Loops

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```r
sum(1, 2, 3, 4, 5)
```

```
## [1] 15
```

```r
sum(19, 11, 04, 27)
```

```
## [1] 61
```

```r
sum(37, 456, 378)
```

```
## [1] 871
```

1.

```r
numbers <- 1:5
numbers <- seq(1, 5, 1)
read.csv(file = "../raw_data.species.csv")
mass <- a * length ^ b
for (item in numbers) {
  print(x = item)
  print("Hello")
}
for (item in 1:5) {
  print(x = item)
  print("New")
}
for (dumpling in 1:5) {
  print(x = dumpling)
  print("New")
}
```

2.

```r
mass_lbs <- c(2.2, 3.5, 9.6, 1.2)
for(items in mass_lbs){
   print(items)
  mass_kg = 2.2 * items
  print(mass_kg)
}
```

```
## [1] 2.2
## [1] 4.84
## [1] 3.5
## [1] 7.7
## [1] 9.6
## [1] 21.12
## [1] 1.2
## [1] 2.64
```

```r
our_names <- c("Azul", "Jai", "Marcos", "Luna")
for(name in our_names) {
  print(name)
}
```

```
## [1] "Azul"
## [1] "Jai"
## [1] "Marcos"
## [1] "Luna"
```

3.

```r
birds <-  c('robin', 'woodpecker', 'blue jay', 'sparrow')
for (i in 1:length(birds)){
  print(birds[i])
}
```

```
## [1] "robin"
## [1] "woodpecker"
## [1] "blue jay"
## [1] "sparrow"
```

4.

```r
radius <- c(1.3, 2.1, 3.5)

areas <- vector(mode = "numeric", length = length(radius))
for (i in 1:length(areas)){
  areas[i] <- pi * radius[i] ^ 2
}
areas
```

```
## [1]  5.309292 13.854424 38.484510
```

5.

```r
lengths = c(1.1, 2.2, 1.6)
widths = c(3.5, 2.4, 2.8)
areas <- vector(length = 3)
for (i in 1:length(areas)) {
  areas[i] <- lengths[i] * widths[i]
}
areas
```

```
## [1] 3.85 5.28 4.48
```

6.

```
dino_lengths <- read.csv(file = "../raw_data/dinosaur_lengths.csv")
species <- read.csv(file = "../raw_data/species.csv")
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
mass_from_length <- function(length, species) {
  if (species == "Stegosauria") {
    a <- 10.95
    b <- 2.64
  } else if (species == "Theropoda") {
  a <- 0.73
  b <- 3.63
  } else if (species == "Sauropoda") {
  a <- 214.44
  b <- 1.46
  } else {
  a <- 25.37
  b <- 2.49
}

mass <- a*length^b
return(mass)
}
```

```r
dino_lengths %>% mutate(dino_mass = mass_from_length(lengths, species))
lengths <- dino_lengths$lengths
species <- dino_lengths$species
masses <- vector(length = length(lengths))
for (i in 1:length(species)) {
  masses[i] <- length[i] * mass_from_length[i]
}
masses
```