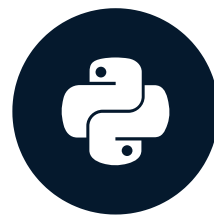


# What is statistics?

INTRODUCTION TO STATISTICS IN PYTHON



**Maggie Matsui**

Content Developer, DataCamp

# 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

# What can statistics do?

## 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

## 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?

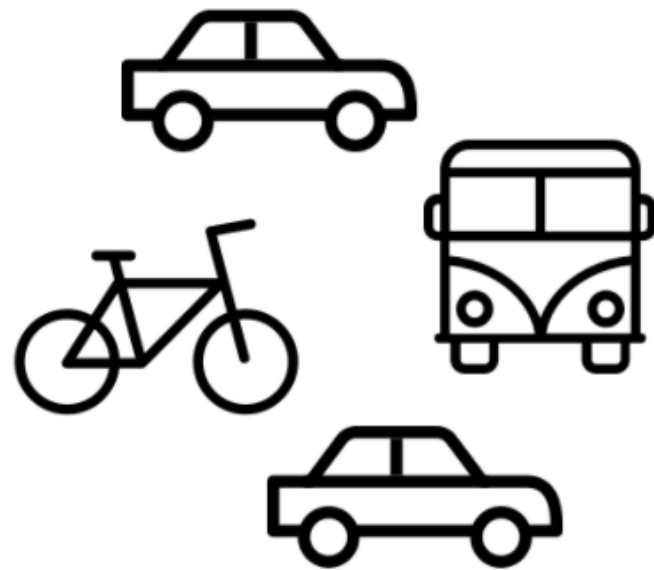
**But...**

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

# Types of statistics

## Descriptive statistics

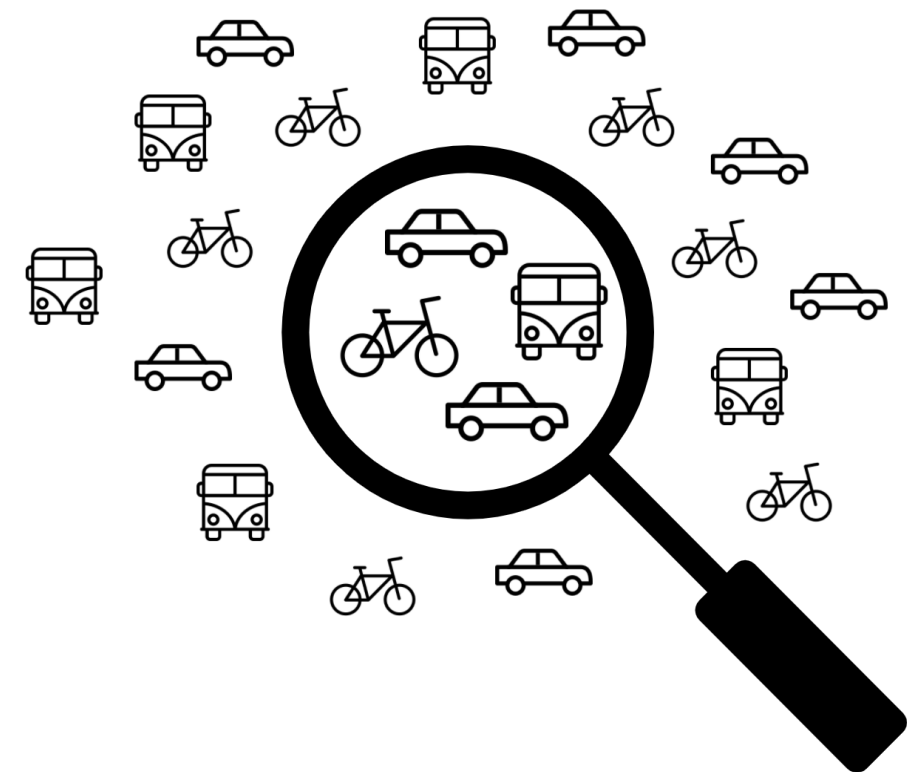
- *Describe* and summarize data



- 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)

