```r
library(tidyverse)
#manipulate your data
#data wrangling
?msleep
glimpse(msleep)
view(msleep)

#how to rename a variable
msleep

msleep %>%
  rename("conserv"="conservation")%>%
  glimpse()
#it get change to conservation to conserv

#reorder variables
msleep %>%
  select(vore,name,everything())

#change a variable type
class(msleep$vore)

msleep$vore <- as.factor(msleep$vore)

glimpse(msleep)
# it change to factor datatype
msleep%>%
  mutate(vore = as.character((vore))) %>%
  glimpse()
#it change to character datatype
#select variable to work with
```

Console   Terminal ×   Background Jobs ×

```
R R 4.2.1 · ~/
#  with 73 more rows, 3 more variables: awake <dbl>,
#   brainwt <dbl>, bodywt <dbl>, and abbreviated variable
#   names 'conservation, 'sleep_total, 'sleep_rem,
#   'sleep_cycle
# i Use `print(n = ...)` to see more rows, and `colnames()` to see all variable names
> msleep %>%
+   rename("conserv"="conservation")%>%
+   glimpse()
Rows: 83
Columns: 11
$ name        <chr> "Cheetah", "Owl monkey", "Mountain beaver", "Greater short-tailed shrew", "Cow", "Three-toed sloth"…
$ genus       <chr> "Acinonyx", "Aotus", "Aplodontia", "Blarina", "Bos", "Bradypus", "Callorhinus", "Calomys", "Canis",…
$ vore        <chr> "carni", "omni", "herbi", "omni", "herbi", "herbi", "carni", NA, "carni", "herbi", "herbi", "herbi"…
$ order       <chr> "Carnivora", "Primates", "Rodentia", "Soricomorpha", "Artiodactyla", "Pilosa", "Carnivora", "Rodent…
$ conserv     <chr> "lc", NA, "nt", "lc", "domesticated", NA, "vu", NA, "domesticated", "lc", "lc", "domesticated", "lc…
$ sleep_total <dbl> 12.1, 17.0, 14.4, 14.9, 4.0, 14.4, 8.7, 7.0, 10.1, 3.0, 5.3, 9.4, 10.0, 12.5, 10.3, 8.3, 9.1, 17.4…
$ sleep_rem   <dbl> NA, 1.8, 2.4, 2.3, 0.7, 2.2, 1.4, NA, 2.9, NA, 0.6, 0.8, 0.7, 1.5, 2.2, 2.0, 1.4, 3.1, 0.5, 4.9, NA…
$ sleep_cycle <dbl> NA, NA, NA, 0.1333333, 0.6666667, 0.7666667, 0.3833333, 0.3333333, NA, NA, 0.2166667, NA, 0.116…
$ awake       <dbl> 11.90, 7.00, 9.60, 9.10, 20.00, 9.60, 15.30, 17.00, 13.90, 21.00, 18.70, 14.60, 14.00, 11.50, 13.70…
$ brainwt     <dbl> NA, 0.01550, NA, 0.00029, 0.42300, NA, NA, NA, 0.07000, 0.09820, 0.11500, 0.00550, NA, 0.00640, 0.0…
$ bodywt      <dbl> 50.000, 0.480, 1.350, 0.019, 600.000, 3.850, 20.490, 0.045, 14.000, 14.800, 33.500, 0.728, 4.750, 0…
>
```

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name

  common name

genus
vore

  carnivore, omnivore or herbivore?

order
conservation

  the conservation status of the animal

```r
library(tidyverse)
#manipulate your data
#data wrangling
?msleep
glimpse(msleep)
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#how to rename a variable
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msleep %>%
  rename("conserv"="conservation")%>%
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msleep %>%
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#change a variable type
class(msleep$vore)

msleep$vore <- as.factor(msleep$vore)

glimpse(msleep)
# it change to factor datatype
msleep%>%
  mutate(vore = as.character((vore))) %>%
  glimpse()
#it change to character datatype
#select variable to work with
```

Console   Terminal ×   Background Jobs ×

```
R R 4.2.1 · ~/
> #reorder variables
> msleep %>%
+   select(vore,name,everything())
# A tibble: 83 × 11
   vore  name                      genus      order        conservation sleep_… ' sleep_… ' sleep_… ' awake brainwt bodywt
   <chr> <chr>                     <chr>      <chr>         <chr>          <dbl>    <dbl>    <dbl>   <dbl>   <dbl>  <dbl>
 1 carni Cheetah                   Acinonyx   Carnivora    lc              12.1   NA       NA       11.9   NA        50
 2 omni  Owl monkey                Aotus      Primates     NA              17      1.8     NA        7      0.0155   0.48
 3 herbi Mountain beaver           Aplodontia Rodentia     nt              14.4    2.4     NA        9.6   NA        1.35
 4 omni  Greater short-tailed shrew Blarina   Soricomorpha lc              14.9    2.3      0.133    9.1    0.00029  0.019
 5 herbi Cow                       Bos        Artiodactyla domesticated     4      0.7      0.667   20      0.423  600
 6 herbi Three-toed sloth          Bradypus   Pilosa       NA              14.4    2.2      0.767    9.6   NA        3.85
 7 carni Northern fur seal         Callorhinus Carnivora   vu               8.7    1.4      0.383   15.3   NA       20.5
 8 NA    Vesper mouse              Calomys    Rodentia     NA               7     NA       NA       17     NA        0.045
 9 carni Dog                       Canis      Carnivora    domesticated    10.1    2.9      0.333   13.9    0.07    14
10 herbi Roe deer                  Capreolus  Artiodactyla lc               3     NA       NA       21      0.0982  14.8
# … with 73 more rows, and abbreviated variable names 'sleep_total, 'sleep_rem, 'sleep_cycle
# i Use `print(n = ...)` to see more rows
> #change a variable type
> class(msleep$vore)
[1] "character"
>
```

