Introduction_to_R

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Welcome to "Understanding taxonomy," a module in the "Using phylogenies to study trait evolution" series.

In this module, we will learn how to download a list of taxa and their corresponding Taxon IDs from an online database: the Open Tree of Life.

In future modules, we will use these taxa to create phylogenies and study how morphological or ecological traits have evolved for these taxa.

Before completing this module, if you have no prior experience with R, it is best if you watch this short *youtube video* describing the RStudio interface. Beginners may also choose to read through either *Getting Started with R and RStudio* or *Introduction to R with Biodiversity Data Chapter 3*. You do not need to complete the steps in these tutorial portions for this module (all code and packages for this module are provided within this project), but these resources should provide relevant introductory background on RStudio, R Projects, running scripts, writing code, and troubleshooting.

This course has several streams and several difficulty levels. Please choose the appropriate datafiles and scripts according to your goals.

Data for each module are generally included as **csv** files. These files are able to be opened manually or using an R script. Each **csv** file contains columns separated by **commas** (,) and rows separated by **new line characters**.

Navigate to the "Data" folder in the "Files" tab (bottom right corner of the screen) and within that, to the "Introduction_example" folder. Open the file "Acer_rubrum.csv" **manually** by clicking on it and selecting "View File" and check it out. It should look like this:

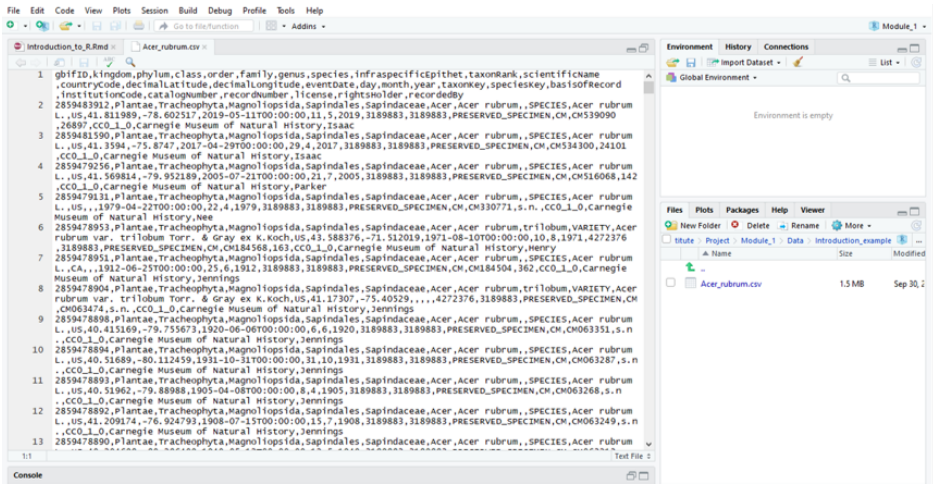

Figure 1: Screenshot of csv file as opened manually

Now, make sure you have the Introduction_to_R.R script open in the Script tab (found in the Scripts folder in the Files tab, open by clicking on it). Using the first lines of code, open the same **csv** file using **R** code.

To run the code, select (highlight) the row(s) of text and click the "Run" button above and "Run Selected Lines". Alternatively, selected lines of code can be run by simultaneously pressing the *ctrl* (*control*) and *enter* keys (Windows) or the *command* (*cmd*) and *enter* (or *return*) keys (Mac).

