

# Exercise: Data Frames

## Day 1, Part C

For this exercise, we will use the `msleep` data frame from the `ggplot2` library. This can be loaded using the following code:

```
library(ggplot2)
data("msleep")
msleep <- data.frame(msleep)
```

Some information about the data set is available in the help file for `msleep`.

1. Check that `msleep` is a data frame.

```
> is.data.frame(msleep)
[1] TRUE
```

```
> class(msleep)
[1] "data.frame"
```

2. Use each of the following functions to explore the data frame: `head()`, `tail()`, `summary()`, and `View()`.

```
> head(msleep)
name      genus  vore      order conservation sleep_total
1          Cheetah  Acinonyx carni    Carnivora      lc      12.1
2      Owl monkey    Aotus  omni    Primates      <NA>      17.0
3  Mountain beaver Aplodontia herbi    Rodentia      nt      14.4
4 Greater short-tailed shrew Blarina omni Soricomorpha      lc      14.9
5          Cow      Bos  herbi Artiodactyla domesticated      4.0
6  Three-toed sloth  Bradypus herbi      Pilosa      <NA>      14.4
  sleep_rem sleep_cycle awake brainwt  bodywt
1      NA      NA  11.9      NA  50.000
2    1.8      NA  7.0 0.01550  0.480
3    2.4      NA  9.6      NA  1.350
4    2.3 0.1333333  9.1 0.00029  0.019
5    0.7 0.6666667 20.0 0.42300 600.000
6    2.2 0.7666667  9.6      NA  3.850
```

```
> tail(msleep)
name      genus  vore      order conservation sleep_total
78      Tenrec  Tenrec  omni  Afrosoricida      <NA>      15.6
79  Tree shrew  Tupaia  omni    Scandentia      <NA>      8.9
80 Bottle-nosed dolphin Tursiops carni    Cetacea      <NA>      5.2
81      Genet  Genetta carni    Carnivora      <NA>      6.3
82  Arctic fox  Vulpes carni    Carnivora      <NA>      12.5
83  Red fox    Vulpes carni    Carnivora      <NA>      9.8
  sleep_rem sleep_cycle awake brainwt  bodywt
78    2.3      NA  8.4 0.0026  0.900
79    2.6 0.2333333 15.1 0.0025  0.104
80      NA      NA 18.8      NA 173.330
81    1.3      NA 17.7 0.0175  2.000
82      NA      NA 11.5 0.0445  3.380
83    2.4 0.3500000 14.2 0.0504  4.230
```

```
> summary(msleep)
name          genus          vore          order
Length:83     Length:83     Length:83     Length:83
Class :character Class :character Class :character Class :character
Mode  :character Mode  :character Mode  :character Mode  :character

conservation    sleep_total    sleep_rem    sleep_cycle    awake
Length:83      Min.   : 1.90    Min.   :0.100  Min.   :0.1167  Min.   : 4.10
Class :character 1st Qu.: 7.85    1st Qu.:0.900  1st Qu.:0.1833  1st Qu.:10.25
Mode  :character Median :10.10    Median :1.500  Median :0.3333  Median :13.90
                Mean  :10.43    Mean  :1.875   Mean  :0.4396   Mean  :13.57
                3rd Qu.:13.75    3rd Qu.:2.400  3rd Qu.:0.5792  3rd Qu.:16.15
                Max.   :19.90    Max.   :6.600   Max.   :1.5000   Max.   :22.10
                NA's   :22      NA's   :51

    brainwt    bodywt
Min.   :0.00014 Min.   : 0.005
1st Qu.:0.00290 1st Qu.: 0.174
Median :0.01240 Median : 1.670
Mean   :0.28158 Mean   :166.136
3rd Qu.:0.12550 3rd Qu.: 41.750
Max.   :5.71200 Max.   :6654.000
NA's   :27
```

```
> View(msleep)
```

3. How many rows and columns does this data frame have?

```
> nrow(msleep)
[1] 83
```

```
> ncol(msleep)
[1] 11
```

```
> dim(msleep)
[1] 83 11
```

