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R for Bioinformatics and HDS

R & RStudio:

Working with Data frames



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Course Structure

- Introduction to R & RStudio
- Syntax, Comments, Variables, Data Types and Operators
- Conditions, Loops, Functions and Data Structures
- Working with Data frames



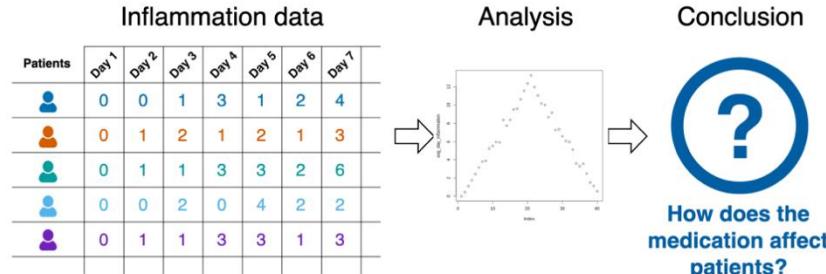
Getting started

- The best way to learn how to work with data frames is to do something useful, so this session is built around a common scientific task: data analysis.
- To do that, we will use the following case scenario, borrowed by the Carpentries:



Arthritis Inflammation

- We are studying **inflammation in patients** who have been given a new treatment for arthritis.
- There are 60 patients, who had their inflammation levels recorded for 40 days. We want to analyse these recordings to study the effect of the new arthritis treatment.
- To see how the treatment is affecting the patients in general, we would like to:
 1. Calculate the average inflammation per day across all patients.
 2. Plot the result to discuss and share with colleagues.



Loading the inflammation data

- To begin processing data, we need to load them.
- Loading our inflammation data

```
read.csv(file = "data/inflammation-01.csv", header = FALSE)
```

- **Don't forget!** Store them into a variable to reuse them

```
data <- read.csv(file = "data/inflammation-01.csv", header = FALSE)
```



What is the structure of the "data" object?

- **Data frame:**
- Think of this structure as a spreadsheet in MS Excel that many of us are familiar with.
- Data frames are very useful for storing data and you will use them frequently when programming in R.
- A typical data frame of experimental data contains individual observations in **rows** and variables in **columns**.



Data Inspection

- Let's see the data

```
data
```

- What's the type of our data

```
class(data)
```

- What's the shape? (How many days? How many patients?)

```
dim(data)
```



Data Navigation

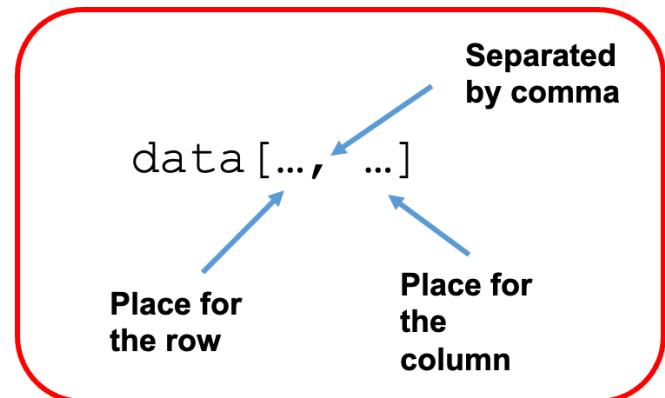
- What is the inflammation value of the first patient in the first day?

