Class06: R Functions

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Background

Functions are at the heart of using R. Everything we do involves calling and using functions (from data input, analysis to results output).

All functions in R have at least three things:

1. a **name** the thing we use to call the function.
2. one or more input **arguments** that are comma separated
3. the **body**, lines of code between curly brackets {} that does the work of the function.

A first function

Let's write a silly wee fucntion to add some numbers.

```
add <- function(x) {
  x + 1
}
```

Let's try it out

```
add(100)
```

```
[1] 101
```

Will this work?

```
add( c(100, 200, 300))
```

```
[1] 101 201 301
```

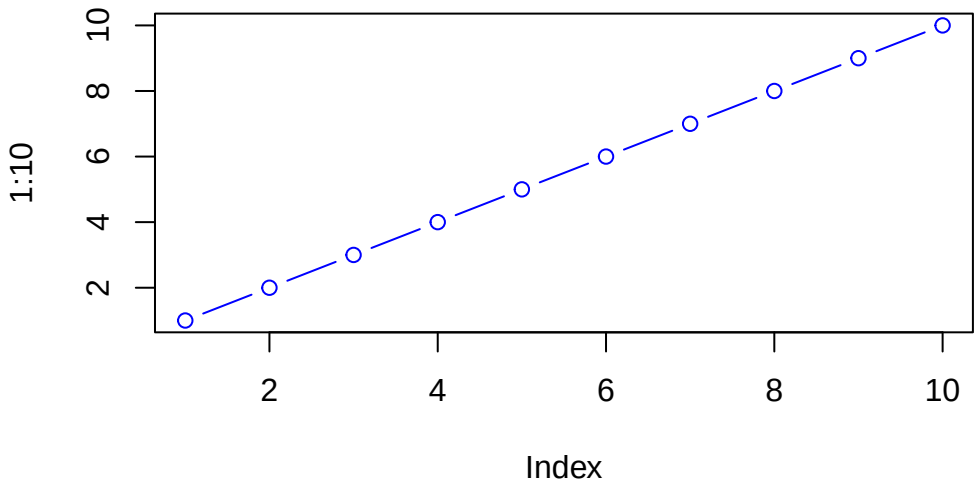
Modify to be more useful and add more than just 1

```
add <- function(x, y) {
  x + y
}
```

```
add(100, 10)
```

```
[1] 110
```

```
plot(1:10, col="blue", typ= "b")
```



```
log(10, base=10)
```

```
[1] 1
```

Given y a default, so if we don't give a value for y, it will automatically think 1.

```
add <- function(x, y=1) {
  x + y
}
```

```
add(100)
```

```
[1] 101
```

> **N.B** Input arguments can either be **required** or *optional*. The latter have a fall-back default that is specified in the function code with an equal sign.

```
#add(x=100, y=200, z=300)
```

A Second Function

All funcitons in R look like this

```
name <- function(arg) {
body
}
```

The `sample()` function in R

```
sample(1:10, size=4)
```

```
[1] 7 6 9 3
```

> Q. Return 12 numbers picked randomly from the input 1:10

```
sample(1:10, size=10, replace=TRUE)
```

```
 [1] 9 7 9 7 3 7 9 6 9 9
```

you have to replace to TRUE, when wanting to generate more numbers than the size you have.

Q. Write the code to generate a random 12 nucleotide long DNA sequence

```
DNA <- c("A", "C", "T", "G")
sample(DNA, size=12, replace=TRUE)
```

```
 [1] "T" "T" "A" "C" "C" "G" "A" "T" "A" "T" "C" "G"
```

Q. Write a first version function called `generate_dna()` that generates a user specified length `n` random DNA sequence?

```
generate_dna <- function(n=6){
  DNA <- c("A", "C", "T", "G")
sample(DNA, size=n, replace=TRUE)
}
```

```
generate_dna()
```

```
[1] "G" "T" "G" "C" "A" "C"
```

```
generate_dna(100)
```

```
  [1] "G" "T" "G" "C" "T" "G" "C" "C" "C" "A" "A" "A" "G" "A" "A" "G" "T" "C"
 [19] "G" "T" "A" "C" "G" "A" "A" "T" "C" "G" "C" "G" "C" "C" "C" "A" "A" "C"
 [37] "A" "A" "G" "T" "C" "G" "T" "T" "T" "G" "G" "A" "G" "C" "T" "C" "G" "A"
 [55] "G" "A" "C" "G" "C" "G" "G" "T" "C" "C" "T" "C" "A" "G" "A" "G" "A" "G"
 [73] "A" "A" "T" "G" "G" "C" "C" "T" "T" "A" "T" "T" "C" "C" "C" "T" "C" "A"
 [91] "T" "T" "A" "T" "T" "G" "A" "C" "A" "G"
```