4. What are the names of the columns? What data type is each column?

```
> names(msleep)
[1] "name"      "genus"      "vore"      "order"      "conservation"
[6] "sleep_total" "sleep_rem"  "sleep_cycle" "awake"      "brainwt"
[11] "bodywt"
```

```
> str(msleep)
'data.frame':   83 obs. of  11 variables:
 $ name      : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed shrew" ...
 $ genus     : chr  "Acinonyx" "Aotus" "Aplodontia" "Blarina" ...
 $ vore      : chr  "carni" "omni" "herbi" "omni" ...
 $ order     : chr  "Carnivora" "Primates" "Rodentia" "Soricomorpha" ...
 $ conservation: chr  "lc" NA "nt" "lc" ...
 $ sleep_total : num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
 $ sleep_rem  : num  NA 1.8 2.4 2.3 0.7 2.2 1.4 NA 2.9 NA ...
```

```
$ sleep_cycle : num NA NA NA 0.133 0.667 ...
$ awake       : num 11.9 7 9.6 9.1 20 9.6 15.3 17 13.9 21 ...
$ brainwt     : num NA 0.0155 NA 0.00029 0.423 NA NA NA 0.07 0.0982 ...
$ bodywt      : num 50 0.48 1.35 0.019 600 ...
```

5. Select the name column three different ways.

```
> msleep[, 1]
[1] "Cheetah" "Owl monkey"
[3] "Mountain beaver" "Greater short-tailed shrew"
[5] "Cow" "Three-toed sloth"
[7] "Northern fur seal" "Vesper mouse"
[9] "Dog" "Roe deer"
[11] "Goat" "Guinea pig"
[13] "Grivet" "Chinchilla"
[15] "Star-nosed mole" "African giant pouched rat"
[17] "Lesser short-tailed shrew" "Long-nosed armadillo"
[19] "Tree hyrax" "North American Opossum"
[21] "Asian elephant" "Big brown bat"
[23] "Horse" "Donkey"
[25] "European hedgehog" "Patas monkey"
[27] "Western american chipmunk" "Domestic cat"
[29] "Galago" "Giraffe"
[31] "Pilot whale" "Gray seal"
[33] "Gray hyrax" "Human"
[35] "Mongoose lemur" "African elephant"
[37] "Thick-tailed opossum" "Macaque"
[39] "Mongolian gerbil" "Golden hamster"
[41] "Vole " "House mouse"
[43] "Little brown bat" "Round-tailed muskrat"
[45] "Slow loris" "Degu"
[47] "Northern grasshopper mouse" "Rabbit"
[49] "Sheep" "Chimpanzee"
[51] "Tiger" "Jaguar"
[53] "Lion" "Baboon"
[55] "Desert hedgehog" "Potto"
[57] "Deer mouse" "Phalanger"
[59] "Caspian seal" "Common porpoise"
[61] "Potoroo" "Giant armadillo"
[63] "Rock hyrax" "Laboratory rat"
[65] "African striped mouse" "Squirrel monkey"
[67] "Eastern american mole" "Cotton rat"
[69] "Mole rat" "Arctic ground squirrel"
[71] "Thirteen-lined ground squirrel" "Golden-mantled ground squirrel"
[73] "Musk shrew" "Pig"
[75] "Short-nosed echidna" "Eastern american chipmunk"
[77] "Brazilian tapir" "Tenrec"
[79] "Tree shrew" "Bottle-nosed dolphin"
[81] "Genet" "Arctic fox"
[83] "Red fox"
```

```
> msleep[, "name"]
[1] "Cheetah" "Owl monkey"
```