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name

  common name

genus
vore

  carnivore, omnivore or herbivore?

order
conservation

  the conservation status of the animal

Top screenshot — Source editor (classlab04.R / msleep)

```r
1
2  library(tidyverse)
3  #manipulate your data
4  #data wrangling
5  ?msleep
6  glimpse(msleep)
7  view(msleep)
8
9  #how to rename a variable
10 msleep
11
12 msleep %>%
13   rename("conserv"="conservation")%>%
14   glimpse()
15 #it get change to conservation to conserv
16
17 #reorder variables
18 msleep %>%
19   select(vore,name,everything())
20
21 #change a variable type
22 class(msleep$vore)
23
24 msleep$vore <- as.factor(msleep$vore)
25
26 glimpse(msleep)
27 # it change to factor datatype
28 msleep%>%
29   mutate(vore = as.character((vore))) %>%
30   glimpse()
31 #it change to character datatype
32 #select variable to work with
```

Top screenshot — Console

```
10 herbi Roe deer          Capreolus  Artiodactyla lc          3  NA   NA    21  0.0982  14.8
# ... with 73 more rows, and abbreviated variable names 'sleep_total, 'sleep_rem, 'sleep_cycle
# i use `print(n = ...)` to see more rows
> #change a variable type
> class(msleep$vore)
[1] "character"
> msleep$vore <- as.factor(msleep$vore)
> glimpse(msleep)
Rows: 83
Columns: 11
$ name         <chr> "Cheetah", "Owl monkey", "Mountain beaver", "Greater short-tailed shrew", "Cow", "Three-toed sloth...
$ genus        <chr> "Acinonyx", "Aotus", "Aplodontia", "Blarina", "Bos", "Bradypus", "Callorhinus", "Calomys", "Canis"...
$ vore         <fct> carni, omni, herbi, omni, herbi, herbi, carni, NA, carni, herbi, herbi, omni, herbi, omni,...
$ order        <chr> "Carnivora", "Primates", "Rodentia", "Soricomorpha", "Artiodactyla", "Pilosa", "Carnivora", "Roden...
$ conservation <chr> "lc", NA, "nt", "lc", "domesticated", NA, "vu", NA, "domesticated", "lc", "lc", "domesticated", "l...
$ sleep_total  <dbl> 12.1, 17.0, 14.4, 14.9, 4.0, 14.4, 8.7, 7.0, 10.1, 3.0, 5.3, 9.4, 10.0, 12.5, 10.3, 8.3, 9.1, 17.4...
$ sleep_rem    <dbl> NA, 1.8, 2.4, 2.3, 0.7, 2.2, 1.4, NA, 2.9, NA, 0.6, 0.8, 0.7, 1.5, 2.2, 2.0, 1.4, 3.1, 0.5, 4.9, N...
$ sleep_cycle  <dbl> NA, NA, NA, 0.1333333, 0.6666667, 0.7666667, 0.3833333, NA, 0.3333333, NA, NA, 0.2166667, NA, 0.11...
$ awake        <dbl> 11.90, 7.00, 9.60, 9.10, 20.00, 9.60, 15.30, 17.00, 13.90, 21.00, 18.70, 14.60, 14.00, 11.50, 13.7...
$ brainwt      <dbl> NA, 0.01550, NA, 0.00029, 0.42300, NA, NA, NA, 0.07000, 0.09820, 0.11500, 0.00550, NA, 0.00640, 0...
$ bodywt       <dbl> 50.000, 0.480, 1.350, 0.019, 600.000, 3.850, 20.490, 0.045, 14.000, 14.800, 33.500, 0.728, 4.750, ...
>
```

Help panel

R: An updated and expanded version of the mammals sleep dataset

msleep {ggplot2}   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name

genus
vore
    carnivore, omnivore or herbivore?

