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BASIC DATA MANIPULATION

SUBSET, MODIFY AND SHAPE YOUR DATA

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Tutorial aims:

1. Learn base R syntax for data manipulation
   - logical operators for finer control
   - creating and assigning objects
   - specifying factors
2. Turn messy data into tidy data with `tidyr`
3. Use efficient tools from the `dplyr` package to manipulate data

Steps:

1. Subset, extract and modify data with R base operators
2. What is tidy data, and how do we achieve it?

- `join()`

4. Challenge yourself!

Data come in all sorts of different shapes and formats, and what is useful or practical for one application is not necessarily so for another. R has specific requirements about the setup and the types of data that can be passed to functions, so one of the best skills in your coding toolbox is being able to play with your data like putty and give it any shape you need!

This tutorial is an introduction to data manipulation and only requires an understanding of how to import and create objects in R. That said, there's still a lot of content in here for a beginner, so do not hesitate to complete only the base R section in one session, and the `dplyr` section in another. (Remember! The beauty of a script is that you can pick up where you left off, anytime.)

> **Haven't used R before, or need a refresher?** No worries! Check out our Intro to R and RStudio tutorial, and then come back here to master tidy data management!
>
> **Know all of this already?** Fast forward to our Efficient Data Manipulation tutorial for more advanced `dplyr` fun or to Advanced Data Manipulation tutorial for even deeper `dplyr` knowledge.

In this tutorial, we will start by showing some ways to manipulate data using *base R* syntax (without any extra package), because you will often see solutions online using this syntax, and it is good to understand how objects are built (and how to take them apart). After that, we will introduce principles of tidy data to encourage best practice in data collection and organisation. We will then start using packages from the Tidyverse , which is quickly becoming the norm in R data science, and offers a neater, clearer way of coding than using only base R functions.

> All the files you need to complete this tutorial can be downloaded from this repository. Clone and download the repo as a zip file, then unzip it.

Data frames are R objects made of rows and columns containing observations of different variables: you will often be importing your data that way. Sometimes, you might notice some mistakes after importing, need to rename a variable, or keep only a subset of the data that meets some conditions. Let's dive right in and do that on the `EmpetrumElongation.csv` dataset that you have downloaded from the repository.

Create a new, blank script, and add in some information at the top, for instance the title of the tutorial, your name, and the date (remember to use hashtags # to comment and annotate your script).

This dataset represents annual increments in stem growth, measured on crowberry shrubs on a sand dune system. The `Zone` field corresponds to distinct zones going from closest (2) to farthest (7) from the sea.

A crowberry shrub, *Empetrum hermaphroditum*. Isn't it pretty?

We have seen in our intro tutorial that we can access variables in R by using the dollar sign `$`. This is already one way of subsetting, as it essentially reduces your data frame (2

```
# Load the elongation data
elongation <- read.csv("EmpetrumElongation.csv", header = TRUE)

# Check import and preview data
head(elongation)   # first few observations
str(elongation)    # types of variables

# Let's get some information out of this object!
elongation$Indiv   # prints out all the ID codes in the dataset
length(unique(elongation$Indiv))   # returns the number of distinct sh
rubs in the data

# Here's how we get the value in the second row and fifth column
elongation[2,5]

# Here's how we get all the info for row number 6
elongation[6, ]

# And of course you can mix it all together!
elongation[6, ]$Indiv   # returns the value in the column Indiv for th
e sixth observation
# (much easier calling columns by their names than figuring out where
 they are!)
```

Subsetting with brackets using row and column numbers can be quite tedious if you have a large dataset and you don't know where the observations you're looking for are situated! And it's never recommended anyway, because if you hard-code a number in your script and you add some rows later on, you might not be selecting the same observations anymore! That's why we can use **logical operations** to access specific parts of the data that match our specification.