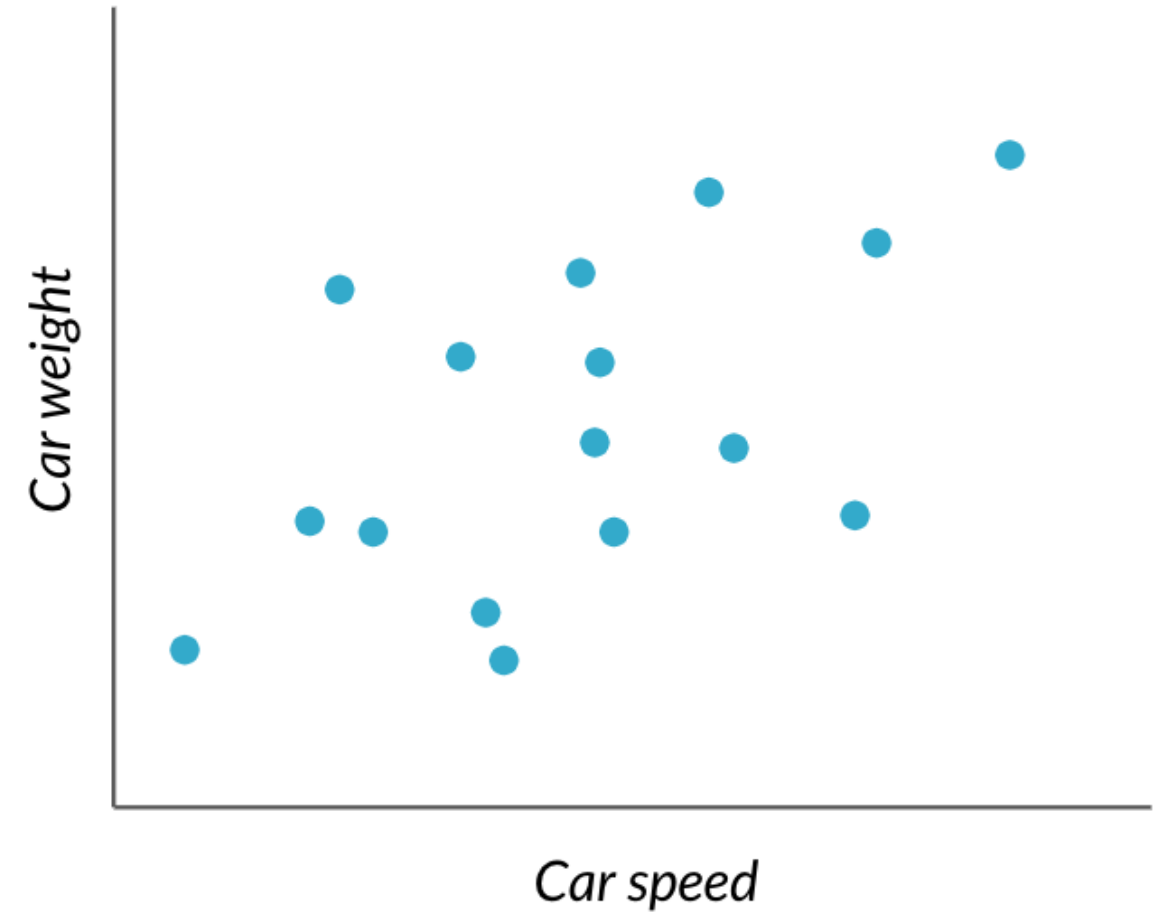
# Why does data type matter?

## Summary statistics

```
import numpy as np  
np.mean(car_speeds['speed_mph'])
```

```
40.09062
```

## Plots





# Why does data type matter?

## Summary statistics

```
demographics['marriage_status'].value_counts()
```

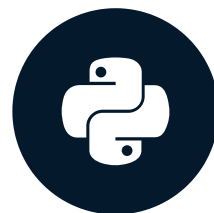
```
single      188  
married     143  
divorced    124  
dtype: int64
```

## Plots



# Measures of center

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**Maggie Matsui**

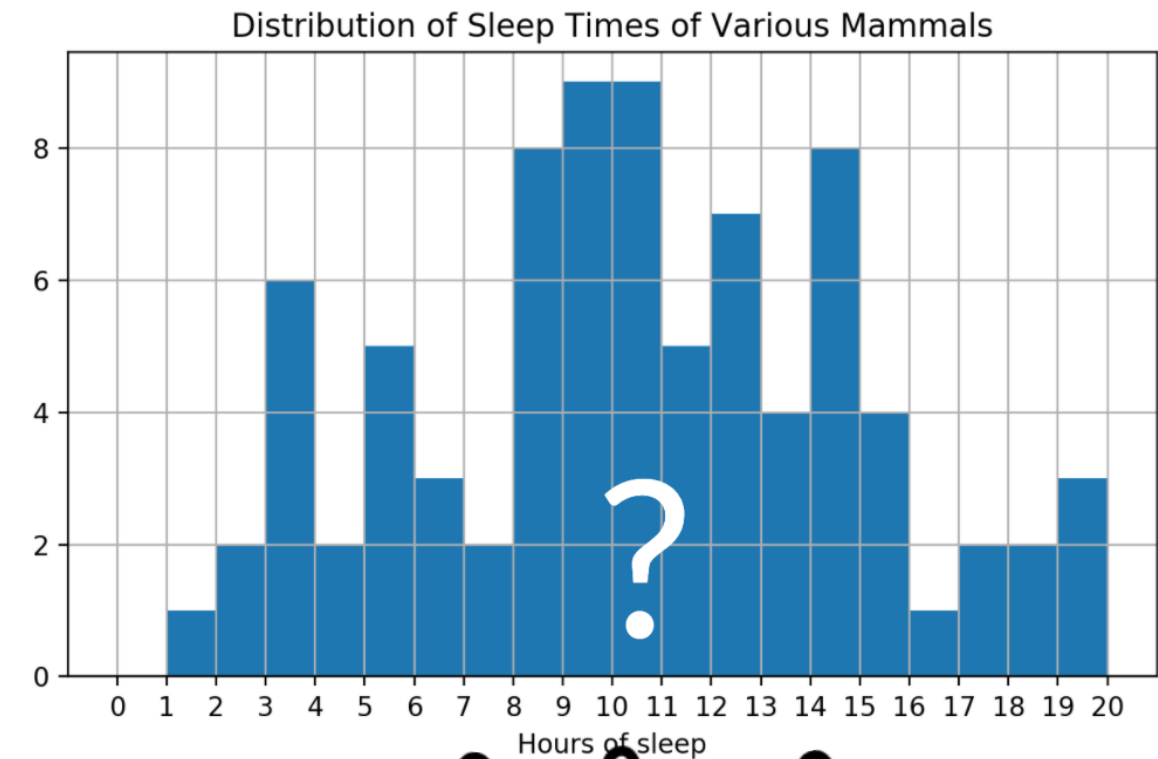
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# How long do mammals in this dataset typically sleep?