order
conservation
    the conservation status of the animal

Environment: msleep 83 obs. of 11 variables

09:41 AM 23-09-2022

Bottom screenshot — Source editor

```r
3  #manipulate your data
4  #data wrangling
5  ?msleep
6  glimpse(msleep)
7  view(msleep)
8
9  #how to rename a variable
10 msleep
11
12 msleep %>%
13   rename("conserv"="conservation")%>%
14   glimpse()
15 #it get change to conservation to conserv
16
17 #reorder variables
18 msleep %>%
19   select(vore,name,everything())
20
21 #change a variable type
22 class(msleep$vore)
23
24 msleep$vore <- as.factor(msleep$vore)
25
26 glimpse(msleep)
27 # it change to factor datatype
28 msleep%>%
29   mutate(vore = as.character((vore))) %>%
30   glimpse()
31 #it change to character datatype
32 #select variable to work with
33 names(msleep)
34 msleep %>%
```

Bottom screenshot — Console

```
$ sleep_cycle  <dbl> NA, NA, NA, 0.1333333, 0.6666667, 0.7666667, 0.3833333, NA, 0.3333333, NA, NA, 0.2166667, NA, 0.11...
$ awake        <dbl> 11.90, 7.00, 9.60, 9.10, 20.00, 9.60, 15.30, 17.00, 13.90, 21.00, 18.70, 14.60, 14.00, 11.50, 13.7...
$ brainwt      <dbl> NA, 0.01550, NA, 0.00029, 0.42300, NA, NA, NA, 0.07000, 0.09820, 0.11500, 0.00550, NA, 0.00640, 0...
$ bodywt       <dbl> 50.000, 0.480, 1.350, 0.019, 600.000, 3.850, 20.490, 0.045, 14.000, 14.800, 33.500, 0.728, 4.750, ...
> # it change to factor datatype
> msleep%>%
+   mutate(vore = as.character((vore))) %>%
+   glimpse()
Rows: 83
Columns: 11
$ name         <chr> "Cheetah", "Owl monkey", "Mountain beaver", "Greater short-tailed shrew", "Cow", "Three-toed sloth...
$ genus        <chr> "Acinonyx", "Aotus", "Aplodontia", "Blarina", "Bos", "Bradypus", "Callorhinus", "Calomys", "Canis"...
$ vore         <chr> "carni", "omni", "herbi", "omni", "herbi", "herbi", "carni", NA, "carni", "herbi", "herbi", "herbi...
$ order        <chr> "Carnivora", "Primates", "Rodentia", "Soricomorpha", "Artiodactyla", "Pilosa", "Carnivora", "Roden...
$ conservation <chr> "lc", NA, "nt", "lc", "domesticated", NA, "vu", NA, "domesticated", "lc", "lc", "domesticated", "l...
$ sleep_total  <dbl> 12.1, 17.0, 14.4, 14.9, 4.0, 14.4, 8.7, 7.0, 10.1, 3.0, 5.3, 9.4, 10.0, 12.5, 10.3, 8.3, 9.1, 17.4...
$ sleep_rem    <dbl> NA, 1.8, 2.4, 2.3, 0.7, 2.2, 1.4, NA, 2.9, NA, 0.6, 0.8, 0.7, 1.5, 2.2, 2.0, 1.4, 3.1, 0.5, 4.9, N...
$ sleep_cycle  <dbl> NA, NA, NA, 0.1333333, 0.6666667, 0.7666667, 0.3833333, NA, 0.3333333, NA, NA, 0.2166667, NA, 0.11...
$ awake        <dbl> 11.90, 7.00, 9.60, 9.10, 20.00, 9.60, 15.30, 17.00, 13.90, 21.00, 18.70, 14.60, 14.00, 11.50, 13.7...
$ brainwt      <dbl> NA, 0.01550, NA, 0.00029, 0.42300, NA, NA, NA, 0.07000, 0.09820, 0.11500, 0.00550, NA, 0.00640, 0...
$ bodywt       <dbl> 50.000, 0.480, 1.350, 0.019, 600.000, 3.850, 20.490, 0.045, 14.000, 14.800, 33.500, 0.728, 4.750, ...
>
```

09:42 AM 23-09-2022

Screenshot 1

```
12  msleep %>%
13    rename("conserv"="conservation")%>%
14    glimpse()
15  #it get change to conservation to conserv
16
17  #reorder variables
18  msleep %>%
19    select(vore,name,everything())
20
21  #change a variable type
22  class(msleep$vore)
23
24  msleep$vore <- as.factor(msleep$vore)
25
26  glimpse(msleep)
27  # it change to factor datatype
28  msleep%>%
29    mutate(vore = as.character((vore))) %>%
30    glimpse()
31  #it change to character datatype
32  #select variable to work with
33  names(msleep)
34  msleep %>%
35    select(2:4,
36           awake,
37           starts_with("sleep"),
38           contains("wt")) %>%
39    names()
40  #selecting a particular variables and manipulate
41  #filter and arrange data
42  unique(msleep$order)
43  msleep %>%
```

