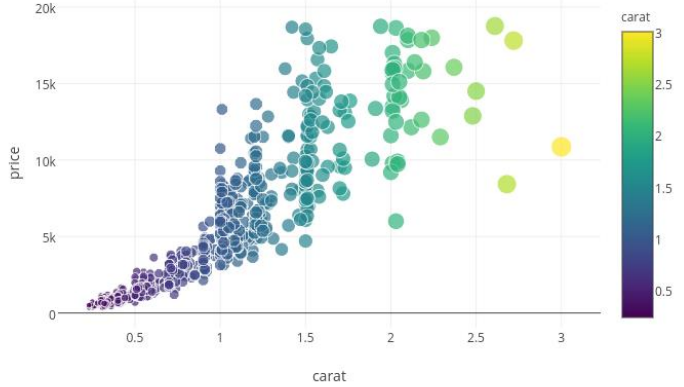












Advantages:

- Fast and free
- Statistical researchers provide their methods as R packages
- Good graphics (MATLAB and python)
- Active user community (great support)
- Excellent data analysis;
- Forces you to think about your analysis
- Functions can be integrated in R packages

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- “Not user friendly at start - steep learning curve, minimal GUI”
- Easy to make mistakes and not know.
- Working with large datasets is limited by RAM

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#I want to calculate the sum of each column
and if it is > 10, print out "column X has
sum greater than 10"

for (i in 1:ncol(t)) {
      f<-sum(t[,i])
      if (f>10) {
            print (paste("Column ", i, "
has a sum greater than 10", sep=""))
      }
      else {
      }
}
```

Advantages:

- **Functions** can be integrated in R packages

```
sum_10 <- function(table) {

for (i in 1:ncol(table)) {
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sum greater than 10", sep=""))
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      }
}

}
```

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dim(t) #number of columns and rows

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sum greater than 10"

sum_10(t)
```
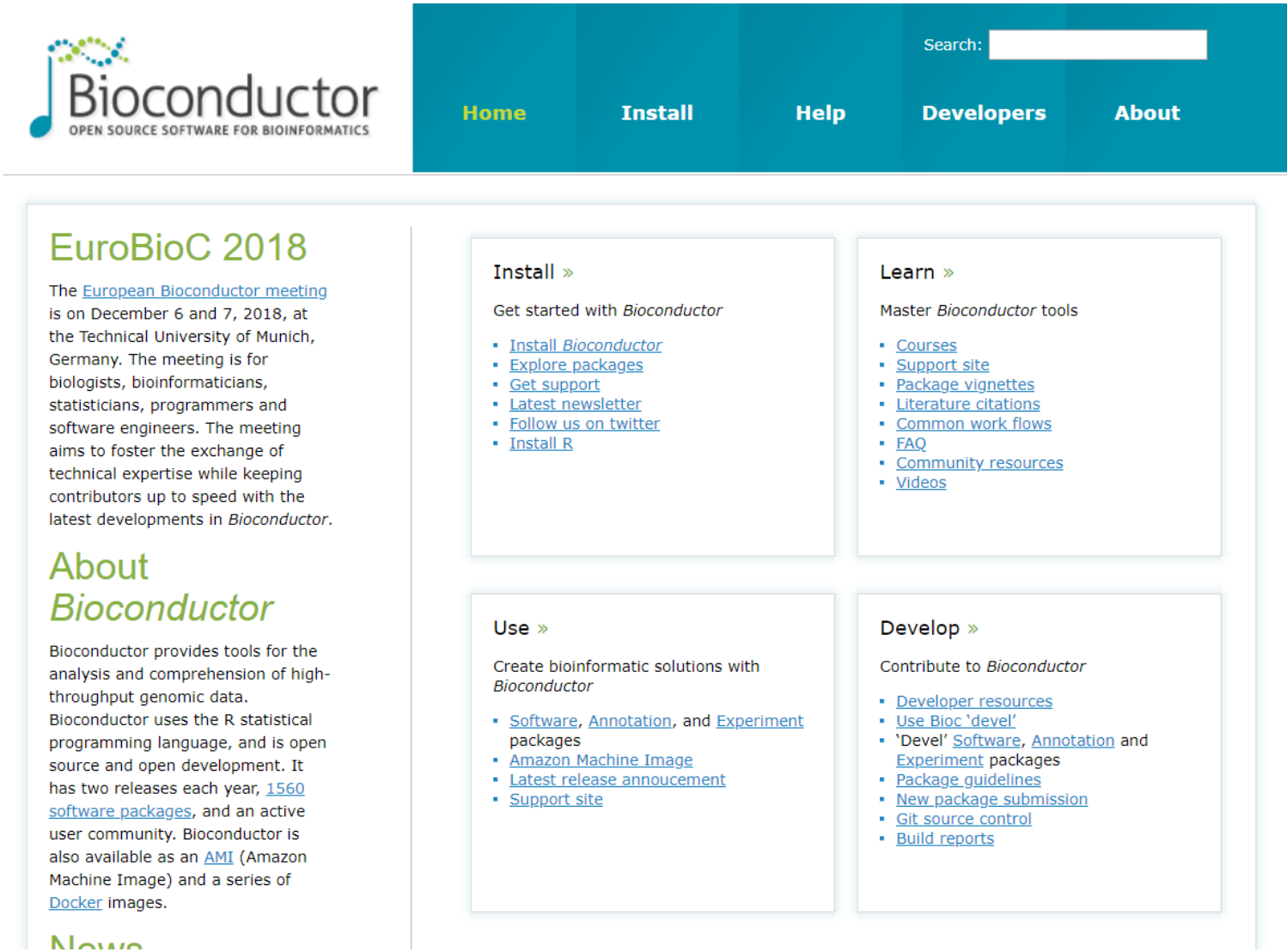

