What is statistics?

INTRODUCTION TO STATISTICS IN R

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What is statistics?

- **The field of statistics** - the practice and study of collecting and analyzing data
- **A summary statistic** - a fact about or summary of some data

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- **The field of statistics** - the practice and study of collecting and analyzing data
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What can statistics do?

- How likely is someone to purchase a product? Are people more likely to purchase it if they can use a different payment system?
- How many occupants will your hotel have? How can you optimize occupancy?
- How many sizes of jeans need to be manufactured so they can fit 95% of the population? Should the same number of each size be produced?
- A/B tests: Which ad is more effective in getting people to purchase a product?

What can't statistics do?

- *Why* is *Game of Thrones* so popular?

Instead...

- Are series with more violent scenes viewed by more people?

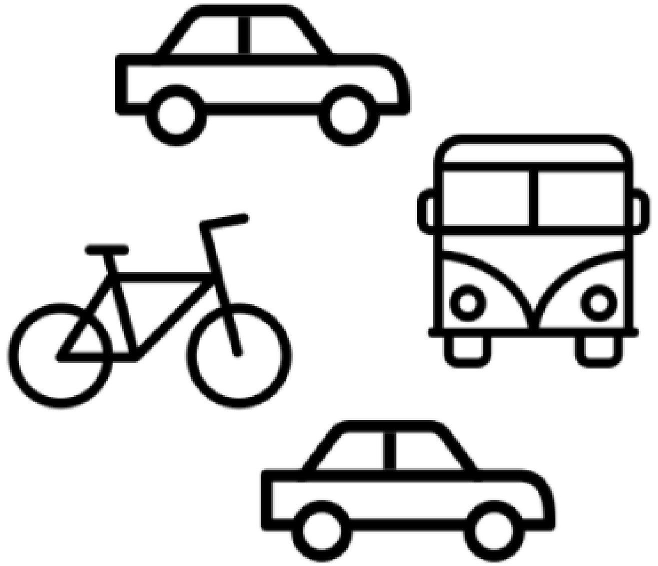
But...

- Even so, this can't tell us if more violent scenes lead to more views

Types of statistics

Descriptive statistics

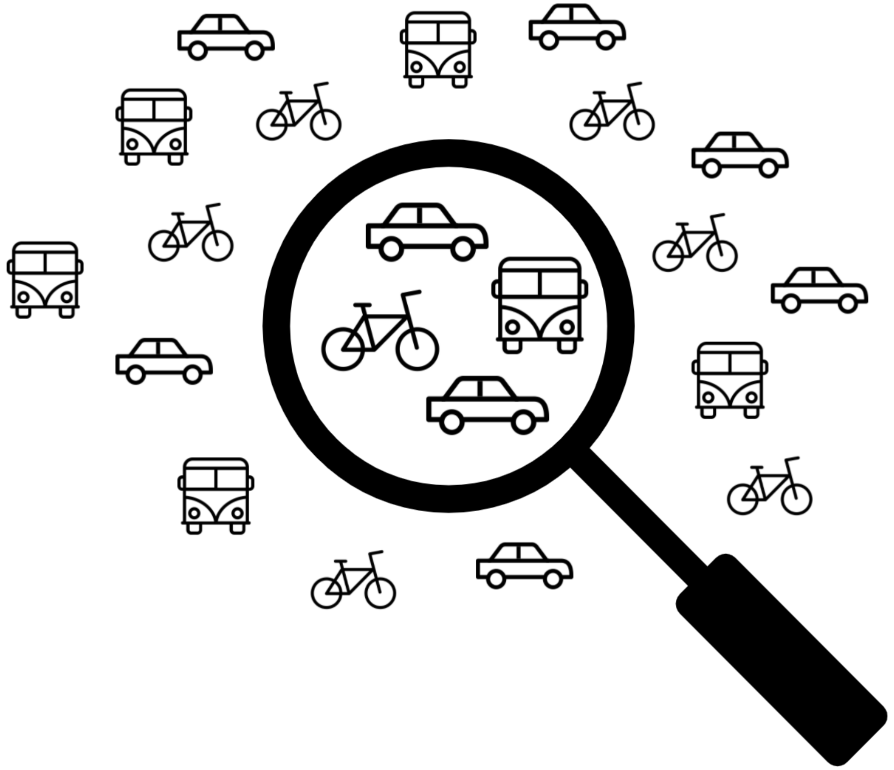
- *Describe* and summarize data



- 50% of friends drive to work
- 25% take the bus
- 25% bike

Inferential statistics

- Use a sample of data to make *inferences* about a larger population



What percent of people drive to work?

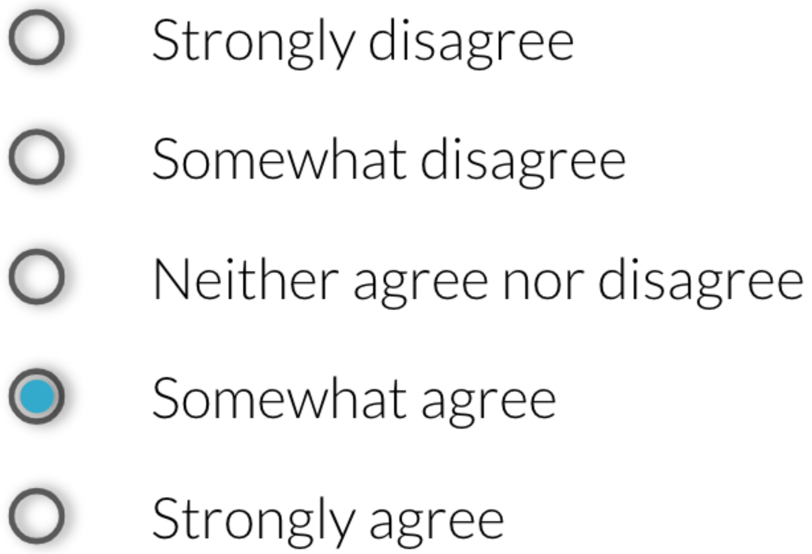
Types of data

Numeric (Quantitative)

- **Continuous (Measured)**
  - Airplane speed
  - Time spent waiting in line
- **Discrete (Counted)**
  - Number of pets
  - Number of packages shipped

Categorical (Qualitative)

- **Nominal (Unordered)**
  - Married/unmarried
  - Country of residence
- **Ordinal (Ordered)**



○ Strongly disagree

○ Somewhat disagree

○ Neither agree nor disagree

● Somewhat agree

○ Strongly agree

Categorical data can be represented as numbers

Nominal (Unordered)

- Married/unmarried (`1` / `0`)
- Country of residence (`1` , `2` , ...)

Ordinal (Ordered)

- Strongly disagree (`1`)
- Somewhat disagree (`2`)
- Neither agree nor disagree (`3`)
- Somewhat agree (`4`)
- Strongly agree (`5`)

