

Making Choices

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Logical and conditional statements

both of them return TRUE or FALSE values some examples of logical statements

```
1 == 1
```

```
## [1] TRUE
```

```
1 > 1
```

```
## [1] FALSE
```

```
1 < 1
```

```
## [1] FALSE
```

```
1 >= 1
```

```
## [1] TRUE
```

```
1 <= 1
```

```
## [1] TRUE
```

```
"a"=="a"
```

```
## [1] TRUE
```

```
"a"<"a"
```

```
## [1] FALSE
```

```
"a">"a"
```

```
## [1] FALSE
```

```
"apple" < "banana"
```

```
## [1] TRUE
```

```
c(1, 2, 3, 4, 1, 1) == 1
```

```
## [1] TRUE FALSE FALSE FALSE TRUE TRUE
```

```
letters < "m"
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [25] FALSE FALSE
```

```
letters[letters < "m"]
```

```
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l"
```

load data from the uhuru dataset

```
surveys <- read.csv(file = "../raw-data/surveys.csv")
species <- read.csv(file = "../raw-data/species.csv")
```

```
colnames(surveys)
```

```
## [1] "record_id"      "month"          "day"            "year"
## [5] "plot_id"        "species_id"     "sex"            "hindfoot_length"
## [9] "weight"
```

```
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
```

```
combined <- dplyr::inner_join(surveys, species, by = "species_id")
```

```
#combined$year
```

```
#combined[,4]
```

```
#combined[]
```

```
combined$year == 1977
```

```
combined$genus == "Dipodomys"
```

```
data.frame(combined$genus, combined$genus == "Dipodomys")
```

```
data.frame(combined$genus, combined$genus == "Dipodomys")
```

a vector that test species to

```
combined$species == "merriami"  
data.frame(combined$species, combined$species == "merriami")
```

examples of conditional statements uses the symbols & , |

```
1 == 1 & 1 < 2
```

```
## [1] TRUE
```

```
1 == 1 & 1 == 2
```

```
## [1] FALSE
```

```
1 == 1 | 1 == 2
```

```
## [1] TRUE
```

```
#combined$year == 1977 & combined$genus == "Dipodomys" & combined$species == "merriami"
```

```
#1
```

```
w <- 10.2  
x <- 1.3  
y <- 2.8  
z <- 17.5  
colors <- c("red", "blue", "green")  
masses <- c(45.2, 36.1, 27.8, 81.6, 42.4)  
dna1 <- "attattaggaccaca"  
dna2 <- "attattaggaacaca"
```

```
w > 10 # TRUE
```

```
## [1] TRUE
```

```
colors == 'green' #FALSE FALSE TRUE short answer is yes green is in the 3rd place
```

```
## [1] FALSE FALSE TRUE
```

```
x > y # FALSE
```

```
## [1] FALSE
```

```
masses > 40 # TRUE FALSE FALSE TRUE TRUE no only 3/5 are greater than 40
```

```
## [1] TRUE FALSE FALSE TRUE TRUE
```

```
2 * x + 0.2 == y #FALSE
```

```
## [1] FALSE
```

```
dna1 == dna2#FALSE
```

```
## [1] FALSE
```

```
dna1 != dna2# TRUE
```

```
## [1] TRUE
```

```
w > x | y > z # TRUE
```

```
## [1] TRUE
```

```
x* w #is between 13.2 and 13.5 TRUE [1] 13.26
```

```
## [1] 13.26
```

```
masses >= 30 & masses <= 50 #TRUE TRUE FALSE FALSE TRUE
```

```
## [1] TRUE TRUE FALSE FALSE TRUE
```

```
#2
```

```
age_class = "sapling"  
if (age_class == "sapling"){  
  y = 10  
}  
y
```

```
## [1] 10
```

```
#3
```

```
age_class <- "seedling"  
if(age_class == "sapling"){  
  y <- 10  
} else{  
  y <- 5  
}  
y
```

```
## [1] 5
```

```
#4
```

```

age_class = "adult"
if (age_class == "sapling"){
  y <- 10
} else if (age_class == "seedling"){
  y <- 5
} else {
  y <- 0
}
y

```

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

```
#5
```

```

get_y = function(age_class){
  if (age_class == "sapling"){
    y <- 10
  } else if (age_class == "seedling"){
    y <- 5
  } else {
    y <- 0
  }
  return(y)
}

```

```
get_y("sapling") #10
```

```
## [1] 10
```

```
get_y("seedling") # 5
```

```
## [1] 5
```

```
get_y("adult") # 0
```

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

```
get_y ("mature") #0
```

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

```
get_y("established")#0
```

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

```
#6
```

```
get_mass_from_length <- function(length, a = 39.9, b = 2.6 ){
  mass <- a * length ^ b
  return(mass)
}
```

Create a new function `get_mass_from_length_by_name()` that: takes two arguments, the length and the name of the dinosaur group. Inside this function use if/else if/else statements to check if the name is one of the following values and if so set a and b to the appropriate values (from Seebacher 2001). Stegosauria: a = 10.95 and b = 2.64. Theropoda: a = 0.73 and b = 3.63. Sauropoda: a = 214.44 and b = 1.46. If the name is not any of these values, the function should return NA. - Once the function has chosen the correct a and b values, have it run `get_mass_from_length()` with the appropriate values and return the estimated mass.

```
#6.1
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 {
    return(NA)
  }
  mass<- get_mass_from_length(length = length, a = a, b = b )
  return(mass)
}

#6.2
get_mass_from_length_by_name(10, "Stegosauria")#4779.848
```

```
## [1] 4779.848
```

```
get_mass_from_length_by_name(8, "Theropoda")#1385.286
```

```
## [1] 1385.286
```

```
get_mass_from_length_by_name(12, "Sauropoda")#8070.685
```

```
## [1] 8070.685
```

```
get_mass_from_length_by_name(13, "Ankylosauria") #NA
```

```
## [1] NA
```

```
#6.3 challenge
```

```

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 {
    message("No known estimation for ", name)
    return(NA)
  }
  mass<- get_mass_from_length(length = length, a = a, b = b )
  return(mass)
}
get_mass_from_length_by_name(13, "Ankylosauria") #No known estimation for Ankylosauria [1] NA

```

```
## No known estimation for Ankylosauria
```

```
## [1] NA
```

```
#6.4 challenge
```

```

get_mass_from_length_by_name = function(length,name) {
  if (name == "Stegosauria"& length > 8) {
    a <- 10.95
    b <- 2.64
  } else if (name == "Stegosauria" & length < 8) {
    a <- 8.5
    b <- 2.8
  } else if (name == "Theropoda") {
    a <- 0.73
    b <- 3.63
  } else if (name == "Sauropoda") {
    a <- 214.44
    b <- 1.46
  } else {
    message("No known estimation for ", name)
    return(NA)
  }
  mass<- get_mass_from_length(length = length, a = a, b = b )
  return(mass)
}
get_mass_from_length_by_name(6, "Stegosauria")# 1283.047

```

```
## [1] 1283.047
```