Advantages:

- Active user community (great support)

R packages for:

- Statistical analysis;
- Plotting;
- Graphs;
- Managing calendar dates;
- Selecting colour palette;
- Machine learning;
- Population genetics;
- …



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Variables:

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Assignment “<-”:

- t<-3, T<-5, X.1<-9;
- In 2001, the “=“ assignment was introduced for compatibility with other languages;

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Assignment “<-”:

- t<-3, T<-5, X.1<-9;
- In 2001, the “=“ assignment was introduced for compatibility with other languages;

```
> t<-3

> k<-“hello”

> a<-1.435275289
```

Arithmetic operators:

- Addition: +
- Subtraction: -
- Division: /
- Multiplication: *
- Exponentiation: ^

- We can use R as a calculator:

```
> (3+2)^2
[1] 25

> (7-5)/2
[1] 1

> 1*2*3*4
[1] 24
```

Data type:

- Numeric, character and logical

```
> t<-2.356  #numeric variable

> t<-”hello” #character variable

> t<-TRUE; f<-FALSE #logical variables
```

Data structure:

- **Vector**: an ordered collection of data;
- **Matrix**: two-dimensional generalisations of vectors
- **Array**: multi-dimensional generalisations of vectors

c function for concatenating values and vectors to create longer vectors

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```
> t<-c(3, 5.6748, 67, 5) #numeric vector

> t<-c(1, 1:3, c(5, 8), 13)
[1] 1  1  2  3  5  8 13

> t<-c("hello", "how", "are", "you", "?") #character vector
```

c function for concatenating values and vectors to create longer vectors

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```
> t<-c(3, 5.6748, 67, 5) #numeric vector

> length(t)
[1] 4
```

c function for concatenating values and vectors to create longer vectors

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```
> matrix(c(1,2,3,4,5,6), ncol=2, nrow=3)

      [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
```

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     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6

> dim(t)
[1] 3 2
```

c function for concatenating values and vectors to create longer vectors

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```
> matrix(c(1,2,3,4,5,6), ncol=2, nrow=3, dimnames=list(c("Variable_1",
"Variable_2", "Variable_3"), c("factor_1","factor_2")))


            factor_1 factor_2
Variable_1        1        4
Variable_2        2        5
Varibale_3        3        6
```

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```
> array(1:24,dim = c(4, 3, 2), dimnames = list(c("one", "two", "three",
"four"),c("apple", "orange", "pear"),
    c("land", "sea")))
```

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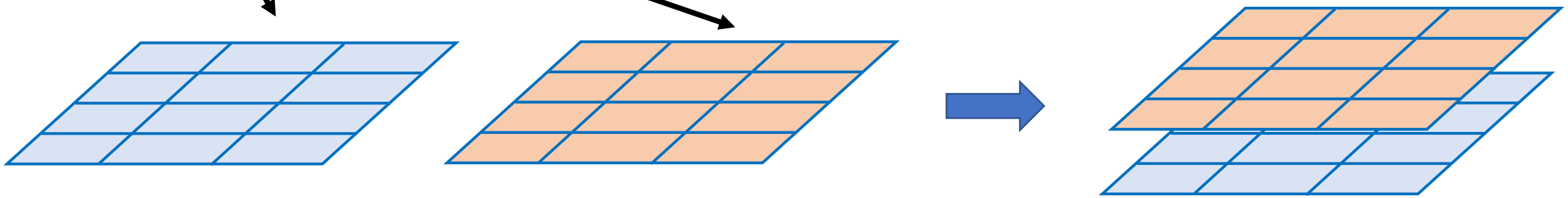

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"four"),c("apple", "orange", "pear"),
    c("land", "sea")))

, , land

      apple orange pear
one       1      5    9
two       2      6   10
three     3      7   11
four      4      8   12

, , sea

      apple orange pear
one      13     17   21
two      14     18   22
three    15     19   23
four     16     20   24
```

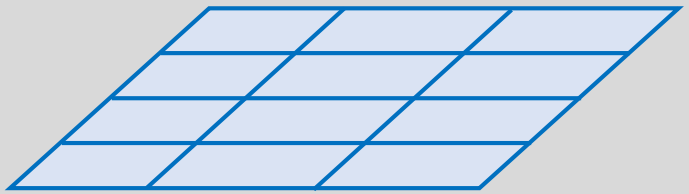

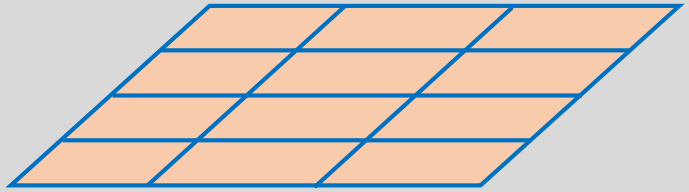

Data structure:

- **Data frame**: are matrix-like structure but the columns can be of different data types (i.e. numerical and character)

