R Functions Class 06

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Today we will get more exposure to functions in R. We call functions to do all our work and today we will learn how to write our own.

```
add<- function(x, y=0) {
 x + y
}

add (5, 6)
```

```
[1] 11
```

```
add (1, c(10, 100))
```

```
[1]  11 101
```

Make sure to send it to the brain if you add a new function

```
add (100)
```

```
[1] 100
```

```
add<- function(x, y=0, z=0) {
 x + y + z
  }

add (8, 17, 45)
```

```
[1] 70
```

Note that arguments can have default values, which allows it to run with less outputs than there are variables.

A second more fun function

Let's write a function that generates random nucleotide sequences.

We can make use of the in-built 'sample()' function in R to help us here.

```
sample(x=1:10, size=9)
```

```
[1]  6  9  8  3  2  4  1  5 10
```

Randomly repeating, but not reusing the same number

```
#{r}    #sample(x=1:10, size=11)
```

Produces error, doesn't work because it's asking for too many outputs and there's not enough option to not repeat one

> Q: Can you use sample() to generate a random nucleotide sequence of length 5?

```
sample(x= c("A", "C", "T", "G"), size= 5, replace = TRUE)
```

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

- Use "replace=TRUE" to be able to repeat values when you're asking for more outputs than you have options.
- Using the small "c" makes your values into a vector

> Q. Write a function called 'generate_dna()' that makes a nucleotide sequence of a user specified length.

Every function in R has at least 3 things:

- a **name** (ie. generate_dna())
- one or more **input arguments** (ie. length of sequence)
- a **body** (what does the work)

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

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

Let's try a way to personalize the length each time.

```r
generate_dna2 <- function(length=12) {
  bases <- c ("A", "C", "G", "T")
  sample(bases, size = length, replace = TRUE)
}
```

```r
generate_dna2(10)
```

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

```r
generate_dna2(100)
```

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

Can you write a 'generate_protein()' function that returns amino acid sequences of a user requested length?

```r
##First, pull in amino acids list from bio3d. 1st line is whole library, 2nd line is more sp

library(bio3d)

bio3d::aa.table$aa1 [1:20]
```

```
 [1] "A" "R" "N" "D" "C" "Q" "E" "G" "H" "I" "L" "K" "M" "F" "P" "S" "T" "W" "Y"
[20] "V"
```

```r
generate_protein <- function(length) {
  AA= c (bio3d::aa.table$aa1 [1:20])
  sample(AA, size=length, replace=TRUE)
}

generate_protein(12)
```

```
 [1] "N" "H" "K" "A" "K" "Y" "S" "A" "N" "D" "A" "D"
```

I want my output of this function not to be a vectore with one amino acid per element but rather a one element single string (ie like a word with all the letters pasted together). The paste() function puts things together; paste (x, collapse=" "). Collapse tells what you want in between the values.

```
bases <- c("A", "C", "G", "T")
paste(bases, collapse="")
```

```
[1] "ACGT"
```

```
paste(generate_protein(), collapse="")
```

```
[1] "EQTMNWDLQKHQDHQGWPLC"
```

```
generate_protein <- function(length=5) {
  AA= c (bio3d::aa.table$aa1 [1:20])
  s<- sample(AA, size=length, replace=TRUE)
  paste(s, collapse="")
}
```

```
  generate_protein()
```

```
[1] "CYHMC"
```

Q. Generate protein sequences from length 6 to 12

We can use the useful utility function 'sapply()' to help us "apply" our function over all the values from 6-12. Want to know more about it? Use ?sapply

```
sapply(6:12, generate_protein)
```

```
[1] "LLILIN"       "YAGNQYK"      "NVRSTNCR"     "NCTVINNEP"    "FCERAMYTYI"
[6] "CIECHHCKLGS"  "RRWQNTTPGLIP"
```

I want teh sequences to be labeled more nicely.

```
paste(">ID", 6:12)
```

```
[1] ">ID 6"  ">ID 7"  ">ID 8"  ">ID 9"  ">ID 10" ">ID 11" ">ID 12"
```

```r
ans <- sapply(6:12, generate_protein)

cat(paste(">ID.", 6:12, sep="", "\n", ans, "\n"), sep="")
```

```
>ID.6
HSNYMG
>ID.7
IDLPAEN
>ID.8
KYYDCFDP
>ID.9
WHTTCPDDY
>ID.10
KQSHERMLKP
>ID.11
GFYFYQVYLHL
>ID.12
ADMNMRWADLYT
```

> Q. Are any of these sequences unique in nature i.e. never found in nature? We can search "refseq-protein" and look for 100% Ide and 100% coverage matches with blastP.

Some sequences did have 100% identity over 100% query coverage. However, there are so many possible amino acid combinations over these varying lengths that it makes sense that there were 4 of the 7 tested sequences that did not have an exact match.