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```
# Let's access the values for Individual number 603
elongation[elongation$Indiv == 603, ]
```

There's a lot to unpack here! We're saying: "Take this dataframe (`elongation`), subset it (`[ , ]`) so as to keep the rows (writing the expression on the left-hand of the comma) for which the value in the column Indiv (`$Indiv`) is exactly (`==`) 603". **Note**: The logical expression works here because the Indiv column contains numeric values: to access data

Here are some of the most commonly used operators to manipulate data. When you use them to create a subsetting condition, R will evaluate the expression, and return only the observations for which the condition is met.

`==`: equals exactly

`<`, `<=`: is smaller than, is smaller than or equal to

`>`, `>=`: is bigger than, is bigger than or equal to

`!=`: not equal to

`%in%`: belongs to one of the following (usually followed by a vector of possible values)

`&`: AND operator, allows you to chain two conditions which must both be met

`|`: OR operator, to chains two conditions when at least one should be met

`!`: NOT operator, to specify things that should be omitted

Let's see them in action!

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```
# Subsetting with one condition

elongation[elongation$Zone < 4, ]    # returns only the data for zones 2-3
elongation[elongation$Zone <= 4, ]   # returns only the data for zones 2-3-4


# This is completely equivalent to the last statement
elongation[!elongation$Zone >= 5, ]   # the ! means exclude


# Subsetting with two conditions
elongation[elongation$Zone == 2 | elongation$Zone == 7, ]    # returns only data for zones 2 and 7
elongation[elongation$Zone == 2 & elongation$Indiv %in% c(300:400), ]
# returns data for shrubs in zone 2 whose ID numbers are between 300 and 400
```

Did you notice that last bit of code: `c(300:400)` ? We saw in our intro tutorial that we can use `c()` to *concatenate* elements in a vector. Using a colon between the two numbers means *counting up from 300 to 400*.

Other useful vector sequence builders are:

`seq()` to create a sequence, incrementing by any specified amount. E.g. try `seq(300, 400, 10)`

`rep()` to create repetitions of elements. E.g. `rep(c(1,2), 3)` will give `1 2 1 2 1 2`.

You can mix and match! What would `rep(seq(0, 30, 10), 4)`give?

And finally, let's say you need to modify some values or factor levels, or want to create a new column? Now that you know how to access parts of a dataframe, you can do all of that. You only need an extra tool: the assign arrow `<-` to overwrite data.

Creating and overwriting objects

Remember how we've been using the arrow `<-` to create new objects? This is a special convention in R that allows you to pick whichever name you want and assign it to an object (vector, list, data frame…).

Something to keep in mind is that **if you use a name again in a same session, it will overwrite the former object**. With experience, you can start making changes to an object and overwrite as you go, to "update" the object rather than creating many intermediaries ("object1", "object2", …). However, when you're starting out, it's a good idea to create these intermediary objects, or at least to create a "working copy" that you can reassign to the main data object once you're satisfied with the changes.

As you will now see, we can also make use of the arrow `<-` to overwrite specific values or range of values we need to change.

```
names() function
# Used on its own, it returns a vector of the names of the columns. Us
ed on the left side of the assign arrow, it overwrites all or some of
 the names to value(s) of your choice.

names(elong2)                 # returns the names of the columns

names(elong2)[1] <- "zone"    # Changing Zone to zone: we call the 1st
element of the names vector using brackets, and assign it a new value
names(elong2)[2] <- "ID"      # Changing Indiv to ID: we call the 2nd
 element and assign it the desired value

# Now suppose there's a mistake in the data, and the value 5.1 for ind
ividual 373 in year 2008 should really be 5.7

## - option 1: you can use row and column number
elong2[1,4] <- 5.7

## - option 2: you can use logical conditions for more control
elong2[elong2$ID == 373, ]$X2008 <- 5.7   # completely equivalent to o
ption 1
```

Can you spot pros and cons of options 1 and 2 above?

Option 1 is compact, but requires you to know exactly where the value to be corrected is. If you reimport your dataset at a later time with new values, it may not be in the same place.

Option 2 is longer and more difficult to read (it uses brackets to extracts the row corresponding to individual #373, and then the dollar sign to access just the column called X2008), but provides fine control, and the code will run even if the observation moves in your dataset.

Using the same techniques, you can specify variable classes, which will be highly useful when we get to designing statistical models and need grouping variables like factors.

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```
## CREATING A FACTOR

# Let's check the classes
str(elong2)

# The zone column shows as integer data (whole numbers), but it's real
```

And what if you're not happy with the factor levels? You can see the names of the factors with the `levels()` function… and yes, overwrite them, too.

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```
## CHANGING A FACTOR'S LEVELS

levels(elong2$zone)  # shows the different factor levels

levels(elong2$zone) <- c("A", "B", "C", "D", "E", "F")   # you can ove
rwrite the original levels with new names

# You must make sure that you have a vector the same length as the num
ber of factors, and pay attention to the order in which they appear!
```

That was a lot, but now you'll be able to adapt these little chunks of code to manipulate your own data. The next sections will hopefully make things even easier, as they'll teach you more intuitive functions to accomplish the same things.

