

# Introduction to R

“How do you turn this thing on?”

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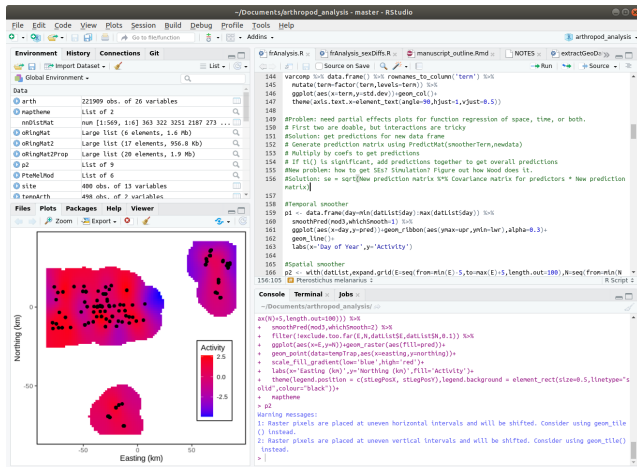
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  - ▶ No point-and-click interface; simple things can take more time
  - ▶ Can be slow if datasets are large\*
- ▶ I am not here to teach you programming, but some basic techniques are useful

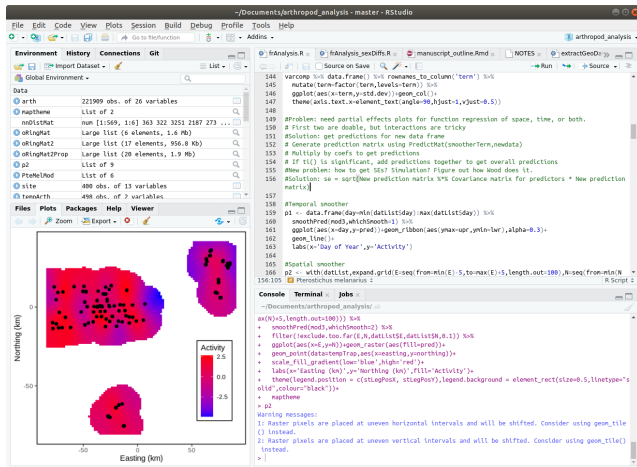
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- The **Console** is the main input into R (where you tell it to do things)



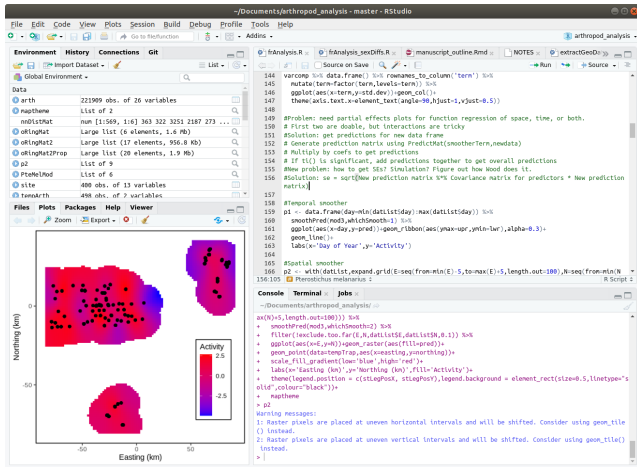
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- ▶ If you're using RStudio, 2 of the 4 panes will be dedicated to the console and scripts



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  - ▶ *plot, summary*
    - ▶ these are polymorphic functions: they do different things to different types of objects
  - ▶ Control flow - *if* and *for*

# Objects

- ▶ Let's make some objects. These are all single objects:

```
myString <- "Hello world"  #A string object  
myNumeric <- 12345         #A numeric object  
myLogical <- TRUE         #A logical object
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- ▶ These are objects joined into a *vector*, joined by the function `c` (concatenate):

```
myCharVec <- c("I like pie", "I like cake", "I like anything you bake")  
myNumVec <- c(1, 2, 3, 4, 5)  
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- ▶ How long are each of these vectors?

```
howLong <- c(length(myCharVec), length(myNumVec), length(myLogVec))
howLong  #This executes the `print` command on `howLong`
```

```
## [1] 3 5 6
```

## Vectors - “getting”

```
myCharVec  #Here's what's inside the whole thing
```

```
## [1] "I like pie"           "I like cake"
```

```
## [3] "I like anything you bake"
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myCharVec[1]
```

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```
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- ▶ Logical vector

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```

- ▶ Results:

```
myCharVec  #Here's what's inside the whole thing
```

```
## [1] "Parakeets" "Cats"      "Dogs"
```

## Class conversions

Vectors (or other data) can be converted between **classes**, usually using *as.something* statements:

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- ▶ Numeric to character

```
as.character(myNumVec)
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```
## [1] "1" "2" "3" "4" "5"
```