```
> data.frame(weight=c(1,23,4,56,32), gender=c("M","F","F","M","F"))

      weight gender
1      1      M
2     23      F
3      4      F
4     56      M
5     32      F
```

Indexing and selecting:

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- **Vector:**

```
> t<-c(3, 5.6748, 67, 5) #numeric vector

> length(t)
[1] 4

> t[3]
[1] 67

> t[c(2,4)]
[1] 5.6748  5
```

Indexing and selecting:

- **Matrix:**

```
> t<- matrix(c(1,2,3,4,5,6), ncol=2, nrow=3)
      [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6

> dim(t)
[1] 3 2

> t[1,] #row 1
[1] 1 4

> t[,2] #column 2
[1] 4 5 6
```

Indexing and selecting:

- **Matrix:**

```
> t<- matrix(c(1,2,3,4,5,6), ncol=2, nrow=3)
      [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6

> dim(t)
[1] 3 2

> t[3,2] #specific cell
[1] 6
```

Indexing and selecting:

- **Matrix:**

```
> t <- matrix(c(1,2,3,4,5,6), ncol=2, nrow=3, dimnames=list(c("Variable_1",
"Variable_2", "Variable_3"), c("factor_1","factor_2")))


            factor_1 factor_2
Variable_1        1        4
Variable_2        2        5
Varibale_3        3        6

> t["Variable_3", "factor_2"]
[1] 6
```

Indexing and selecting: Array

```
> t <- array(1:24,dim = c(4, 3, 2), dimnames = list(c("one", "two",
"three", "four"),c("apple", "orange", "pear"),
    c("land", "sea")))

, , land

      apple orange pear
one       1      5    9
two       2      6   10
three     3      7   11
four      4      8   12

, , sea

      apple orange pear
one      13     17   21
two      14     18   22
three    15     19   23
four     16     20   24
```

Indexing and selecting: Array

```
> t <- array(1:24,dim = c(4, 3, 2), dimnames = list(c("one", "two",
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, , sea

      apple orange pear
one      13     17   21
two      14     18   22
three    15     19   23
four     16     20   24
```

```
> t[3,1,2]
[1] 15

> t["two","orange","land"]
[1] 6
```

Deleting:

```
> t<-10:20 #vector

> t
 [1] 10 11 12 13 14 15 16 17 18 19 20

> t[-2] #remove element in position number 2
 [1] 10 12 13 14 15 16 17 18 19 20

> t1<-t[-2]

> t1
[1] 10 12 13 14 15 16 17 18 19 20
```

Deleting:

```
> t<- matrix(c(1,2,3,4,5,6), ncol=3, nrow=2)

> t
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6

> t[-1,] #remove row1
[1] 2 4 6

> t[,-2] #remove col2
     [,1] [,2]
[1,]    1    5
[2,]    2    6
```

Commands/operations:

- paste text strings together;
- append element to vectors;
- operations between vectors and matrices (sum, difference);
- “apply” a specific rule/function to all columns/rows of a matrix;
- match specific elements;
- subset a vector or a matrix;
- …and many more!!

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- paste text strings together;
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- subset a vector or a matrix;
- …and many more!!

- “which” element satisfies a specific condition…

```
> t<-10:20 #vector
> t
 [1] 10 11 12 13 14 15 16 17 18 19 20

> which(t>15)
[1]  7  8  9 10 11

> t[which(t>15)]
[1] 16 17 18 19 20
```

Loops and conditional execution

Syntax:

```
for (variable in sequence) {
        statements
}
```

Loops and conditional execution

Syntax:

for (variable in sequence) {
statements
}

```
> for (i in 1:10) {
+ print(i)
+ }
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
```

```
> for (i in 1:10) {
+ print(paste("hello to our customer number ",
i, sep=""))
+ }
[1] "hello to our customer number 1"
[1] "hello to our customer number 2"
[1] "hello to our customer number 3"
[1] "hello to our customer number 4"
[1] "hello to our customer number 5"
[1] "hello to our customer number 6"
[1] "hello to our customer number 7"
[1] "hello to our customer number 8"
[1] "hello to our customer number 9"
[1] "hello to our customer number 10"
```

Loops and conditional execution

Comparison operators

equal: ==
not equal: !=
greater: >
less than: <
greater or equal: >=
less than or equal: <=

Logical operators

and: &
or: |
not: !

Loops and conditional execution

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and: &
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Syntax:

```
If (condition) {

        statement

} else {

        alternative

}
```

Loops and conditional execution

Syntax:

If (condition) {

statement

} else {

alternative

}

```
> x<--4

> if(x>0){

+ print("Positive number")

+ } else if (x==0) {

+ print("Zero")

+ } else {

+ print("Negative number")

