

Introduction to R

“How do you turn this thing on?”

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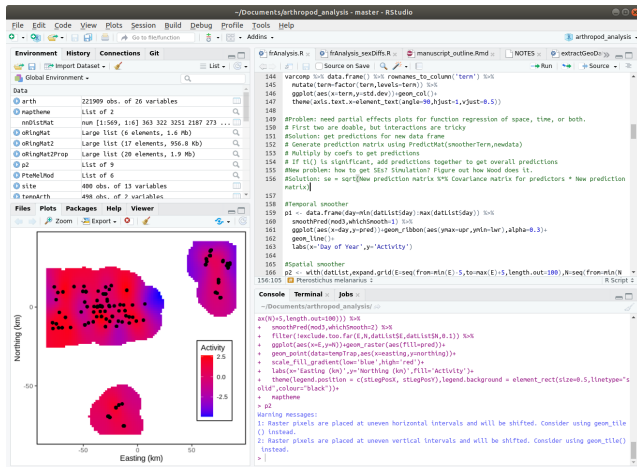
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- ▶ I am not here to teach you programming, but some basic techniques are useful

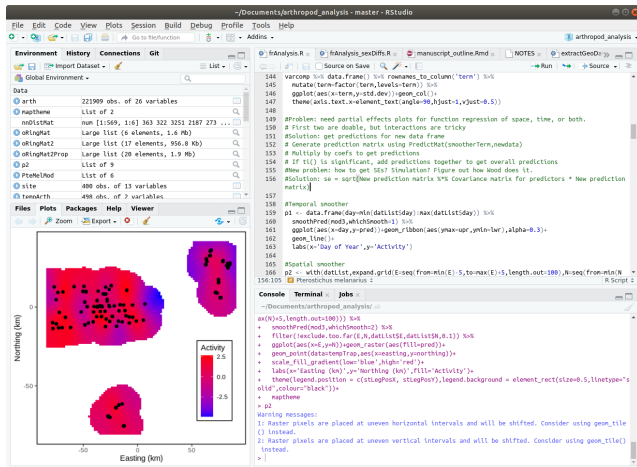
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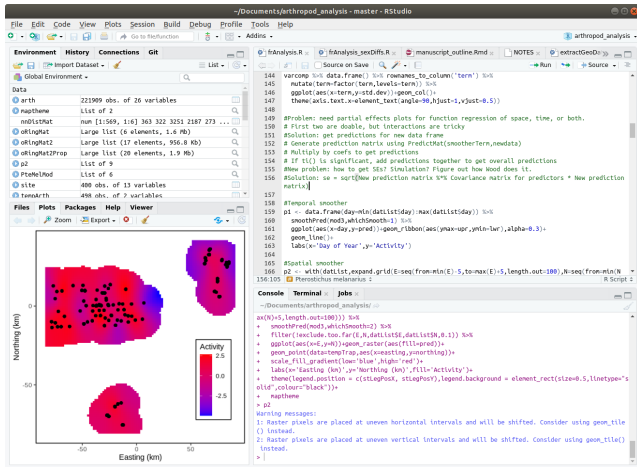
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- ▶ If you're using RStudio, 2 of the 4 panes will be dedicated to the console and scripts



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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):

```
myStringVec <- c("I like pie", "I like cake", "I like anything you bake")  
myNumericVec <- c(1, 2, 3, 4, 5)  
myLogicalVec <- c(TRUE, TRUE, FALSE, TRUE, FALSE, FALSE)
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```

- ▶ How long are each of these vectors?

```
howLong <- c(length(myStringVec), length(myNumericVec), length(myLogicalVec))
howLong  #This executes the `print` command on `howLong`
```

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

Vectors

- How do I get stuff out of the vectors I just made?

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

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

```
myStringVec[1]  #Uses a single numeric
```

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

```
myStringVec[c(2, 3)]  #Uses a vector of numerics
```

```
## [1] "I like cake"           "I like anything you bake"
```

```
myStringVec[c(TRUE, FALSE, TRUE)]  #Uses a logical vector of same length
```

```
## [1] "I like pie"           "I like anything you bake"
```

Matrices

- ▶ Matrices are rectangular structures that hold values inside them:

```
(myMatrix <- matrix(1:9, ncol = 3))
```

```
##      [,1] [,2] [,3]  
## [1,]    1    4    7  
## [2,]    2    5    8  
## [3,]    3    6    9
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## [3,]    3    6    9
```

- ▶ Matrices are indexed by *rows* and *columns* (in that order):

```
myMatrix[1, 3]  #1st row, 3rd col
```

```
## [1] 7
```

```
myMatrix[, 3]  #All rows, 3rd column
```

```
## [1] 7 8 9
```

Dataframes

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

```
# Each column has a unique name, and must be the same length
```

```
myDF <- data.frame(stringCol = myStringVec, numCol = myNumericVec[c(1:3)], logCol = my  
myDF
```