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```

- ▶ Characters to **factors**: these represent *categories* or experimental levels

```
as.factor(myCharVec) #Default order is alphabetical
```

```
## [1] Parakeets Cats      Dogs
```

```
## Levels: Cats Dogs Parakeets
```



# Dataframes

- Dataframes look similar to matrices, but can hold different data types in each column:

```
myDF <- data.frame(stringCol = myCharVec, numCol = myNumVec[c(1:3)],  
  logCol = myLogVec[c(1:3)])  
myDF
```

```
##  stringCol numCol logCol  
## 1 Parakeets      1  TRUE  
## 2      Cats      2  TRUE  
## 3      Dogs      3 FALSE
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```
##   stringCol numCol logCol  
## 1 Parakeets     1   TRUE  
## 2      Cats     2   TRUE  
## 3      Dogs     3  FALSE
```

- `summary(myDF)` *#This function summarizes each column*

```
##   stringCol           numCol       logCol  
## Length:3           Min.      :1.0     Mode :logical  
## Class :character   1st Qu.:1.5     FALSE:1  
## Mode  :character   Median  :2.0     TRUE  :2  
##                   Mean       :2.0  
##                   3rd Qu.:2.5  
##                   Max.      :3.0
```

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

▶ `myDF[1, "numCol"]`

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

▶ `myDF$numCol[1]`

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

## Reading csv files

- One very common practice is to read in your own data from a csv file. Excel files can be read in directly, but present other problems.

```
testDat <- read.csv("test_results.csv")  
head(testDat)  #head shows only first 6 rows of dataframe
```

##	Concentration	Treatment	Lab.Member	Time.of.Day
## 1	2.9	Control	Will	Morning
## 2	3.2	Control	Will	Morning
## 3	3.6	Control	Will	Morning
## 4	5.6	A	Will	Morning
## 5	6.8	A	Will	Morning
## 6	7.0	A	Will	Morning



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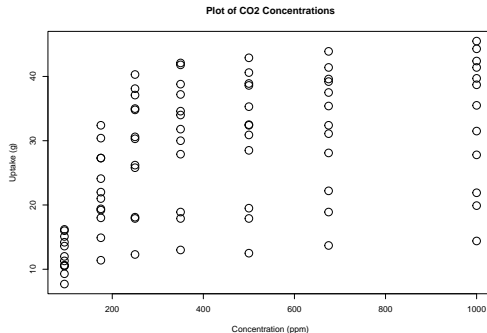
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## 4           5.6      A        Will    Morning  
## 5           6.8      A        Will    Morning  
## 6           7.0      A        Will    Morning
```

- ▶ R can't handle spaces or other special characters in the column headers (replaces them with periods). It also tries to guess the proper data type for each column, but sometimes gets this wrong.

# Plotting

- The *plot* command is useful for quickly looking at sets of data. The following CO2 dataset is built-in to R. To see others, type `data()`

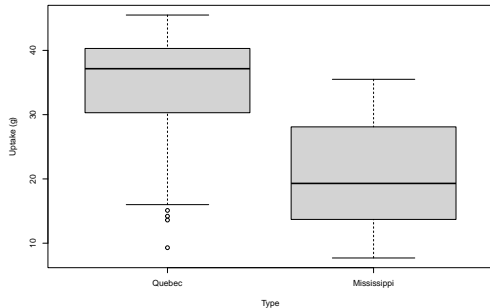
```
#Makes a plot of the uptake (y) and  
# concentration (x) columns of CO2  
# dataframe, and customizes axis labels  
plot(x = CO2$conc, y = CO2$uptake,  
      xlab = 'Concentration (ppm)',  
      ylab = 'Uptake (g)',  
      main = 'Plot of CO2 Concentrations',  
      cex = 2)
```



## Plotting (cont.)

- The boxplot command can summarize *continuous* and *categorical* data

```
# Boxplot uses a formula  
# rather than x,y vectors  
  
# Formula: uptake depends on  
# (~) Type  
boxplot(CO2$uptake ~ CO2$Type,  
        xlab = "Type", ylab = "Uptake (g)")
```



## First challenge

Your supervisor has just given you a dataset (*test\_results.csv*) recorded by two undergrads. However, these undergrads were in a hurry and have made some mistakes:

- ▶ Make a **script** in R, and use this to record what you do
- ▶ Read the *csv* file and fix any mistakes. Bonus if you do this without using Excel!
- ▶ Plot the concentration data by treatment group, then plot it for each undergrad. Does there look like much of a difference?
- ▶ Some useful commands: **read.csv**, **boxplot**, **is.na**, **as.factor**, **summary**

# Lists

- ▶ Lists look similar to vectors, but can hold anything in each slot, including other lists.
- ▶ LOTS of things in R (e.g. model output) are specially-structured lists at their core

```
myList <- list(charSlot = myCharVec,  
              numSlot = myNumVec, logSlot = myLogVec,  
              dfSlot = myDF)
```