Remember! We start counting from “1”!

```
data[1, 1]
```

- What about the middle one?

```
data[30, 20]
```



Slicing data

- We can take more than one values from the dataset

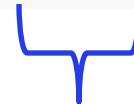
The inflammation scores of the first 4 patients across the first 10 days:

```
data[1:4, 1:10]
```

Or

The inflammation scores of 5 -10 patients across the first 10 days:

```
print(data[5:10, 1:10])
```



Range



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Analyzing Data

- We use functions (“canned scripts” that automate something complicated)
- Functions take inputs as arguments and return values as outputs (not in all cases!)
- How can we find the average of all the inflammation scores:

```
mean(data)
```

We use the function “mean” and our data as input



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Analyzing data – Descriptive functions

- We can apply many descriptive statistics
maxval, minval, stdval = max(data), min(data), sd(data)
- We can focus on the stats of one patient, or of one day

Like:

```
max(data[1,] #The maximum inflammation of patient 1
min(data[,1] #The minimum inflammation of day 1
median(data[,7]) #The median inflammation of day 7
```



Analysing data - summary

- We can have a summary of the descriptive statistics of all our data

```
summary(data[, 1:4]) # Summarize function summary
```

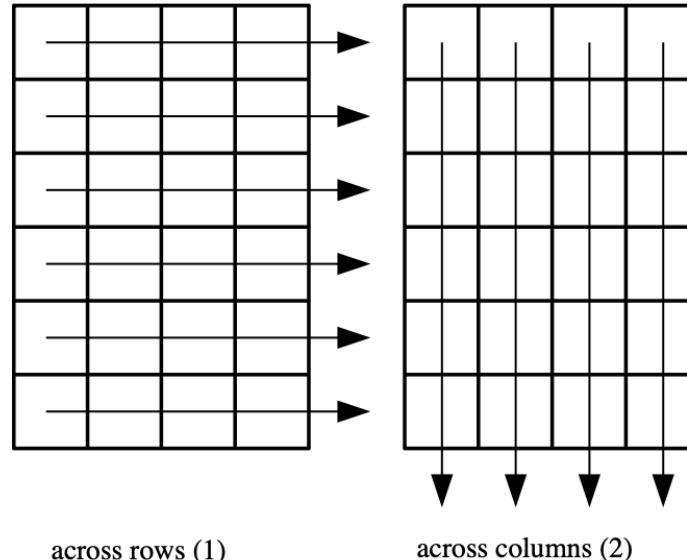
OUTPUT<>

| | V1 | V2 | V3 | V4 |
|--|-----------|--------------|---------------|--------------|
| | Min. :0 | Min. :0.00 | Min. :0.000 | Min. :0.00 |
| | 1st Qu.:0 | 1st Qu.:0.00 | 1st Qu.:1.000 | 1st Qu.:1.00 |
| | Median :0 | Median :0.00 | Median :1.000 | Median :2.00 |
| | Mean :0 | Mean :0.45 | Mean :1.117 | Mean :1.75 |
| | 3rd Qu.:0 | 3rd Qu.:1.00 | 3rd Qu.:2.000 | 3rd Qu.:3.00 |
| | Max. :0 | Max. :1.00 | Max. :2.000 | Max. :3.00 |



A little bit more advanced calculations....

- What if we need the maximum inflammation for each patient over all days or the average inflammation score for each day?



The *apply()* function

- If we want to calculate the average across the rows

```
apply(data, 1, mean)
```

- If we want to calculate the average across the columns

```
apply(data, 2, mean)
```

- And we can store them to a variable to reuse them...

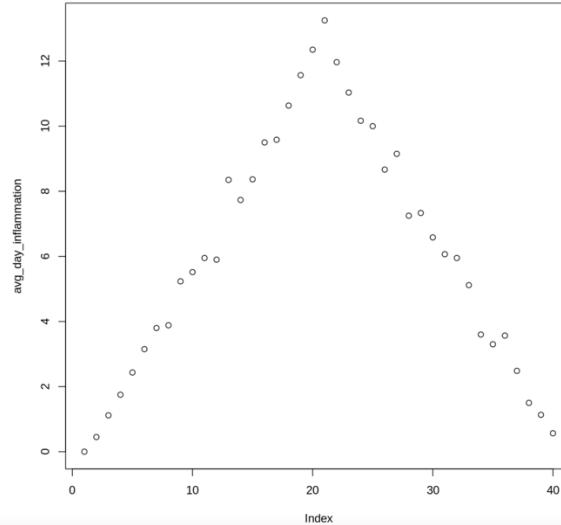
```
avg_patient_inflammation <- apply(data, 1, mean)  
avg_day_inflammation <- apply(data, 2, mean)
```

