Introduction to R "How do you turn this thing on?"

Samuel Robinson, Ph.D.

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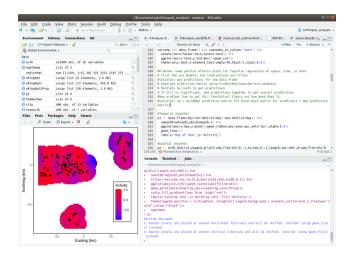
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- ► This is not a course in R programming (see here, here, here , but you do need some basic techniques

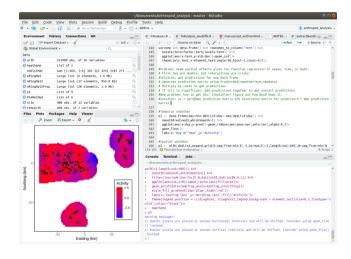
RStudio GUI

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



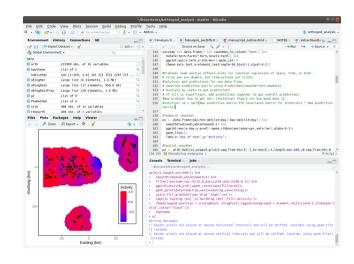
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- Scripts are lists of commands that get passed into the console
- If you're using RStudio, 2 of the 4 panes will be dedicated to the console and scripts



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Objects

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

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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
```

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

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➤ Single number: myCharVec[1]

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Vector of numbers

```
myCharVec[c(2,3)]
```

```
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```
Vectors - "getting"
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String vector

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Results:

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

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

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

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Numeric to character

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

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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:

Dataframes

2

3

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

## stringCol numCol logCol
## 1 Parakeets 1 TBUE</pre>
```

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

2 TRUE

3 FALSE

Cats

Dogs

```
stringCol
                                   logCol
##
                        numCol
   Length:3
                                 Mode :logical
##
            Min. :1.0
   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
```

```
myDF[1,2]
## [1] 1
```

```
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myDF$numCol #This gets all of the column "numCol"
## [1] 1 2 3
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myDF[1,"numCol"]
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```

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  ## [1] 1 2 3
  myDF[1,"numCol"]
  ## [1] 1
  myDF$numCol[1]
  ## [1] 1
```

Like other objects, you can alter dataframes

► You can add columns

```
myDF$numCol2 <- myDF$numCol*3 #Multiplies numCol by 3</pre>
```

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▶ You can also alter columns in place, or elements within columns

```
myDF$numCol <- (myDF$numCol)^2 #Square of numCol
myDF$numCol[3] <- myDF$numCol[3] - myDF$numCol[2] #Subtracts 2nd from 3rd
```

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You can delete columns by subsetting the dataframe, or assigning the column to NULL

```
myDF <- myDF[,c(1,2)] #Selects only column 1 and 2
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We'll learn easier ways of doing this next week using the tidyverse

Reading csv files

▶ One common practice is to read in your own dataframe from a csv file ²

```
testDat <- read.csv('test_results.csv') #Path to csv file
head(testDat) #head shows only the 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
               5.6
                                             Morning
## 4
                            Α
                                    Will
               6.8
## 5
                                    Will
                                             Morning
## 6
               7.0
                                    Will
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```

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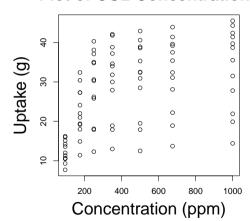
- R can't handle spaces or other special characters in the column headers (replaces them with periods). It also tries to guess the proper data type for each column
- Make sure that the csv file is in your working directory

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Plotting

► The plot command is useful for quickly looking at sets of data. The following CO2 dataset is built-in to R.³

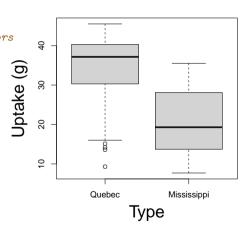
Plot of CO2 Concentrations



³To see others, type data() in the console

More Plotting

The boxplot command can summarize continuous and categorical data



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

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
```