```
## $charSlot  
## [1] "Parakeets" "Cats"      "Dogs"  
##  
## $numSlot  
## [1] 1 2 3 4 5  
##  
## $logSlot  
## [1] TRUE TRUE FALSE TRUE FALSE FALSE  
##  
## $dfSlot  
##   stringCol numCol logCol  
## 1 Parakeets      1  TRUE  
## 2      Cats      2  TRUE  
## 3      Dogs      3 FALSE
```

## Accessing Lists

Lists can be accessed numerically or logically, or by their name slots:

```
myList[[2]] #Needs 2 square brackets to isolate object
```

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

```
myList[["numSlot"]]
```

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

```
myList$numSlot
```

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

```
myList[[4]][, 3] #Same as myList$dfSlot$logCol
```

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

# Functions

- Functions take objects as **arguments** (input) and return other **objects** (output)

```
myNumVec <- c(1, 2, 3, 4, 5)
meanVec <- mean(myNumVec)  #Arithmetic mean (average)
sdVec <- sd(myNumVec)      #Standard deviation (sqrt(variance))
meanSdVec <- c(meanVec, sdVec)  #Joins mean and SD into a vector
meanSdVec
```

```
## [1] 3.000000 1.581139
```

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```

- If you can't remember how a command works, use ? to access the help files

```
`?`(median)
```



# Homemade Functions

- You can make your own functions! This is useful if you have to do the same thing to many different input objects.

```
myFun <- function(input) {  
  # Takes a vector of numbers  
  A <- mean(input) #Take the mean of INPUT  
  B <- sd(input)   #Take the SD of INPUT  
  C <- c(A, B)    #Join A and B into a vector C  
  return(C)      #Return (output) C, then end the function  
}  
myFun(myNumVec)  #Same as previous slide  
  
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}  
myFun(myNumVec)   #Same as previous slide
```

```
## [1] 3.000000 1.581139
```

- ▶ The objects inside of functions (A, B, C in the one above) disappear after the function runs. However, *functions can see objects in the outer environment*, so beware of the Steve Problem\*

## Summary statistics

Often we want to get the mean of one columns, but split it up by other things in the dataframe. Using the CO2 plant example, how does *uptake* differ between *Type*?

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```
options(width = 10)
```

```
# Split up uptake by Type and Treatment, then take the mean  
tapply(CO2$uptake, list(CO2$Type, CO2$Treatment), mean)
```

```
##           nonchilled  
## Quebec          35.33333  
## Mississippi    25.95238  
##           chilled  
## Quebec          31.75238  
## Mississippi    15.81429
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Typing “CO2” over and over again is annoying. You can use *with* to avoid this (avoid using *attach*):

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```
# Runs command
# inside the name
# space of the CO2
# object
with(CO2, tapply(uptake,
                  list(Type, Treatment),
                  sd))
```

```
##                nonchilled
## Quebec         9.596371
## Mississippi    7.402136
##                chilled
## Quebec         9.644823
## Mississippi    4.058976
```

## if statements

- R can be told to do things only *if* certain conditions apply. This is useful inside of functions for error handling:

```
myFun2 <- function(x) {  
  xClass <- class(x)  #What class is x? (Numeric, character, boolean)  
  
  if (xClass == "character") {  
    # == means  
    # 'are  
    # these  
    # things  
    # equal'?  
    return("This is a string")  #If x is a character, returns a message  
  } else {  
    return(mean(x))  #If x isn't a character, returns the mean of x  
  }  
}
```

myFun2(myCharVec)

```
## [1] "This is a string"
```

## for loops

- R can be told to do things *repeatedly*, using an index:

```
classVec <- rep("", length(myList))  #Storage vector
```

```
# i will take on
```

```
# values 1 to 4,
```

```
# each time the
```

```
# loop repeats
```

```
for (i in 1:length(myList)) {
```

```
  # ith slot of
```

```
  # classVec
```

```
  # becomes class
```

```
  # from ith slot
```

```
  # of myList
```

```
  classVec[i] <- class(myList[[i]])
```

```
}
```

```
classVec
```

```
## [1] "character"
```

```
## [2] "numeric"
```



## Second challenge

Population growth models are common in ecology, and usually often take the form  $n_t = n_{t-1} + rn_{t-1}$ , where  $n$  is the number of critters at some time point  $t$ , and  $r$  is the change in  $n$  from one point to the next ( $r = 0$ : no change). Using a for loop, write a simple population simulation using the following models:

- ▶ Exponential growth:  $n_t = n_{t-1}(1 + r)$
- ▶ Logistic growth:  $n_t = n_{t-1}(1 + r(1 - \frac{n_{t-1}}{k}))$
- ▶ Predator-prey cycles (Lotka-Volterra):

```
>- $\text{prey}_t = \text{prey}_{t-1}(1 + r_1 - a_1\text{pred}_{t-1})$  
>- $\text{pred}_t = \text{pred}_{t-1}(1 + a_2\text{prey}_{t-1} - d)$
```