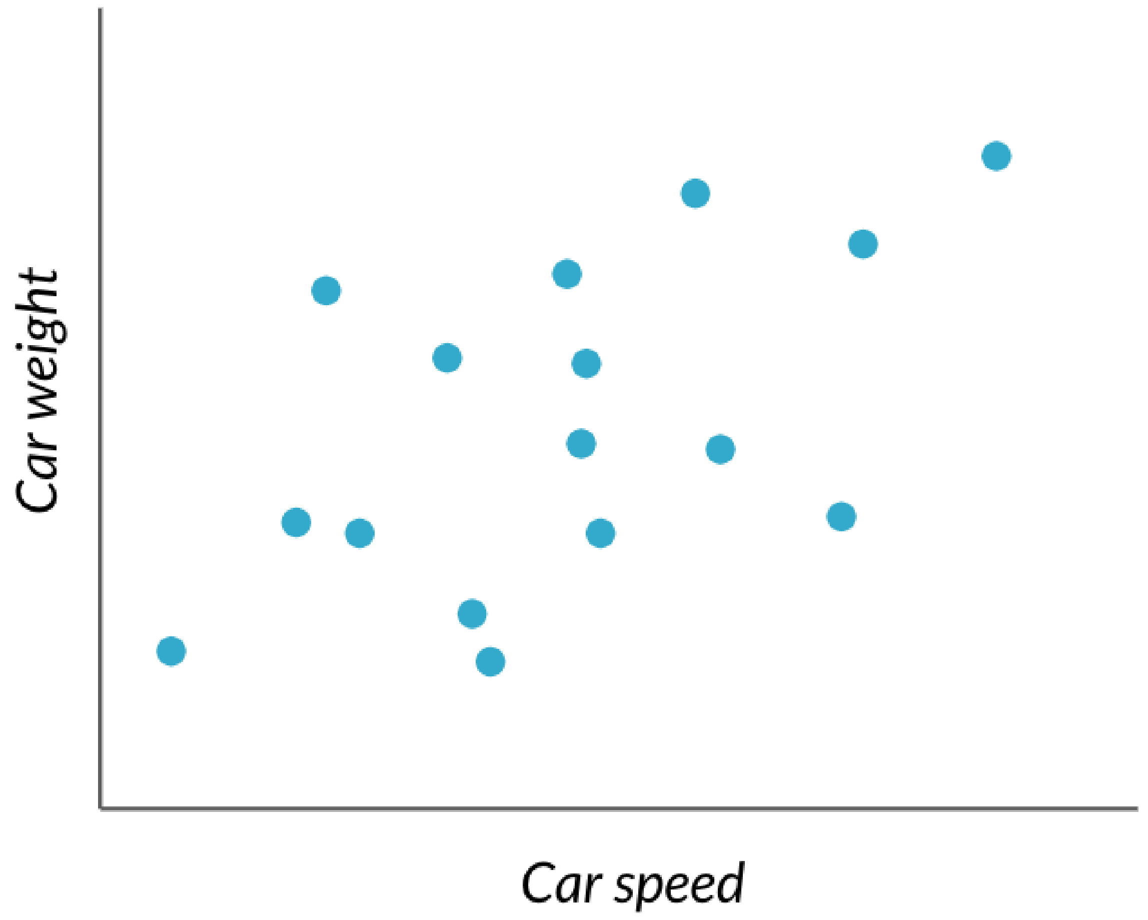
Why does data type matter?

Summary statistics

```
car_speeds %>%
  summarize(avg_speed = mean(speed_mph))
```

```
  avg_speed
1  40.09062
```

Plots



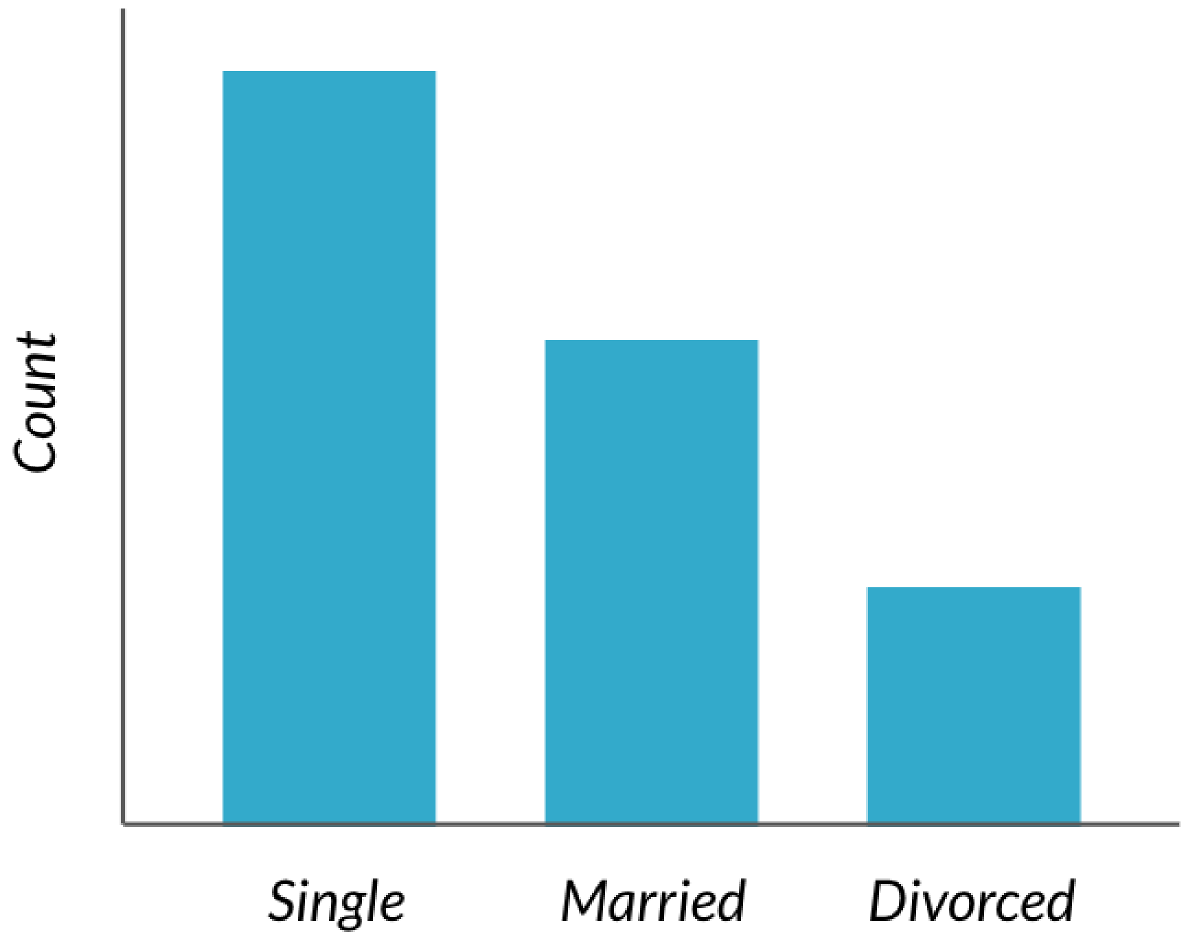
Why does data type matter?

Summary statistics

```
demographics %>%
  count(marriage_status)
```

```
  marriage_status    n
1          single  188
2         married  143
3        divorced  124
```

Plots



Let's practice!