Console / Terminal / Background Jobs

R 4.2.1 · ~/

```
$ order        <chr> "Carnivora", "Primates", "Rodentia", "Soricomorpha", "Artiodactyla", "Pilosa", "Carnivora", "Roden...
$ conservation <chr> "lc", NA, "nt", "lc", "domesticated", NA, "vu", NA, "domesticated", "lc", "lc", "domesticated", "l...
$ sleep_total  <dbl> 12.1, 17.0, 14.4, 14.9, 4.0, 14.4, 8.7, 7.0, 10.1, 3.0, 5.3, 9.4, 10.0, 12.5, 10.3, 8.3, 9.1, 17.4...
$ sleep_rem    <dbl> NA, 1.8, 2.4, 2.3, 0.7, 2.2, 1.4, NA, 2.9, NA, 0.6, 0.8, 0.7, 1.5, 2.2, 2.0, 1.4, 3.1, 0.5, 4.9, N...
$ sleep_cycle  <dbl> NA, NA, NA, 0.1333333, 0.6666667, 0.7666667, 0.3833333, NA, 0.3333333, NA, NA, 0.2166667, NA, 0.11...
$ awake        <dbl> 11.90, 7.00, 9.60, 9.10, 20.00, 9.60, 15.30, 17.00, 13.90, 21.00, 18.70, 14.60, 14.00, 11.50, 13.7...
$ brainwt      <dbl> NA, 0.01550, NA, 0.00029, 0.42300, NA, NA, NA, 0.07000, 0.09820, 0.11500, 0.00550, NA, 0.00640, 0...
$ bodywt       <dbl> 50.000, 0.480, 1.350, 0.019, 600.000, 3.850, 20.490, 0.045, 14.000, 14.800, 33.500, 0.728, 4.750, ...
> #it change to character datatype
> #select variable to work with
> names(msleep)
 [1] "name"        "genus"       "vore"        "order"                     "conservation" "sleep_total" "sleep_rem"
 [8] "sleep_cycle" "awake"       "brainwt"     "bodywt"
> msleep %>%
+   select(2:4,
+          awake,
+          starts_with("sleep"),
+          contains("wt")) %>%
+   names()
 [1] "genus"       "vore"        "order"       "awake"       "sleep_total" "sleep_rem"   "sleep_cycle" "brainwt"
 [9] "bodywt"
>
```

Global Environment — Data — msleep — 83 obs. of 11 variables

R: An updated and expanded version of the mammals sleep dataset

msleep {ggplot2}   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

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Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name
genus
vore
    carnivore, omnivore or herbivore?
order
conservation
    the conservation status of the animal

Type here to search   09:43 AM 23-09-2022

Screenshot 2

```
22  class(msleep$vore)
23
24  msleep$vore <- as.factor(msleep$vore)
25
26  glimpse(msleep)
27  # it change to factor datatype
28  msleep%>%
29    mutate(vore = as.character((vore))) %>%
30    glimpse()
31  #it change to character datatype
32  #select variable to work with
33  names(msleep)
34  msleep %>%
35    select(2:4,
36           awake,
37           starts_with("sleep"),
38           contains("wt")) %>%
39    names()
40  #selecting a particular variables and manipulate
41  #filter and arrange data
42  unique(msleep$order)
43  msleep %>%
44    filter((order == "Carnivora" |
45            order == "Primates") &
46            sleep_total > 8)%>%
47    select(name,order,sleep_total)%>%
48    arrange(-sleep_total)%>%
49    view
50  #the above code is filters out carnivous and primates from order variable
51  #it arranges the sleep_total variable in descending order
52  #alternate way to filter and arrange
53  msleep%>%
```

Console / Terminal / Background Jobs

R 4.2.1 · ~/

```
+   select(2:4,
+          awake,
+          starts_with("sleep"),
+          contains("wt")) %>%
+   names()
 [1] "genus"       "vore"        "order"       "awake"       "sleep_total" "sleep_rem"   "sleep_cycle" "brainwt"
 [9] "bodywt"
> #selecting a particular variables and manipulate
> #filter and arrange data
> unique(msleep$order)
 [1] "Carnivora"      "Primates"       "Rodentia"       "Soricomorpha"    "Artiodactyla"    "Pilosa"
 [7] "Cingulata"      "Hyracoidea"     "Didelphimorphia" "Proboscidea"     "Chiroptera"      "Perissodactyla"
[13] "Erinaceomorpha" "Cetacea"        "Lagomorpha"      "Diprotodontia"   "Monotremata"     "Afrosoricida"
[19] "Scandentia"
> msleep %>%
+   filter((order == "Carnivora" |
+           order == "Primates") &
+           sleep_total > 8)%>%
+   select(name,order,sleep_total)%>%
+   arrange(-sleep_total)%>%
+   view
>
```

Global Environment — Data — msleep — 83 obs. of 11 variables

R: An updated and expanded version of the mammals sleep dataset

msleep {ggplot2}   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

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Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name
genus
vore
    carnivore, omnivore or herbivore?
order
conservation
    the conservation status of the animal

