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
```

Exercise 1:

Part 1.

```r
numbers <- c(1, 2, 3, 4, 5)
numbers <- 1:5
numbers <- seq(1, 5, 0.3)
read.csv(file = "../data-raw/species.csv")
```

```
##    species_id            genus          species    taxa
## 1          AB        Amphispiza        bilineata    Bird
## 2          AH  Ammospermophilus          harrisi  Rodent
## 3          AS        Ammodramus        savannarum    Bird
## 4          BA           Baiomys          taylori  Rodent
## 5          CB    Campylorhynchus  brunneicapillus    Bird
## 6          CM        Calamospiza      melanocorys    Bird
## 7          CQ         Callipepla         squamata    Bird
## 8          CS          Crotalus        scutalatus Reptile
## 9          CT     Cnemidophorus           tigris Reptile
## 10         CU     Cnemidophorus        uniparens Reptile
## 11         CV          Crotalus          viridis Reptile
## 12         DM         Dipodomys         merriami  Rodent
## 13         DO         Dipodomys            ordii  Rodent
## 14         DS         Dipodomys       spectabilis  Rodent
## 15         DX         Dipodomys              sp.  Rodent
## 16         EO           Eumeces         obsoletus Reptile
## 17         GS          Gambelia            silus Reptile
## 18         NL           Neotoma         albigula  Rodent
## 19         NX           Neotoma              sp.  Rodent
## 20         OL         Onychomys      leucogaster  Rodent
## 21         OT         Onychomys          torridus  Rodent
## 22         OX         Onychomys              sp.  Rodent
## 23         PB        Chaetodipus          baileyi  Rodent
## 24         PC            Pipilo         chlorurus    Bird
```

```
## 25         PE        Peromyscus        eremicus   Rodent
## 26         PF        Perognathus         flavus   Rodent
## 27         PG         Pooecetes        gramineus     Bird
## 28         PH        Perognathus        hispidus   Rodent
## 29         PI        Chaetodipus     intermedius   Rodent
## 30         PL        Peromyscus        leucopus   Rodent
## 31         PM        Peromyscus      maniculatus   Rodent
## 32         PP        Chaetodipus     penicillatus   Rodent
## 33         PU           Pipilo          fuscus     Bird
## 34         PX        Chaetodipus          sp.   Rodent
## 35         RF  Reithrodontomys      fulvescens   Rodent
## 36         RM  Reithrodontomys       megalotis   Rodent
## 37         RO  Reithrodontomys        montanus   Rodent
## 38         RX  Reithrodontomys          sp.   Rodent
## 39         SA        Sylvilagus       audubonii   Rabbit
## 40         SB         Spizella         breweri     Bird
## 41         SC        Sceloporus          clarki  Reptile
## 42         SF         Sigmodon      fulviventer   Rodent
## 43         SH         Sigmodon        hispidus   Rodent
## 44         SO         Sigmodon      ochrognathus   Rodent
## 45         SS        Spermophilus      spilosoma   Rodent
## 46         ST        Spermophilus   tereticaudus   Rodent
## 47         SU        Sceloporus       undulatus  Reptile
## 48         SX         Sigmodon          sp.   Rodent
## 49         UL           Lizard          sp.  Reptile
## 50         UP           Pipilo          sp.     Bird
## 51         UR           Rodent          sp.   Rodent
## 52         US          Sparrow          sp.     Bird
## 53         ZL        Zonotrichia     leucophrys     Bird
## 54         ZM          Zenaida        macroura     Bird
```

```r
# mass <- a * length ^ b
for (k in 1:5) {
  print(x = k)
  print("k")
}
```

```
## [1] 1
## [1] "k"
## [1] 2
## [1] "k"
## [1] 3
## [1] "k"
## [1] 4
## [1] "k"
## [1] 5
## [1] "k"
```

```r
our_names <- c("Azul", "Jai", "Marcos", "Luna")
print(our_names)
```

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

```r
for (items in our_names) {
  print(items)
}
```

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

Part 2. Write a for loop that loops over the following vector and prints out the mass in kilograms (mass_kg = 2.2 * mass_lb)

```
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
```

Part 3. Complete the code below so that it prints out the name of each bird one line at a time.

```
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"
```

Part 4. Complete the code below so that it stores one area for each radius.

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

areas <- vector(mode = "numeric", length = length(radius))

for (i in 1:length(radius)){
  print(areas)
  areas[i] <- pi * radius[i] ^ 2
  print(areas)
}
```

```
## [1] 0 0 0
## [1] 5.309292 0.000000 0.000000
## [1] 5.309292 0.000000 0.000000
## [1]  5.309292 13.854424  0.000000
## [1]  5.309292 13.854424  0.000000
## [1]  5.309292 13.854424 38.484510
```

```
areas
```

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

Part 5. Complete the code below to calculate an area for each pair of lengths and widths, store the areas in a vector, and after they are all calculated print them out:

```
lengths = c(1.1, 2.2, 1.6)
widths = c(3.5, 2.4, 2.8)
areas <- vector(length = length(lengths), mode = "numeric")
length(areas)
```

```
## [1] 3
```
```
areas
```

```
## [1] 0 0 0
```

```
for (i in 1:length(lengths)) {
  areas[i] <- lengths[i] * widths[i]
}
areas
```

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

Exercise 2.

Part 1. Write a function `mass_from_length()` that uses the equation `mass <- a * length^b` to estimate the size of a dinosaur from its length. This function should take two arguments, `length` and `species`. For each of the following inputs for species, use the given values of a and b for the calculation from Seebacher 2001:

For Stegosauria: a = 10.95 and b = 2.64 For Theropoda: a = 0.73 and b = 3.63 For Sauropoda: a = 214.44 and b = 1.46 For any other value of species: a = 25.37 and b = 2.49

Part 2. Use this function and a for loop to calculate the estimated mass for each dinosaur, store the masses in a vector, and after all of the calculations are complete show the first few items in the vector using head().

Part 3. Add the results in the vector back to the original data frame. Show the first few rows of the data frame using `head()`.

Part 4. Calculate the mean mass for each species using `dplyr`.