Class 06: R Functions

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Table of contents

Background

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

All functions in R have at least 3 things:

1. A **name** the thing we use to call the function.
2. One or more input **arguments** that are a comma separared
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 function to add some numbers:

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

Let's try it out

```r
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=1){
  x + y
}
```

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

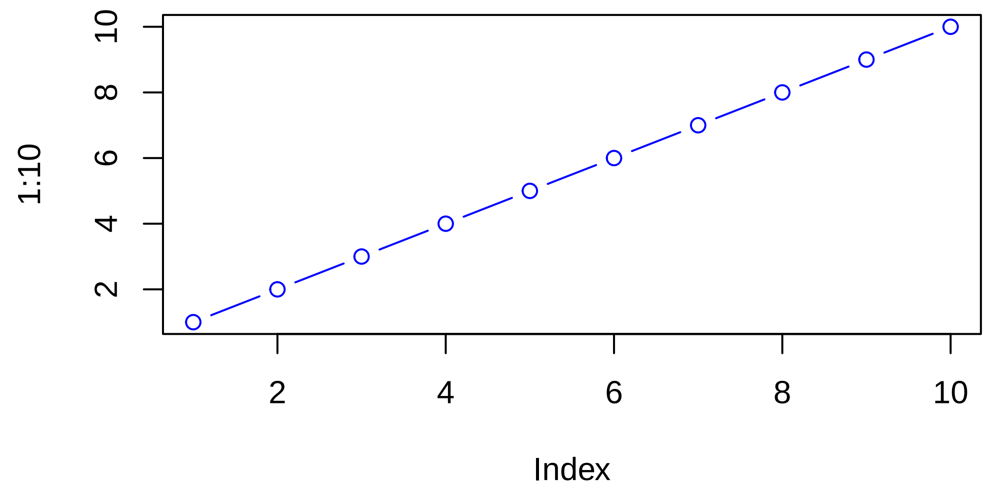
```
[1] 110
```

Will this work?

```
add(100)
```

```
[1] 101
```

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



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

```
[1] 1
```

> **N.B.** Input arguments can be either **required** or **optional**. The later 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 functions in R look like this

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

The `sample()` function in R...?

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

```
[1]  7  3 10  4
```

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

```r
sample(1:10, size=12, replace=TRUE)
```

```
 [1]  5  3  6 10  9  5  2  9  4  6  1  5
```

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

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

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

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

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

```r
generate_dna(100)
```

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

> Q. Modify your function to return a FASTA like sequence so rather than [1] " "A" "T" "C" "C" "G" we want "ATCCG"

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

```r
generate_dna(10)
```

```
[1] "GGATTGGGGG"
```

```r
x<- 100
x<- 10
x<- 300
x
```

```
[1] 300
```

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

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

 if(fasta){
   ans <- paste(ans, collapse = "")
   cat("Hello...")
 }else {
   cat("...is it me you are looking for...")
 }

 return(ans)
}
```

```r
generate_dna(10)
```

```
Hello...
```

```
[1] "GTAGATGTAA"
```

```r
generate_dna(10, fasta=F)
```

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

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

A new cool function

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

```r
generate_protein <- function(n){

 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=T)
 ans <- paste (ans, collapse= "")
 return (ans)
}
```

```r
generate_protein(10)
```

```
[1] "HPYGLCYCNK"
```

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

```r
generate_protein(6)
```

```
[1] "EIGSFH"
```

```r
generate_protein(7)
```

```
[1] "KVKYDFI"
```

```r
generate_protein(8)
```

```
[1] "ACYWRHEY"
```

```r
generate_protein(9)
```

```
[1] "LGMESNGHY"
```

```r
generate_protein(10)
```

```
[1] "NCDLWVNMPI"
```

```r
generate_protein(11)
```

```
[1] "KTPEPEAIIIR"
```

```r
generate_protein(12)
```

```
[1] "SCWFSLHCIQKI"
```

Or we could do a `for()` loop:

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

```
>6
EQTAGP
>7
LEMFTAQ
>8
VLEGYVGV
>9
HGSDSHLKQ
>10
RGHDFSGMIT
```

```
>11
CMWCKMRDPCV
>12
GNYKKKAEQMGM
```

Results: Only 6-8 were found within the NCBI database.