Measures of center

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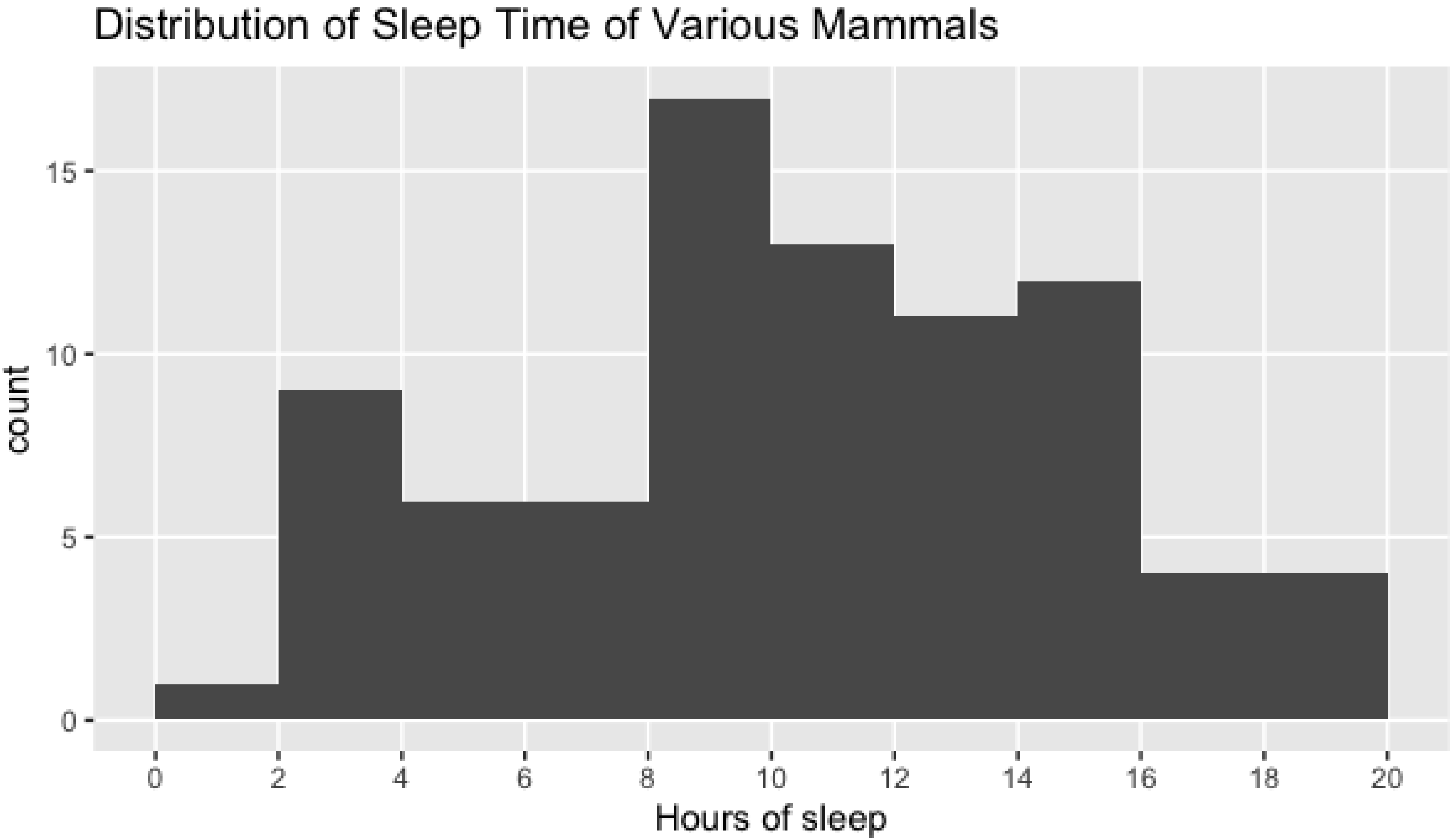
Mammal sleep data

```r
msleep
```

```
# A tibble: 83 x 11
   name             genus       vore  order        sleep_total sleep_rem sleep_cycle awake
   <chr>            <chr>       <chr> <chr>              <dbl>     <dbl>       <dbl> <dbl>
 1 Cheetah          Acinonyx    carni Carnivora           12.1      NA        NA      11.9
 2 Owl monkey       Aotus       omni  Primates            17         1.8      NA       7
 3 Mountain beaver  Aplodontia  herbi Rodentia            14.4       2.4      NA       9.6
 4 Greater short... Blarina     omni  Soricomorpha        14.9       2.3       0.133   9.1
 5 Cow              Bos         herbi Artiodactyla         4         0.7       0.667  20
 6 Three-toed sloth Bradypus    herbi Pilosa              14.4       2.2       0.767   9.6
 7 Northern fur...  Callorhinus carni Carnivora            8.7       1.4       0.383  15.3
# ... with 76 more rows, and 2 more variables: brainwt <dbl>, bodywt <dbl>
```

Histograms

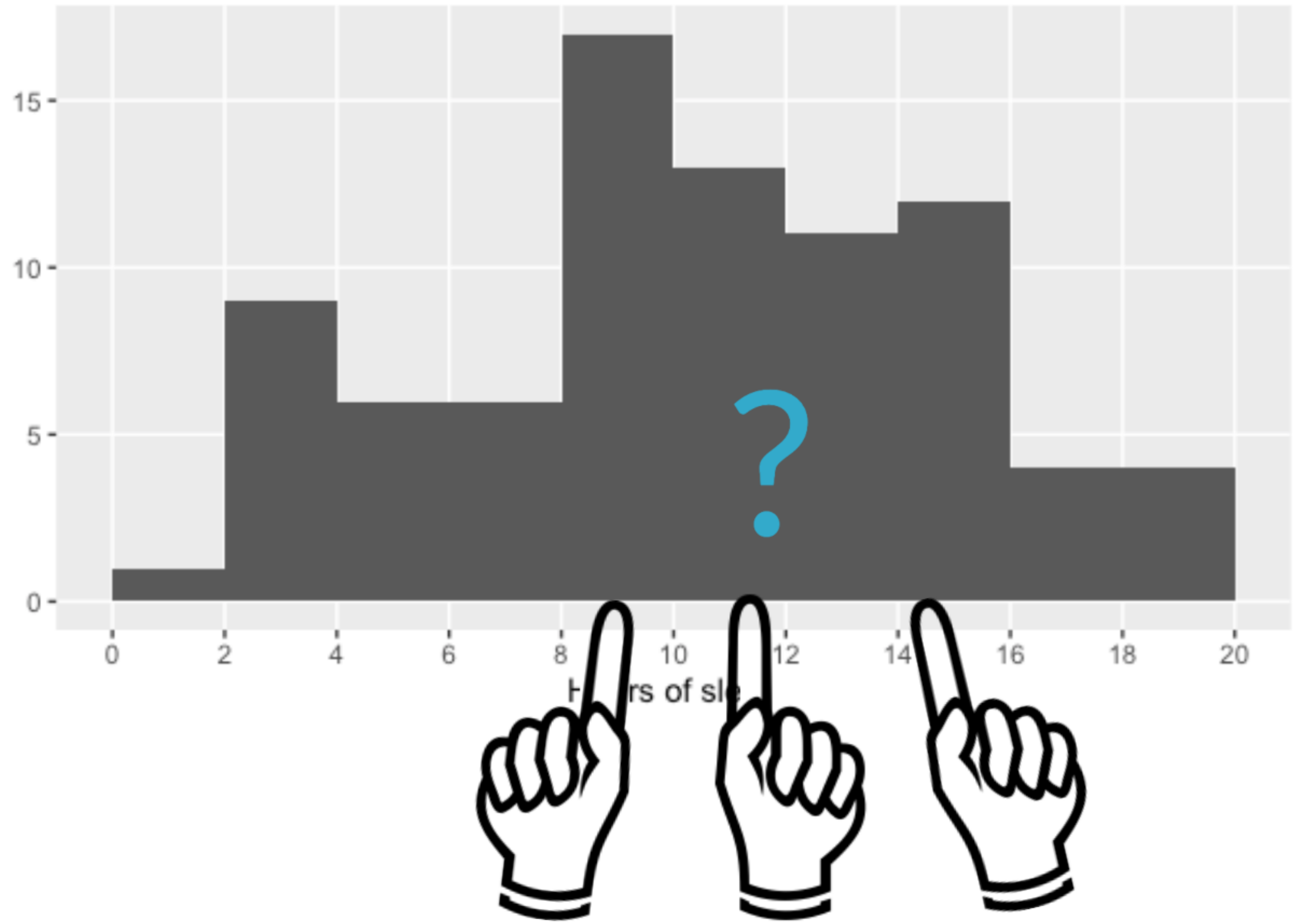

Distribution of Sleep Time of Various Mammals
count
0
5
10
15
0
2
4
6
8
10
12
14
16
18
20
Hours of sleep

How long do mammals in this dataset typically sleep?

What's a typical value?

Where is the center of the data?

- Mean
- Median
- Mode



Measures of center: mean

```
  name                          sleep_total
1 Cheetah                              12.1
2 Owl monkey                           17.0
3 Mountain beaver                      14.4
4 Greater short-tailed shrew           14.9
...
```

$$\text{Mean sleep time} = \frac{12.1 + 17.0 + 14.4 + 14.9 + ...}{83} = 10.43$$

```
mean(msleep$sleep_total)
```

```
10.43373
```

Measures of center: median

```
sort(msleep$sleep_total)
```

```
 [1]  1.9  2.7  2.9  3.0  3.1  3.3  3.5  3.8  3.9  4.0  4.4  5.2  5.3  5.3  5.4  5.6  6.2
...
[52] 11.5 12.1 12.5 12.5 12.5 12.5 12.8 12.8 13.0 13.5 13.7 13.8 14.2 14.3 14.4 14.4 14.5
[69] 14.6 14.9 14.9 15.6 15.8 15.8 15.9 16.6 17.0 17.4 18.0 18.1 19.4 19.7 19.9
```

```
sort(msleep$sleep_total)[42]
```

```
10.1
```

```
median(msleep$sleep_total)
```

```
10.1
```