Type here to search   09:44 AM 23-09-2022

```r
#it change to character datatype
#select variable to work with
names(msleep)
msleep %>%
  select(2:4,
         awake,
         starts_with("sleep"),
         contains("wt")) %>%
  names()
#selecting a particular variables and manipulate
#filter and arrange data
unique(msleep$order)
msleep %>%
  filter((order == "Carnivora" |
            order == "Primates") &
           sleep_total > 8)%>%
  select(name,order,sleep_total)%>%
  arrange(-sleep_total)%>%
  view
#the above code is filters out carnvious and primates from order variable
#it arranges the sleep_total variable in descending order
#alternate way to filter and arrange
msleep%>%
  filter(order %in% c("Carnivora", "Primates") &
           sleep_total > 8) %>%
  select(name,order,sleep_total) %>%
  arrange(order) %>%
  view
#mutate function usage
#here the mutate function is used for changing the oberservation
msleep %>%
  mutate(brainwt=brainwt*1000) %>%
```

Console output:

```
> unique(msleep$order)
 [1] "Carnivora"       "Primates"       "Rodentia"       "Soricomorpha"   "Artiodactyla"   "Pilosa"
 [7] "Cingulata"       "Hyracoidea"     "Didelphimorphia" "Proboscidea"    "Chiroptera"     "Perissodactyla"
[13] "Erinaceomorpha"  "Cetacea"        "Lagomorpha"     "Diprotodontia"  "Monotremata"    "Afrosoricida"
[19] "Scandentia"
> msleep %>%
+   filter((order == "Carnivora" |
+            order == "Primates") &
+           sleep_total > 8)%>%
+   select(name,order,sleep_total)%>%
+   arrange(-sleep_total)%>%
+   view
> #the above code is filters out carnvious and primates from order variable
> #it arranges the sleep_total variable in descending order
> #alternate way to filter and arrange
> msleep%>%
+   filter(order %in% c("Carnivora", "Primates") &
+            sleep_total > 8) %>%
+   select(name,order,sleep_total) %>%
+   arrange(order) %>%
+   view
> |
```

	name	order	sleep_total
1	Owl monkey	Primates	17.0
2	Tiger	Carnivora	15.8
3	Lion	Carnivora	13.5
4	Domestic cat	Carnivora	12.5
5	Arctic fox	Carnivora	12.5
6	Cheetah	Carnivora	12.1
7	Slow loris	Primates	11.0
8	Potto	Primates	11.0
9	Patas monkey	Primates	10.9
10	Jaguar	Carnivora	10.4
11	Dog	Carnivora	10.1
12	Macaque	Primates	10.1
13	Grivet	Primates	10.0
14	Galago	Primates	9.8
15	Red fox	Carnivora	9.8
16	Chimpanzee	Primates	9.7
17	Squirrel monkey	Primates	9.6
18	Mongoose lemur	Primates	9.5

```r
        awake,
        starts_with("sleep"),
        contains("wt")) %>%
  names()
#selecting a particular variables and manipulate
#filter and arrange data
unique(msleep$order)
msleep %>%
  filter((order == "Carnivora" |
          order == "Primates") &
          sleep_total > 8)%>%
  select(name,order,sleep_total)%>%
  arrange(-sleep_total)%>%
  view
#the above code is filters out carnvious and primates from order variable
#it arranges the sleep_total variable in descending order
#alternate way to filter and arrange
msleep%>%
  filter(order %in% c("Carnivora", "Primates") &
          sleep_total > 8) %>%
  select(name,order,sleep_total) %>%
  arrange(order) %>%
  view
#mutate function usage
#here the mutate function is used for changing the oberservation
msleep %>%
  mutate(brainwt=brainwt*1000) %>%
  view
#here the code is changing the kilogram to gram
#it can be done only by multiping it by 1000
msleep %>%
  mutate(brainwt_in_grams = brainwt*1000)%>%
```

R: An updated and expanded version of the mammals sleep dataset

msleep {ggplot2}   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name

  common name

genus
vore

  carnivore, omnivore or herbivore?

order
conservation

  the conservation status of the animal

Console output:

```
> msleep %>%
+   filter((order == "Carnivora" |
+           order == "Primates") &
+           sleep_total > 8)%>%
+   select(name,order,sleep_total)%>%
+   arrange(-sleep_total)%>%
+   view
> #the above code is filters out carnvious and primates from order variable
> #it arranges the sleep_total variable in descending order
> #alternate way to filter and arrange
> msleep%>%
+   filter(order %in% c("Carnivora", "Primates") &
+           sleep_total > 8) %>%
+   select(name,order,sleep_total) %>%
+   arrange(order) %>%
+   view
> #mutate function usage
> #here the mutate function is used for changing the oberservation
> msleep %>%
+   mutate(brainwt=brainwt*1000) %>%
+   view
>
```

brainwt
NA
15.50
NA
0.29
423.00
NA
NA
NA
70.00
98.20
115.00
5.50
NA
6.40
1.00
6.60
0.14
10.80

brainwt	bodywt	brainwt_in_grams
NA	50.000	NA
0.01550	0.480	15.50
NA	1.350	NA
0.00029	0.019	0.29
0.42300	600.000	423.00
NA	3.850	NA
NA	20.490	NA
NA	0.045	NA
0.07000	14.000	70.00
0.09820	14.800	98.20
0.11500	33.500	115.00
0.00550	0.728	5.50
NA	4.750	NA
0.00640	0.420	6.40
0.00100	0.060	1.00
0.00660	1.000	6.60
0.00014	0.005	0.14
0.01080	3.500	10.80

