

JW_Loops

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Loops

Loops, not dissimilar to those in Python, help you iterate a task for a given set of intervals. For loops are another way that we can tell a computer to repeat tasks for us. They are versatile and very explicit, so that means that we are controlling everything that is run on each iteration of the loop (mostly).

The general structure: `for ([value] in [list]) { do_something_with(values) }`

```
lengths <- c(13.3,15,100)

for (value in lengths) {
  mass <- 0.73 * value^2
  print(mass)
  ## `return()` does not work in loops ##
}
```

```
## [1] 129.1297
## [1] 164.25
## [1] 7300
```

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

```
## [1] 4.84
## [1] 7.7
## [1] 21.12
## [1] 2.64
```

What is an index in R? It is the numeric position of values inside any data structure in R. We can use indexes to sort through the full length of a

```
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"
```

How do we save the results from a For Loop? When using `vector()`, we don't need insert the mode or length

```
flowers <- c("daisies","lilacs","lillies")
my_results <- vector(mode = "character", length = length(flowers))
for (i in 1:length(flowers)) {
  upper <- toupper(flowers[i])
  my_results[i] <-(upper)
}
my_results
```

```
## [1] "DAISES" "LILACS" "LILLIES"
```

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

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

```
#1#

dino_dat <- read.csv("197-raw_storage/dinosaur_lengths.csv")

get_mass_from_length_by_name <-function(length,name){
  if(name == "Stegosauria"){
    a = 10.95
    b = 2.64
  }
  else if(name == "Theropoda"){
    a = 0.73
    b = 3.63
  }
  else if(name == "Sauropoda"){
    a = 214.44
    b = 1.46
  }
  else{
    a = NA
    b = NA
  }
  mass <- a * length^b
  return(mass)
}
```

```

#2#

results <- vector()
for (i in 1:length(dino_dat$lengths)) {
  myresults <- get_mass_from_length_by_name(length = dino_dat$lengths[i], name = dino_dat$species[i])
  results[i] <- myresults
}

#3#

head(dino_dat)

```

```

##      species  lengths
## 1 Stegosauria 18.52588
## 2 Ankylosauria 16.43598
## 3 Ankylosauria 23.73421
## 4   Sauropoda 23.93411
## 5 Ankylosauria 21.68718
## 6 Ankylosauria 21.38363

```

```

dino_dat$mass <- results

```

```

#4#

dino_dat %>%
  group_by(species) %>%
  summarize(mean_mass = (sum(mass)/length(lengths)))

```

```

## # A tibble: 4 x 2
##   species      mean_mass
##   <chr>         <dbl>
## 1 Ankylosauria         NA
## 2 Sauropoda         16104.
## 3 Stegosauria         31924.
## 4 Theropoda          45572.

```

```

#download.file("http://www.datacarpentry.org/semester-biology/data/individual_collar_data.zip.")

#file <- unzip("197-raw_storage/individual_collar_data.zip")
#list.files(file)

```