Measures of center: mode

Most frequent value

```
msleep %>% count(sleep_total, sort = TRUE)
```

```
  sleep_total     n
        <dbl> <int>
1        12.5     4
2        10.1     3
3         5.3     2
4         6.3     2
...
```

```
msleep %>% count(vore, sort = TRUE)
```

```
  vore        n
  <chr>   <int>
1 herbi      32
2 omni       20
3 carni      19
4 NA          7
5 insecti     5
```

Adding an outlier

```
msleep %>%
  filter(vore == "insecti")
```

```
  name                   genus        vore     order        sleep_total
  <chr>                  <chr>        <chr>    <chr>              <dbl>
1 Big brown bat          Eptesicus    insecti  Chiroptera          19.7
2 Little brown bat       Myotis       insecti  Chiroptera          19.9
3 Giant armadillo        Priodontes   insecti  Cingulata           18.1
4 Eastern american mole  Scalopus     insecti  Soricomorpha         8.4
```

Adding an outlier

```r
msleep %>%
  filter(vore == "insecti") %>%
  summarize(mean_sleep = mean(sleep_total),
            median_sleep = median(sleep_total))
```

```
  mean_sleep median_sleep
       <dbl>        <dbl>
1      16.52         18.9
```

Adding an outlier

```r
msleep %>%
  filter(vore == "insecti")
```

```
  name                  genus        vore    order        sleep_total
  <chr>                 <chr>        <chr>   <chr>              <dbl>
1 Big brown bat         Eptesicus    insecti Chiroptera          19.7
2 Little brown bat      Myotis       insecti Chiroptera          19.9
3 Giant armadillo       Priodontes   insecti Cingulata           18.1
4 Eastern american mole Scalopus     insecti Soricomorpha         8.4
5 Mystery insectivore   ...          ...     ...                  0.0
```

Adding an outlier

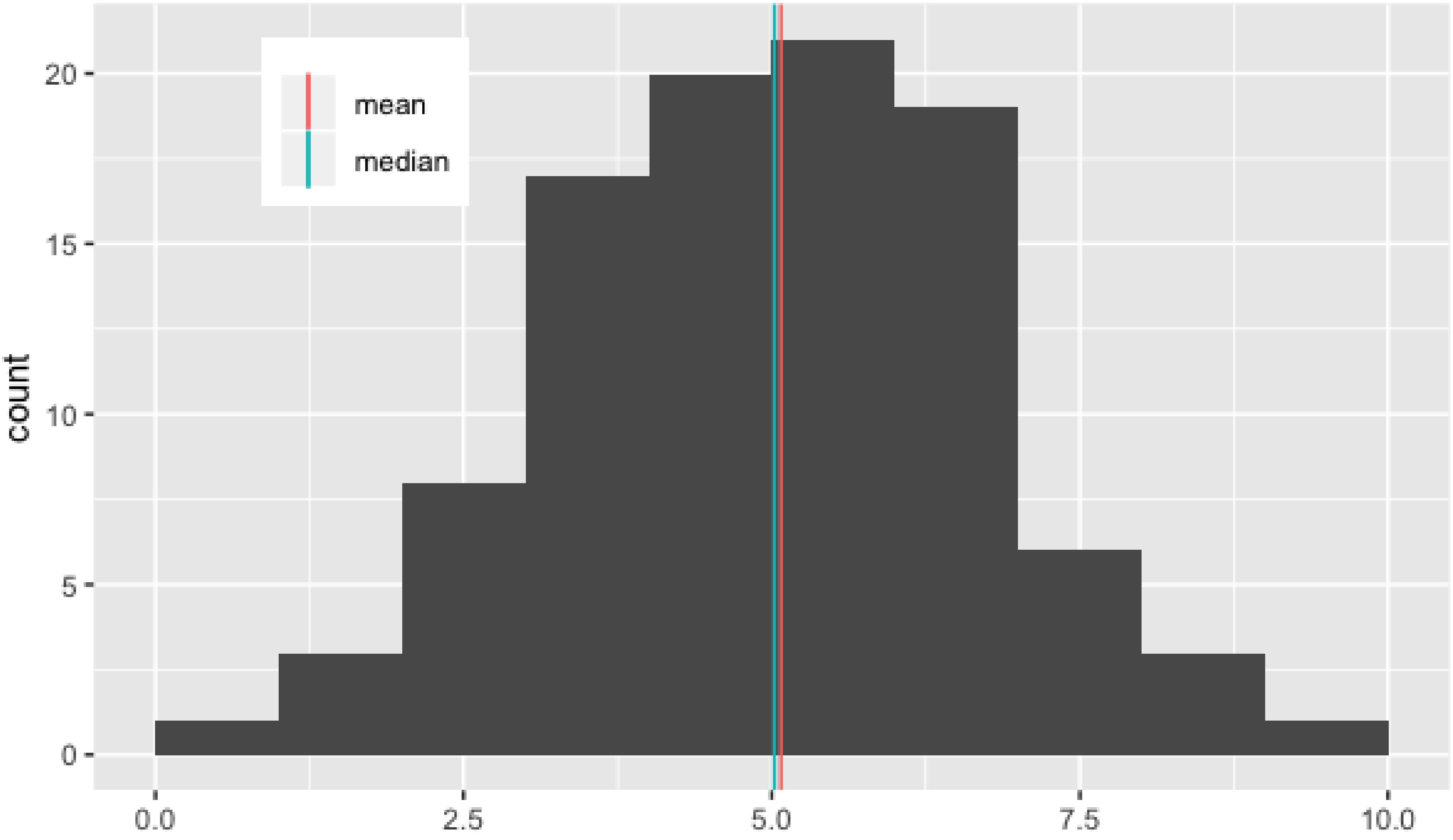
```r
msleep %>%
  filter(vore == "insecti") %>%
  summarize(mean_sleep = mean(sleep_total),
            median_sleep = median(sleep_total))
```

```
  mean_sleep median_sleep
       <dbl>        <dbl>
1      13.22         18.1
```

