



Tools for biologists

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How organizing an R script

A well-organized R script is essential for readability, reproducibility and collaboration with colleagues that are or not proficient in R.

1. Each script should answer one main question
2. Avoid “monster script”
3. If needed, split the workflow into multiple scripts or sections.
 - I. 01_data_cleaning_210126.R
 - II. 03_data_analysis_230126.R
 - III. 04_plots_150126.R

Hints:

- Separated words by “underscore” (_) (snake_case)
- Use the functions save() and load() to export and import data
- Add the date in the name of the file.

The functions save and load

Create an R studio project

Create a data frame

Save the data.frame using the function *save()*

e.g. *save(yourobject, file = "path.rda")*

Clean objects from the workspace

Load the object using the function *load()*

e.g. *load(file = "path.rda")*

How organizing an R script

4. Start with a header

5. Load packages at the beginning

6. Add customized R functions

7. Organize code into logical sections

```
# 1. Data import  
# 2. Data cleaning  
# 3. Exploratory analysis  
# 4. Statistical analysis  
# 5. Visualization  
# 6. Export results
```

8. Avoid manual steps

9. Save, run, rerun

```
1 ###### ##### ##### ##### ##### ##### ##### ##### ##### ##### ##### ##### #####  
2 ##### Mapping sexual dimorphism signal in the human cranium #####  
3 ##### ##### ##### ##### R code ##### ##### ##### ##### ##### ##### #####  
4 ##### ##### ##### ##### ##### ##### ##### ##### ##### ##### ##### #####  
5  
6 #load libraries  
7 { }  
22  
23 #load functions  
24 { }  
350  
351 #load data  
352 { }  
361  
362 #Figure 1 - R code  
363 { }  
414  
415 #Figure 2 - R code  
416 { }  
444  
445 #Figure 4 - R code  
446 { }  
477  
478 #Figure 5 - R code - frontal region  
479 { }  
583 |  
584 #Figure 6 - R code - module definition  
585 { }  
608  
609 #Figure 6 - nasal region module  
610 { }  
698  
699 #Figure 6 - frontal region module  
700 { }  
786  
787 #Figure 6 - mastoid process module  
788 { }  
876
```

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```
362 #Figure 1 - R code  
363 {  
364 PCA<-procSym(lset,sizeshape = TRUE)  
365 PCscores<-PCA$PCscores  
366 Variance<-PCA$Variance  
367 PCx<-1  
368 PCy<-2  
369 xlim<-c(-1*max(abs(PCscores[,PCx])),max(abs(PCscores[,PCx])))  
370 ylim<-c(-1*max(abs(PCscores[,PCy])),max(abs(PCscores[,PCy])))  
371 xlab<-paste("PC",PCx," ",round(Variance[PCx,2],2), "%",sep="")  
372 Ylab<-paste("PC",PCy," ",round(Variance[PCy,2],2), "%",sep="")  
373 dir.create("Figure_1")  
374 t.test(PCscores[,1]~group)  
375 t.test(PCscores[,2]~group)  
376 summary(procD.lm(PCscores~group))  
377 summary(procD.lm(PCscores~PCA$size))  
378 summary(procD.lm(PCscores~PCA$size*group))  
379 summary(procD.lm(PCscores[,1]~group))  
380 summary(procD.lm(PCscores[,1]~PCA$size))  
381 summary(procD.lm(PCscores[,2]~group))  
382 summary(procD.lm(PCscores[,2]~PCA$size))  
383  
384  
385 tiff("Figure_1/Fig. 1 - PCA_formspace.tiff",width = 1500,height = 1500,pointsize = 6,res = 300)  
386 par(mar = c(5, 5, 5, 5))  
387 plot(NA,xlim=extendrange(xlim),ylim=extendrange(ylim),xlab=xlab,ylab=Ylab,asp=1,  
388 main="",cex.axis=1.5,cex.main=2.5,cex.lab=2,  
389 cex=2)  
390 abline(v=0,lty=2,lwd=0.7)  
391 abline(h=0,lty=2,lwd=0.7)  
392  
393 cols<-c("deepskyblue3","khaki2")  
394 sex<-group  
395 for(i in 1:2){  
396 sel<-which(sex==levels(as.factor(sex))[[i]])  
397 pchi<-sex[sel]  
398 pchi[pchi=="M"]<-19  
399 pchi[pchi=="F"]<-19  
400 mat<-PCscores[sel,c(PCx,PCy)]  
401 conv<-chull(mat)  
402 polygon(mat[c(conv,conv[1]),],col=adjustcolor(cols[i],alpha.f=0.3))  
403 points(mat,col=cols[i],pch=as.numeric(pchi),cex=1.5)  
404 }  
405 dev.off()
```

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371 xlab<-paste("PC",PCx," ",round(Variance[PCx,2],2), "%",sep="")  
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373 dir.create("Figure_1")  
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386 par(mar = c(5, 5, 5, 5))  
387 plot(NA,xlim=extendrange(xlim),ylim=extendrange(ylim),xlab=xlab,ylab=Ylab,asp=1,  
      main="",cex.axis=1.5,cex.main=2.5,cex.lab=2,  
      cex=2)  
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390  
391 cols<-c("deepskyblue3","khaki2")  
392 sex<-group  
393 for(i in 1:2){  
394   sel<-which(sex==levels(as.factor(sex))[[i]])  
395   pchi<-sex[sel]  
396   pchi[pchi=="M"]<-19  
397   pchi[pchi=="F"]<-19  
398   mat<-PCscores[sel,c(PCx,PCy)]  
399   conv<-chull(mat)  
400   polygon(mat[c(conv,conv[1]),],col=adjustcolor(cols[i],alpha.f=0.3))  
401   points(mat,col=cols[i],pch=as.numeric(pchi),cex=1.5)  
402 }  
403 dev.off()
```