```
##           stringCol numCol logCol  
## 1           I like pie      1  TRUE  
## 2           I like cake      2  TRUE  
## 3 I like anything you bake      3 FALSE
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## 1           I like pie      1  TRUE  
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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
```

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(stringSlot = myStringVec,  
  numSlot = myNumericVec,  
  logSlot = myLogicalVec,  
  dfSlot = myDF)
```

```
## $stringSlot  
## [1] "I like pie" "I like cake"  
## [3] "I like anything you bake"  
##  
## $numSlot  
## [1] 1 2 3 4 5  
##  
## $logSlot  
## [1] TRUE TRUE FALSE TRUE FALSE FALSE  
##  
## $dfSlot  
##           stringCol numCol logCol  
## 1           I like pie      1  TRUE  
## 2           I like cake      2  TRUE  
## 3 I like anything you bake      3 FALSE
```

Accessing Dataframes

- Dataframes can be accessed numerically, by their name slots, or with a mixture of the two:

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

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

```
myDF$numCol #This gets all of the column 'numCol'
```

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

```
myDF[1, "numCol"]
```

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

Accessing Lists

- Similarly, lists can be accessed numerically (see below), 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)

```
myNumericVec
meanVec <- mean(myNumericVec)  #Arithmetic mean (average)
sdVec <- sd(myNumericVec)      #Standard deviation (sqrt(variance))
meanSdVec <- c(meanVec, sdVec)  #Joins mean and SD into a vector
meanSdVec
`?`(median  #If you can't remember how a command works, use '?' to access the help files
)
```

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(myNumericVec)  #Same as previous slide  
  
## [1] 3.000000 1.581139
```

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- ▶ `myFun(myLogicalVec)` *#Logical vector is converted to 1 (TRUE) and 0 (FALSE)*

```
## [1] 0.5000000 0.5477226
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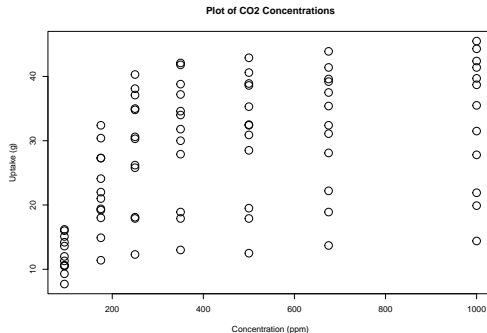
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- ▶ The objects inside of functions (A,B,C in the one above) disappear after the function runs. However, functions can see objects in the outer environment, so beware of the Steve Problem*

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()`

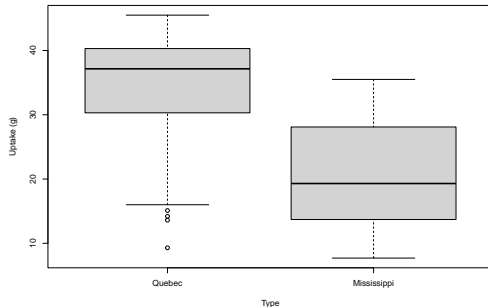
```
#Makes a plot of the uptake (y) and  
# concentration (x) columns of CO2  
# dataframe, and customizes axis labels  
plot(x = CO2$conc, y = CO2$uptake,  
      xlab = 'Concentration (ppm)',  
      ylab = 'Uptake (g)',  
      main = 'Plot of CO2 Concentrations',  
      cex = 2)
```



Plotting (cont.)

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

```
# Boxplot uses a formula  
# rather than x,y vectors  
# Note: plot can also use  
# formulas in lieu of x,y  
boxplot(CO2$uptake ~ CO2$Type,  
        xlab = "Type", ylab = "Uptake (g)")  
# Formula: uptake depends on  
# (~) Type
```



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*?

```
# 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  
## Mississippi     25.95238 15.81429
```

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

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- It's annoying and repetitive to type "CO2" over and over again. You can use *with* to avoid this (avoid using *attach*):

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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(myStringVec)
```

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

```
myFun2(myNumericVec)
```

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

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" "numeric"    "logical"    "data.frame"
```

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 |
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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, but sometimes gets this wrong.

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- ▶ 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:

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

A challenger approaches!

- ▶ 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:
 - ▶ 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**
- ▶ 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:
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 - ▶ Predator-prey system:
 $\text{prey}_t = \text{prey}_{t-1}(1 + r_1 - a_1\text{predators}_{t-1})$; $\text{pred}_t = \text{pred}_{t-1}(1 + a_2\text{prey}_{t-1} - d)$

Solutions (1)

```
dat <- read.csv("test_results.csv", )  
# print(dat)  
dat <- dat[!is.na(dat$Concentration), ] #Remove NA  
dat$Treatment[dat$Treatment == "Bee"] <- "B" #Change Bee to B  
dat$Lab.Member[dat$Lab.Member == "Same"] <- "Sam" #Change Same to Sam  
dat$Treatment <- as.factor(dat$Treatment) #Change characters to factor  
dat$Lab.Member <- as.factor(dat$Lab.Member)  
dat$Concentration[dat$Concentration == 30] <- 3  
  
boxplot(Concentration ~ Treatment, data = dat)
```