+ }

[1] "Negative number”
```

User-defined functions

```
myFunction <- function(arg1, arg2,..) {
        function_body
}

myFunction(arg1=..., arg2=...)
```

User-defined functions

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myFunction <- function(arg1, arg2,..) {
        function_body
}

myFunction(arg1=..., arg2=...)
```

```
> myvar<-function(x) {
+ y<-sum((x-mean(x))^2)/(length(x)-1)
+ return(y)
+ }

> a<-rnorm(6)

> a
[1] -0.9379583  0.6599282  0.6204624
0.4395611  1.0989696  2.4148308

> var(a)
[1] 1.171392

> myvar(a)
[1] 1.171392
```

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- Why R? What can R do?
- Basic commands and operations
- Data analysis in R
- Github and Gitlab

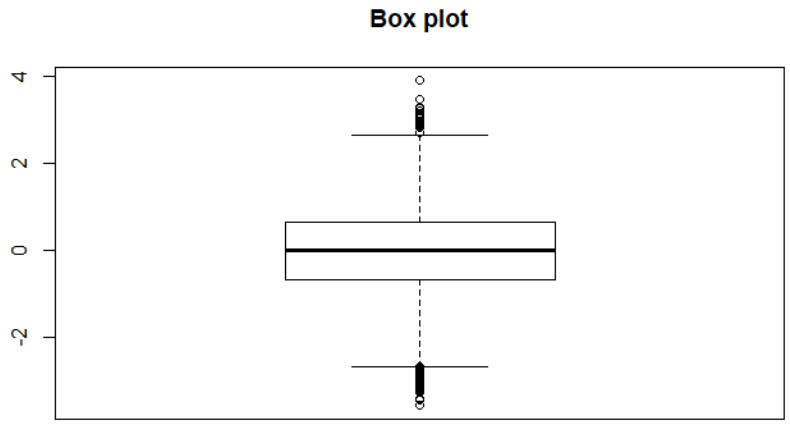
- Descriptive Statistics
- Statistical Modeling
  - Regressions: Linear and Logistic;
  - Time Series;
  - …
- Multivariate Functions
- Bayesian statistics
- Machine learning
- Inbuilt Packages, contributed packages

Basic statistical analysis

```
#generate random number form normal distribution
> x<-rnorm(10000,0,1)

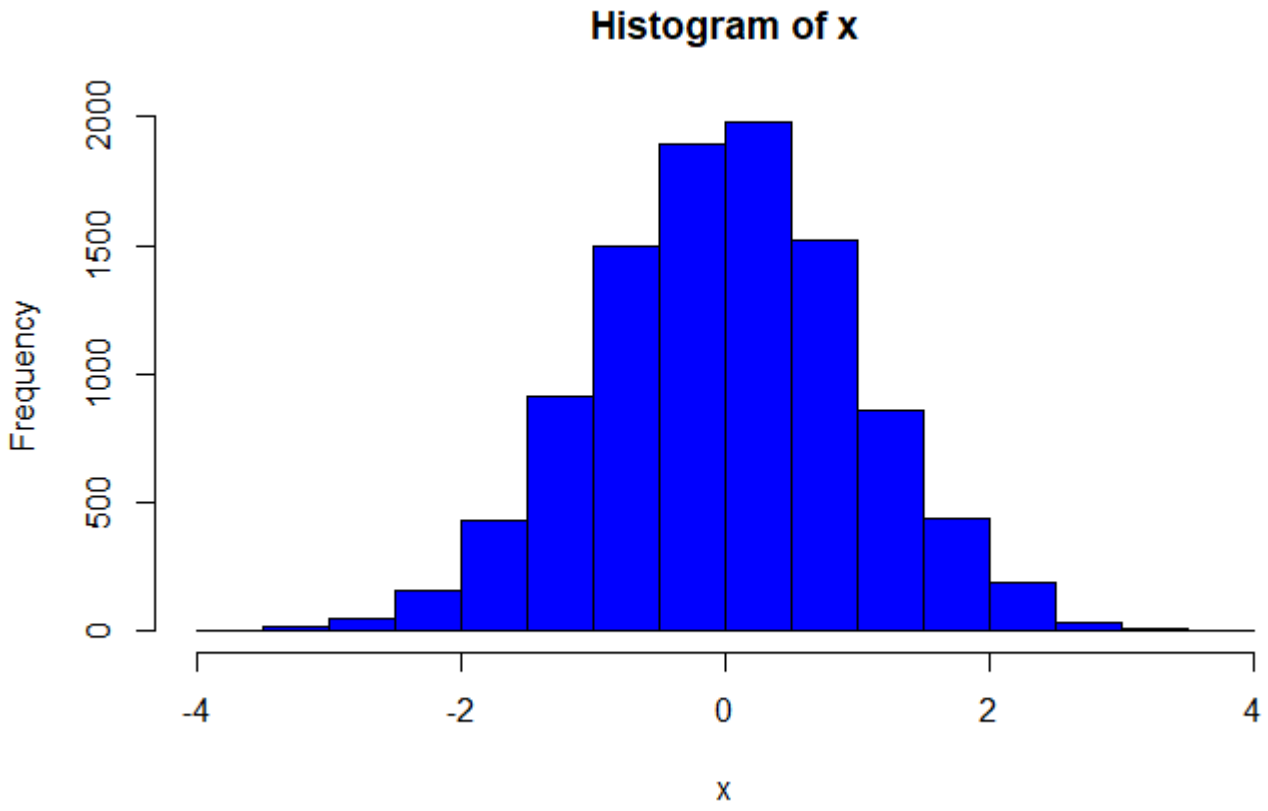
#get a summary of the distribution
> summary(x)
 Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-3.55700 -0.66420  0.00822  0.00131  0.66440  3.90500

> boxplot(x, main="Box plot")
```



