class06

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Table of contents

Background

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

All functions in R have at least 3 things:

- A **name** the thing we use to call the function.
- One or more input **arguments** that are comma seperated
- The ***body**, liens 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:

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

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

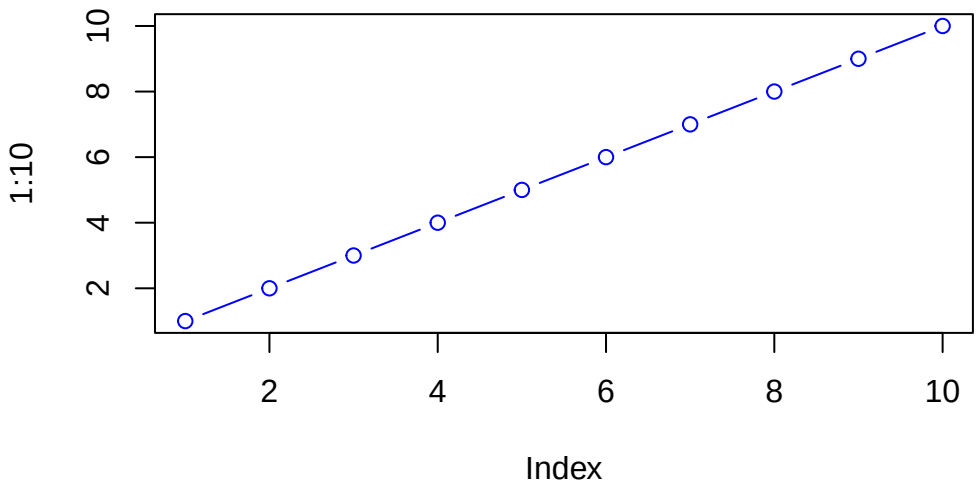
```
[1] 110
```

Will this work?

```
add(100)
```

```
[1] 101
```

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



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

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

```
[1]  6  2  5 10
```

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

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

```
 [1]  8  4  4  4  8 10  3  3  5  5  3  3
```

Q. Write the code that generates a random 12 nucleotide long DNA sequence?

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

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

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

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

```
generate_dna <- function(n=3) {
  sample( c("A","T","G","C"), size=n, replace=TRUE )
}
```

```
generate_dna(100)
```

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

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

```
generate_dna <- function(n=3) {
  ans <- sample( c("A","T","G","C"), size=n, replace=TRUE )
  ans <- paste(ans, collapse ="")
  return(ans)
}
```

```
generate_dna(10)
```

```
[1] "GCATAAAGCG"
```

An example

```
# Example pattern (not using your bases)
x <- c("H","E","L","L","O")

paste(x, collapse = "****")
```

```
[1] "H****E****L****L****O"
```

```
# returns "HELLO"
```

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

```
generate_dna <- function(n=3, fasta=TRUE) {
  ans <- sample( c("A","T","G","C"), 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] "GGGACCATGA"
```

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

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

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

A new cool function

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

```
generate_protein <- function(n=3, fasta=TRUE) {
  aa <- c( "A","R","N","D",
           "C","Q","E","G",
           "H","I","L","K",
           "M","F","P","S",
           "T","W","Y","V")
  gen <- sample(aa,size=n, replace=TRUE)

  if(fasta) {
```

```
    prn <- paste(gen, collapse = "")
  }

  return(prn)

}
```

```
generate_protein(10)
```

```
[1] "HNSKNKWAKQ"
```

Q. Use your new 'generate_protein()' function to generate sequences between lengths 6 and 12 amino acids in length and check of any of these are unique in nature (i.e. found in the MR database at NCBI)?

```
generate_protein(6)
```

```
[1] "SSIFEA"
```

```
generate_protein(7)
```

```
[1] "KYMFACN"
```

```
generate_protein(8)
```

```
[1] "ADDRCCGR"
```

```
generate_protein(9)
```

```
[1] "NFLTAMEDH"
```

```
generate_protein(10)
```

```
[1] "VYYWRLPFYV"
```

```
generate_protein(11)
```

```
[1] "WFTPMNRAADQ"
```

```
generate_protein(12)
```

```
[1] "IRPEEDGKHTEM"
```

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

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

```
>6
LGMEIA
>7
NLILACP
>8
SFEMLNPY
>9
NHGNQLESG
>10
QRSYYARLNP
>11
CFEFKDAETMT
>12
RNYLKGRFIENS
```