Class6

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Background

Functions are at the heart of using R. Evrything we do involves calling and sing functions (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 comma separated
3. The **body**, lines of code between curly bracketa { }, that does the work of the function

A First Function

Let's write a function to add some numbers:

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

Let's try it out

```r
add(100)
```

```
[1] 101
```

Will this work:

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

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

We want to modify the code, for it to be more useful and add more than just 1:

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

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

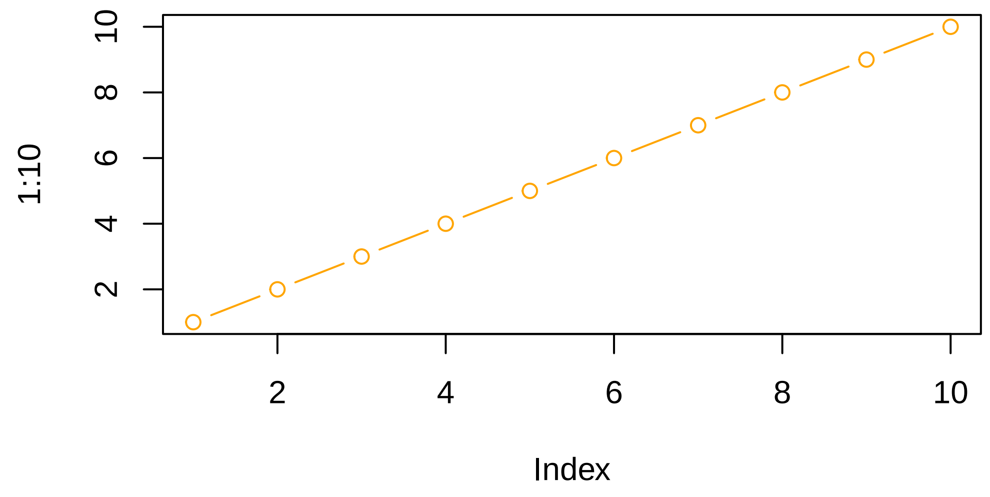
```
[1] 110
```

```r
add(100)
```

```
[1] 101
```

We cannot run the code as we need y!

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



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

```
[1] 1
```

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

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

A Second Function

All R functions in R look like this:

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

The `sample()` function in R …

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

```
[1]  5  3  8 10
```

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

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

```
 [1]  3  8  1  7  9  4  3  3 10  2 10  5
```

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

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

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

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

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

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

```r
generate_dna(25)
```

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

Q. Modify our function to return a FASTA-like sequence. So, rather than "A" "A" "C" "T", we want to get "AACT". (Use `collapse`)

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

```r
generate_dna (100)
```

```
[1] "AGGGTCTGCCATTGGTGTAAACCGCTTACACGAAGAGCACAACAGTGTGTAAATTAGGACGATACGAACCTATGATAGAAGAGAACGC
```

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

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

if(FASTA) {
 ans<-paste(ans, collapse = "")
 cat("Hello>>>")
} else {
  cat("LALALALLA")
}
 return(ans)
}
```

```r
generate_dna(10)
```

```
Hello>>>

[1] "CACCTGCATT"
```

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

```
LALALALLA

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

A third, 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, FASTA=T) {
  amino_acids <- c ("A","R","N","D","C","E","Q","G","H","I",
                    "L","K","M","F","P","S","T","W","Y","V")
  ans <- sample(amino_acids, size=n, replace = T)
 ans<-paste(ans, collapse = "")
 return(ans)
}
```

```r
generate_protein (7)
```

```
[1] "RLVEQHN"
```

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

```r
generate_protein(6)
```

```
[1] "GGEFHI"
```

```r
generate_protein(7)
```

```
[1] "MKEMWTQ"
```

```r
generate_protein(8)
```

```
[1] "SGGPRPHL"
```

```r
generate_protein(9)
```

```
[1] "GCKNCVRCF"
```

```r
generate_protein(10)
```

```
[1] "YPGYIVRITK"
```

```r
generate_protein(11)
```

```
[1] "IVFRGVKPCSK"
```

```r
generate_protein(12)
```

```
[1] "THRRFNAFLLKF"
```

Or.. we could fo a `for()` loop:

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

```
>6
YRWWQK
>7
GNEMHFG
>8
LVDYEQWQ
>9
NATWIKWDH
>10
HRYQHLHKQE
>11
KNTNRCVKVLI
>12
STDARNKMHERR
```