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▶ If you can't remember how a command works, use ? in the console to access the help files (e.g. ?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</pre>
```

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► 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*

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Using the CO2 plant example, how does uptake differ between Type?

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

```
## nonchilled chilled
## Quebec 35.33333 31.75238
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► Typing "CO2" over and over again is annoying. You can use *with* to avoid repeating the name of the dataframe (avoid using *attach*)

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

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)</pre>
```

```
## [1] "This is a string"
myFun2(myNumVec)
## [1] 3
```

for loops

R can be told to do things repeatedly, using an *index* inside a loop:

```
classVec <- rep(0,10) #Storage vector of zeros, 10 long
classVec[c(1,2)] <- 1 #Set first two slots to 1

#Each time the loop repeats, i will take on values 3 to 10
for(i in 3:length(classVec)){
   #ith slot of classVec becomes the sum of the previous two slots
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classVec #First 10 numbers in the Fibbonaci sequence

```
## [1] 1 1 2 3 5 8 13 21 34 55
```

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).

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 - Exponential growth: $n_t = n_{t-1}(1+r)$
 - Logistic growth: $n_t = n_{t-1}(1 + r(1 \frac{n_{t-1}}{k}))$

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).

- ▶ Write a function (with a for loop inside) that performs a simple population simulation using the following models:
 - Exponential growth: $n_t = n_{t-1}(1+r)$
 - Logistic growth: $n_t = n_{t-1}(1 + r(1 \frac{n_{t-1}}{k}))$
- ► Make a simple plot of your results

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

```
## $charSlot
## [1] "Parakeets" "Cats"
                                 "Dogs"
##
## $numSlot.
   [1] 1 2 3 4 5
##
## $logSlot
                           TRUE FALSE FALSE
   Γ1]
        TRUE
              TRUE FALSE
##
## $dfSlot
##
     stringCol numCol logCol
## 1 Parakeets
                         TRUE
## 2
          Cats
                         TRUE
## 3
          Dogs
                        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
```

lapply and sapply

Loops can be slow: using a **functional** is generally better (if each step doesn't depend on the previous one)

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```
input <- c(1,2,3) #Input vector
pFun <- function(N,type='normal'){
  if(type=='poisson') rpois(N,3) else rnorm(N,3)
}
lapply(input,pFun,type='poisson') #Generates a list of N Poisson random numbers
## [[1]]
## [1] 4
##
## [[2]]
## [1] 3 2
##
## [[3]]
## [1] 4 0 3
```

lapply and sapply

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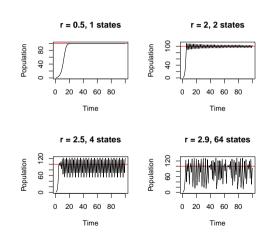
Different output formats: lapply uses a list, sapply uses a vector (or matrix)

Third challenge

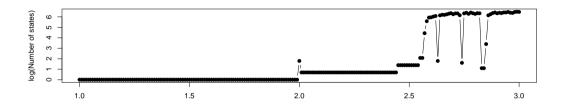
The discrete logistic growth equation has some interesting mathematical properties (see here and here). At certain values of r the population converges to the carrying capacity K, while at other values it cycles between multiple values.

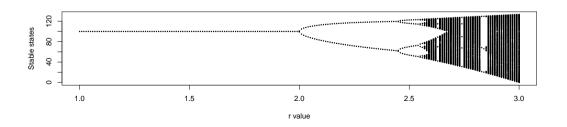
Using *lapply*, *sapply* and the logistic function you wrote for the second challenge:

- Write a script that iterates across a range of r values: 1 < r < 3
- ► At each *r* value, how many unique values exist?
- ▶ Keep K at 100 and n_0 at 1 for now. Use a simulation time of t = 1000, but discard the first 100 points



Complex behaviour from a simple system





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1. Your own dataset that you want to analyze

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- Take a look at a data repository like Dryad