Introduction to R

“How do you turn this thing on?”

Samuel Robinson, Ph.D.

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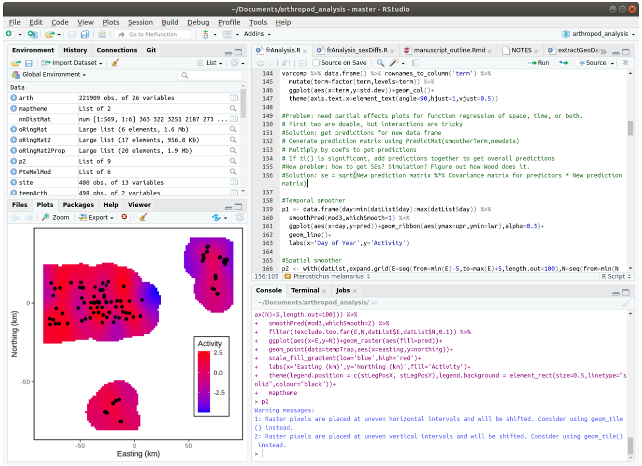
- "What is R bad at?"
  - No point-and-click interface; simple things can take more time
  - Can be slow if datasets are large
- This is not a course in R programming (see here, here, here , but you do need some basic techniques

RStudio GUI

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


~/Documents/arthropod_analysis - master - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
arthropod_analysis
Environment History Connections Git
Import Dataset
List
Global Environment
Files Plots Packages Help Viewer
Zoom Export
Northing (km)
Easting (km)
Activity
2.5
0.0
-2.5
0
-50
50
frAnalysis.R frAnalysis_sexDiffs.R manuscript_outline.Rmd NOTES extractGeoDa
Source on Save
Run
Source
156:105
Pterostichus melanarius
R Script
Console Terminal Jobs
~/Documents/arthropod_analysis/

```
Data
arth           221909 obs. of 26 variables
maptheme       List of 2
nnDistMat      num [1:569, 1:6] 363 322 3251 2187 273 ...
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varcomp %>% data.frame() %>% rownames_to_column('term') %>%
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#Problem: need partial effects plots for function regression of space, time, or both.
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#Temporal smoother
p1 <- data.frame(day=min(datList$day):max(datList$day)) %>%
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#Spatial smoother
p2 <- with(datList,expand.grid(E=seq(from=min(E)-5,to=max(E)+5,length.out=100),N=seq(from=min(N
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```
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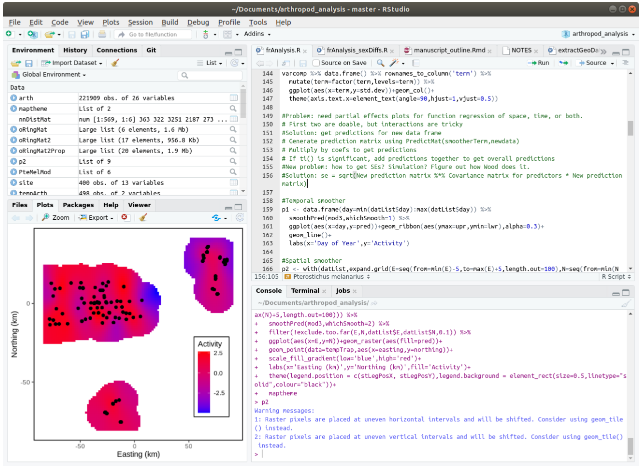

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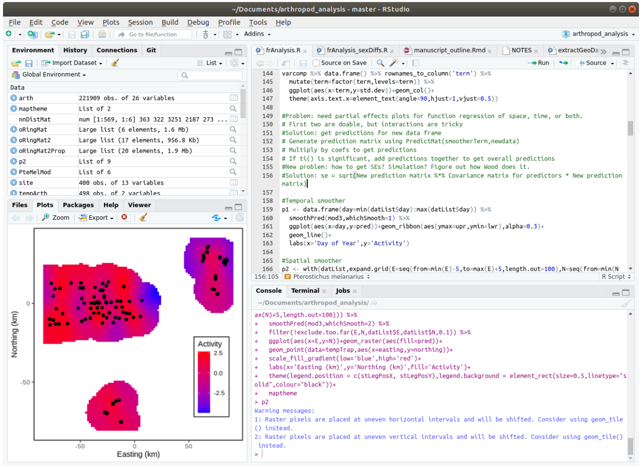

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  - Control flow - *if* and *for*

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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”

```r
myCharVec  #Here's what's inside the whole thing
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## [1] "I like pie"                    "I like cake"
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- Logical vector