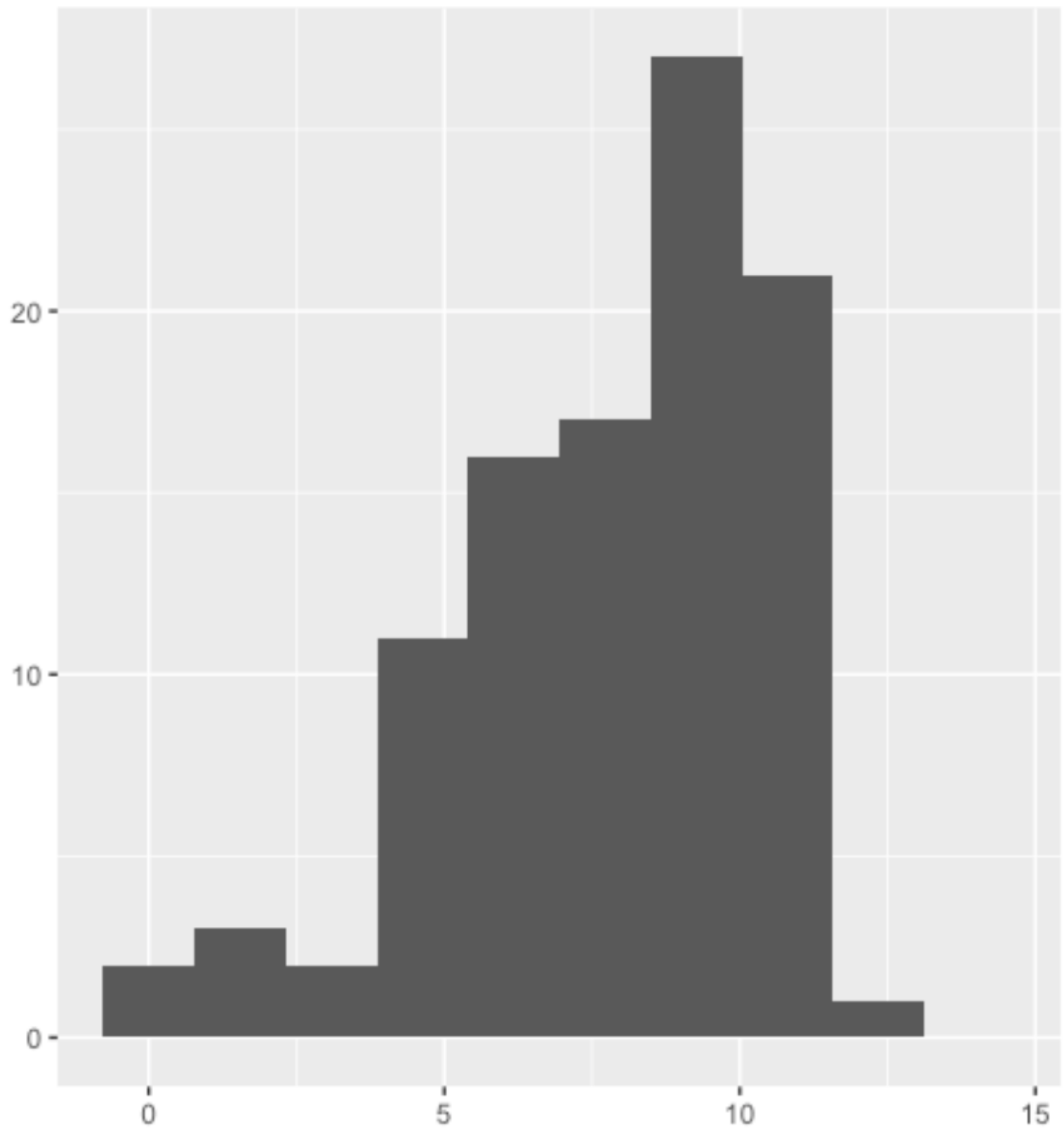
Mean: 16.5 → 13.2

Median: 18.9 → 18.1

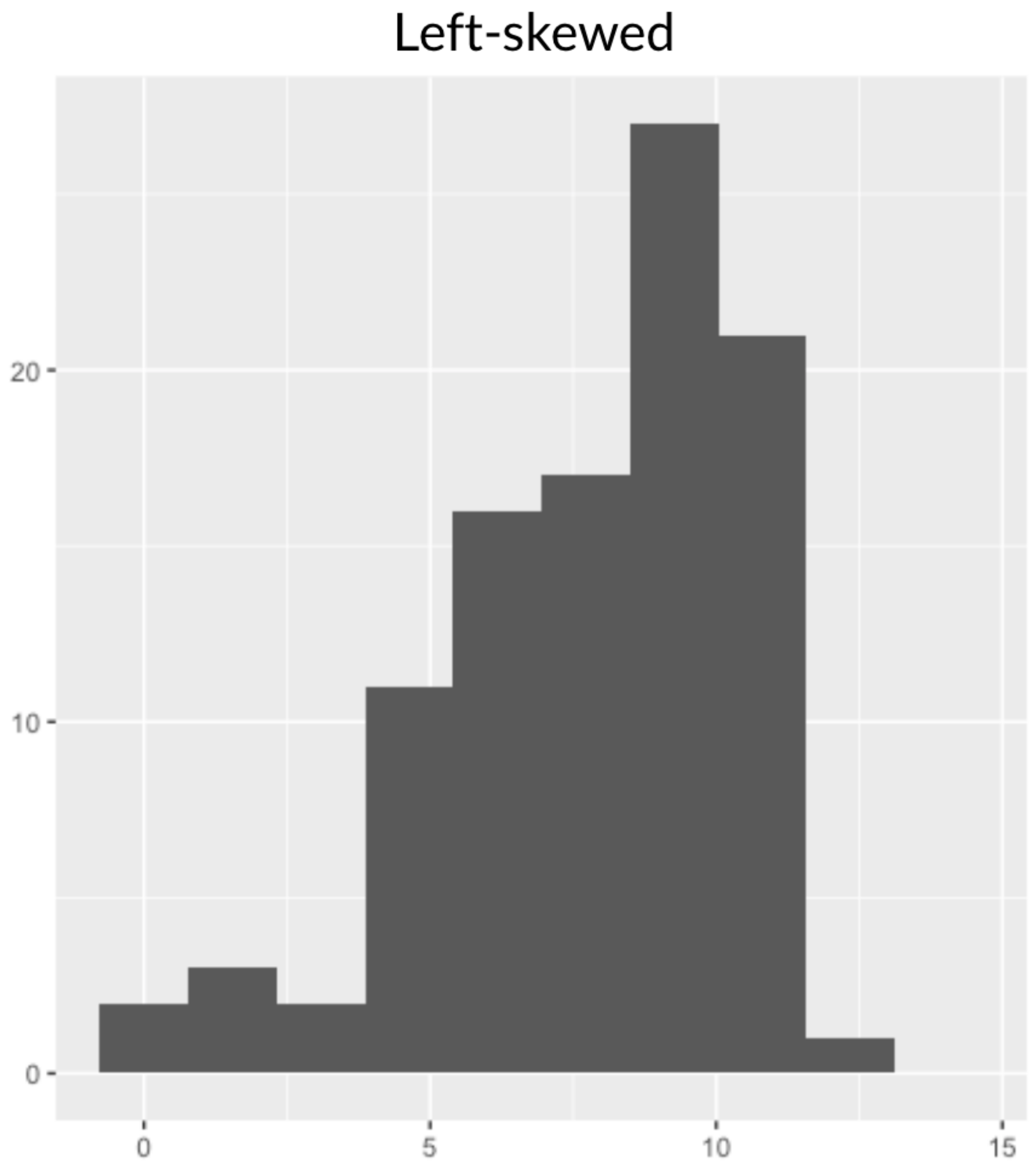
Which measure to use?