Screenshot 1 (top):

Script editor:
```
57     arrange(order) %>%
58     view
59  #mutate function usage
60  #here the mutate function is used for changing the oberservation
61  msleep %>%
62     mutate(brainwt=brainwt*1000) %>%
63     view
64  #here the code is changing the kilogram to gram
65  #it can be done only by multiplying it by 1000
66  msleep %>%
67     mutate(brainwt_in_grams = brainwt*1000)%>%
68     view
69  #the above code creates a column "brainwt_in_grams" and stores the gram values
70
71
72  msleep$brainwt
73  # it displays the all the values present in brainwt column
74  msleep$brainwt >0.01
75  # as the above code we can see that NA is present in the column and few value are present
76  #conditionalchange (if_else)
77  ##logical vector based on a condition
78  size_of_brain <- msleep %>%
79     select(name,brainwt) %>%
80     drop_na(brainwt) %>%
81     mutate(brain_size = if_else(brainwt > 0.01 ,
82                        "large",
83                        "small"))
84
85  size_of_brain
86  # this code drops/eliminates  NA value and it is been sagrated the values which are greater than 0.01
87
88  #recode data and rename a variable
```

Console:
```
[15] 0.00100 0.00660 0.00014 0.01080 0.01230 0.00630 4.60300 0.00030 0.65500 0.41900 0.00350 0.11500      NA 0.02560
[29] 0.00500      NA      NA 0.32500 0.01227 1.32000      NA 5.71200      NA 0.17900      NA 0.00100      NA 0.00040
[43] 0.00025      NA 0.01250      NA      NA 0.01210 0.17500 0.44000      NA 0.15700      NA 0.18000 0.00240      NA
[57]      NA 0.01140      NA      NA      NA 0.08100 0.02100 0.00190      NA 0.02000 0.00120 0.00118 0.00300 0.00570
[71] 0.00400      NA 0.00033 0.18000 0.02500      NA 0.16900 0.00260 0.00250      NA 0.01750 0.00450 0.03040
> # it displays the all the values present in brainwt column
> msleep$brainwt >0.01
  [1]      NA  TRUE      NA FALSE  TRUE      NA      NA      NA  TRUE  TRUE  TRUE FALSE      NA FALSE FALSE FALSE FALSE  TRUE  TRUE
 [20] FALSE  TRUE FALSE  TRUE  TRUE FALSE  TRUE      NA  TRUE FALSE      NA  TRUE  TRUE  TRUE  TRUE      NA  TRUE      NA  TRUE
 [39]      NA FALSE      NA FALSE  TRUE FALSE  TRUE      NA  TRUE  TRUE  TRUE      NA  TRUE      NA  TRUE FALSE      NA      NA
 [58]  TRUE      NA      NA      NA  TRUE  TRUE FALSE      NA  TRUE FALSE FALSE FALSE FALSE      NA FALSE  TRUE  TRUE      NA      NA
 [77]  TRUE FALSE FALSE      NA  TRUE  TRUE  TRUE
> # as the above code we can see that NA is present in the column and few value are present
> #conditionalchange (if_else)
> ##logical vector based on a condition
> size_of_brain <- msleep %>%
+    select(name,brainwt) %>%
+    drop_na(brainwt) %>%
+    mutate(brain_size = if_else(brainwt > 0.01 ,
+                       "large",
+                       "small"))
> |
```

Environment pane:
```
Data
 msleep        83 obs. of 11 variables
 size_of_brain 56 obs. of 3 variables
```

Help pane:
An updated and expanded version of the mammals sleep dataset
msleep (ggplot2)   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
      common name
genus
vore
      carnivore, omnivore or herbivore?
order
conservation
      the conservation status of the animal

Screenshot 2 (bottom):

Script editor:
```
58     view
59  #mutate function usage
60  #here the mutate function is used for changing the oberservation
61  msleep %>%
62     mutate(brainwt=brainwt*1000) %>%
63     view
64  #here the code is changing the kilogram to gram
65  #it can be done only by multiplying it by 1000
66  msleep %>%
67     mutate(brainwt_in_grams = brainwt*1000)%>%
68     view
69  #the above code creates a column "brainwt_in_grams" and stores the gram values
70
71
72  msleep$brainwt
73  # it displays the all the values present in brainwt column
74  msleep$brainwt >0.01
75  # as the above code we can see that NA is present in the column and few value are present
76  #conditionalchange (if_else)
77  ##logical vector based on a condition
78  size_of_brain <- msleep %>%
79     select(name,brainwt) %>%
80     drop_na(brainwt) %>%
81     mutate(brain_size = if_else(brainwt > 0.01 ,
82                        "large",
83                        "small"))
84
85  size_of_brain
86  # this code drops/eliminates  NA value and it is been sagrated the values which are greater than 0.01
87
88  #recode data and rename a variable
89  size_of_brain %>%
```

