'This is a string with a closing quote'

c("one", "two", "three")

my\_dna <- "ATGCGTA"

my\_dna

stringExample <- c("one", "two", "three")

stringExample #check the string content

#Select the first part of string:

stringExample[1]

**Upper and Lower Case**

DNA1 <- "atcg"

toupper(DNA1) # Convert to upper case letters

DNA2 <- "AATT"

tolower(DNA2) # Convert to lower case letters

Concatenation strings str\_c()

a <- "R you"

b <- "Ready"

c <- "for"

d <- "Molecular Biology"

str\_c(a,b,c,d, sep = " ")

**Concatenation strings str\_c()**

stringExample <- c("one", "two", "three")

str\_c(stringExample[1],stringExample[2],stringExample[3], sep = " ")

FirstDNA <- "AAGG"

SecondDNA <- "TTCC"

str\_c(FirstDNA, SecondDNA, sep = "") # sep="", without any spaces

str\_c(FirstDNA, SecondDNA, sep = ",") #sep=",", the comma make

my\_dna <- str\_c("AAGG","TTCC")

my\_dna

FirstDNA <- "AAGG"

SecondDNA <- "TTCC"

my\_dna <- str\_c(FirstDNA, "Exon", SecondDNA)

my\_dna

# Now add a space as separator

my\_dna <- str\_c(FirstDNA, "Exon", SecondDNA, sep = " ")

my\_dna

**length of a string (str\_length() Function):**

DNA <- "AACTCGCCTTAGCT"

# nchar(DNA)

str\_length(DNA)

**Exercise 1.a and 1.b**

**Count Number of Occurrences**

exp <- "R You Ready For Molecular Biology?"

#Number of o in this sentence

str\_count(exp, pattern = "o")

**Exercise 1c:**

**Replacement:**

Name <- "Nolecular Biologi and Nolecular Oncology"

# replace the first N with M

str\_replace(Name, "N", "M")

# replace all N with M

str\_replace\_all(Name, "N", "M")

# let's save this replacement by some name

New\_Name <- str\_replace(Name, "N", "B")

New\_Name

str\_c("The name of new Name is: ", New\_Name)

my\_dna <- "ACTG"

*# replace A with T*

replacement1 <- str\_replace\_all(my\_dna, "A", "T")

replacement2 <- str\_replace\_all(replacement1, "C", "G")

replacement3 <- str\_replace\_all(replacement2, "T", "A")

replacement4 <- str\_replace\_all(replacement3, "G", "C")

replacement4

dna <- "ACTG"

*# replace A with T*

replacement1 <- str\_replace\_all(my\_dna, "A", "t")

replacement2 <- str\_replace\_all(replacement1, "C", "g")

replacement3 <- str\_replace\_all(replacement2, "T", "a")

replacement4 <- str\_replace\_all(replacement3, "G", "c")

replacement4

toupper(replacement4)

dna <- str\_replace\_all(dna, c("A" = "t", "C" ="g", "G"= "c", "T"= "a"))

toupper(dna)