Introduction to R

"How do you turn this thing on?"

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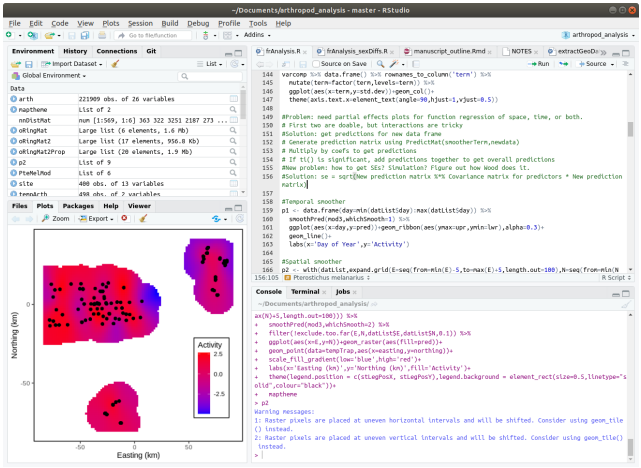
- "What is R bad at?"
  - No point-and-click interface; simple things can take more time
  - Can be slow if datasets are large*
- I am not here to teach you programming, but some basic techniques are useful

RStudio GUI

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



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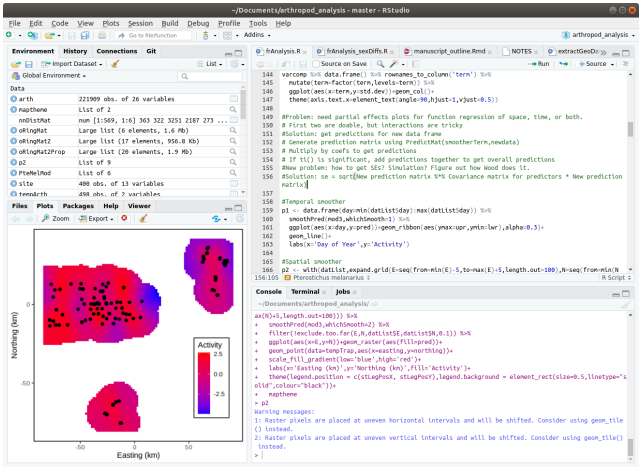

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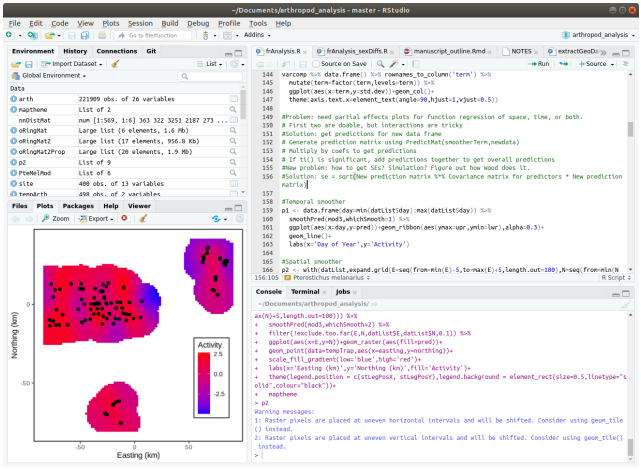
- If you're using RStudio, 2 of the 4 panes will be dedicated to the console and scripts



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

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- 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
```

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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```

```
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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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```

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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:

```
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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## 1 Parakeets      1   TRUE
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## 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
```

Accessing Dataframes

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

  ```
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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]
  ```

  ```
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Manipulating dataframe

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- You can add columns

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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
myDF$numCol <- NULL #Removes numCol
```

Reading csv files

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

```
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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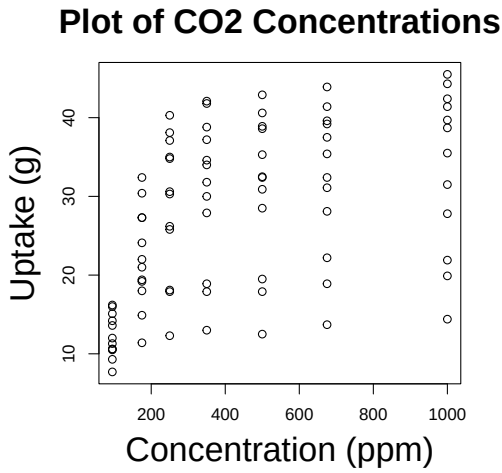
```

- 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, 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.[1]

```
#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)
```



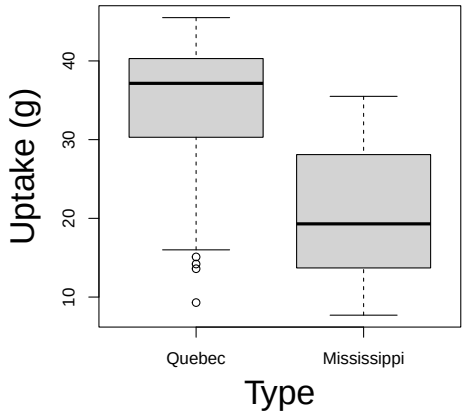
[1] To see others, type `data()` in the console

More Plotting

- 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)',
        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)

```
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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- 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

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

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

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

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

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