What's wrong with this script?

```
library(ggplot2)
x <- read.csv("data.csv", sep=";", dec=",")
mean(x$size)
ggplot(x, aes(size, shape)) +
  geom_point()
x <- x[x$size > 0, ]
library(dplyr)
write.csv(x, "clean_data.csv")
# PCA
pca <- prcomp(x[,3:6], scale.=TRUE)
summary(pca)
setwd("/Users/student/Desktop/project")
library(vegan)
```

What's wrong with this script?

```
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x <- read.csv("data.csv", sep=";", dec=",")
mean(x$size)
ggplot(x, aes(size, shape)) +
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library(dplyr)
write.csv(x, "clean_data.csv")
# PCA
pca <- prcomp(x[,3:6], scale.=TRUE)
summary(pca)
setwd("/Users/student/Desktop/project")
library(vegan)
```

- No header or description
- Working directory set in the middle of the script
- Libraries loaded in different places
- Data cleaning after analysis
- Unclear object names (x)
- No section structure
- Hard-coded file paths

In class exercise

Load the data and prepare a clean and organized version of this script

An introduction to programming

R is an interpreted language; instructions are executed one at a time.

This allows us to:

1. Repeat a group of instructions (*for, while, repeat* loops)
2. Execute instructions in an alternative way (conditional statements)

Examples:

Ex. 1 Copy – rename – paste all files contained within a folder

Ex. 2 Data simulation (coin toss, bootstrap)

Ex. 3 Meta-analysis (e.g., systematic literature review, word cloud)

Create a loop

Create an empty R object (eg. extractions <- NULL)

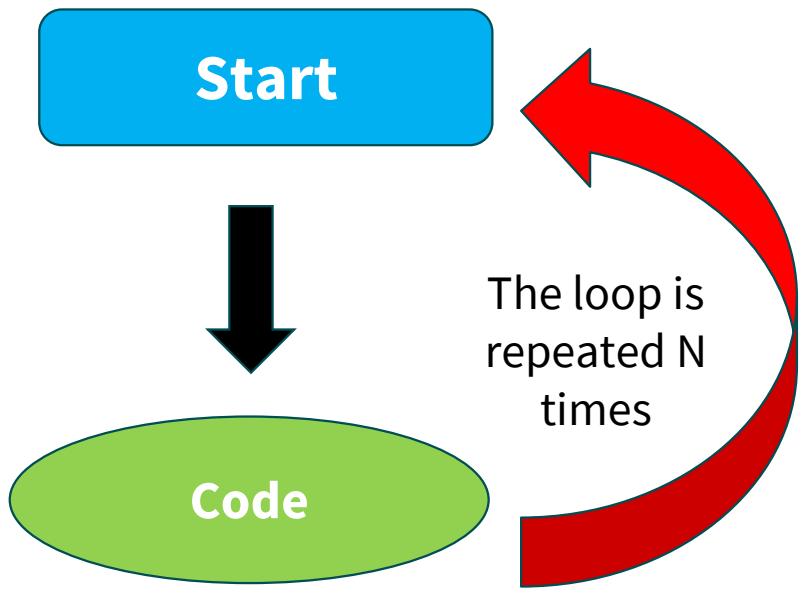
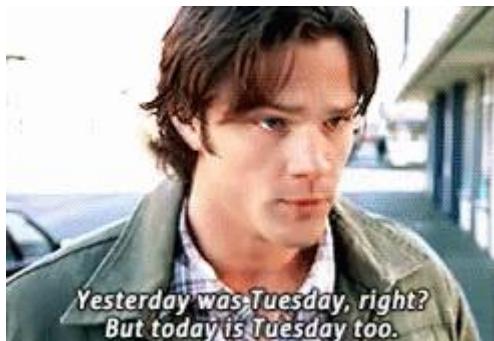
Define how many times the loop will repeat (eg. 100, 1000, etc.)