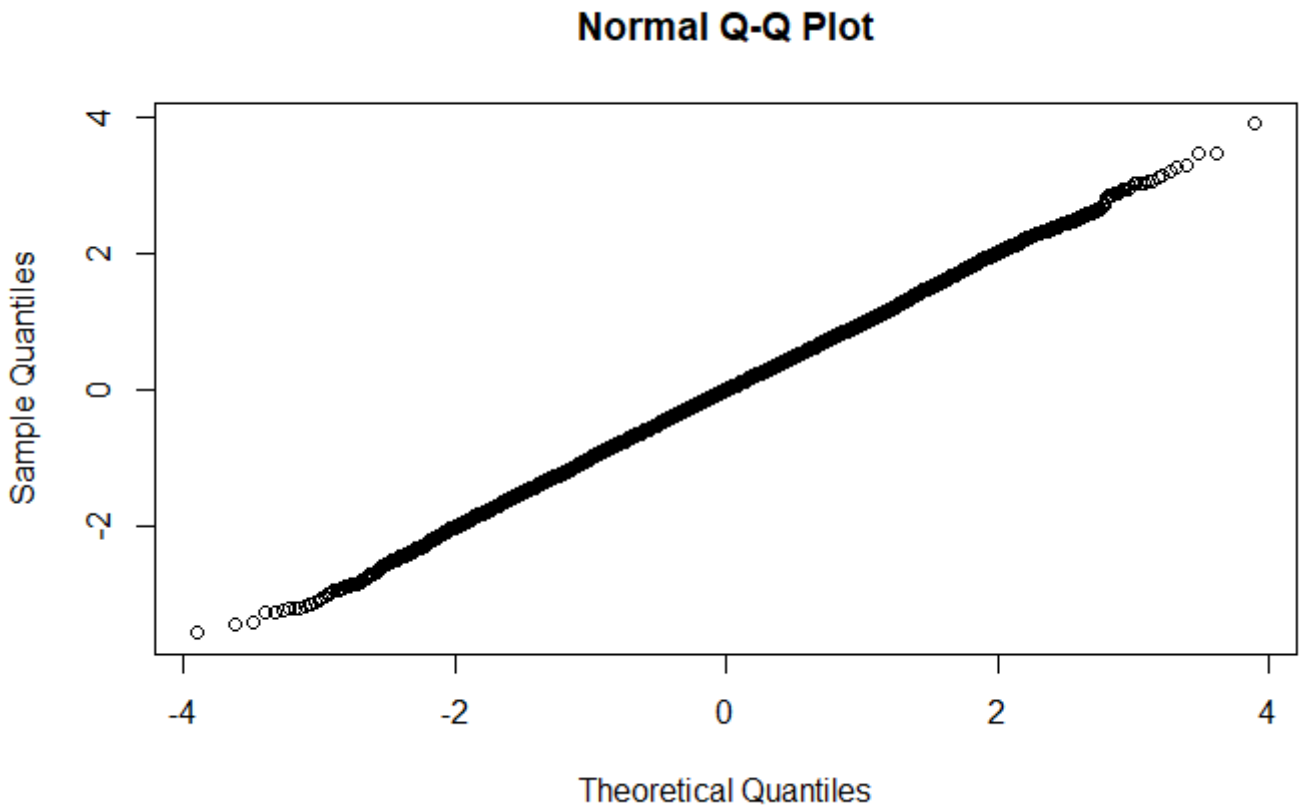
Basic statistical analysis

```
> hist(x, col="blue")
```



Basic statistical analysis

```
> qqnorm(x)
```



Parallel boxplots

```
> set.seed(12345)

> weight<-
round(c(rnorm(10,0,1),rnorm(10,2,
1)),3)

> group<-rep(c("ctrl","case"),
each=10)

> mydata<-data.frame(weight,
group)

> plot(weight~group, mydata)
```

Parallel boxplots

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> set.seed(12345)

> weight<-
round(c(rnorm(10,0,1),rnorm(10,2,
1)),3)

> group<-rep(c("ctrl","case"),
each=10)

> mydata<-data.frame(weight,
group)