*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-t...	14.9
5	Cow	4.0
..	...	...

```
import numpy as np
np.mean(msleep['sleep_total'])
```

```
10.43373
```

Mean sleep time =

$$\frac{12.1 + 17.0 + 14.4 + 14.9 + \dots}{83} = 10.43$$

# Measures of center: median

```
msleep['sleep_total'].sort_values()
```

```
29    1.9
30    2.7
22    2.9
9     3.0
23    3.1
...
19   18.0
61   18.1
36   19.4
21   19.7
42   19.9
```

```
msleep['sleep_total'].sort_values().iloc[41]
```

```
10.1
```

```
np.median(msleep['sleep_total'])
```

```
10.1
```

# Measures of center: mode

*Most frequent value*

```
msleep['sleep_total'].value_counts()
```

```
12.5    4
10.1    3
14.9    2
11.0    2
 8.4    2
...
14.3    1
17.0    1
Name: sleep_total, Length: 65, dtype: int64
```

```
msleep['vore'].value_counts()
```

```
herbi    32
omni     20
carni    19
insecti   5
Name: vore, dtype: int64
```

```
import statistics
statistics.mode(msleep['vore'])
```

```
'herbi'
```

# Adding an outlier

```
msleep[msleep['vore'] == 'insecti']
```

	name	genus	vore	order	sleep_total
22	Big brown bat	Eptesicus	insecti	Chiroptera	19.7
43	Little brown bat	Myotis	insecti	Chiroptera	19.9
62	Giant armadillo	Priodontes	insecti	Cingulata	18.1
67	Eastern american mole	Scalopus	insecti	Soricomorpha	8.4

# Adding an outlier

```
msleep[msleep['vore'] == "insecti"]['sleep_total'].agg([np.mean, np.median])
```

```
mean      16.53  
median    18.9  
Name: sleep_total, dtype: float64
```



# Adding an outlier

```
msleep[msleep['vore'] == 'insecti']
```

	name	genus	vore	order	sleep_total
22	Big brown bat	Eptesicus	insecti	Chiroptera	19.7
43	Little brown bat	Myotis	insecti	Chiroptera	19.9
62	Giant armadillo	Priodontes	insecti	Cingulata	18.1
67	Eastern american mole	Scalopus	insecti	Soricomorpha	8.4
84	Mystery insectivore	...	insecti	...	0.0

# Adding an outlier

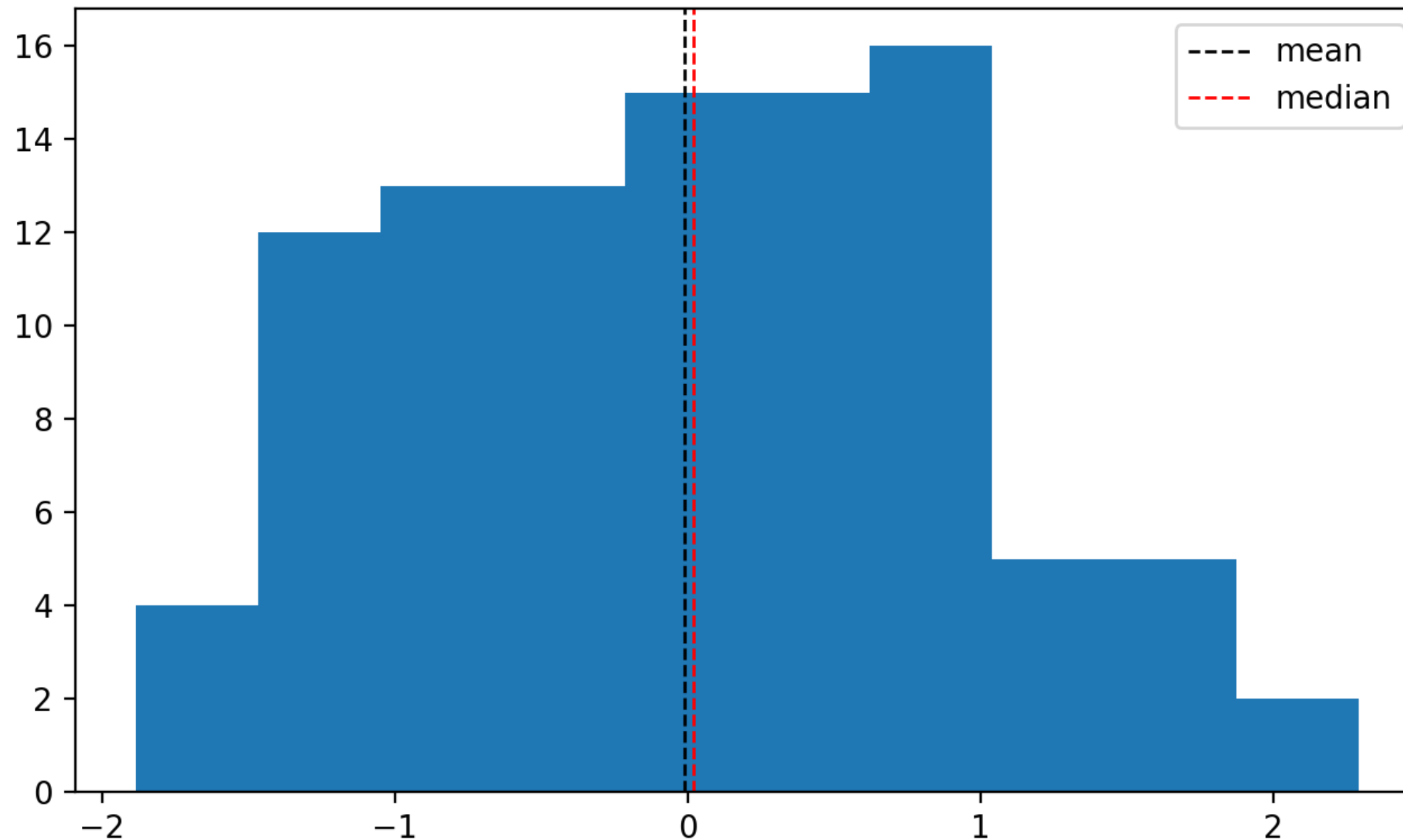
```
msleep[msleep['vore'] == "insecti"]['sleep_total'].agg([np.mean, np.median])
```

```
mean      13.22  
median    18.1  
Name: sleep_total, dtype: float64
```