Insert code to be repeated

```
#Flip a coin
```

```
Flip<-sample(c("Heads", "Tails")
```

```
#Assign the result of the extraction, at each iteration, in the object  
extractions <- c(extractions, extractions)
```



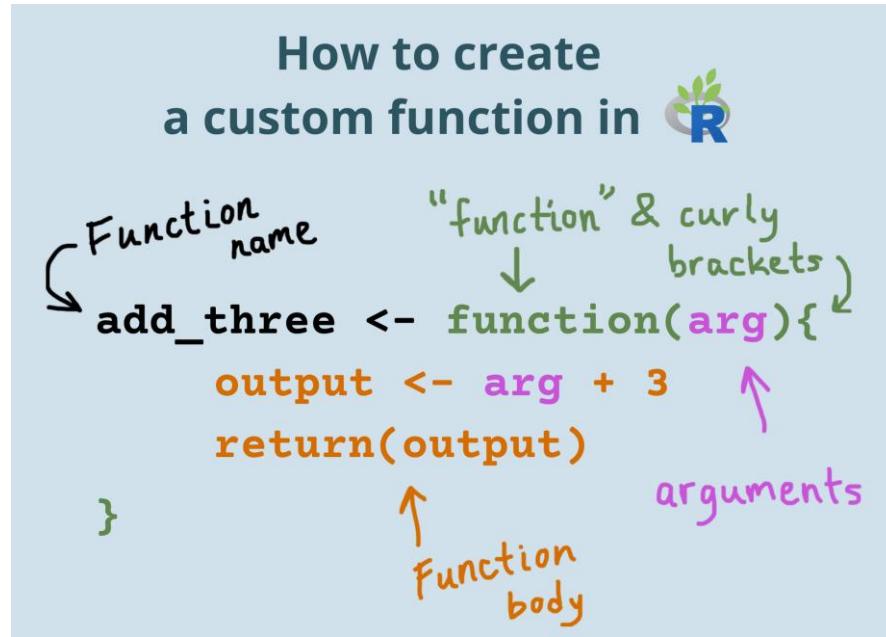
Result of i -th (each iteration)

How writing an R function?

Why writing a function?

1. The function is not embedded in an existing R package
2. Avoid repeating the same code
3. Make analysis reproducible and repeatable
4. Convert workflows into reusable tools

How writing an R function?



Basic structure of a function

1. Use `function()`
2. Define input arguments
3. Write the R code body
4. Return the output

```
add_three <- function(arg) {  
  output <- arg + 3  
  return (output)  
}
```

In class exercise

Load the data and prepare a clean and organized version of this script

How writing an R function?

Goal: Write an R function that calculates the Euclidean distance between two points in a 2D space.

Hints:

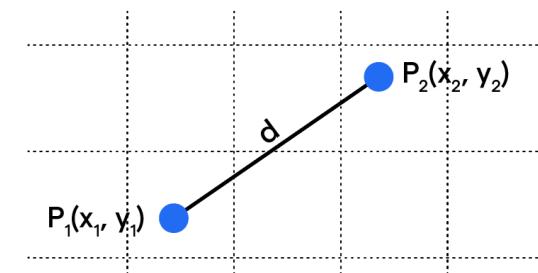
1. A point in 2D space is defined by its coordinates: $P=(x,y)$
2. The Euclidean distance between two points

Euclidean Distance

$$P_1 = (x_1, y_1) \text{ and } P_2 = (x_2, y_2)$$

$$d = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$$

3. use `sqrt()` and `^2`



$$\text{Euclidean Distance (d)} = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$$

The function locator

`locator()` is an interactive function that allows the user to click on a plot and retrieve x and y coordinates of the clicked points

1. `locator(n)` n = number of points to select
2. The output is a list with two elements:
 1. `$x` -> x coordinates
 2. `$y` -> y coordinates

```
plot(c(1:10),c(1:10))
pts<-locator(3)
pts$x
pts$y
```

Write a function - exercise

Write an R function to measure the distance between two points in an interactive way

1 – Generate a matrix with 25 rows and 2 columns

2 – Create a plot

3 – Use the function locator to select 2 points

4 – Calculate the Euclidean distance

5 – Return and print the value