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Transcriptomics 7633
Exercise #1

2.1) How do you start a new R script in RStudio?

I did it by going into RStudio, going to new file, and then pressing new script

2.2) Why is it not a good idea to use MS Word to save your commands?

MS Word does not do a good job of keeping record of indents, spaces or syntax that are required to make the script run properly

2.3) Where does R save the history of your commands?

I believe it saves it to my program files, or wherever I installed R and RStudio

3.1) How do you know when R is ready for your command?

R is ready for your command when the slash is blinking within the terminal

3.2) How do you comment your code?

You can comment on your code using a series of hashtags wherever explanation is needed

3.3) What does it mean then R prompts you with a "+" in the beginning of the line?

The plus sign just stands for an unfinished line

4.1) What is an R workspace? How do you save it and how do you load it?

An R workspace is a just a series of scripts or ways that someone has manipulated data within the R terminal. It saves codes, graphs, calculations, etc.

4.2) What is a working directory? How do you set it and how do you determine which directory is the working directory?

A working directory is the location from which data is being extracted and displayed

4.3) How is an RStudio project related to the R workspace and Working directory?

RStudio is simply a user interface so it just displays the R workspace and information from the directory

5.1) What is the command to install a package from CRAN?

install.packages("package")

5.2) What is the command to retrieve documentation related to a function and its usage?

help("package")

7.1) Create two integer vectors, one called GeneA with the values 3,4,5,7 and the other GeneB with the values 4,6,8,5

7.2) Create a character vector with the words, "control", "nitrogen", "potassium", and "phosphate" and call it Experiments.

8.1) Add vectors GeneA and GeneB and save it as GeneAB

GeneA	num [1:4] 3 4 5 7
GeneAB	num [1:4] 7 10 13 12
GeneB	num [1:4] 4 6 8 5

8.2) Add vectors GeneAB with Experiments. Do you get an error? Why or Why not?

```
> Geneexperiments = GeneAB + Experiments  
Error in GeneAB + Experiments : non-numeric argument to binary operator
```

I believe this error is due to trying to combine numeric and alpha characters

8.3) Add 1 to vector GeneAB and call it GeneABplusOne. Which value has changed and by how much?

Each of the individual values in the vector increased by 1

9.1) Create a matrix called expvalues where GeneA is the first row and GeneB is the second row.

9.2) Assign the Experiments as the column names of the matrix expvalues.

9.3) Subset the matrix to retrieve the control and nitrogen values for GeneA.

10.1) In what situation would you prefer a dataframe over a matrix?

A dataframe would be better if you had a numerical as well as alphabetical data that you want to store in a table

10.2) In what situation would you prefer a list over a dataframe?

A list is useful if you have a series of values or strings that you want stored and don't care about organizing it in rows and columns

11.1) Convert the expvalues matrix into a dataframe and call it expvaluesdf

11.2) Give three different ways to retrieve the “potassium” column from `expvaluesdf`

The first way is you can use `$` like `expvaluesdf$potassium`. The second way is to do `expvaluesdf[, c(potassium)]`, and lastly you can use the numerical index like `expvaluesdf[, c(1,4)]`

12.1) What class of an object is created when using the `read.table()` function to import files?

The object is in a data frame when you use `read.table()` to import files

12.2) Use the help function to look at the details of how `read.table()` function works. Compare `read.table()` and `read.delim()`. Which default options are different for the two commands?

The header command is true for `read.delim` while it is false for `read.table`, also the fill is `blank.lines.skip` for `read.table` while it is true for `read.delim`

12.3) What does the `stringsAsFactors` option do?

It converts character strings into an alternate data type for data.frames