2. What is tidy data, and how do we achieve it?

The way you record information in the field or in the lab is probably very different to the way you want your data entered into R. In the field, you want tables that you can ideally draw up ahead of time and fill in as you go, and you will be adding notes and all sorts of information in addition to the data you want to analyse. For instance, if you monitor the height of seedlings during a factorial experiment using warming and fertilisation treatments, you might record your data like this:

		Warm		Fertilised		Warm + Fertilised		Control	
	seedling	Species 1	Species 2	Species 1	Species 2	Species 1	Species 2	Species 1	Species 2
Week 1	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
Week 2	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
Week 3 etc									

Let's say you want to run a test to determine whether warming and/or fertilisation affected seedling growth. You may know how your experiment is set up, but R doesn't! At the moment, with 8 measures per row (combination of all treatments and species for one replicate, or block), you cannot run an analysis. On the contrary, tidy datasets are arranged so that each **row** represents an **observation** and each **column** represents a **variable**. In our case, this would look something like this:

Week	Species	Block	Treatment	Length (cm)
1	1	1	Warmed	
1	1	1	Fertilised	
1	1	1	W + F	
1	1	1	Control	
1	2	1	Warmed	
1	2	1	Fertilised	
1	2	1	W + F	
1	2	1	Control	
1	1	2	Warmed	
1	1	2	Fertilised	
1	1	2	W + F	
1	1	2	Control	

This makes a much longer dataframe row-wise, which is why this form is often called *long format*. Now if you wanted to compare between groups, treatments, species, etc., R would be able to split the dataframe correctly, as each grouping factor has its own column.

Based on this, do you notice something not quite tidy with our previous object `elongation`? We have observation of the same variable, i.e. stem length, spread across multiple columns representing different years.

The `gather()` function from the `tidyr` package will let us convert this wide-format table to a tidy dataframe. We want to create a single column **Year** that will have years currently in the columns (2007-2012) repeated for each individual. From this, you should be able to work out that the dataframe will be six times longer than the original. We also want a column **Length** where all the growth data associated to each year and individual will go.

Note: This function is slightly unusual as you are making up your own column names in the second (key) and third (value) arguments, rather than passing them pre-defined objects or values like most R functions. Here, year is our key and length is our value.

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```
install.packages("tidyr")  # install the package
library(tidyr)             # load the package


elongation_long <- gather(elongation, Year, Length,
# in this order: data frame, key, value
                          c(X2007, X2008, X2009, X2010, X2011, X2012))
# we need to specify which columns to gather