**Mean:** 16.5 → 13.2

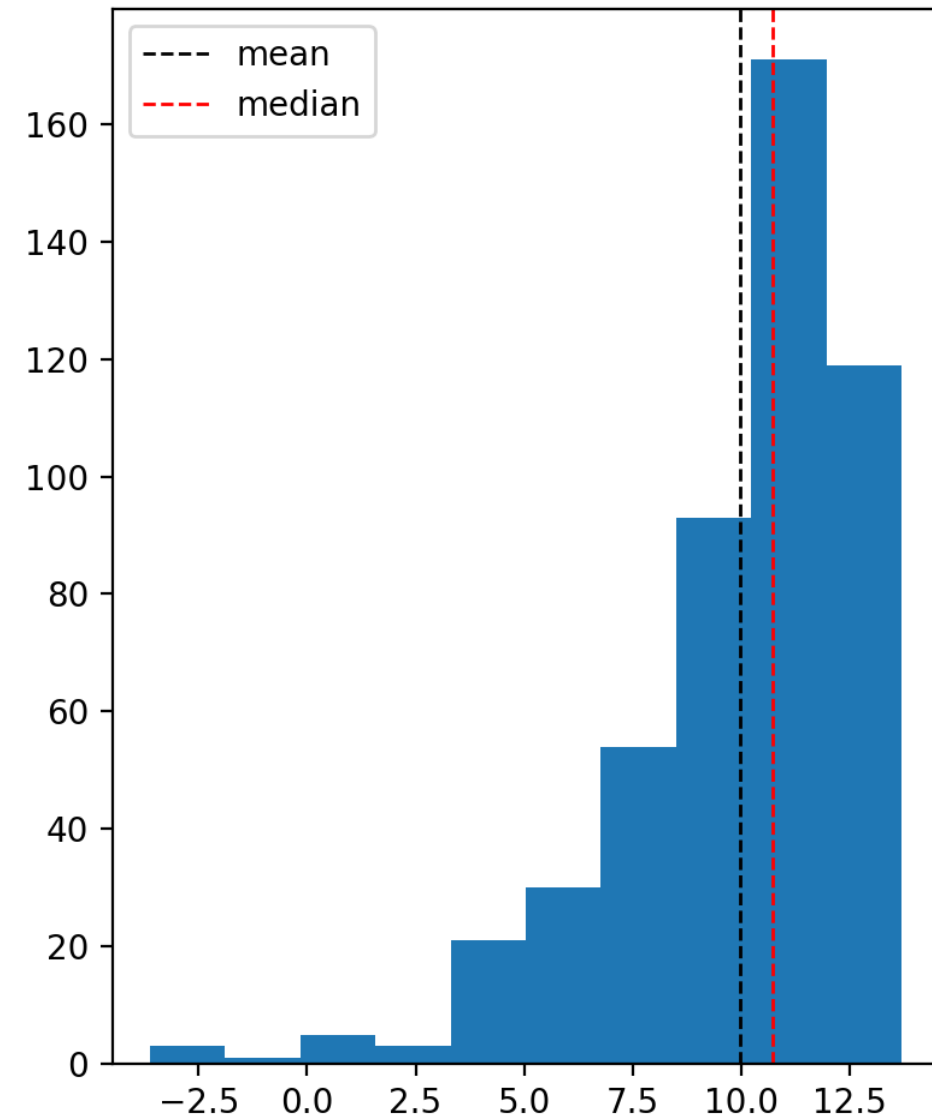
**Median:** 18.9 → 18.1