> plot(weight~group, mydata)
```

```
 weight group
1   0.586  ctrl
2   0.709  ctrl
3  -0.109  ctrl
4  -0.453  ctrl
5   0.606  ctrl
6  -1.818  ctrl
7   0.630  ctrl
8  -0.276  ctrl
9  -0.284  ctrl
10 -0.919  ctrl
11  1.884  case
12  3.817  case
13  2.371  case
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17  1.114  case
18  1.668  case
19  3.121  case
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```
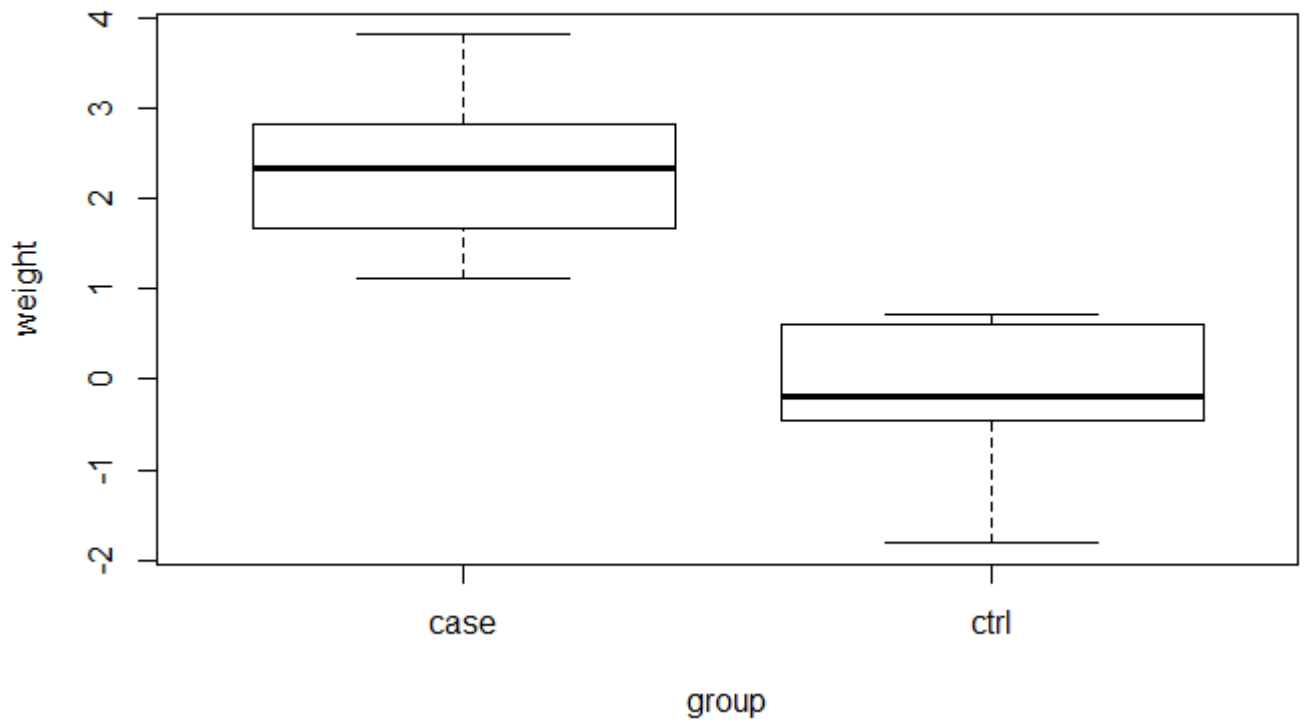

Parallel boxplots

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T-test

```
> t.test(weight~group, mydata)

      Welch Two Sample t-test

data:  weight by group
t = 6.5335, df = 17.979, p-value = 3.873e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 1.640945 3.196655
sample estimates:
mean in group case mean in group ctrl
            2.2860            -0.1328
```