Q. Modify your function to retunr a FASTA like sequence so rather than [1] “G” “C” etc we want GCAAT.

```
generate_dna <- function(n=6){
  DNA <- c("A", "C", "T", "G")
sample(DNA, size=n, replace=TRUE)
}
```

```
hello <- c("H", "E", "L", "L", "O")
paste(hello, collapse="")
```

```
[1] "HELLO"
```

THIS is how you get the quotations marks out of the way.

```
paste(generate_dna(20), collapse="")
```

```
[1] "CTGGATCCGTTACCTGTTCT"
```

or

```
generate_dna <- function(n=6){
  DNA <- c("A", "C", "T", "G")
ans <- sample(DNA, size=n, replace=TRUE)
ans <- paste(ans, collapse="")
return(ans)
}
```

```
generate_dna(10)
```

```
[1] "CAGAAGAGCA"
```

> Q. Give the user an option to return FASTA format output sequence or standard multi-element vector format.

```
generate_dna <- function(n=6, fasta=TRUE){
  DNA <- c("A", "C", "T", "G")
ans <- sample(DNA, size=n, replace=TRUE)

if(fasta) {
  ans <- paste(ans, collapse="")
}
return(ans)
}
```

```
generate_dna(10)
```

```
[1] "ATTTTTTCCC"
```

```
generate_dna(10, fasta=FALSE)
```

```
 [1] "G" "T" "T" "A" "A" "G" "G" "T" "G" "T"
```

just to show how it works:

```
generate_dna <- function(n=6, fasta=TRUE){
  DNA <- c("A", "C", "T", "G")
ans <- sample(DNA, size=n, replace=TRUE)

if(fasta) {
  ans <- paste(ans, collapse="")
  cat("Hello...")
}
return(ans)
}
```

```
generate_dna(10)
```

```
Hello...
```

```
[1] "GTACCGTGAC"
```

```
generate_dna(10, fasta=FALSE)
```

```
 [1] "G" "G" "G" "A" "C" "T" "G" "A" "C" "T"
```

```
generate_dna <- function(n=6, fasta=TRUE){
  DNA <- c("A", "C", "T", "G")
ans <- sample(DNA, size=n, replace=TRUE)

if(fasta) {
  ans <- paste(ans, collapse="")
  cat("Hello...")
```

```
} else {
  cat("...is it me you are looking for")
}
return(ans)
}
```

```
generate_dna(10)
```

```
Hello...
```

```
[1] "ACGGTTGGGG"
```

```
generate_dna(10, fasta=FALSE)
```

```
...is it me you are looking for
```

```
 [1] "T" "G" "A" "A" "T" "C" "G" "A" "A" "T"
```

A new cool function

> Q. Write a function called `generate_protein()` that generates a use specified length protein sequence in FASTA like format

```
generate_protein <- function(n=6){
  aa <- c("A", "R", "N", "D", "C", "Q", "E", "G", "H", "I", "L", "K", "M", "F", "P", "S", "T
ans <- sample(aa, size=n, replace=TRUE)
ans <- paste(ans, collapse="")
return(ans)
}
```

```
generate_protein(10)
```

```
[1] "NKTKIFNEMA"
```

> Q. Use your new `generate_protein()` function to generate all sequences between length 6 and 12 amino acids in length and check that any of these are unique in nature (ie found in the NR database at NBI)

```
generate_protein(6)
```

```
[1] "DDDMHY"
```

this is found in NBI

```
generate_protein(12)
```

```
[1] "LADYKGQYRPMD"
```

there is no 100% cover and identity

```
generate_protein(10)
```

```
[1] "RIQWRQCGSI"
```

to not keep repeating yourself, using the for() loop

```
for(i in 6:12) {
  cat(i, "\n")
  cat(generate_protein(i), "\n")
}
```

```
6
QNEEPN
7
LFETDVQ
8
WDDTPSYG
9
QCHVTHVYG
10
ALCVFCPTIH
11
WKPDISCPCTT
12
QWYYGWWVFKST
```

what a FASTA format looks like: >id AGKRTST >next GKSTR

sep is for getting rid of the space between the > and the numbers

```
for(i in 6:12) {
  cat(">", i, sep="", "\n")
  cat(generate_protein(i), "\n")
}
```

```
>6
RKNRAF
>7
LTLWLWQ
>8
SSNWPVLR
>9
PTDGFMYIG
>10
TNNQVWNDNY
>11
QNNNILLFFAV
>12
QDGGYKELIKQS
```

number 9, 10, 11, 12 does not have a match