Exercise 1.
Numeric vector manipulation

First create a script "exercise1.R" and save it to the "Rintro/day1" directory: you will save all your commands in it for that exercise.
Remember you can comment the code using #.

1. Create vector **y** as:
y <- 8:22

2. How many elements does **y** contain?
length()

3. Remove the 7th element of y.

4. Select all elements of **y** that are **inferior to** 12.
* First get the indices: y < 12
* Then get the actual values: y[?]

5. Select all elements of **y** that are **equal to** 22.
y[?]

6. Select all elements of **y** that are superior to 12 **and** inferior to 18, both included.
y[? & ?]

7. Select all elements of **y** that are **either inferior to** 10, or **superior to** 20.
y[? | ?]

8. Create vector **x** of 1000 random numbers from the random distribution:
First read the help page of **rnorm** function.

9. What are the mean, median, minimum and maximum values of **x**?
mean(); median(); min(); max()

10. What additional information do you get with the **summary**() function?

11. Create vector **y2** as:
y2 <- c(1, 11, 130, 62, 18, 2, 37)

12. Which elements of **y2** are present in **y**?
*Note: remember **%in%**.*

13. Add 2 to each element of **y2**: **reassign the new values to the y2 object**!

--- OPTIONAL FROM HERE ON FOR EXERCISE 1 ---

14. Create vector **myvector** such as:
myvector <- c(1, 2, 3, 1, 2, 3, 1, 2, 3)
* Create it the way shown above.
* Create the same vector using the **rep** function.

15. Replace the 5th, 6th and 7th element of **myvector** with 8, 12 and 32 values.

16. Calculate the **fraction/percentage** of each element of myvector relative to the total sum of the vector.
sum() can be useful.

17. Add vector c(2, 4, 6, 7) to the end of **myvector**: reassign!

<u>**Exercise 2.**</u>
Character vector manipulation.

First create a script "exercise2.R" and save it to the "Rintro/day1" directory: you will save all your commands in it for that exercise.

1. Create vector **w** as:
w <- rep(c("miRNA", "mRNA"), c(3, 2))

2. View vector **w** in the console: what is function **rep**() doing?

3. Type **table**(w). What do you obtain?

4. Type **w[grep("mRNA", w)]** and **w[w == "mRNA"]**
Is there a difference between the two outputs?

5. Now type **w[grep("RNA", w)]** and **w[w == "RNA"]**
Is there a difference between the two ouputs?

6. Create vector **g** as:
g <- c("hsa-let-7a", "hsa-mir-1", "CLC", "DKK1", "LPA")

7. How many elements do **w** and **g** contain?
length()

8. Assign names to each element of **g**: the names of **g** will be the characters contained in **w!**
names()

--- OPTIONAL FROM HERE ON FOR EXERCISE 2 ---

9. Replace all column names of **g** that are "mRNA" with "Gene"

10. Count how many miRNAs and how many Genes there are based on the column names.

Exercise 3.

First create a script “exercise3.R” and save it to the “Rintro/day1” directory: you will save all your commands in it for that exercise.

1. Create a directory “**exercise3**” (in Rintro/day1/exercise3)
dir.create()

2. Go to directory “**exercise3**”
setwd()

3. Scan elements from **ex3_input.txt**, and save into object **z**.
ex3_input.txt is in: /users/bi/public-docs/sbonnin/Rcourse/ex3_input.txt
scan()

4. Sort elements of **z** and save into object **zsorted**.
sort()

5. Write **zsorted** into file **ex3_output.txt.**
write()
*Note: set option **ncolumns** to 1.*

6. Go back to the **Rintro** directory in the home directory.
setwd("~/Rintro")
Note: ~ is the home directory. Your home directory in the Isilon storage where we work on now is /users/[yourgroup]/[yourpseudo]. e.g. /users/bi/sbonnin.

7. Save **exercise3.R** file and source it.
Code -> Source

Do you get any error? Time to debug!
Does directory “**exercise3**” contain “ex3_output.txt” file? Check its contents!