Lab2_answers

sbsambado

1/16/2021

#Answers for Lab 2

Question 1 (6 points: 2 points code is correct, 1 point for correct response) A. The ground squirrel has the largest brain size:body ratio of 40 g/kg. B. The African elephant has the smallest brain size:body ratio of 0.858431 g/kg. C. The mean brain size:body ratio is 9.516999 g/kg. This is less than the human ratio of 21.29032. D. Anything coherent that explains their findings about the data not supporting scientist hypothesis in complete sentencees.

Question 2 (2 points: 1 point for code, 1 point for response) There are 16 species of desert birds that are considered rare.

Question 3 (2 points: 1 point for code, 1 point for response) 27% of endangered species are vertebrates.

Notes

- ALL HOMEWORK SHOULD BE SUBMITTED AS A KNITTED HOMEWORK FILE (.PDF or .HTML)
  - Reduce 20% off HW not in right format (-2 points)
- Take the time to nail in homework format since this is first graded assignment
  - -.25 point if code is not annotated
  - -.25 point if answers are not in complete sentences
  - -.25 point if code does not seem adequate to answer question

Some potential code to answer questions

Question 1.

```
# load in required data
mammal <- read_csv("mammals.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   name = col_character(),
##   `body mass (kg)` = col_double(),
##   `brain mass (g)` = col_double()
## )
```

```r
# let's look at file
#View(mammal)

names(mammal) <- c("name", "body", "brain")

# A. Which mammal has the largest brain size:body ratio?

# make new variable column
mammal$ratio <- mammal$brain / mammal$body

# / divide
# * multiply
# exp is exponential


# find max ratio
# dataframe[which.function(df$variable),]

mammal[which.max(mammal$ratio),] # don't forget the comma post ()!!!
```

```
## # A tibble: 1 x 4
##   name             body brain ratio
##   <chr>           <dbl> <dbl> <dbl>
## 1 Ground squirrel   0.1     4    40
```

```r
# B. Which mammal has the smallest ratio?
mammal[which.min(mammal$ratio),] # don't forget the comma post ()!!!
```

```
## # A tibble: 1 x 4
##   name              body brain ratio
##   <chr>            <dbl> <dbl> <dbl>
## 1 African elephant  6654  5712 0.858
```

```r
# C. What is the mean brain size:body ratio? Are humans above or below the mean?
mean(mammal$ratio)
```

```
## [1] 9.516999
```

```r
# find human ratio

# Option 1 (prefered)
mammal[mammal$name == "Human",] # make sure the spelling is the exact same!
```

```
## # A tibble: 1 x 4
##   name   body brain ratio
##   <chr> <dbl> <dbl> <dbl>
## 1 Human    62  1320  21.3
```

```r
# Option 2
mammal[mammal$name == "Human", "ratio"] # if you have a lot of variable columns
```

```
## # A tibble: 1 x 1
##   ratio
##   <dbl>
## 1  21.3
```

```r
# Option 3 (less prefered)
# make new dataframe for humans and analyze that
human <- mammal[which(mammal$name == "Human"),]
mean(human$ratio)
```

```
## [1] 21.29032
```

Question 2

```r
# load data

birds <- read_csv("desert_birds.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   Species = col_character(),
##   Count = col_double()
## )
```

```r
#View(birds)

# A. How many desert bird species are rare (<= 10 counts)

# make subset

rare <- subset(birds, Count <= 10)
#find how many rows there are in subset

# Option 1. Look at length of vector
length(rare$Count)
```

```
## [1] 16
```

```r
dim(rare)
```

```
## [1] 16  2
```

```r
nrow(rare)
```

```
## [1] 16
```

```r
# Option 2. Look at dataset summary
print(rare)
```

```
## # A tibble: 16 x 2
##    Species                 Count
##    <chr>                   <dbl>
##  1 Harris's Hawk               3
##  2 American Kestrel            7
##  3 Rock Dove                   7
##  4 Greater Roadrunner          1
##  5 Great Horned Owl            2
##  6 Black-chin. Hummingbird     1
##  7 Costa's Hummingbird         2
##  8 Western Kingbird            1
##  9 Loggerhead Shrike           3
## 10 Bell's Vireo               10
## 11 Canyon Wren                 2
## 12 Northern Mockingbird        5
## 13 Canyon Towhee               2
## 14 Great-tailed Grackle        1
## 15 Bronzed Cowbird             1
## 16 Hooded Oriole               4
```

```
summary(rare)
```

```
##    Species              Count
##  Length:16          Min.   : 1.00
##  Class :character   1st Qu.: 1.00
##  Mode  :character   Median : 2.00
##                     Mean   : 3.25
##                     3rd Qu.: 4.25
##                     Max.   :10.00
```

```
# This is different than finding the total sum of birds within these rare species
sum(rare$Count)
```

```
## [1] 52
```

Question 3

```
# load data
endangered <- read_csv("endangered.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   vertebrate = col_character(),
##   taxon = col_character(),
##   no.species = col_double()
## )
```

```
#View(endangered)

# A. What proportion of endangered species are vertebrates?
```

```r
# Option 1

Verts <- subset(endangered, vertebrate == "yes")
sum(Verts$no.species) / sum(endangered$no.species) # 0.26
```

```
## [1] 0.2684086
```

```r
# / divide
# * multiple
# exp is exponential


# Option 2

verts <- sum(endangered$no.species[endangered$vertebrate == "yes"])
prop <- verts/sum(endangered$no.species)
print(prop) # 0.27
```

```
## [1] 0.2684086
```

```r
# Option 3
# make new dataframe

vertebrate <- subset(endangered, vertebrate == "yes")

# find sum of vertebrates
vertebrate_count <- sum(vertebrate$no.species)
print(vertebrate_count) # 399
```

```
## [1] 339
```

```r
# find sum of all endangered species (verts & inverts)
endangered_count <- sum(endangered$no.species)
print(endangered_count) # 1263
```

```
## [1] 1263
```

```r
# find proportion of vertebrates
proportion <- vertebrate_count/endangered_count
print(proportion) # 0.27
```

```
## [1] 0.2684086
```