*Note: copying code from the pdf instructions into the console or a new script will likely not work due to formatting errors. Please open the script provided and run the code directly from there.

```
example_file <- read.csv("../Data/Introduction_example/Acer_rubrum.csv",
    stringsAsFactors = FALSE, header = TRUE)
head(example_file)
```

```
##       gbifID kingdom       phylum          class       order       family
    genus
## 1 2859483912 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 2 2859481590 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 3 2859479256 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 4 2859479131 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 5 2859478953 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 6 2859478951 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
##       species infraspecificEpithet taxonRank
## 1 Acer rubrum                        SPECIES
## 2 Acer rubrum                        SPECIES
## 3 Acer rubrum                        SPECIES
## 4 Acer rubrum                        SPECIES
## 5 Acer rubrum             trilobum   VARIETY
## 6 Acer rubrum                        SPECIES
##                                   scientificName countryCode
    decimalLatitude
## 1                                  Acer rubrum L.          US
    41.81199
## 2                                  Acer rubrum L.          US
    41.35940
## 3                                  Acer rubrum L.          US
    41.56981
## 4                                  Acer rubrum L.          US
                NA
## 5 Acer rubrum var. trilobum Torr. & Gray ex K.Koch          US
    43.58838
## 6                                  Acer rubrum L.          CA
                NA
##   decimalLongitude           eventDate day month year taxonKey speciesKey
## 1        -78.60252 2019-05-11T00:00:00  11     5 2019  3189883    3189883
## 2        -75.87470 2017-04-29T00:00:00  29     4 2017  3189883    3189883
## 3        -79.95219 2005-07-21T00:00:00  21     7 2005  3189883    3189883
## 4               NA 1979-04-22T00:00:00  22     4 1979  3189883    3189883
## 5        -71.51202 1971-08-10T00:00:00  10     8 1971  4272376    3189883
## 6               NA 1912-06-25T00:00:00  25     6 1912  3189883    3189883
##       basisOfRecord institutionCode catalogNumber recordNumber license
## 1 PRESERVED_SPECIMEN             CM       CM539090        26897 CC0_1_0
```

```
## 2 PRESERVED_SPECIMEN                CM       CM534300        24101 CC0_1_0
## 3 PRESERVED_SPECIMEN                CM       CM516068          142 CC0_1_0
## 4 PRESERVED_SPECIMEN                CM       CM330771         s.n. CC0_1_0
## 5 PRESERVED_SPECIMEN                CM       CM184568          163 CC0_1_0
## 6 PRESERVED_SPECIMEN                CM       CM184504          362 CC0_1_0
##                                rightsHolder recordedBy
## 1 Carnegie Museum of Natural History      Isaac
## 2 Carnegie Museum of Natural History      Isaac
## 3 Carnegie Museum of Natural History     Parker
## 4 Carnegie Museum of Natural History        Nee
## 5 Carnegie Museum of Natural History      Henry
## 6 Carnegie Museum of Natural History   Jennings
```

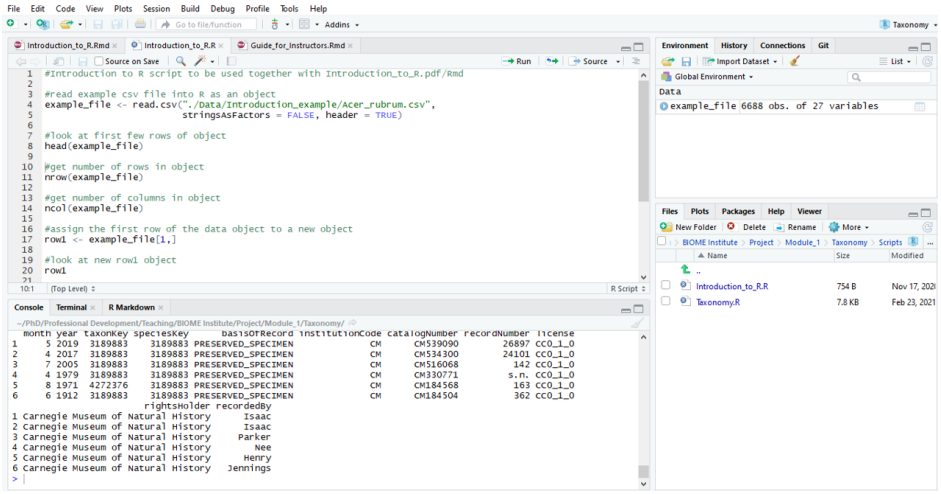

Figure 2: Screenshot of RStudio interface with head of *examplefile*

We can use several functions to learn more about our dataset. For example, we can use *nrow()* to count how many rows there are in the dataset. Try it now. How many rows are there? What about columns?

```
nrow(example_file)
```

```
## [1] 6688
```

```
ncol(example_file)
```

```
## [1] 27
```

You will notice that we are using the **object** *example_file* to refer to the dataset. **Objects** are easy ways to assign large amounts of information to a single string of letters and/or numbers.