Console:
```
+    select(name,brainwt) %>%
+    drop_na(brainwt) %>%
+    mutate(brain_size = if_else(brainwt > 0.01 ,
+                       "large",
+                       "small"))
> size_of_brain
# A tibble: 56 × 3
   name                     brainwt brain_size
   <chr>                      <dbl> <chr>
 1 Owl monkey                0.0155 large
 2 Greater short-tailed shrew 0.00029 small
 3 Cow                       0.423  large
 4 Dog                       0.07   large
 5 Roe deer                  0.0982 large
 6 Goat                      0.115  large
 7 Guinea pig                0.0055 small
 8 Chinchilla                0.0064 small
 9 Star-nosed mole           0.001  small
10 African giant pouched rat 0.0066 small
# ... with 46 more rows
# i Use `print(n = ...)` to see more rows
> |
```

Environment pane:
```
Data
 msleep        83 obs. of 11 variables
 size_of_brain 56 obs. of 3 variables
```

Help pane:
msleep (ggplot2)   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
      common name
genus
vore
      carnivore, omnivore or herbivore?
order
conservation
      the conservation status of the animal

First screenshot

Script editor:

```
72  msleep$brainwt
73  # it displays the all the values present in brainwt column
74  msleep$brainwt >0.01
75  # as the above code we can see that NA is present in the column and few value are present
76  #conditionalchange (if_else)
77  ##logical vector based on a condition
78  size_of_brain <- msleep %>%
79    select(name,brainwt) %>%
80    drop_na(brainwt) %>%
81    mutate(brain_size = if_else(brainwt > 0.01 ,
82                               "large",
83                               "small"))
84
85  size_of_brain
86  # this code drops/eliminates  NA value and it is been sagrated the values which are greater than 0.01
87
88  #recode data and rename a variable
89  size_of_brain %>%
90    mutate(brain_size= recode(brain_size,
91                             "large"=1,
92                             "small"=2))
93  #this code it change the brain_size column into 1 and 2 where  1 states that it has large brain
94  #and 2 states that it has small brain
95  #reshape the data from wide to long or long to wide
96  #install.packages("gapminder")
97  library(gapminder)
98  view(gapminder)
99
100 data <- select(gapminder,country,year,lifeExp)
101 # it selects the particular columns it is store in dataframe called data
102 view(data)
103
```

Console:

```
> view(gapminder)
> #recode data and rename a variable
> size_of_brain %>%
+   mutate(brain_size= recode(brain_size,
+                            "large"=1,
+                            "small"=2))
# A tibble: 56 x 3
   name                        brainwt brain_size
   <chr>                         <dbl>      <dbl>
 1 Owl monkey                   0.0155          1
 2 Greater short-tailed shrew   0.00029         2
 3 Cow                          0.423           1
 4 Dog                          0.07            1
 5 Roe deer                     0.0982          1
 6 Goat                         0.115           1
 7 Guinea pig                   0.0055          2
 8 Chinchilla                   0.0064          2
 9 Star-nosed mole              0.001           2
10 African giant pouched rat    0.0066          2
# ... with 46 more rows
# i Use `print(n = ...)` to see more rows
>
```

Global Environment — Data:
- msleep   83 obs. of 11 variables
- size_of_brain   56 obs. of 3 variables

R Documentation panel:

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name
genus
vore
    carnivore, omnivore or herbivore?
order
conservation
    the conservation status of the animal

Second screenshot

Data viewer table:

