

In-class worksheet 6

Feb 7, 2019

In this worksheet, we will continue to work with the tidyverse libraries:

```
library(tidyverse)
```

1. The msleep dataset

The `msleep` dataset, provided with `ggplot2`, contains information about sleep and awake times of different mammals:

```
msleep
```

```
## # A tibble: 83 x 11
##   name  genus vore  order conservation sleep_total sleep_rem sleep_cycle
##   <chr> <chr> <chr> <chr> <chr>          <dbl>    <dbl>    <dbl>
## 1 Chee... Acin... carni Carn... lc           12.1      NA        NA
## 2 Owl ... Aotus omni  Prim... <NA>         17        1.8       NA
## 3 Moun... Aplo... herbi Rode... nt          14.4      2.4       NA
## 4 Grea... Blar... omni  Sori... lc           14.9      2.3       0.133
## 5 Cow   Bos   herbi Arti... domesticated    4        0.7       0.667
## 6 Thre... Brad... herbi Pilo... <NA>         14.4      2.2       0.767
## 7 Nort... Call... carni Carn... vu           8.7      1.4       0.383
## 8 Vesp... Calo... <NA>  Rode... <NA>          7        NA        NA
## 9 Dog   Canis carni Carn... domesticated   10.1      2.9       0.333
## 10 Roe ... Capr... herbi Arti... lc           3        NA        NA
## # ... with 73 more rows, and 3 more variables: awake <dbl>, brainwt <dbl>,
## #   bodywt <dbl>
```

Verify that the sum of total sleep time (column `sleep_total`) and total awake time (column `awake`) adds up to 24h for all animals in the `msleep` dataset.

```
(msleep$sleep_total + msleep$awake) == 24
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [12] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [23] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE
## [34] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [45] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [56] TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [67] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [78] TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

There are two cases where the sum is not equal to exactly 24 hours.

```
msleep %>%
  mutate(day_total = sleep_total + awake) %>%
  filter(day_total != 24) %>%
  select(name, vore, sleep_total, awake, day_total)
```

```
## # A tibble: 2 x 5
##   name          vore  sleep_total awake day_total
##   <chr>         <chr>      <dbl> <dbl>    <dbl>
## 1 Pilot whale   carnivoran  2.7   21.4    24.0
## 2 Common porpoise carnivoran  5.6   18.4    24.0
```

In the pilot whale and the common porpoise, the total sleep and awake times add up to 24.05 hours.

Make a list of all the domesticated species in the `msleep` dataset, in alphabetical order. Hint: Domesticated species have the entry "domesticated" in the column `conservation`.

```
msleep %>%
  filter(conservation == "domesticated") %>%
  select(name) %>%
  arrange(name)
```

```
## # A tibble: 10 x 1
##   name
##   <chr>
## 1 Chinchilla
## 2 Cow
## 3 Dog
## 4 Domestic cat
## 5 Donkey
## 6 Guinea pig
## 7 Horse
## 8 Pig
## 9 Rabbit
## 10 Sheep
```

For the different vore classifications, tally how many species are awake for at least 18 hours. Hint: Use the function `tally()`.

```
msleep %>%
  filter(awake >= 18) %>%
  group_by(vore) %>%
  tally()
```

```
## # A tibble: 3 x 2
##   vore      n
##   <chr> <int>
## 1 <NA>     1
## 2 carni     4
## 3 herbi    11
```

Using the function `top_n()`, identify the top-10 least-awake animals and list them from least awake to most awake. Explain why this analysis gives you 11 results instead of 10. Hint: Before calling `top_n()`, use the function `select()` to extract the two columns `name` and `sleep_total`, in that order.