Let's assign a single individual row to a new object: *row1*

```
row1 <- example_file[1,]
```

In this example, we are assigning the **object** *row1* the value of *example_file[1,]* which represents the first row and all columns of the **object** *example_file* using the **operator** <- . Let's see what that looks like. Here, rather than asking to see a subset of the data, as we did above with the *head()* **function**, we can run the **object** itself and see the whole thing.

```
row1
```

```
##        gbifID kingdom        phylum         class       order        family
    genus
## 1 2859483912 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
##        species infraspecificEpithet taxonRank scientificName countryCode
## 1 Acer rubrum                       SPECIES Acer rubrum L.           US
##   decimalLatitude decimalLongitude           eventDate day month year
    taxonKey
## 1        41.81199        -78.60252 2019-05-11T00:00:00  11     5 2019
    3189883
##   speciesKey      basisOfRecord institutionCode catalogNumber recordNumber
## 1    3189883 PRESERVED_SPECIMEN              CM       CM539090        26897
##   license                        rightsHolder recordedBy
## 1 CC0_1_0 Carnegie Museum of Natural History      Isaac
```

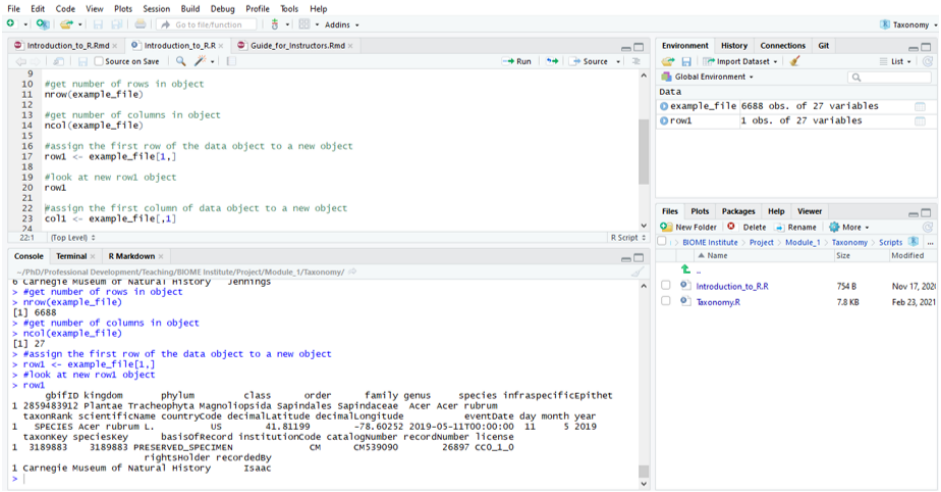

Figure 3: Screenshot of *nrow*, *ncol*, and *row*1 lines of code

Let's see what just the first column of the original data would look like.

```
col1 <- example_file[,1]
head(col1)
```

```
## [1] 2859483912 2859481590 2859479256 2859479131 2859478953 2859478951
```

