

Class 6: R Functions

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All functions in R have at least 3 things:

- A **name**, we pick this and use it to call our function,
- Input **arguments** (there can be multiple)
- The **body** lines of R code that do the work

Our first (silly) function

Write a function to add some numbers

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

Note: The y=1 means that if we don't provide a value for y, it will default to 1.

Now we call this function:

```
add(5,10)
```

```
[1] 15
```

```
add(5)
```

```
[1] 6
```

Input values as vectors

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

```
[1] 11 11 101
```

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

```
[1] 110 110
```

Our second function

Write a function to generate random nucleotide sequences of a user specified length

The `sample()` function can be helpful here

```
sample(c("A","T","G","C"), size = 50, replace = TRUE)
```

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

*Replace = TRUE fixes the size issue

I want the a 1 element long character vector that looks have no gaps like “ATCGCTA”

```
v <- sample(c("A","T","G","C"), size = 50, replace = TRUE)
paste(v, collapse = "")
```

```
[1] "TACTAATAGGCCTGTACGGGTATAGGTGCCTTCACCCTCAACCCAAGTCA"
```

*The `paste(x, collapse = “”) function removes the gap`

Turn the above into a function that takes input length and generates nucleotide sequence of that input length

```
generate_DNA <- function(x){
  v <- sample(c("A","T","G","C"), size = x, replace = TRUE)
  paste(v, collapse = "")
}
```

Calling the function above

```
generate_DNA(20)
```

```
[1] "AGTATTGTCCAGTTTAAGCA"
```

The if statement has the following structure:

```
if(TRUE){
  cat("HELLO you!")
} else{
  cat("No you don't")
}
```

HELLO you!

Add the ability to return a multi-element vector or a single element fasta like vector

```
generate_fasta <- function(size = 50, fasta = TRUE){
  v <- sample(c("A","T","G","C"), size = size, replace = TRUE)
  s <- paste(v, collapse = "")

  if(fasta){
    return(s)
  } else{
    return(v)
  }
}
```

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

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

```
generate_fasta()
```

```
[1] "CCCTGGGCTAAACCTTATGGTACCAAACCTCGGCCCTCGGATTGAGTGAAA"
```

```
generate_fasta(10)
```

```
[1] "CCAATAGCTC"
```

A protein generating function

```
generate_protein <- function(size = 50, fasta = TRUE){  
  aa <- c("A","R","N","D","C","Q","E","G","H","I",  
          "L","K","M","F","P","S","T","W","Y","V")  
  v <- sample(aa, size = size, replace = TRUE)  
  s <- paste(v, collapse = "")  
  
  if(fasta){  
    return(s)  
  } else{  
    return(v)  
  }  
}
```

```
generate_protein(60)
```

```
[1] "IGPYINRHVSAKNIQYYDFFMPTTTVHQNDWLNDALKEYDGWKKRNLKWCKISQVFHNHF"
```

Use our new `generate_protein()` function to make random protein sequences of length 6 to 12 (i.e. one length = 6, one length = 7...)

Using for loop

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

```
>6
PASGPR
>7
HWFVGA
>8
ICVDRKQR
>9
HVAEPIKDD
>10
KQKNCQAALP
>11
DNaCTPITAPY
>12
SMNPWATPWAHK
```

```
sapply(6:10, generate_protein)
```

```
[1] "YLIKIH"      "PTHCKAG"     "EFISRIYF"    "SYSREHIWE"   "YVFRQNMKCH"
```