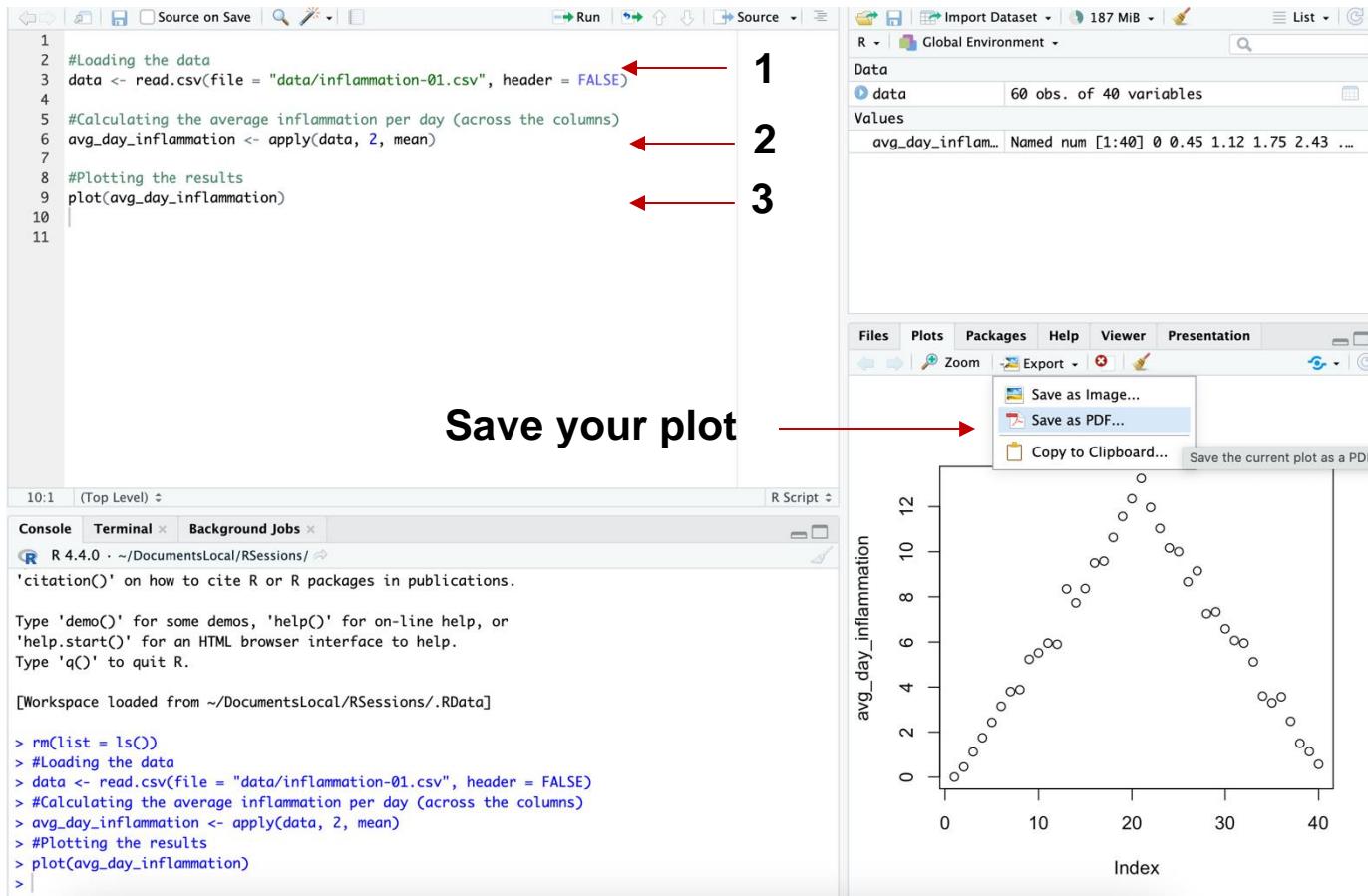


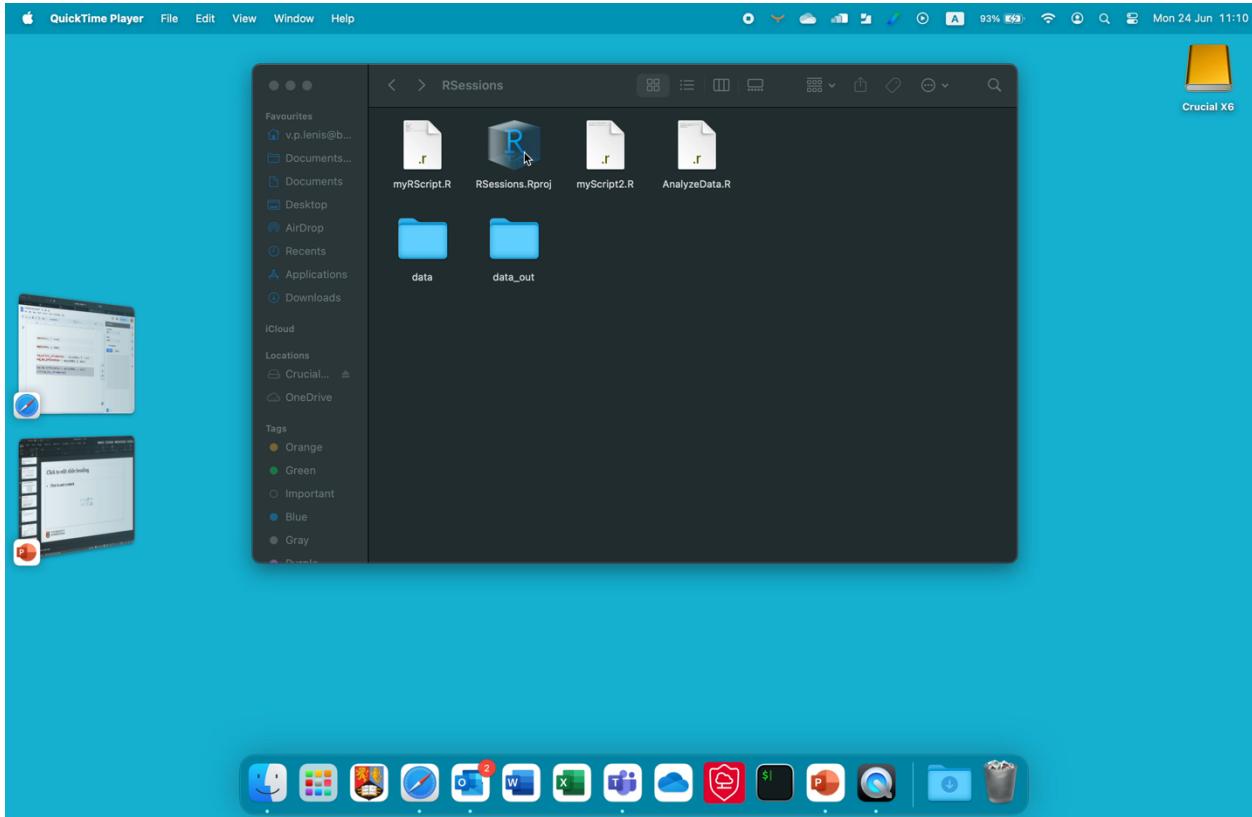
Let's plot!

- Let's have a look at the average inflammation over time:

```
avg_day_inflammation <- apply(data, 2, mean)  
plot(avg_day_inflammation)
```







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