Sometimes it's hard to visualize lots of data at once, which is why the summary tools, viewing a subset, or viewing the structure of the dataset can be useful.

```
str(example_file)
```

```
## 'data.frame':    6688 obs. of  27 variables:
##  $ gbifID              : num  2.86e+09 2.86e+09 2.86e+09 2.86e+09 2.86e+09
    ...
##  $ kingdom             : chr  "Plantae" "Plantae" "Plantae" "Plantae" ...
##  $ phylum              : chr  "Tracheophyta" "Tracheophyta" "Tracheophyta"
    "Tracheophyta" ...
##  $ class               : chr  "Magnoliopsida" "Magnoliopsida" "
    Magnoliopsida" "Magnoliopsida" ...
##  $ order               : chr  "Sapindales" "Sapindales" "Sapindales" "
    Sapindales" ...
```

```
## $ family              : chr  "Sapindaceae" "Sapindaceae" "Sapindaceae" "
   Sapindaceae" ...
## $ genus               : chr  "Acer" "Acer" "Acer" "Acer" ...
## $ species             : chr  "Acer rubrum" "Acer rubrum" "Acer rubrum" "
   Acer rubrum" ...
## $ infraspecificEpithet: chr  "" "" "" "" ...
## $ taxonRank           : chr  "SPECIES" "SPECIES" "SPECIES" "SPECIES" ...
## $ scientificName      : chr  "Acer rubrum L." "Acer rubrum L." "Acer
   rubrum L." "Acer rubrum L." ...
## $ countryCode         : chr  "US" "US" "US" "US" ...
## $ decimalLatitude     : num  41.8 41.4 41.6 NA 43.6 ...
## $ decimalLongitude    : num  -78.6 -75.9 -80 NA -71.5 ...
## $ eventDate           : chr  "2019-05-11T00:00:00" "2017-04-29T00:00:00"
   "2005-07-21T00:00:00" "1979-04-22T00:00:00" ...
## $ day                 : int  11 29 21 22 10 25 NA 6 31 8 ...
## $ month               : int  5 4 7 4 8 6 NA 6 10 4 ...
## $ year                : int  2019 2017 2005 1979 1971 1912 NA 1920 1931
   1905 ...
## $ taxonKey            : int  3189883 3189883 3189883 3189883 4272376
   3189883 4272376 3189883 3189883 3189883 ...
## $ speciesKey          : int  3189883 3189883 3189883 3189883 3189883
   3189883 3189883 3189883 3189883 3189883 ...
## $ basisOfRecord       : chr  "PRESERVED_SPECIMEN" "PRESERVED_SPECIMEN" "
   PRESERVED_SPECIMEN" "PRESERVED_SPECIMEN" ...
## $ institutionCode     : chr  "CM" "CM" "CM" "CM" ...
## $ catalogNumber       : chr  "CM539090" "CM534300" "CM516068" "CM330771"
   ...
## $ recordNumber        : chr  "26897" "24101" "142" "s.n." ...
## $ license             : chr  "CC0_1_0" "CC0_1_0" "CC0_1_0" "CC0_1_0" ...
## $ rightsHolder        : chr  "Carnegie Museum of Natural History" "
   Carnegie Museum of Natural History" "Carnegie Museum of Natural History" "
   Carnegie Museum of Natural History" ...
## $ recordedBy          : chr  "Isaac" "Isaac" "Parker" "Nee" ...
```

Another important element is the concept of **classes** of **objects**. If the data is a number, it is often stored as a *numeric* or *integer* **class** while words or other groups of letters are stored as *character* **classes**. If you look at column *kingdom*, for example, you can see that it has the **class** *character* while the *gbifID* which is composed of numbers, is stored as *numeric*.