# Which measure to use?

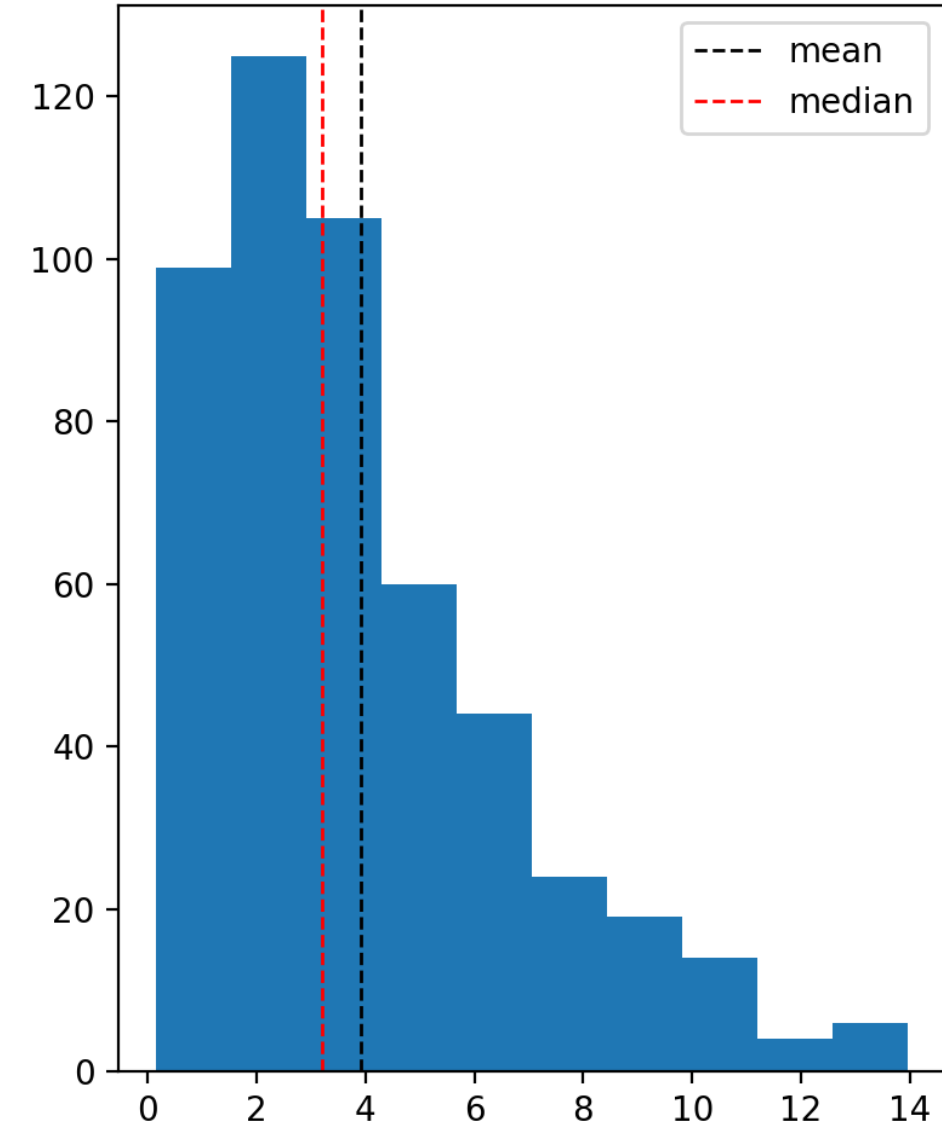


# Skew