A t-test is a linear regression…

```
> summary(lm(weight~group, mydata))

Call:
lm(formula = weight ~ group, data = mydata)

Residuals:
    Min      1Q  Median      3Q     Max 
-1.6852 -0.4560  0.0184  0.7238  1.5310 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   2.2860     0.2618   8.733 6.89e-08 ***
groupctrl    -2.4188     0.3702  -6.534 3.85e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8278 on 18 degrees of freedom
Multiple R-squared:  0.7034,	Adjusted R-squared:  0.6869 
F-statistic: 42.69 on 1 and 18 DF,  p-value: 3.85e-06
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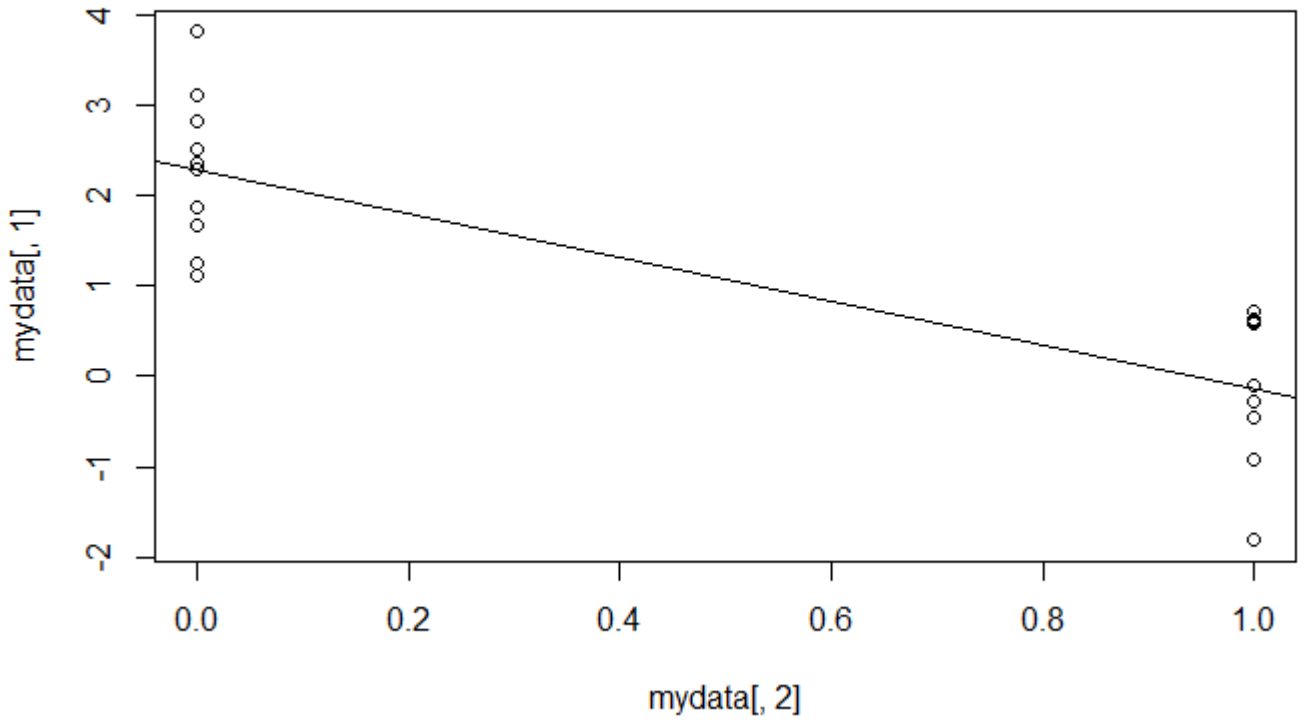


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```

- Logistic regression;
- Bayesian analysis (Bayer factor, library(BayesFactor);
- ANOVA;
- Approximate Bayesian Computation (ABC) framework;
- ….

Outline:

- Why R? What can R do?
- Basic commands and operations
- Data analysis in R
- Github and Gitlab

- Github: “GitHub is a development platform inspired by the way you work. From open source to business, you can host and review code, manage projects, and build software alongside 31 million developers.”

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Coding

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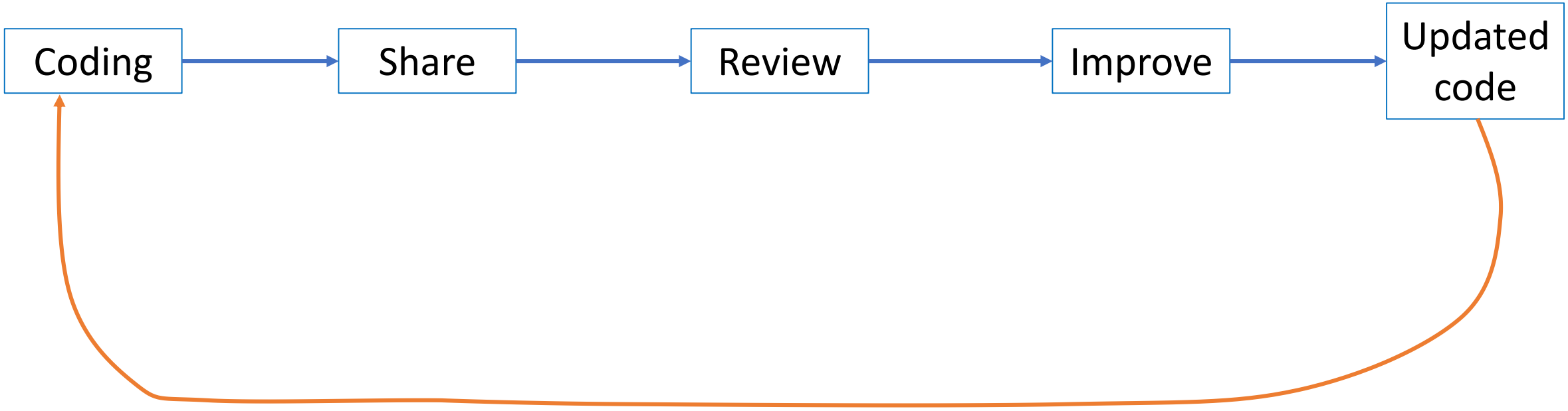

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David Reich Lab

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Thibaut Jombart
thibautjombart

Lecturer in genetic analysis & outbreak response at Imperial College London. R geek. Muay Thai enthusiast. Vocalist of the grind/hardcore band The Brood.

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Basic Tools for the Analysis of Disease Outbreaks
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apex
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R 4 2

adephylo
exploratory analyses for the phylogenetic comparative method
R 3

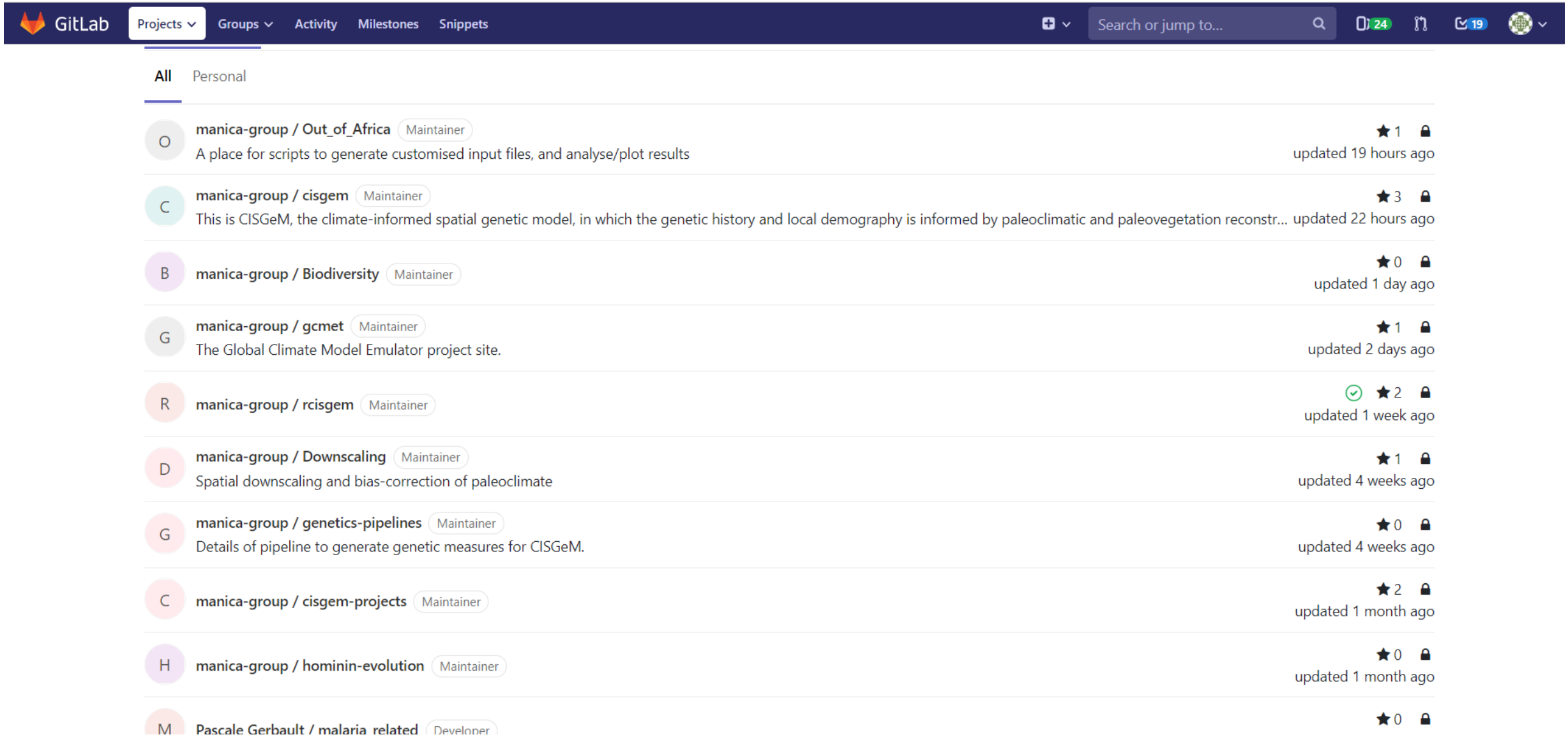
1,198 contributions in the last year