# Here we want the lengths (value) to be gathered by year (key)

# Let's reverse! spread() is the inverse function, allowing you to go
 from long to wide format
elongation_wide <- spread(elongation_long, Year, Length)
```

Notice how we used the column names to tell `gather()` which columns to reshape. This is handy if you only have a few, and if the columns change order eventually, the function will still work. However, if you have a dataset with columns for 100 genes, for instance, you might be better off specifying the column numbers:

However, these functions have limitations and will not work on every data structure. To quote Hadley Wickham, **“every messy dataset is messy in its own way”**. This is why giving a bit of thought to your dataset structure *before* doing your digital entry can spare you a lot of frustration later!

Once you have the data in the right format, it’s much easier to analyse them and visualise the results. For example, if we want to find out if there is inter-annual variation in the growth of *Empetrum hermaphroditum*, we can quickly make a boxplot:

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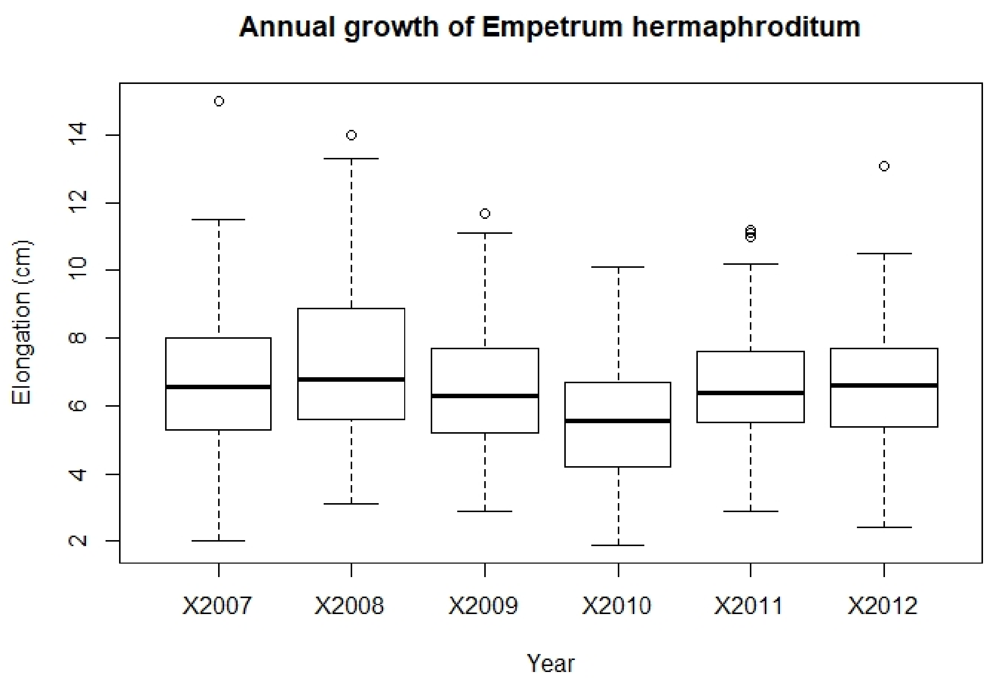
```
boxplot(Length ~ Year, data = elongation_long,
        xlab = "Year", ylab = "Elongation (cm)",
        main = "Annual growth of Empetrum hermaphroditum")
```



Annual growth of *Empetrum hermaphroditum*.

.

From looking at the boxplot, there is a fairly big overlap between the annual growth in each year - nothing special to see. (Don’t worry, we’ll learn to make much prettier and interesting

The package dplyr is a fantastic bundle of intuitive functions for data manipulation, named after the action they perform. A big advantage of these functions is that they take your **data frame** as a first argument, so that you can refer to columns without explicitly having to refer to the full object (so you can drop those $ signs!). Let's meet the most common and useful functions by working on the long format object we just created, elongation_long. First, install and load the package.

```
install.packages("dplyr")  # install the package
library(dplyr)              # load the package
```

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3a. rename() variables

This lets you change the name(s) of a column or columns. The first argument is the data frame, the second (and third, etc.) takes the form **New name = Old name**.

```
elongation_long <- rename(elongation_long, zone = Zone, indiv = Indiv, year = Year, length = Length)
# changes the names of the columns (getting rid of capital letters) and overwriting our data frame

# As we saw earlier, the base R equivalent would have been
names(elongation_long) <- c("zone", "indiv", "year", "length")
```

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3b. filter() rows and select() columns

These are some of the most routine functions that let you reduce your data frame to just the rows and columns you need. The filter() function works great for subsetting rows with logical operations. The select() function lets you specify which columns to keep. **Note: the select() function often clashes with functions of the same name in other packages, and for that reason it is recommended to always use the notation dplyr::select() when calling it.**

```
# For comparison, the base R equivalent would be (not assigned to an o
bject here):
elongation_long[elongation_long$zone %in% c(2,3) & elongation_long$yea
r %in% c("X2009", "X2010", "X2011"), ]
```

Note that here, we use `%in%` as a logical operator because we are looking to match a list of exact (character) values. If you want to keep observations within a range of *numeric* values, you either need two logical statements in your `filter()` function, e.g. `length > 4 & length <= 6.5` or you can use the convenient `between()` function, e.g. `between(length, 4, 6.5)`.

See how `dplyr`is already starting to shine by avoiding repetition and calling directly the column names without needing to call the object every time?

To quote or not to quote?

You may have noticed how we sometimes call values in quotes `""`, and sometimes not. This depends on:

- *Whether the value you are calling is a character or numeric value*: above, `zone` is of class *integer* (a number), so we don't need quotes around the values it takes, but `year` is a *character* (letters), so needs them.
- *Whether you are calling an existing object or referring to a value that R does not yet know about. Compare:*
    - `new.object <- elongation_long` and
    - `new.object <- "elongation_long"`

The first creates a duplicate of our object, because R recognises the name as an object in our environment. In the second case, you're creating an object consisting of one character value.

It takes time and practice to get used to these conventions, but just keep an eye out for error messages and you'll get there.

Now that we know how to subset rows, let's do the same with columns!