[3]	"Mountain beaver"	"Greater short-tailed shrew"
[5]	"Cow"	"Three-toed sloth"
[7]	"Northern fur seal"	"Vesper mouse"
[9]	"Dog"	"Roe deer"
[11]	"Goat"	"Guinea pig"
[13]	"Grivet"	"Chinchilla"
[15]	"Star-nosed mole"	"African giant pouched rat"
[17]	"Lesser short-tailed shrew"	"Long-nosed armadillo"
[19]	"Tree hyrax"	"North American Opossum"
[21]	"Asian elephant"	"Big brown bat"
[23]	"Horse"	"Donkey"
[25]	"European hedgehog"	"Patas monkey"
[27]	"Western american chipmunk"	"Domestic cat"
[29]	"Galago"	"Giraffe"
[31]	"Pilot whale"	"Gray seal"
[33]	"Gray hyrax"	"Human"
[35]	"Mongoose lemur"	"African elephant"
[37]	"Thick-tailed opossum"	"Macaque"
[39]	"Mongolian gerbil"	"Golden hamster"
[41]	"Vole "	"House mouse"
[43]	"Little brown bat"	"Round-tailed muskrat"
[45]	"Slow loris"	"Degu"
[47]	"Northern grasshopper mouse"	"Rabbit"
[49]	"Sheep"	"Chimpanzee"
[51]	"Tiger"	"Jaguar"
[53]	"Lion"	"Baboon"
[55]	"Desert hedgehog"	"Potto"
[57]	"Deer mouse"	"Phalanger"
[59]	"Caspian seal"	"Common porpoise"
[61]	"Potoroo"	"Giant armadillo"
[63]	"Rock hyrax"	"Laboratory rat"
[65]	"African striped mouse"	"Squirrel monkey"
[67]	"Eastern american mole"	"Cotton rat"
[69]	"Mole rat"	"Arctic ground squirrel"
[71]	"Thirteen-lined ground squirrel"	"Golden-mantled ground squirrel"
[73]	"Musk shrew"	"Pig"
[75]	"Short-nosed echidna"	"Eastern american chipmunk"
[77]	"Brazilian tapir"	"Tenrec"
[79]	"Tree shrew"	"Bottle-nosed dolphin"
[81]	"Genet"	"Arctic fox"
[83]	"Red fox"	

```
> msleep$name
```

[1]	"Cheetah"	"Owl monkey"
[3]	"Mountain beaver"	"Greater short-tailed shrew"
[5]	"Cow"	"Three-toed sloth"
[7]	"Northern fur seal"	"Vesper mouse"
[9]	"Dog"	"Roe deer"
[11]	"Goat"	"Guinea pig"
[13]	"Grivet"	"Chinchilla"
[15]	"Star-nosed mole"	"African giant pouched rat"
[17]	"Lesser short-tailed shrew"	"Long-nosed armadillo"
[19]	"Tree hyrax"	"North American Opossum"

```

[21] "Asian elephant"      "Big brown bat"
[23] "Horse"               "Donkey"
[25] "European hedgehog"   "Patas monkey"
[27] "Western american chipmunk" "Domestic cat"
[29] "Galago"              "Giraffe"
[31] "Pilot whale"         "Gray seal"
[33] "Gray hyrax"          "Human"
[35] "Mongoose lemur"      "African elephant"
[37] "Thick-tailed opossum" "Macaque"
[39] "Mongolian gerbil"    "Golden hamster"
[41] "Vole "               "House mouse"
[43] "Little brown bat"    "Round-tailed muskrat"
[45] "Slow loris"          "Degu"
[47] "Northern grasshopper mouse" "Rabbit"
[49] "Sheep"               "Chimpanzee"
[51] "Tiger"               "Jaguar"
[53] "Lion"                "Baboon"
[55] "Desert hedgehog"     "Potto"
[57] "Deer mouse"          "Phalanger"
[59] "Caspian seal"        "Common porpoise"
[61] "Potoroo"             "Giant armadillo"
[63] "Rock hyrax"          "Laboratory rat"
[65] "African striped mouse" "Squirrel monkey"
[67] "Eastern american mole" "Cotton rat"
[69] "Mole rat"            "Arctic ground squirrel"
[71] "Thirteen-lined ground squirrel" "Golden-mantled ground squirrel"
[73] "Musk shrew"          "Pig"
[75] "Short-nosed echidna" "Eastern american chipmunk"
[77] "Brazilian tapir"     "Tenrec"
[79] "Tree shrew"          "Bottle-nosed dolphin"
[81] "Genet"               "Arctic fox"
[83] "Red fox"

```

6. Select just rows where the order column is "Carnivora."

```

> msleep[msleep$order == "Carnivora", ]
name      genus vore      order conservation sleep_total sleep_rem
1         Cheetah  Acinonyx  carni  Carnivora          lc      12.1      NA
7 Northern fur seal Callorhinus carni  Carnivora          vu       8.7     1.4
9          Dog      Canis  carni  Carnivora  domesticated    10.1     2.9
28 Domestic cat     Felis  carni  Carnivora  domesticated    12.5     3.2
32      Gray seal Haliochoerus carni  Carnivora          lc       6.2     1.5
51         Tiger   Panthera carni  Carnivora          en     15.8     NA
52         Jaguar   Panthera carni  Carnivora          nt     10.4     NA
53         Lion     Panthera carni  Carnivora          vu     13.5     NA
59 Caspian seal     Phoca  carni  Carnivora          vu       3.5     0.4
81         Genet   Genetta carni  Carnivora      <NA>      6.3     1.3
82 Arctic fox      Vulpes carni  Carnivora      <NA>     12.5     NA
83 Red fox         Vulpes carni  Carnivora      <NA>      9.8     2.4

sleep_cycle awake brainwt bodywt
1         NA  11.9      NA  50.000
7  0.3833333  15.3      NA  20.490
9  0.3333333  13.9  0.0700  14.000

