

# Lab 6

Janie Chang-Weinberg (PID: A69037446)

title: “Lab 6” author: “Janie Chang-Weinberg (PID: A69037446)” format: pdf editor: visual

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

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

```
[1] 2
```

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

```
[1] 2
```

Q1: Define a function “Generate\_DNA()” that makes a random nucleotide sequence of any length

## A second Function

```
#generate_dna <- function()  
bases <- c("A","C","T","G")  
sequence <- sample(bases, replace=TRUE, size=5)
```

~the above are code snippets that can be stitched together for function building

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

```
generate_dna(10)
```

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

tadaa

```
aas <- unique(bio3d::aa.table$aa1)[1:20]
aaseq <- sample(aas, size=5, replace= TRUE)
```

Now make a similar function to the “generate\_dna” function, but with amino acids.

```
generate_pep <- function(length){
  aas <- unique(bio3d::aa.table$aa1)[1:20]
  aaseq <- sample(aas,size=length,replace=TRUE)
  aaseq <- paste(aaseq, collapse="") #collapse command will remove spaces between returned v
  return(aaseq)
}
```

Q2: Generate random protein sequences of length 6-13 AAs.

```
generate_pep(6)
```

```
[1] "LPYRKP"
```

Generate random sequences of length 6-12 AAs

```
answer <- sapply(6:12, generate_pep)
answer
```

```
[1] "GDNMGP"      "IMPLHAG"      "MDSVHRMH"      "NNSFWHMF"      "YMQWATGIEK"
[6] "EYYTTILFHRQ" "HNTPSRDMHPPV"
```

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

```
>id.6  
GDNMGP  
>id.7  
IMPLHAG  
>id.8  
MDSVHRMH  
>id.9  
NNSFWHMF  
>id.10  
YMQWATGIEK  
>id.11  
EYYTTILFHRQ  
>id.12  
HNTPSRDMHPPV
```