

# class06 Lab - Functions

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## Functions!

```
fname <- function(arg1, arg2) { paste(arg1,arg2)}
```

My first function:

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

```
w <- c(1,3)
```

```
v <- c(2,4)
```

```
add(w,v)
```

```
[1] 3 7
```

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

```
[1] 2
```

```
add(x=1, y=2)
```

```
[1] 3
```

```
add(c(1,2,3), 3)
```

```
[1] 4 5 6
```

To set a default value:

```
add <- function(x,y=5) {  
  x + y  
}  
  
w <- c(1,3)  
v <- c(2,4)  
  
add(w,v)
```

```
[1] 3 7
```

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

```
[1] 2
```

```
add(x=1, y=2)
```

```
[1] 3
```

```
add(c(1,2,3), 3)
```

```
[1] 4 5 6
```

```
add(10)
```

```
[1] 15
```

**New Task:** To make a function *generatedna()* that makes a random nucleotide sequence

```
generatedata <- function(length) {  
  bases <- c("A","T","C","G")  
  dna_sequence <- sample(x=bases, size = length, replace = TRUE)  
  return(dna_sequence)  
}  
  
generatedata(5)
```

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

To make a function *generateprotein()* that makes a random amino acid sequence.

```
generateprotein <- function(length) {  
  residues <- unique(bio3d::aa.table$aa1)  
  aa_sequence <- paste(sample(x=residues, size = length, replace = TRUE),  
                        collapse = "")  
  return(aa_sequence)  
}  
  
# Generate a sequence of 5 amino acids  
generateprotein(5)
```

```
[1] "CAYMM"
```

To generate many sequences:

generate protein sequences of lengths 6 to 12 in fasta format

```
sequences <- sapply(6:12, generateprotein)  
  
cat(paste(">id.length", 6:12, "\n", sequences, sep=""), sep="\n")
```

```
>id.length6  
DDDTMC  
>id.length7  
RRPXPXI  
>id.length8  
YGACIPFT  
>id.length9  
HRLXXHHMK  
>id.length10  
NPGELLADHR  
>id.length11  
XGEHEAYPKSA  
>id.length12  
MPHFYNESSNRY
```