```

```

28  0.4166667  11.5  0.0256  3.300
32      NA  17.8  0.3250  85.000
51      NA   8.2      NA 162.564
52      NA  13.6  0.1570 100.000
53      NA  10.5      NA 161.499
59      NA  20.5      NA  86.000
81      NA  17.7  0.0175   2.000
82      NA  11.5  0.0445   3.380
83  0.3500000  14.2  0.0504   4.230

```

7. Select just rows for animals with body weight > 200kg.

```

> msleep[msleep$bodywt > 200, ]
name      genus vore      order conservation sleep_total
5         Cow      Bos herbi  Artiodactyla domesticated      4.0
21  Asian elephant Elephas herbi  Proboscidea          en      3.9
23         Horse      Equus herbi Perissodactyla domesticated      2.9
30        Giraffe  Giraffa herbi  Artiodactyla          cd      1.9
31  Pilot whale Globicephalus carni  Cetacea          cd      2.7
36 African elephant Loxodonta herbi  Proboscidea          vu      3.3
77 Brazilian tapir  Tapirus herbi Perissodactyla          vu      4.4
      sleep_rem sleep_cycle awake brainwt  bodywt
5         0.7    0.6666667 20.00    0.423  600.000
21        NA         NA 20.10    4.603 2547.000
23         0.6    1.0000000 21.10    0.655  521.000
30         0.4         NA 22.10     NA  899.995
31         0.1         NA 21.35     NA  800.000
36        NA         NA 20.70    5.712 6654.000
77         1.0    0.9000000 19.60    0.169  207.501

```

8. Create a new variable for the total amount of sleep in minutes (sleep\_total\_min).

```

> msleep$sleep_total_min <- msleep$sleep_total * 60

```

- a. What is the longest time any animal sleeps (in minutes)?

```

> max(msleep$sleep_total_min)
[1] 1194

```

- b. Which animal sleeps this long?

```

> msleep[msleep$sleep_total_min == max(msleep$sleep_total_min), "name"]
[1] "Little brown bat"

> msleep$name[msleep$sleep_total_min == max(msleep$sleep_total_min)]
[1] "Little brown bat"

```

9. Create a new variable for the proportion of total sleep spent in REM (prop\_rem).

```

> msleep$prop_rem <- msleep$sleep_rem/msleep$sleep_total

```

- a. What is the minimum proportion? (hint, look at the argument options in the help file for min())

```

> min(msleep$prop_rem, na.rm = T)
[1] 0.03703704

> min(msleep$prop_rem[!is.na(msleep$prop_rem)])
[1] 0.03703704

```

- b. How long is REM sleep for the animal with the smallest proportion REM? (hint, this requires two conditions be met: `prop_rem` is NOT missing, and `prop_rem` is the minimum value)

```
> msleep$sleep_rem[msleep$prop_rem == min(msleep$prop_rem, na.rm = T) & !is.na(msleep$prop_r  
[1] 0.1
```

10. Create a new variable for the ratio of body weight to brain weight (`bdy_brn_ratio`).

```
> msleep$bdy_brn_ratio <- msleep$bodywt/msleep$brainwt
```

- a. What is the median body-to-brain weight ratio?

```
> median(msleep$bdy_brn_ratio, na.rm = T)  
[1] 143.7799
```

- b. What is the variance of the body-to-brain weight ratio?

```
> var(msleep$bdy_brn_ratio, na.rm = T)  
[1] 90841.86
```

11. Drop the `conservation`, `sleep_cycle`, and `bodywt` variables from the `msleep` object.

```
> msleep[, c("conservation", "sleep_cycle", "bodywt")] <- NULL
```

12. Create a new object (`msleep_carni`) that contains just the data for carnivores and only the `name`, `genus`, `order`, `sleep_total`, and `brainwt` variables.

```
> msleep_carni <- msleep[msleep$vore == "carni", c("name", "genus", "order", "sleep_total",  
+ "brainwt")]
```