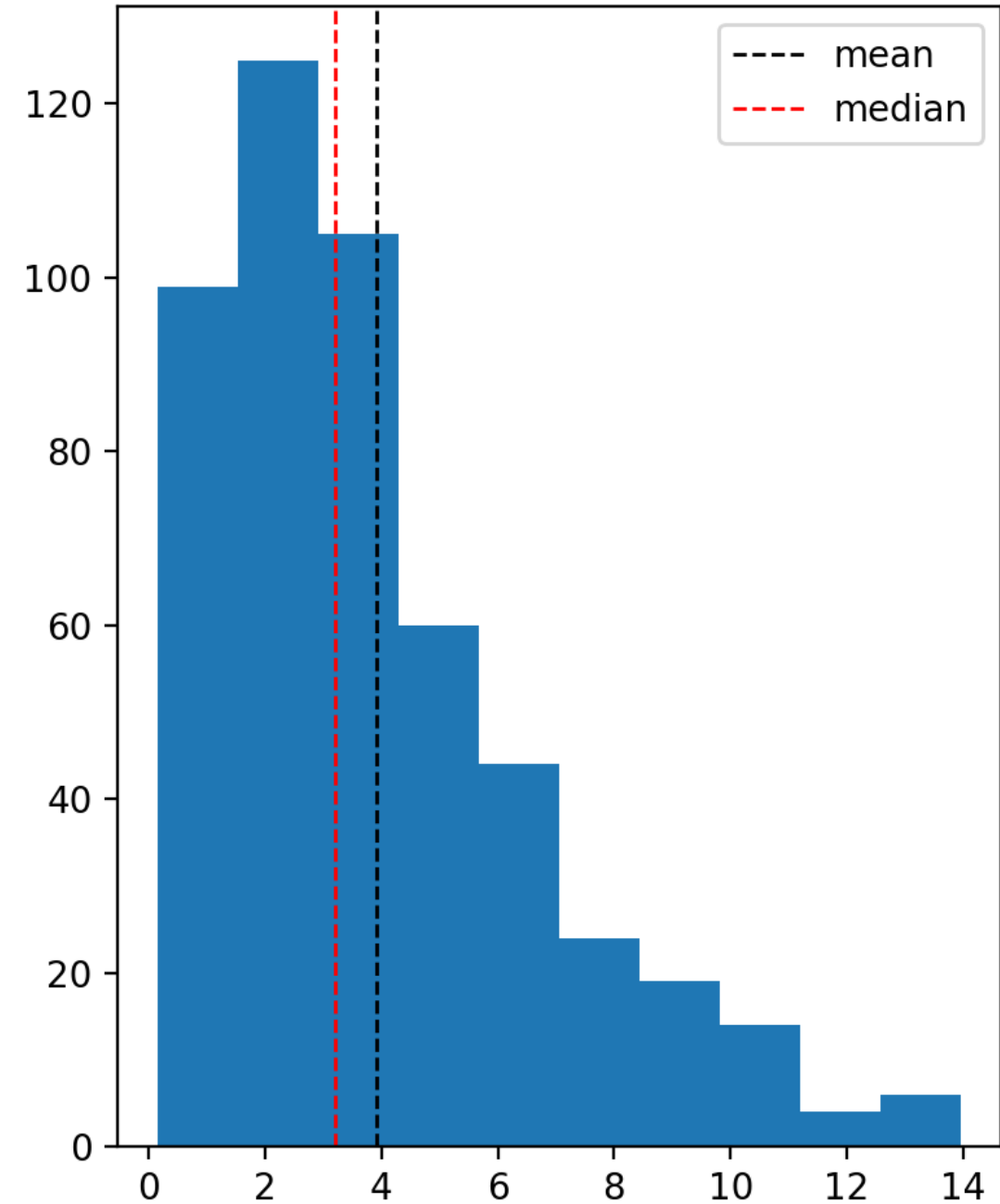
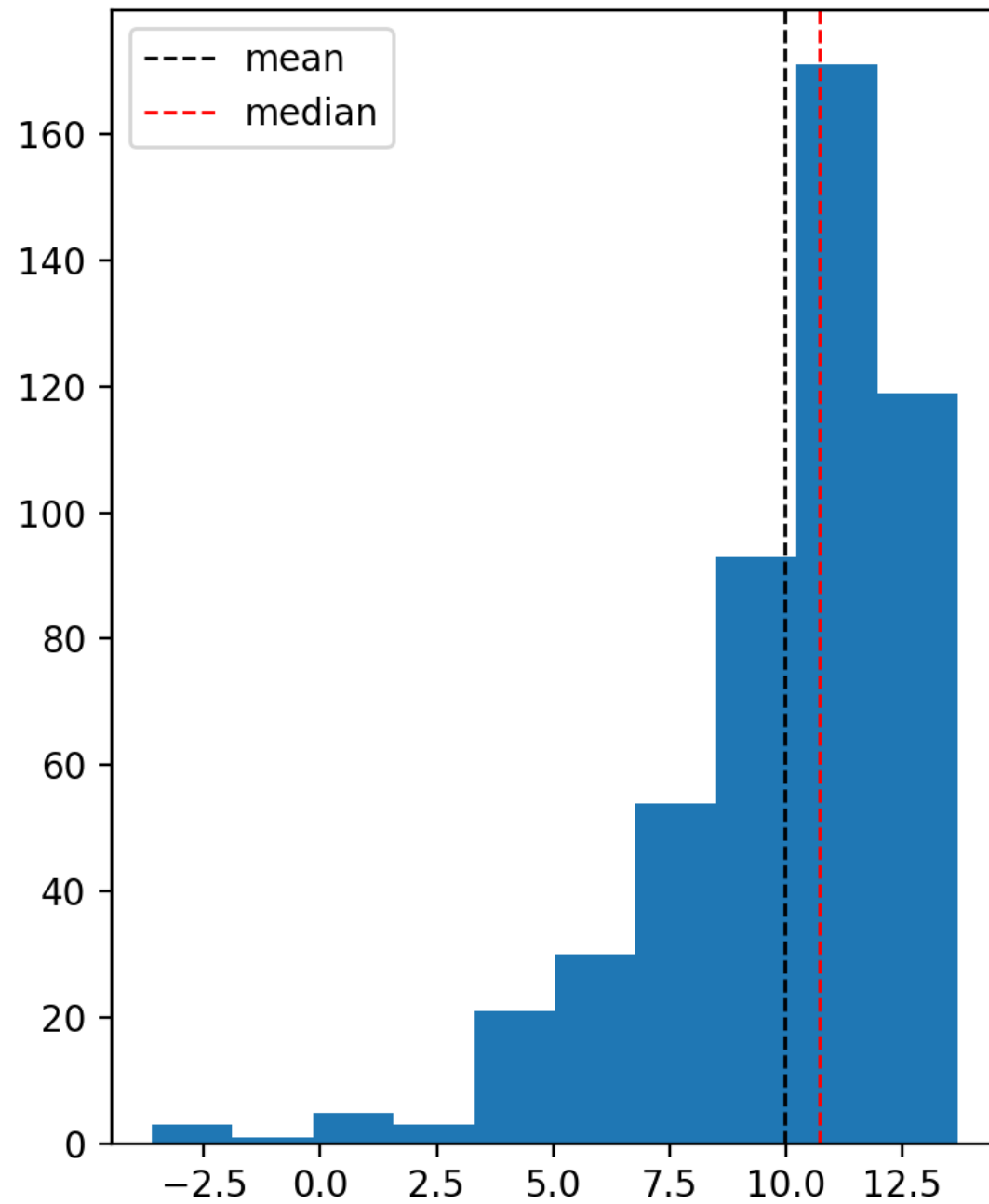
## Left-skewed