```
n removes the column

# For comparison, the base R equivalent would be (not assigned to an o
bject here):
elongation_long[ , -1]  # removes first column

# A nice hack! select() lets you rename and reorder columns on the fly
elong_no.zone <- dplyr::select(elongation_long, Year = year, Shrub.ID
= indiv, Growth = length)

# Neat, uh?
```

3c. `mutate()` your dataset by creating new columns

Something we have not yet touched on is how to create a new column. This is useful when you want to perform an operation on multiple columns, or perhaps reclassify a factor. The `mutate()` function does just that, and also lets you define the name of the column. Here let's use our old wide-format object `elongation` and create a column representing total growth for the period 2007-2012:

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```
# CREATE A NEW COLUMN

elong_total <- mutate(elongation, total.growth = X2007 + X2008 + X2009
+ X2010 + X2011 + X2012)
```

Now, let's see how we could accomplish the same thing on our long-format data `elongation_long` by using two functions that pair extremely well together: `group_by()` and `summarise()`.

3d. `group_by()` certain factors to perform operations on chunks of data

```
# GROUP DATA

elong_grouped <- group_by(elongation_long, indiv)   # grouping our dat
aset by individual
```

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Compare `elong_grouped` and `elongation_long` : they should look exactly the same. But now, let's use `summarise()` to calculate total growth of each individual over the years.

3e. `summarise()` data with a range of summary statistics

This function will always aggregate your original data frame, i.e. the output data frame will be shorter than the input. Here, let's contrast summing growth increments over the study period on the original dataset vs our new **grouped** dataset.

```
# SUMMARISING OUR DATA

summary1 <- summarise(elongation_long, total.growth = sum(length))
summary2 <- summarise(elong_grouped, total.growth = sum(length))
```

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The first summary corresponds to the sum of **all** growth increments in the dataset (all individuals and years). The second one gives us a breakdown of total growth **per individual**, our grouping variable. Amazing! We can compute all sorts of summary statistics, too, like the mean or standard deviation of growth across years:

```
summary3 <- summarise(elong_grouped, total.growth =
sum(length),
                                     mean.growth = mean(length),
                                     sd.growth = sd(length))
```

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Less amazing is that we lose all the other columns not specified at the grouping stage or in a summary operation. For instance, we lost the column year because there are 5 years for

Sometimes you have multiple data files concerning a same project: one for measurements taken at various sites, others with climate data at these sites, and perhaps some metadata about your experiment. Depending on your analytical needs, it may be very useful to have all the information in one table. This is where merging, or joining, datasets comes in handy.

Let's imagine that the growth data we have been working with actually comes from an experiment where some plants where warmed with portable greenhouses (W), others were fertilised (F), some received both treatments (WF) and some were control plants (C). We will import this data from the file `EmpetrumTreatments.csv`, which contains the details of which individuals received which treatments, and join it with our main dataset `elongation_long`. We can do this because both datasets have a column representing the ID of each plant: this is what we will merge by.

There are many types of joins you can perform, which will make sense to you if you are familiar with the SQL language. They differ in how they handle data that is not shared by both tables, so always ask yourself which observations you need to keep and which you want to drop, and look up the help pages if necessary (in doubt, `full_join()` will keep everything). In the following example, we want to keep all the information in `elong_long` and have the treatment code repeated for the five occurrences of every individual, so we will use `left_join()`.

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```
# Load the treatments associated with each individual

treatments <- read.csv("EmpetrumTreatments.csv", header = TRUE, sep = ";")
head(treatments)

# Join the two data frames by ID code. The column names are spelled differently, so we need to tell the function which columns represent a match. We have two columns that contain the same information in both datasets: zone and individual ID.

experiment <- left_join(elongation_long, treatments, by = c("indiv" = "Indiv", "zone" = "Zone"))

# We see that the new object has the same length as our first data frame, which is what we want. And the treatments corresponding to each plant have been added!
```

ensures more control over the function. The equivalent base R function is `merge()` and actually works very well, too:

```
experiment2 <- merge(elongation_long, treatments, by.x = c("zone", "indiv"), by.y = c("Zone", "Indiv"))
# same result!
```

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Now that we have gone to the trouble of adding treatments into our data, let's check if they affect growth by drawing another box plot.

