

# Class 6: R functions

Medhini Sosale (PID: A69034757)

My first function :)

```
add <- function(x,y=1,z=0){  
  x + y + z  
}
```

Can I just use it?

```
add(1, 1)
```

```
[1] 2
```

```
add(x=1, y=100)
```

```
[1] 101
```

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

```
[1] 101    2 101
```

```
add(10) # works because we set y to a default value
```

```
[1] 11
```

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

```
[1] 20
```

```
add(1, 1, z=1)
```

```
[1] 3
```

Write a function “generate\_dna” that makes a random nucleotide sequence of any length

```
# generate_dna <- function(){  
  
# }  
  
bases <- c("A", "C", "G", "T")  
sequence <- sample(bases, size=50, replace = TRUE)
```

Turning working snippet into a function:

```
generate_dna <- function(length){  
  bases <- c("A", "C", "G", "T")  
  sequence <- sample(bases, size=length, replace = TRUE)  
  return(sequence)  
}
```

```
generate_dna(10)
```

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

Then I installed the bio3d package.

```
aa <- unique(bio3d::aa.table$aa1)[1:20] # pull out the amino acid table but only unique la  
  
generate_protein <- function(length){  
  aa <- unique(bio3d::aa.table$aa1)[1:20]  
  sequence <- sample(aa, size=length, replace = TRUE)  
  sequence <- paste(sequence, collapse = '') # gets rid of spaces  
  return(sequence)  
}  
  
generate_protein(10)
```

```
[1] "MPAPKNMIIY"
```

```

for (len in 6:13)
{
  seq <- generate_protein(len)
  print(seq)
}

```

```

[1] "SNLKHP"
[1] "RKKLLFE"
[1] "KLNQMENS"
[1] "THAATLYQL"
[1] "LCDMEKWLYF"
[1] "TSYPSCWGNAT"
[1] "FTYRAHEWVPYS"
[1] "DVCYINYKPMNIP"

```

```

answer <- sapply(6:12, generate_protein)
paste(c("barry", "alice", "amy", "chandra"), "loves R", sep='')

```

```

[1] "barryloves R"   "aliceloves R"   "amyloves R"     "chandraloves R"

```

```

cat(paste('>id.', 6:12, '\n', answer, sep='', '\n')) # prepping the sequences to be FASTA

```

```

>id.6
RIMNRA
>id.7
KEPACAC
>id.8
QSTHSPNA
>id.9
EWAVPKHGF
>id.10
DGTDILNLTM
>id.11
DTFFCYGWNMR
>id.12
NSYNVMCEAMDS

```