## Right-skewed

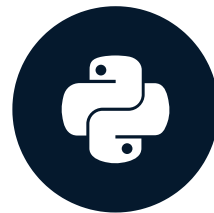


# Which measure to use?



# Measures of spread

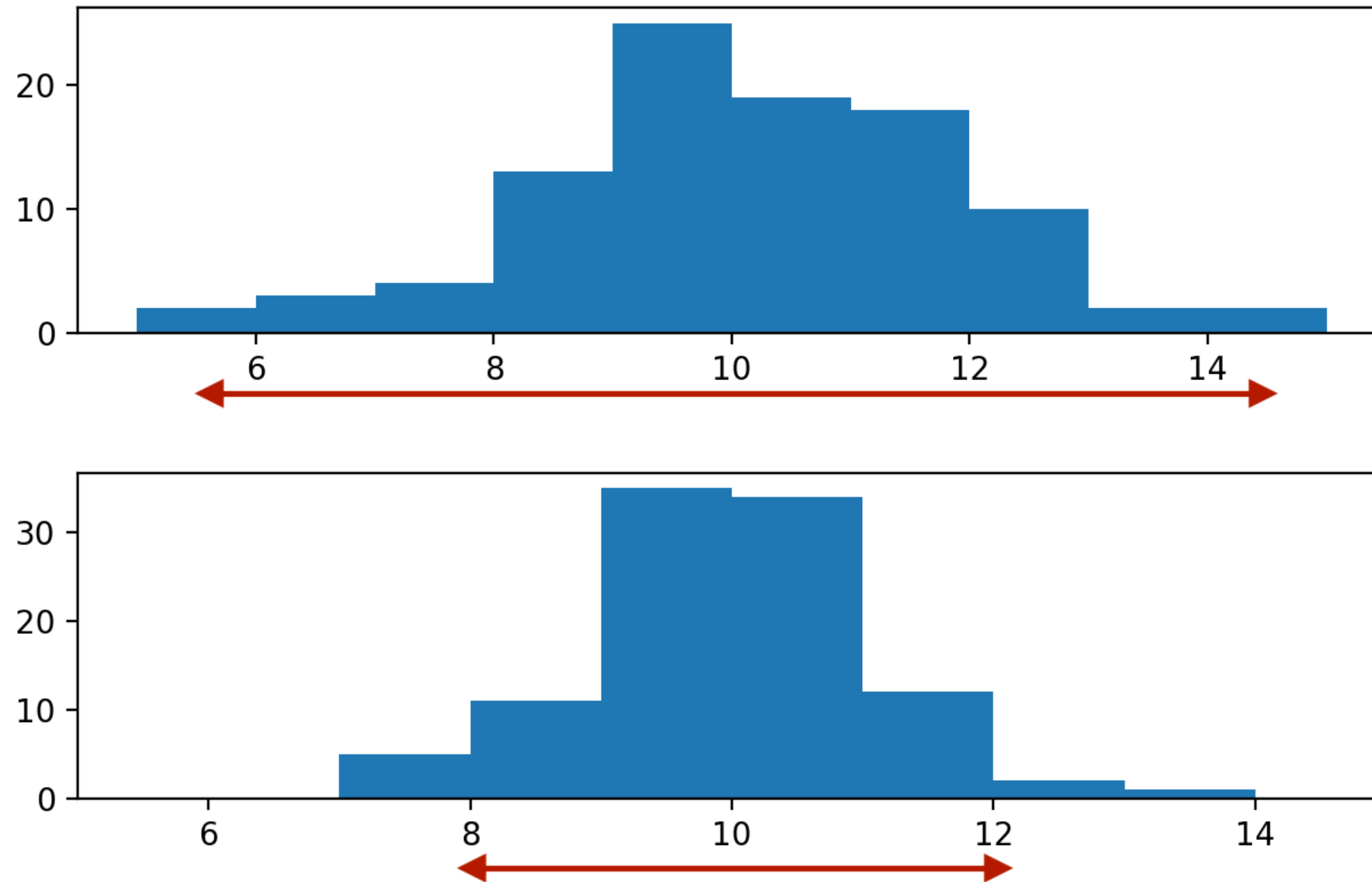
INTRODUCTION TO STATISTICS IN PYTHON



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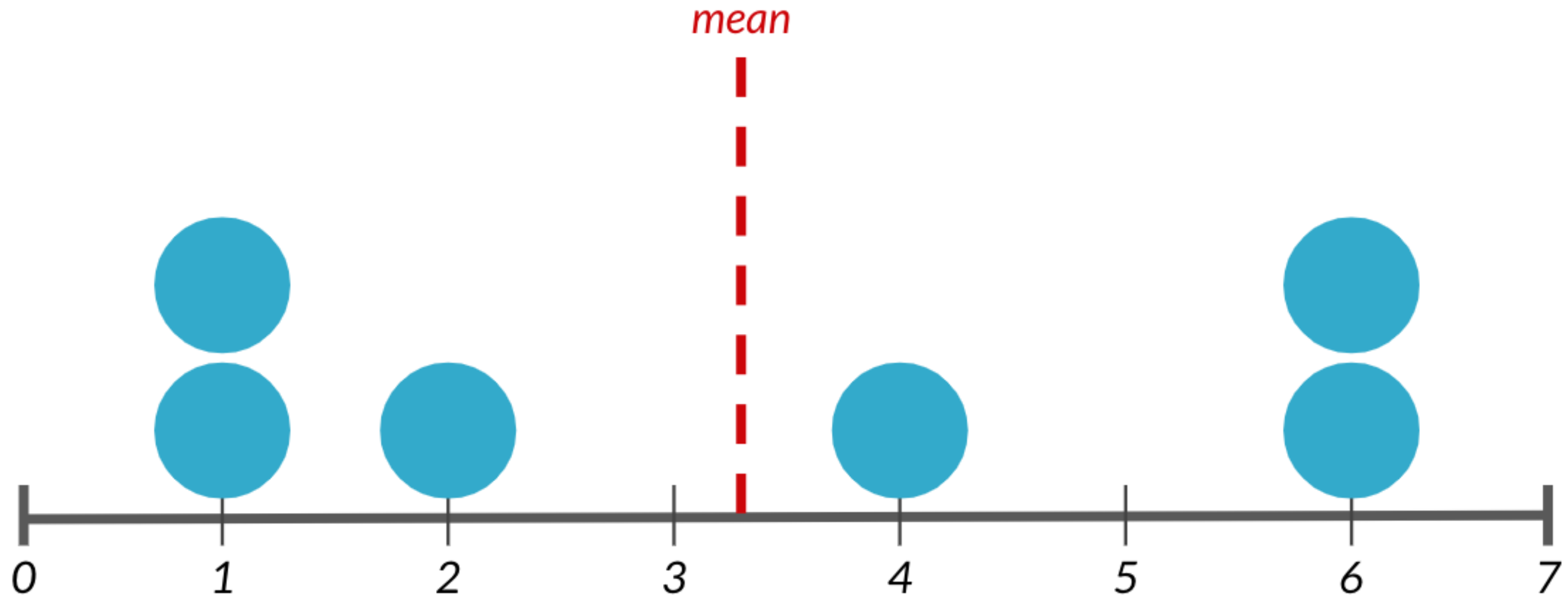
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# What is spread?