File formats and file typs are very important when manipulating data. As described above, **csv** files are **comma** delimited, meaning that columns are separated by **commas** (,) and rows are separated by **new line characters**. Another file type is **tab** delimited files, where columns are separated by **tabs** (a type of **white space**). The ending of a filename often gives a clue to what type of file it is; **comma** delimited files are typically saved as *.csv* while **tab** delimited files are often saved as *.txt*. To compare with the **csv** file we looked at earlier, let's look at a **txt** file.

```
#Read in the tab-delimited file using the read.delim function - you need to
   specify that the character "\t" is used to separate columns (the backslash
    is used to "excape" the t, which means that you are referring to a tab,
   not the letter t)
txt_file_example_1 <- read.delim("../Data/Introduction_example/Birthdates.txt"
   , sep = "\t", stringsAsFactors = FALSE, header = TRUE)

head(txt_file_example_1)
```

```
##       Name  Birthdate
## 1     John 2000-04-22
## 2    Maria 1996-11-02
## 3   Sophia 1999-07-14
## 4    Ahmet 2001/08/08
## 5 Fernanda 1998/06/29
## 6   Takumi 1997/02/12

#If you specify that the separator is a space (" "), the file is not imported
    correctly, because the separator is actually a tab
txt_file_example_2 <- read.delim("../Data/Introduction_example/Birthdates.txt"
    , sep = "␣", stringsAsFactors = FALSE, header = TRUE)

head(txt_file_example_2)

##        Name.Birthdate
## 1     John\t2000-04-22
## 2    Maria\t1996-11-02
## 3   Sophia\t1999-07-14
## 4    Ahmet\t2001/08/08
## 5 Fernanda\t1998/06/29
## 6   Takumi\t1997/02/12

#Alternatively, if the separator is actually a space and not a tab, the
    separator needs to be specified as sep = " "
#If you specify that the separator is a space (" "), the file is not imported
    correctly, because the separator is actually a tab
txt_file_example_3 <- read.delim("../Data/Introduction_example/Birthdates_
    space.txt", sep = "␣", stringsAsFactors = FALSE, header = TRUE)

head(txt_file_example_3)

##       Name  Birthdate
## 1     John 2000-04-22
## 2    Maria 1996-11-02
## 3   Sophia 1999-07-14
## 4    Ahmet 2001/08/08
## 5 Fernanda 1998/06/29
## 6   Takumi 1997/02/12

#To compare, read in the original csv file using the read.delim function,
    specifying that the separator is a comma
example_file_delim <- read.delim("../Data/Introduction_example/Acer_rubrum.csv
    ", sep = ",", stringsAsFactors = FALSE, header = TRUE)

head(example_file_delim)

##       gbifID kingdom       phylum       class       order       family
    genus
## 1 2859483912 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 2 2859481590 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 3 2859479256 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
```

```
## 4 2859479131 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 5 2859478953 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
## 6 2859478951 Plantae Tracheophyta Magnoliopsida Sapindales Sapindaceae
    Acer
##       species infraspecificEpithet taxonRank
## 1 Acer rubrum                         SPECIES
## 2 Acer rubrum                         SPECIES
## 3 Acer rubrum                         SPECIES
## 4 Acer rubrum                         SPECIES
## 5 Acer rubrum             trilobum    VARIETY
## 6 Acer rubrum                         SPECIES
##                                     scientificName countryCode
    decimalLatitude
## 1                                   Acer rubrum L.          US
    41.81199
## 2                                   Acer rubrum L.          US
    41.35940
## 3                                   Acer rubrum L.          US
    41.56981
## 4                                   Acer rubrum L.          US
                NA
## 5 Acer rubrum var. trilobum Torr. & Gray ex K.Koch          US
    43.58838
## 6                                   Acer rubrum L.          CA
                NA
##   decimalLongitude           eventDate day month year taxonKey speciesKey
## 1        -78.60252 2019-05-11T00:00:00  11     5 2019  3189883    3189883
## 2        -75.87470 2017-04-29T00:00:00  29     4 2017  3189883    3189883
## 3        -79.95219 2005-07-21T00:00:00  21     7 2005  3189883    3189883
## 4               NA 1979-04-22T00:00:00  22     4 1979  3189883    3189883
## 5        -71.51202 1971-08-10T00:00:00  10     8 1971  4272376    3189883
## 6               NA 1912-06-25T00:00:00  25     6 1912  3189883    3189883
##       basisOfRecord institutionCode catalogNumber recordNumber license
## 1 PRESERVED_SPECIMEN              CM      CM539090        26897 CC0_1_0
## 2 PRESERVED_SPECIMEN              CM      CM534300        24101 CC0_1_0
## 3 PRESERVED_SPECIMEN              CM      CM516068          142 CC0_1_0
## 4 PRESERVED_SPECIMEN              CM      CM330771         s.n. CC0_1_0
## 5 PRESERVED_SPECIMEN              CM      CM184568          163 CC0_1_0
## 6 PRESERVED_SPECIMEN              CM      CM184504          362 CC0_1_0
##                          rightsHolder recordedBy
## 1 Carnegie Museum of Natural History      Isaac
## 2 Carnegie Museum of Natural History      Isaac
## 3 Carnegie Museum of Natural History     Parker
## 4 Carnegie Museum of Natural History        Nee
## 5 Carnegie Museum of Natural History      Henry
## 6 Carnegie Museum of Natural History   Jennings
```