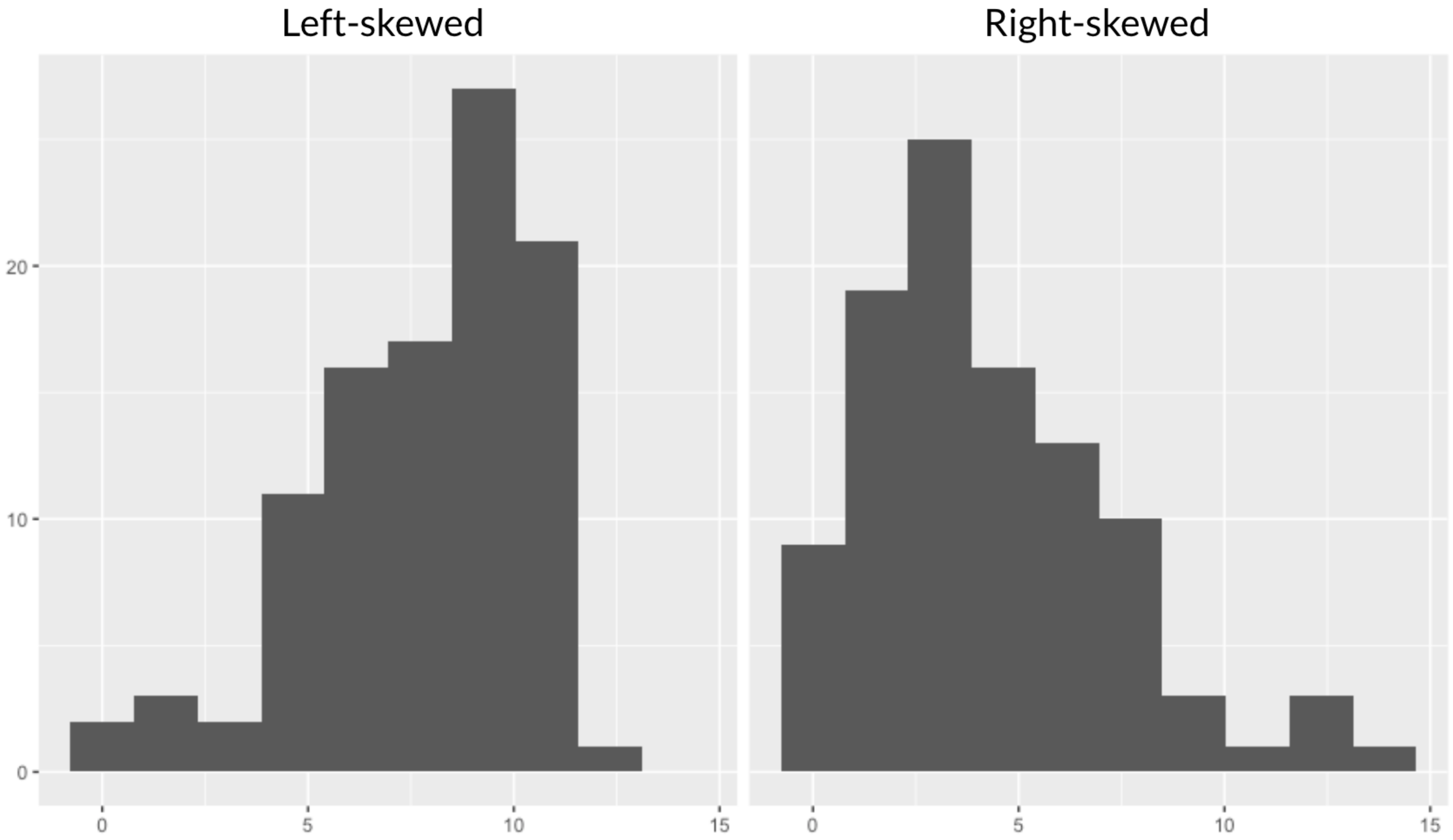
Skew



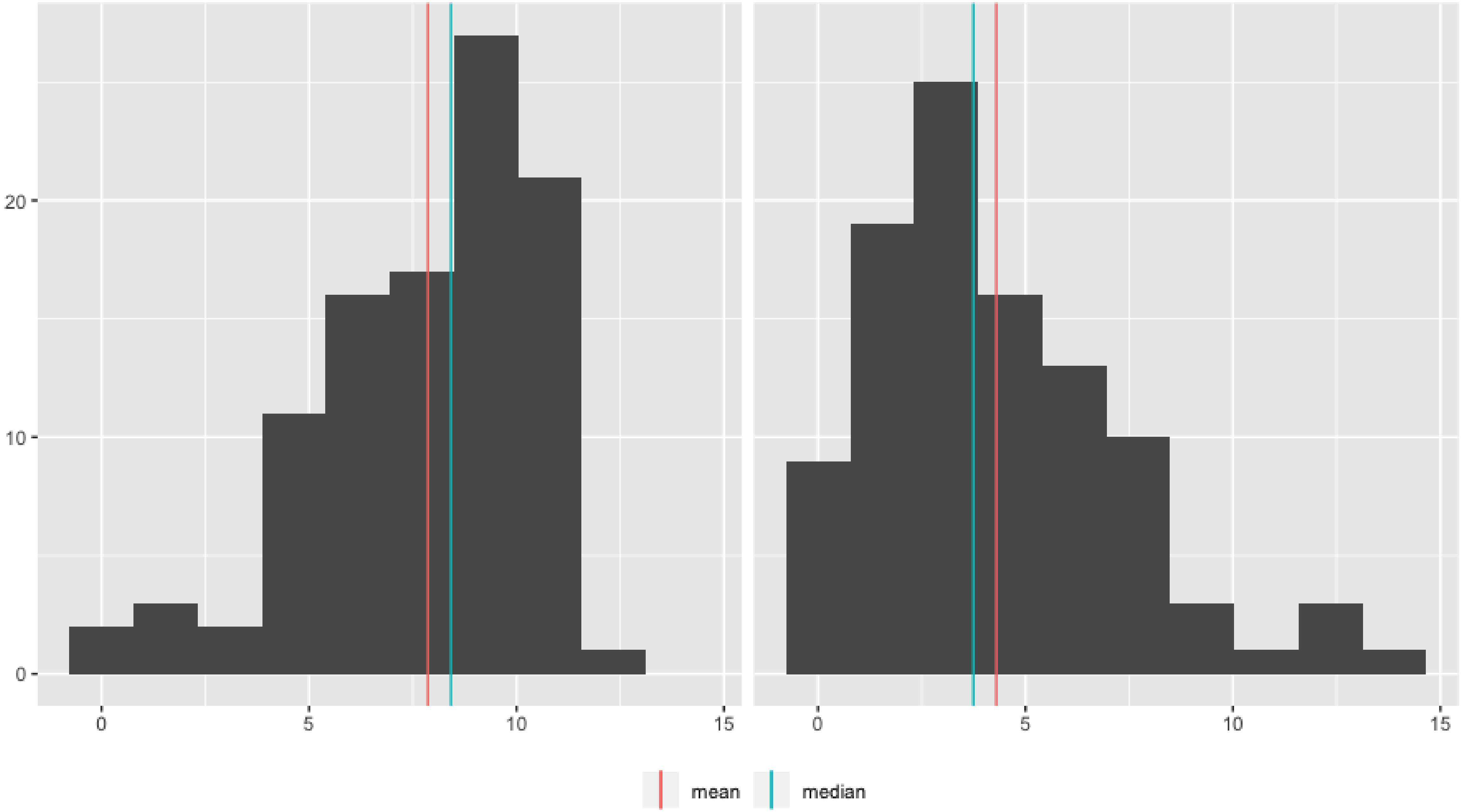
Skew



Skew



Which measure to use?



Let's practice!