```
boxplot(length ~ Treatment, data = experiment)
```

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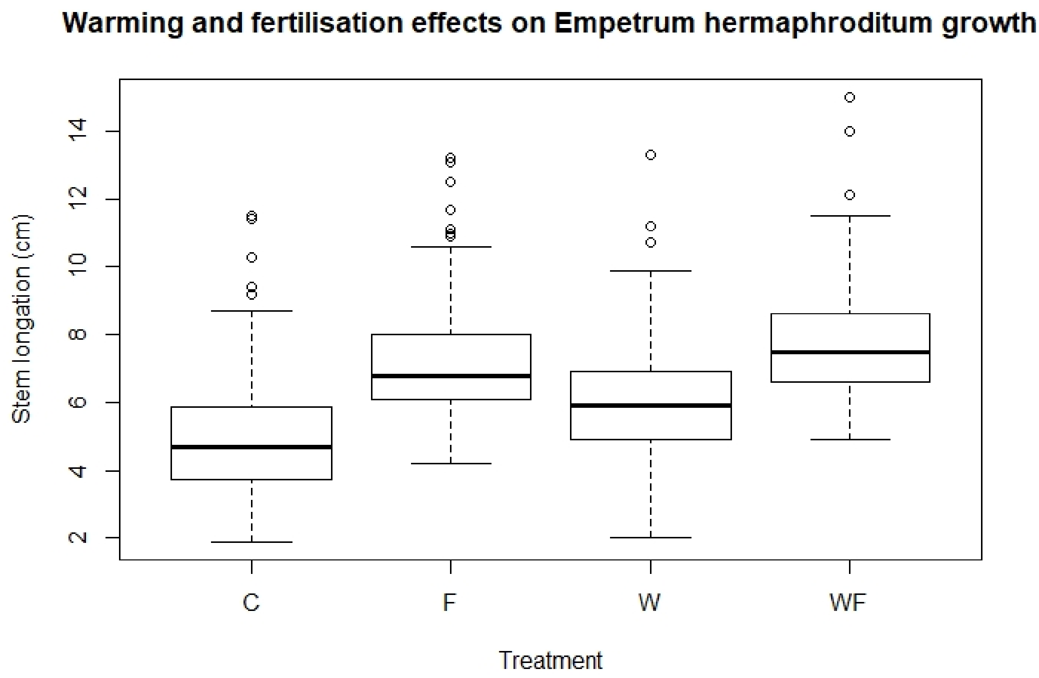

Effects of warming (W) and fertilisation (F) treatments on crowberry growth (fictional data!).

Are these differences statistically significant? We'll find out how to test this in our modelling tutorial!

But for now, don't you think it's enough for one tutorial? Congratulations for powering

Let's see if you can apply some of the functions we have learned today in a different context. In the repository, you will find the file `dragons.csv`, which gives the length (in cm) of the fire plumes breathed by dragons of different species when fed different spices.

Your challenge is to make the data tidy (long format) and to create a boxplot **for each species** showing the effect of the spices on plume size, so you can answer the questions: **Which spice triggers the most fiery reaction? And the least?**

However, you find out that your field assistant was a bit careless during data collection, and let slip many mistakes which you will need to correct.

1. The fourth treatment wasn't paprika at all, it was turmeric.
2. There was a calibration error with the measuring device for the tabasco trial, but only for the Hungarian Horntail species. All measurements are 30 cm higher than they should be.
3. The lengths are given in centimeters, but really it would make sense to convert them to meters.

Now let's see what you can do!

Stuck? Click for a few hints

Click to see the solution

Tutorial Outcomes:

1. You can use `$`and `[]` operators to subset elements of data frames in the classic R notation
2. You understand the format required for analyses in R, and can use the package `tidyr` to achieve it.
3. You can manipulate, subset, create and merge data with `dplyr`

When you're ready for more `dplyr` tips and workflows, follow up with our Efficient data manipulation tutorial!

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