If you have trouble importing a file into R, check to make sure that the formatting of the file matches the format that you are specifying in your R code. Additionally, check to make sure that **white spaces** are being interpreted correctly (you can check for white spaces by toggling the "Show All Characters" or "Show White Space Characters" options in a text editor such as Notepad++). Spaces are typically represented by dots while tabs are represented by arrows. It is generally easiest to import files that contain multiple

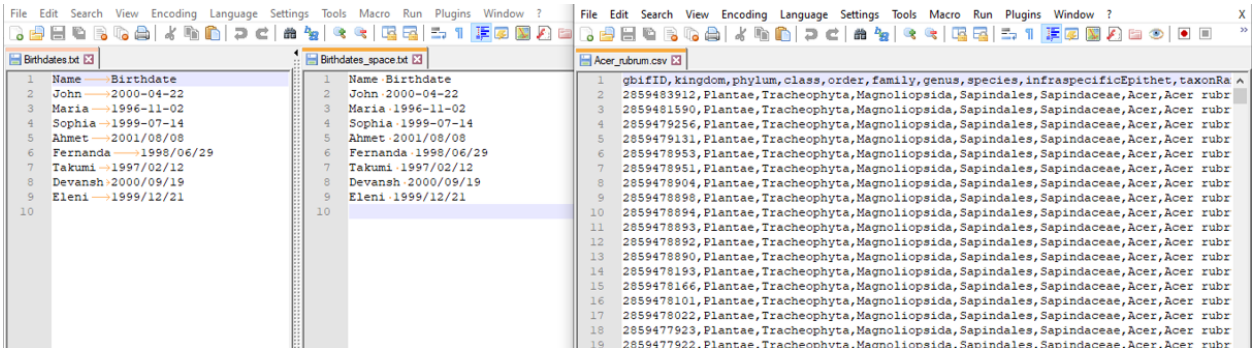

Figure 4: Screenshot of different file types in text editor

columns into R as **csv** files. To save your own data as a **csv** file, in Excel, you can go to "Save As" and for file type, specify "CSV (Comma delimited)" rather than "Excel Workbook" or whatever file type it was originally.

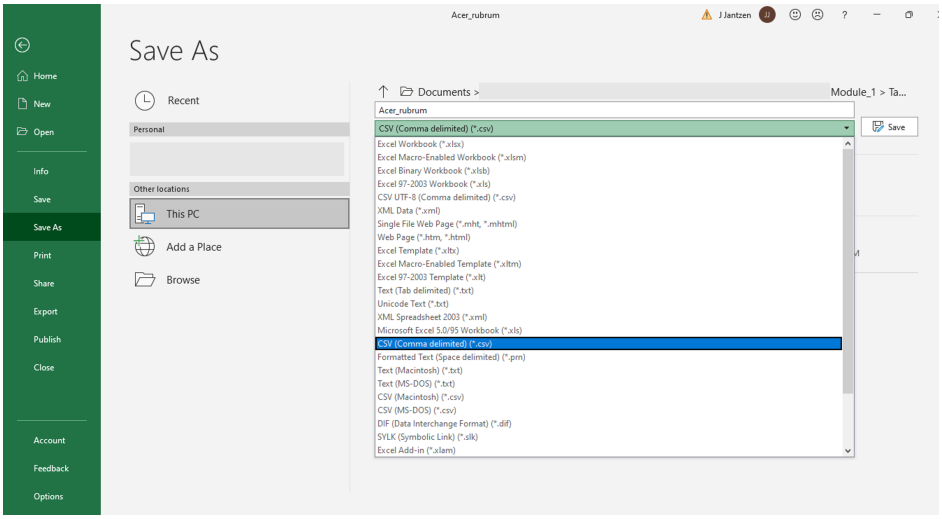

Figure 5: Screenshot of how to save as .csv in Excel

To check if R has correctly imported your file, make sure you inspect it using the summary functions we introduced in this tutorial. You may need to reformat the resulting object to ensure it is in the right format for your analyses (as demonstrated in the Taxonomy.R script).

I think that is enough of an introduction for now so let's get into this module!