```
msleep %>%
  select(name, sleep_total) %>%
  top_n(10) %>%
  arrange(desc(sleep_total))
```

```
## Selecting by sleep_total
```

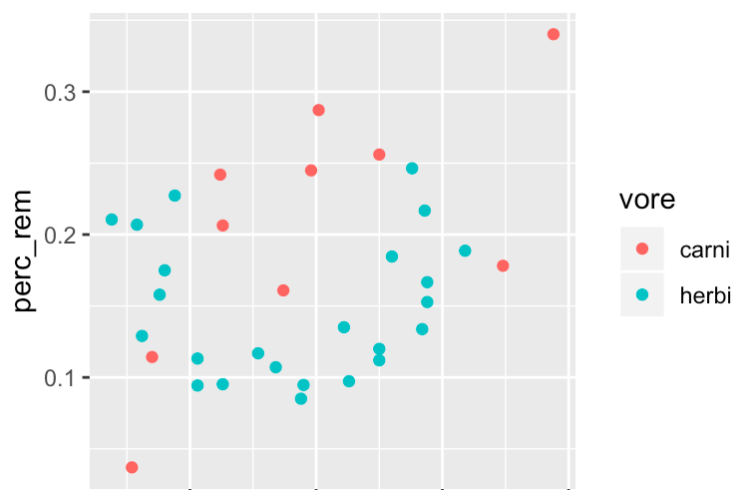
```
## # A tibble: 11 x 2
##   name                sleep_total
##   <chr>                <dbl>
## 1 Little brown bat      19.9
## 2 Big brown bat         19.7
## 3 Thick-tailed opossum  19.4
## 4 Giant armadillo       18.1
## 5 North American Opossum 18
## 6 Long-nosed armadillo  17.4
## 7 Owl monkey            17
## 8 Arctic ground squirrel 16.6
## 9 Golden-mantled ground squirrel 15.9
## 10 Tiger                15.8
## 11 Eastern american chipmunk 15.8
```

There are 11 results because there is a tie. Both the Tiger and the Eastern american chipmunk have a total sleep time of 15.8h, and they are in positions 10 and 11 of the list. Note that by default, `top_n()` orders based on the last variable in the table. Since we selected `sleep_total` as the last column before we called `top_n()`, we get the desired result.

Considering only carnivores and herbivores, make a plot of the percent of time each animal is in REM sleep (out of the total sleep time) vs. the animal's total sleep time. Hint: Use the operator `|` to indicate logical OR in the `filter()` function.

```
msleep %>%
  filter(vore == "carni" | vore == "herbi") %>%
  mutate(perc_rem = sleep_rem / sleep_total) %>%
  ggplot(aes(x = sleep_total, y = perc_rem, color = vore)) +
  geom_point()
```

```
## Warning: Removed 17 rows containing missing values (geom_point).
```



5 10 15 20
sleep_total

2. The diamonds dataset

The `diamonds` dataset provided by `ggplot2` provides information about quality and price of 53940 diamonds:

```
head(diamonds)
```

```
## # A tibble: 6 x 10
##   carat cut      color clarity depth table price     x     y     z
##   <dbl> <ord>    <ord> <ord>   <dbl> <dbl> <int> <dbl> <dbl> <dbl>
## 1 0.23 Ideal    E      SI2     61.5   55   326  3.95  3.98  2.43
## 2 0.21 Premium E      SI1     59.8   61   326  3.89  3.84  2.31
## 3 0.23 Good    E      VS1     56.9   65   327  4.05  4.07  2.31
## 4 0.290 Premium I      VS2     62.4   58   334  4.2   4.23  2.63
## 5 0.31 Good    J      SI2     63.3   58   335  4.34  4.35  2.75
## 6 0.24 Very Good J      VVS2     62.8   57   336  3.94  3.96  2.48
```

The best cuts of diamonds are “Very Good”, “Premium”, and “Ideal”. Make a table that selects only those diamonds, and find the minimum, median, and maximum price for each cut. Hint: The operator `%in%` is helpful for selecting the diamond cuts.