	country	1952	1957	1962	1967	1972	1977	1982	1987	1992	1997	2002	2007
1	Afghanistan	28.801	30.33200	31.99700	34.02000	36.08800	38.43800	39.854	40.822	41.674	41.763	42.129	43.828
2	Albania	55.230	59.28000	64.82000	66.22000	67.69000	68.93000	70.420	72.000	71.581	72.950	75.651	76.423
3	Algeria	43.077	45.68500	48.30300	51.40700	54.51800	58.01400	61.368	65.799	67.744	69.152	70.994	72.301
4	Angola	30.015	31.99900	34.00000	35.98500	37.92800	39.48300	39.942	39.906	40.647	40.963	41.003	42.731
5	Argentina	62.485	64.39900	65.14200	65.63400	67.06500	68.48100	69.942	70.774	71.868	73.275	74.340	75.320
6	Australia	69.120	70.33000	70.93000	71.10000	71.93000	73.49000	74.740	76.320	77.560	78.830	80.370	81.235
7	Austria	66.800	67.48000	69.54000	70.14000	70.63000	72.17000	73.180	74.940	76.040	77.510	78.980	79.829
8	Bahrain	50.939	53.83200	56.92300	59.92300	63.30000	65.59300	69.052	70.750	72.601	73.925	74.795	75.635
9	Bangladesh	37.484	39.34800	41.21600	43.45300	45.25200	46.92300	50.009	52.819	56.018	59.412	62.013	64.062
10	Belgium	68.000	69.24000	70.25000	70.94000	71.44000	72.80000	73.930	75.350	76.460	77.530	78.320	79.441
11	Benin	38.223	40.35800	42.61800	44.88500	47.01400	49.19000	50.904	52.337	53.919	54.777	54.406	56.728
12	Bolivia	40.414	41.89000	43.42800	45.03200	46.71400	50.02300	53.859	57.251	59.957	62.050	63.883	65.554
13	Bosnia and Herzegovina	53.820	58.45000	61.93000	64.79000	67.45000	69.86000	70.690	71.140	72.178	73.244	74.090	74.852
14	Botswana	47.622	49.61800	51.52000	53.29800	56.02400	59.31900	61.484	63.622	62.745	52.556	46.634	50.728
15	Brazil	50.917	53.28500	55.66500	57.63200	59.50400	61.48900	63.336	65.205	67.057	69.388	71.006	72.390
16	Bulgaria	59.600	66.61000	69.51000	70.42000	70.90000	70.81000	71.080	71.340	71.190	70.320	72.140	73.005
17	Burkina Faso	31.975	34.90600	37.81400	40.69700	43.59100	46.13700	48.122	49.557	50.260	50.324	50.650	52.295
18	Burundi	39.031	40.53300	42.04500	43.54800	44.05700	45.91000	47.471	48.211	44.736	45.326	47.360	49.580

Showing 1 to 19 of 142 entries, 13 total columns

Console:

```
 4 Dog                       0.07          1
 5 Roe deer                  0.0982        1
 6 Goat                      0.115         1
 7 Guinea pig                0.0055        2
 8 Chinchilla                0.0064        2
 9 Star-nosed mole           0.001         2
10 African giant pouched rat 0.0066        2
# ... with 46 more rows
# i Use `print(n = ...)` to see more rows
> #this code it change the brain_size column into 1 and 2 where  1 states that it has large brain
> #and 2 states that it has small brain
> #reshape the data from wide to long or long to wide
> #install.packages("gapminder")
> library(gapminder)
> view(gapminder)
> data <- select(gapminder,country,year,lifeExp)
> # it selects the particular columns it is store in dataframe called data
> view(data)
> wide_data <-data %>%
+   pivot_wider(names_from =year, values_from = lifeExp)
> view(wide_data)
>
```

Global Environment — Data:
- data   1704 obs. of 3 variables
- msleep   83 obs. of 11 variables
- size_of_brain   56 obs. of 3 variables
- wide_data   142 obs. of 13 variables

R Documentation panel:

An updated and expanded version of the mammals sleep dataset

Description

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Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name
genus
vore
    carnivore, omnivore or herbivore?
order
conservation
    the conservation status of the animal

Data viewer (top-left panel):

	country	year	lifeExp
1	Afghanistan	1952	28.801
2	Afghanistan	1957	30.332
3	Afghanistan	1962	31.997
4	Afghanistan	1967	34.020
5	Afghanistan	1972	36.088
6	Afghanistan	1977	38.438
7	Afghanistan	1982	39.854
8	Afghanistan	1987	40.822
9	Afghanistan	1992	41.674
10	Afghanistan	1997	41.763
11	Afghanistan	2002	42.129
12	Afghanistan	2007	43.828
13	Albania	1952	55.230
14	Albania	1957	59.280
15	Albania	1962	64.820
16	Albania	1967	66.220
17	Albania	1972	67.690
18	Albania	1977	68.930

Showing 1 to 19 of 1,704 entries, 3 total columns

Environment panel (top-right):

Data
- data — 1704 obs. of 3 variables
- long_data — 1704 obs. of 3 variables
- msleep — 83 obs. of 11 variables
- size_of_brain — 56 obs. of 3 variables
- wide_data — 142 obs. of 13 variables

Help panel:

msleep {ggplot2}   R Documentation

An updated and expanded version of the mammals sleep dataset

Description

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
    common name
genus
vore
    carnivore, omnivore or herbivore?
order
conservation
    the conservation status of the animal

Console panel:

```
  9 Star-nosed mole          0.001        2
 10 African giant pouched rat 0.0066      2
# ... with 46 more rows
# i Use `print(n = ...)` to see more rows
> #this code it change the brain_size column into 1 and 2 where  1 states that it has large brain
> #and 2 states that it has small brain
> #reshape the data from wide to long or long to wide
> #install.packages("gapminder")
> library(gapminder)
> view(gapminder)
> data <- select(gapminder,country,year,lifeExp)
> # it selects the particular columns it is store in dataframe called data
> view(data)
> wide_data <-data %>%
+   pivot_wider(names_from =year, values_from = lifeExp)
> view(wide_data)
> long_data <-wide_data %>%
+   pivot_longer(2:13,
+                names_to = "year",
+                values_to = "lifeExp")
> view(long_data)
> |
```

Bar charts and Histograms