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Measures of spread

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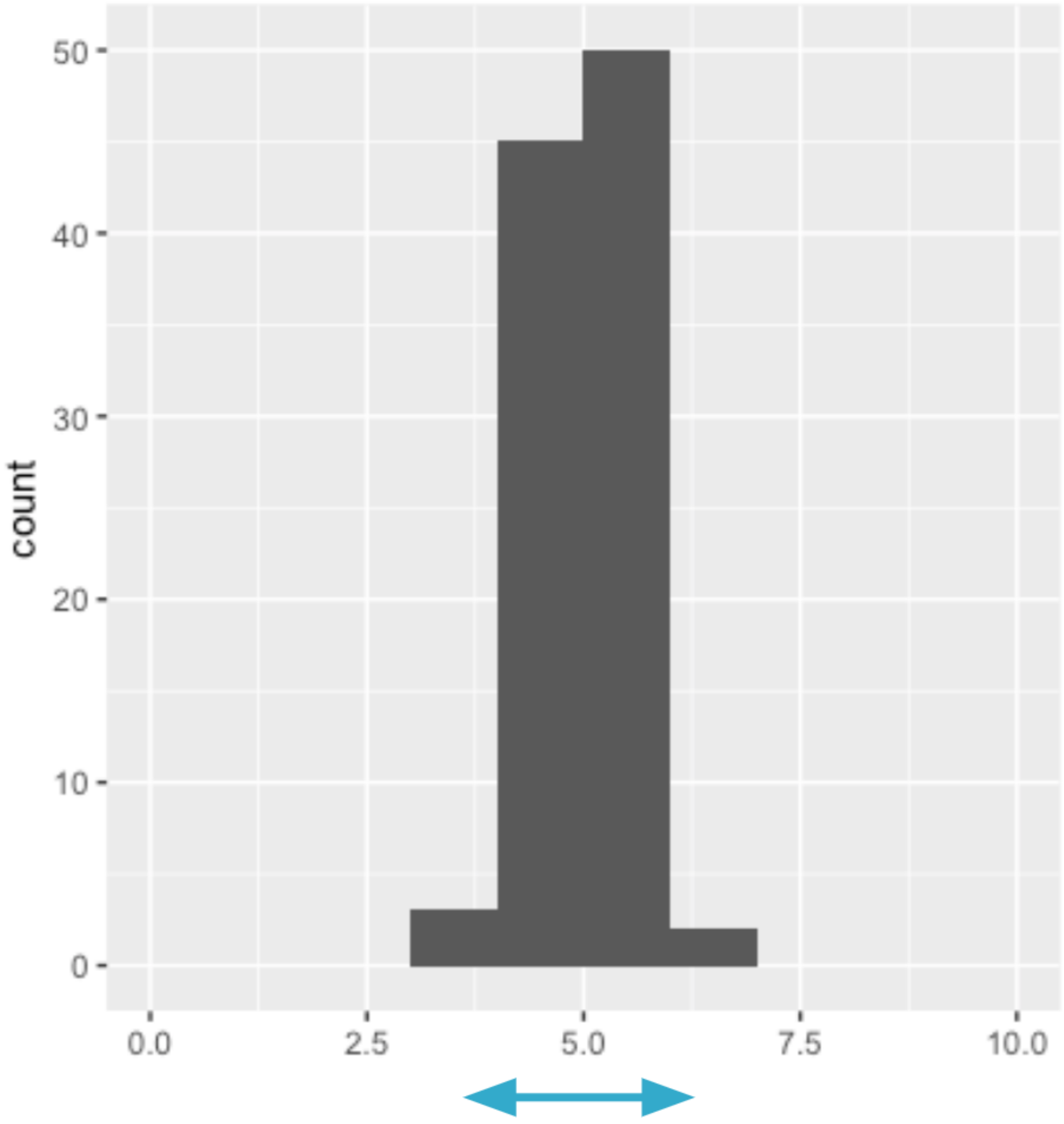
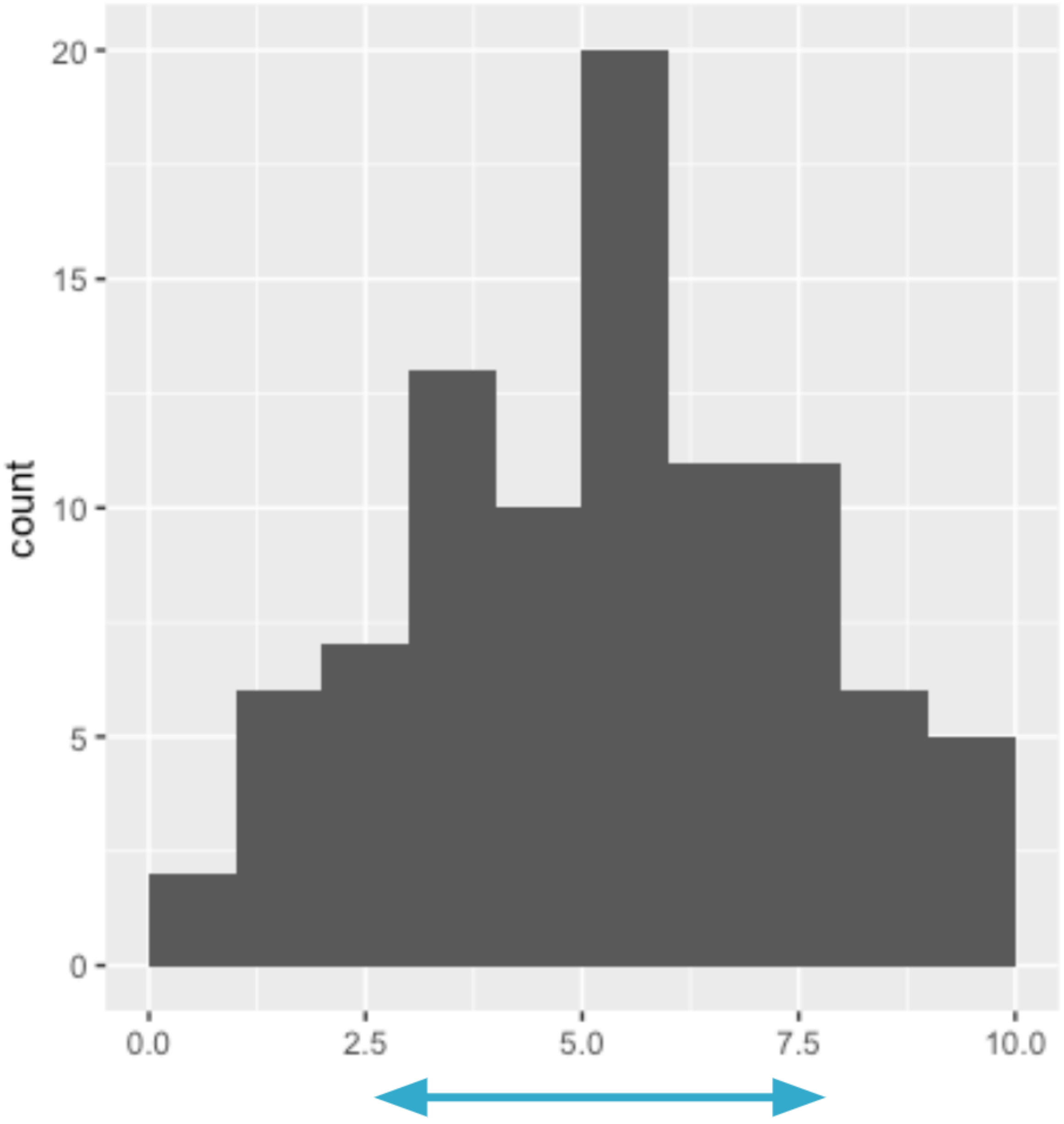
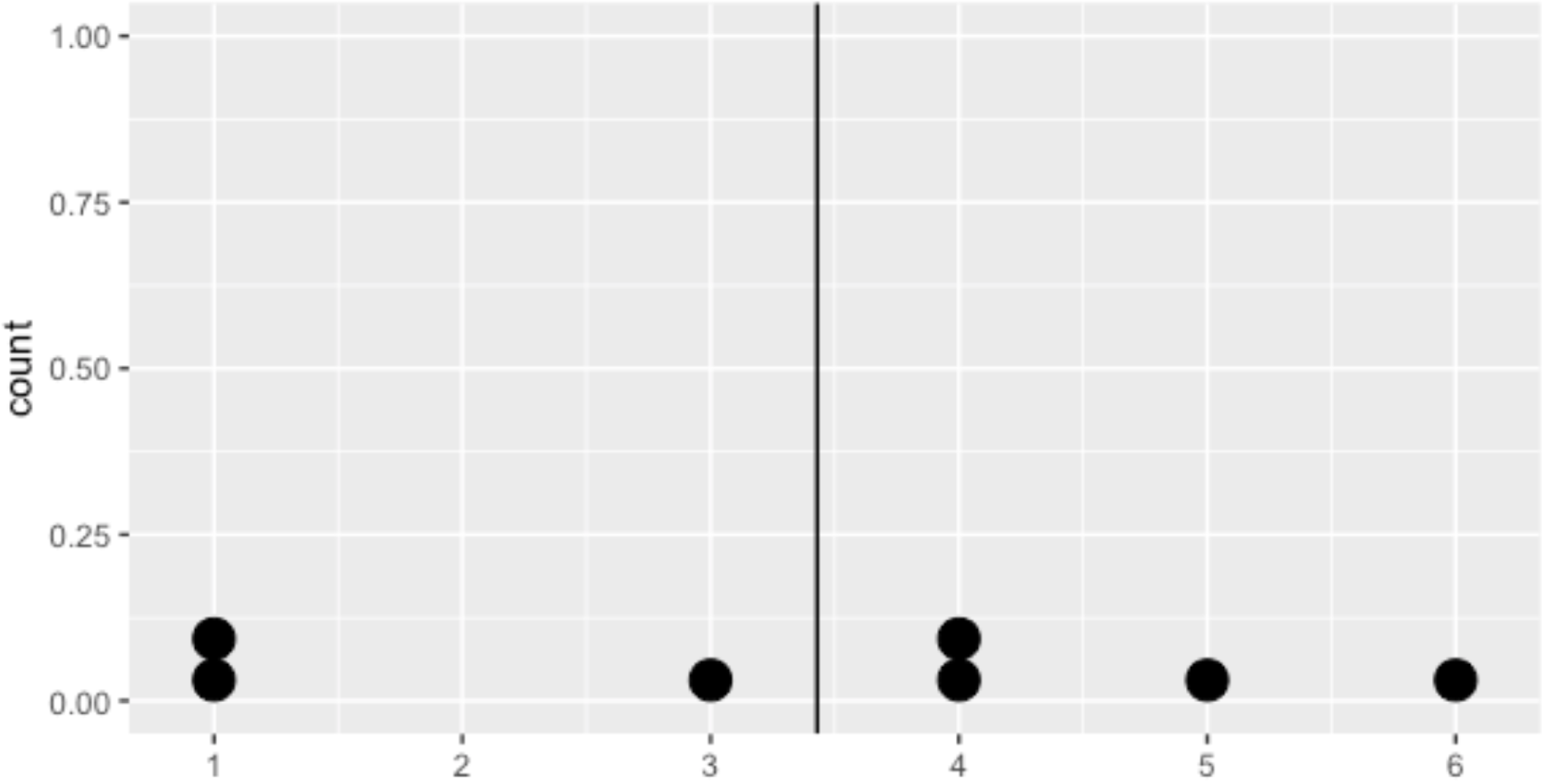
What is spread?