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- Results:

```
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```

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

-
  ```
  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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Accessing Dataframes

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  myDF[1, 2]
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  ```r
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  ```

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Manipulating dataframe

Like other objects, you can alter dataframes

- You can add columns

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

Manipulating dataframe

Like other objects, you can alter dataframes

- You can add columns

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myDF$numCol2 <- myDF$numCol * 3  #Multiplies numCol by 3
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- You can also alter columns in place, or elements within columns

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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]

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

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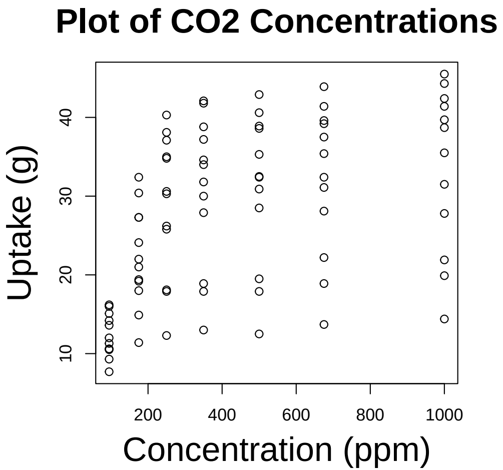
- R can't handle spaces or other special characters in the column headers (replaces them with periods). It also tries to guess the proper data type for each column
- Make sure that the csv file is in your *working directory*

[2] Excel files can be read in, but can cause problems

Plotting

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

```
#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.lab = 2, cex.main=2)
```



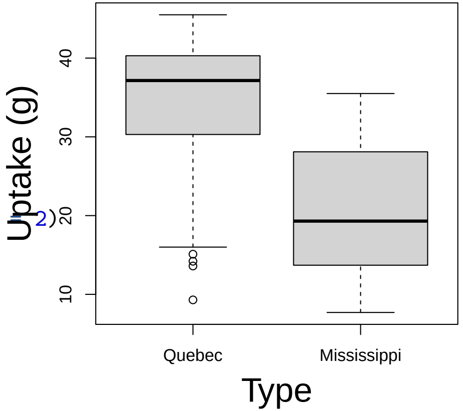
[3]To see others, type `data()` in the console

More Plotting

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

```r
# Boxplot uses a formula rather than
# x,y vectors

# Formula: uptake depends on (~) Type
boxplot(CO2$uptake ~ CO2$Type, xlab = "Type",
    ylab = "Uptake (g)", cex.lab = 2, cex.main = 2)
```



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)

```r
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 ? 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
```

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

```
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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*

Summary statistics

Often we want to get the mean of one columns, but split it up by other things in the dataframe.

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

```r
# 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)
```

```
## [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:

```r
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
    classVec[i] <- classVec[i - 1] + classVec[i - 2]
}
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}
```

-
  ```
  classVec  #First 10 numbers in the Fibbonaci sequence
  ```

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

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).

- Write a `function` (with a `for` loop inside) that performs a simple population simulation using the following models:

Hint: functions need input variables that tell them what to do. The input variables here could be things like *starting population* (n_0), *growth rate* (r), and *number of time steps* (T) to simulate

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

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- Make a simple plot of your results

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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
```

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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```r
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] 3
##
## [[2]]
## [1] 4 2
##
## [[3]]
## [1] 2 0 4
```

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##
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##
## [[3]]
## [1] 2 0 4
```

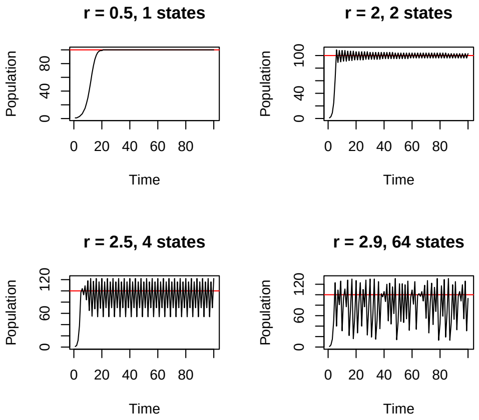
Different output formats: *lapply* uses a list, *sapply* uses a vector (or matrix)

Third challenge

The discrete logistic growth equation has some interesting mathematical properties (see here). 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: $1 \leq r \leq 3$
- 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



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Get a dataset to work with! This can be:

1. Your own dataset that you want to analyze

Try loading this data into R and play around with it: make some simple plots, or get some summary statistics. Bring it next week and we'll continue using it.

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- Take a look at a data repository like Dryad

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