Nov Dec Jan Feb Mar Apr May Jun Jul Aug Sep Oct

- Gitlab: Github for companies, university group, enterprises

    - More interaction between users;
    - You can create different projects;
    - You can submit issues and assign them to different lab members;
    - You can use as lab notebook;
    - You can set up mile stones;
    - ….

Github and Gitlab



Github and Gitlab

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Pi and D outputs in statistics
#59 · opened 1 month ago by Robert Beyer
0 updated 1 month ago

Hunter-gatherer carrying capacity
#58 · opened 3 months ago by Robert Beyer
4 updated 4 days ago

cell distance is hardcoaded, it shoudl be a paramater from the environment file
#57 · opened 4 months ago by Andrea Manica New feature
1 updated 4 months ago

Add MD5 checksum for input files to output streams
#52 · opened 4 months ago by Mario Krapp Version 1.0 New feature
1 updated 3 months ago

rename variable names for consistency with input variables
#50 · opened 4 months ago by Mario Krapp
2 updated 4 months ago

Add Continuous Integration
#42 · opened 5 months ago by Mario Krapp
1 updated 5 months ago

Add parameter values + input file names to output files (demography_output.nc, genealogy_trees.txt)
#40 · opened 5 months ago by Robert Beyer
2 updated 3 months ago

adding extra information to genetics nc file
#38 · opened 5 months ago by Eppie Jones New feature
0 updated 5 months ago

Find optimal number for genealogy trees to decrease overall runtime of MC sweep
#37 · opened 5 months ago by Mario Krapp New feature
0 updated 5 months ago

- Github and gitlab…why???

- It helps to promote reproducible science;
- More transparent and clear specifically for data analysis;
- Working together (with other users) helps to improve and grow faster;

Conclusions:

- R is a flexible language for data analysis, summary, visualisation and modelling;
- R community is vast, lots of support and developers (R package);
- Sharing code, science reproducibility and help the scientific community to grow faster;