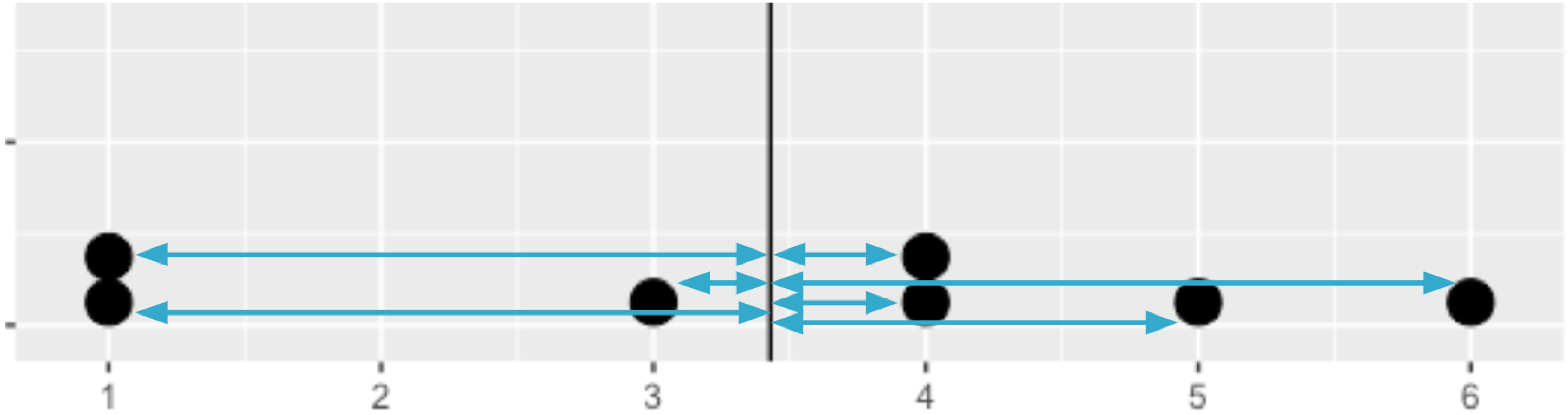


Variance

Average distance from each data point to the data's mean



Variance



```
dists <- msleep$sleep_total - mean(msleep$sleep_total)
dists
```

```
1.66626506  6.56626506 ... -4.13373494  2.06626506 -0.63373494
```

Variance

```
squared_dists <- (dists)^2
```

```
2.776439251 43.115836841 ... 17.087764552  4.269451299  0.401619974
```

```
sum_sq_dists <- sum(squared_dists)
sum_sq_dists
```

```
1624.066
```

Variance

```
sum_sq_dists/82
```

```
19.80568
```

```
var(msleep$sleep_total)
```

```
19.80568
```

Standard deviation

```
sqrt(var(msleep$sleep_total))
```

```
4.450357
```

```
sd(msleep$sleep_total)
```

```
4.450357
```

Mean absolute deviation

```
dists <- msleep$sleep_total - mean(msleep$sleep_total)
mean(abs(dists))
```

```
3.566701
```

Standard deviation vs. mean absolute deviation

- SD squares distances, penalizing longer distances more than shorter ones.
- MAD penalizes each distance equally.
- One isn't better than the other, but SD is more common than MAD.

Quartiles

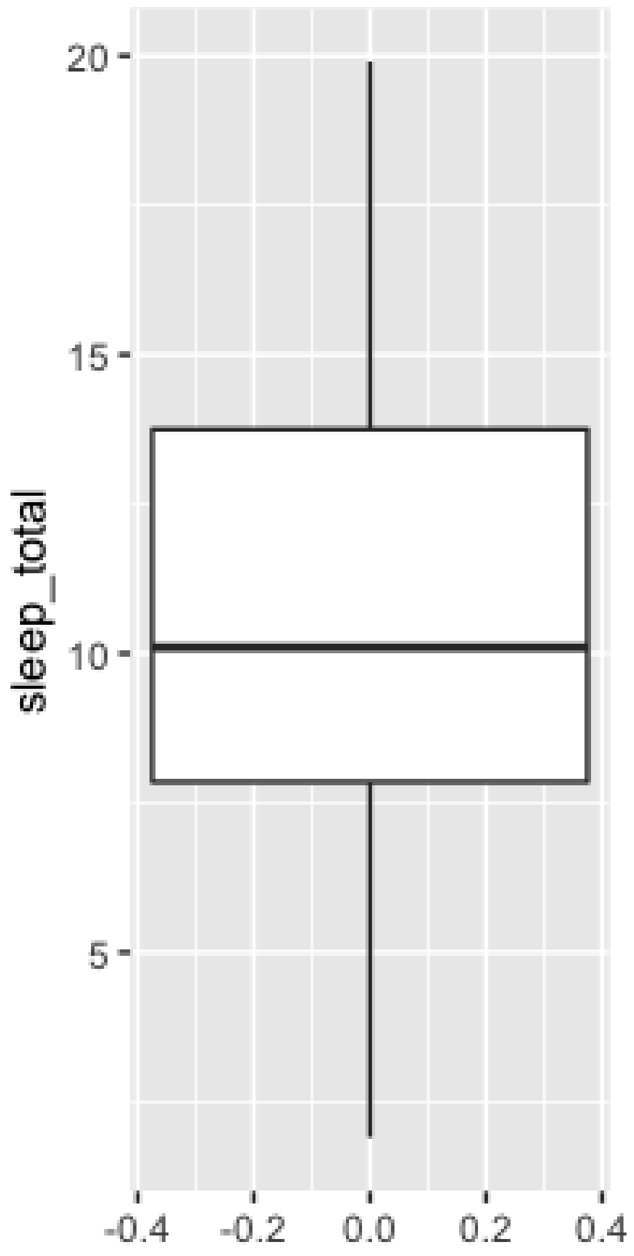
```
quantile(msleep$sleep_total)
```

```
   0%   25%   50%   75%  100%
 1.90  7.85 10.10 13.75 19.90
```

Second quartile/50th percentile = median

Boxplots use quartiles

```
ggplot(msleep, aes(y = sleep_total)) +
  geom_boxplot()
```



Quantiles

```r
quantile(msleep$sleep_total, probs = c(0, 0.2, 0.4, 0.6, 0.8, 1))
```

```
   0%   20%   40%   60%   80%  100% 
 1.90  6.24  9.48 11.14 14.40 19.90 
```

`seq(from, to, by)`

```r
quantile(msleep$sleep_total, probs = seq(0, 1, 0.2))
```

```
   0%   20%   40%   60%   80%  100% 
 1.90  6.24  9.48 11.14 14.40 19.90 
```

Interquartile range (IQR)

Height of the box in a boxplot

```r
quantile(msleep$sleep_total, 0.75) - quantile(msleep$sleep_total, 0.25)
```

```
5.9
```

Outliers

Outlier: data point that is substantially different from the others

How do we know what a substantial difference is? A data point is an outlier if:

- $\text{data} < \text{Q1} - 1.5 \times \text{IQR}$ or
- $\text{data} > \text{Q3} + 1.5 \times \text{IQR}$

Finding outliers

```
iqr <- quantile(msleep$bodywt, 0.75) - quantile(msleep$bodywt, 0.25)
lower_threshold <- quantile(msleep$bodywt, 0.25) - 1.5 * iqr
upper_threshold<- quantile(msleep$bodywt, 0.75) + 1.5 * iqr
```

```
msleep %>% filter(bodywt < lower_threshold | bodywt > upper_threshold ) %>%
  select(name, vore, sleep_total, bodywt)
```

```
# A tibble: 11 x 4
   name                 vore  sleep_total bodywt
 1 Cow                  herbi         4      600
 2 Asian elephant       herbi         3.9   2547
 3 Horse                herbi         2.9    521
 ...
```

Let's practice!

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