```
diamonds %>%
  filter(cut %in% c("Very Good", "Premium", "Ideal")) %>%
  group_by(cut) %>%
  summarize(
    min_price = min(price),
    med_price = median(price),
    max_price = max(price)
  )
```

```
## # A tibble: 5 x 4
##   cut      min_price med_price max_price
##   <ord>      <dbl>      <dbl>      <dbl>
## 1 Fair          Inf         NA        -Inf
## 2 Good          Inf         NA        -Inf
## 3 Very Good    336       2648     18818
## 4 Premium     326       3185     18823
## 5 Ideal       326       1810     18806
```

For each of the different diamond cuts, calculate the mean carat level among the diamonds whose price falls within 10% of the most expensive diamond for that cut.

```
diamonds %>%
  group_by(cut) %>%
  filter(price > 0.9 * max(price)) %>%
  summarize(mean_carat = mean(carat))
```

```
## # A tibble: 5 x 2
##   cut      mean_carat
##   <ord>      <dbl>
## 1 Fair        2.73
## 2 Good        2.08
## 3 Very Good   1.97
## 4 Premium     2.08
## 5 Ideal       1.99
```

For each of the different diamond cuts, calculate the mean carat level among the top-10% most expensive diamonds.

```
diamonds %>%
  group_by(cut) %>%
  mutate(price_rank = rank(desc(price))) %>% # rank diamonds by price, in descending order
  filter(price_rank < 0.1 * max(price_rank)) %>% # pick the top 10%
  summarize(mean_carat = mean(carat))
```

```
## # A tibble: 5 x 2
##   cut      mean_carat
##   <ord>      <dbl>
## 1 Fair        2.04
## 2 Good        1.76
## 3 Very Good   1.71
## 4 Premium     1.88
## 5 Ideal       1.58
```

Make a table that contains the median price for each combination of `cut` and `clarity`, and arrange the final table in descending order of median price.

```
diamonds %>%
  group_by(cut, clarity) %>%
  summarize(med_price = median(price)) %>%
  arrange(desc(med_price))
```

```
## # A tibble: 40 x 3
## # Groups:   cut [5]
##   cut      clarity med_price
##   <ord>    <ord>      <dbl>
## 1 Premium SI2         4291
## 2 Ideal   SI2        4060.
## 3 Very Good SI2        4042
## 4 Good    SI2        3770
## 5 Fair    SI2        3681
## 6 Ideal   I1         3674.
## 7 Premium SI1        3618
## 8 Fair    SI1        3528.
## 9 Very Good I1        3283
## 10 Premium I1        3261
## # ... with 30 more rows
```

Now arrange the same table first by cut and then within each cut group by median price.

```
diamonds %>%
  group_by(cut, clarity) %>%
  summarize(med_price = median(price)) %>%
  arrange(desc(cut), desc(med_price))
```

```
## # A tibble: 40 x 3
## # Groups:   cut [5]
##   cut      clarity med_price
##   <ord>    <ord>      <dbl>
## 1 Ideal   SI2        4060.
## 2 Ideal   I1         3674.
## 3 Ideal   SI1        2537
## 4 Ideal   VS1        1813
## 5 Ideal   VS2        1689
## 6 Ideal   VVS2        1330
## 7 Ideal   VVS1        1114
## 8 Ideal   IF         1022.
## 9 Premium SI2        4291
## 10 Premium SI1        3618
## # ... with 30 more rows
```

3. If this was easy

For the `diamonds` data set, separately for each diamond cut, calculate the percentage of diamonds with a price above \$10,000, and the median carat value for diamonds priced \$10,000 or more.

```
diamonds %>%
  group_by(cut) %>%
  summarize(
    percent_above_10k = round(100 * sum(price >= 10000) / n(), 1),
    median_carat_above_10k = median(carat[price >= 10000])
  )
```

```
## # A tibble: 5 x 3
##   cut      percent_above_10k median_carat_above_10k
##   <ord>          <dbl>          <dbl>
## 1 Fair           9.1           2.01
## 2 Good           7.6           2
## 3 Very Good      9.3           1.7
## 4 Premium       13.1           1.72
## 5 Ideal          8.2           1.57
```