# Variance

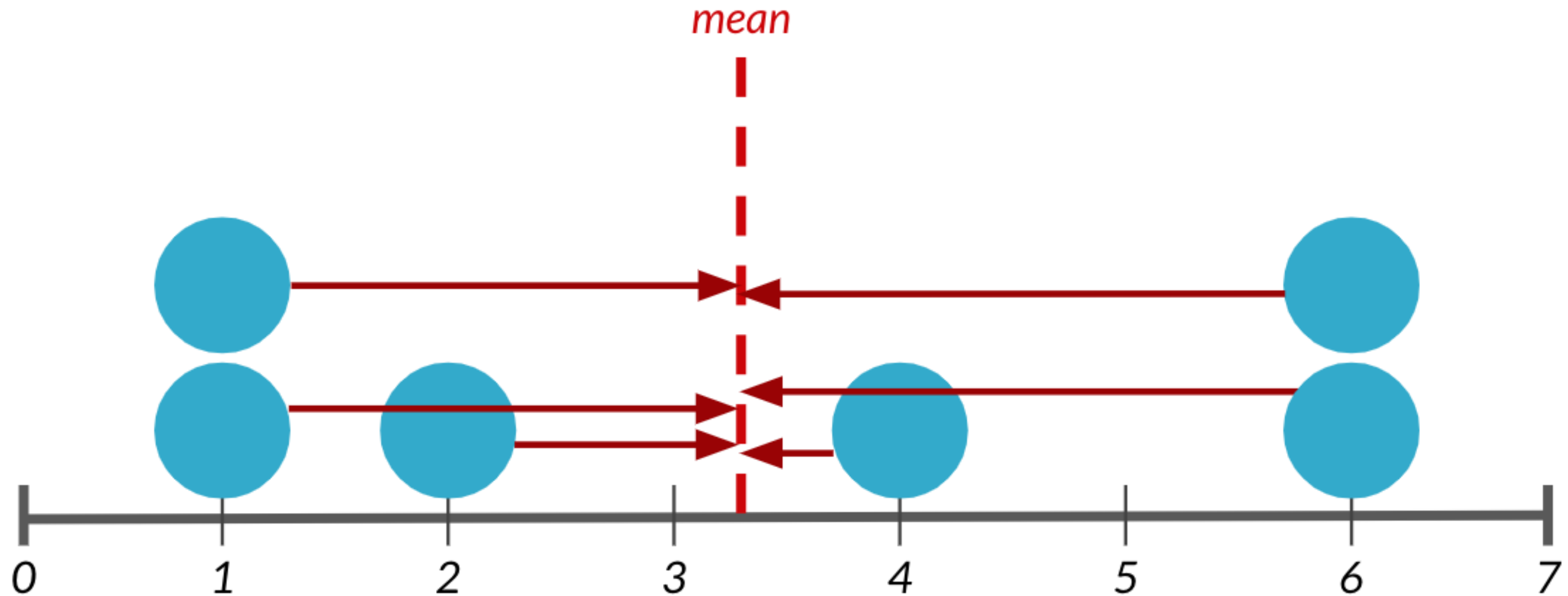
*Average distance from each data point to the data's mean*





# Variance

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



# Calculating variance

## 1. Subtract mean from each data point

```
dists = msleep['sleep_total'] -  
        np.mean(msleep['sleep_total'])  
print(dists)
```

```
0    1.666265  
1    6.566265  
2    3.966265  
3    4.466265  
4   -6.433735  
...
```

## 2. Square each distance

```
sq_dists = dists ** 2  
print(sq_dists)
```

```
0    2.776439  
1   43.115837  
2   15.731259  
3   19.947524  
4   41.392945  
...
```

# Calculating variance

## 3. Sum squared distances

```
sum_sq_dists = np.sum(sq_dists)
print(sum_sq_dists)
```

```
1624.065542
```

## 4. Divide by number of data points - 1

```
variance = sum_sq_dists / (83 - 1)
print(variance)
```

```
19.805677
```

Use `np.var()`

```
np.var(msleep['sleep_total'], ddof=1)
```

```
19.805677
```

*Without `ddof=1`, **population variance** is calculated instead of **sample variance**:*

```
np.var(msleep['sleep_total'])
```

```
19.567055
```

# Standard deviation

```
np.sqrt(np.var(msleep['sleep_total'], ddof=1))
```

```
4.450357
```

```
np.std(msleep['sleep_total'], ddof=1)
```

```
4.450357
```

# Mean absolute deviation

```
dists = msleep['sleep_total'] - mean(msleep$sleep_total)
np.mean(np.abs(dists))
```

```
3.566701
```

## Standard deviation vs. mean absolute deviation

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

# Quantiles

```
np.quantile(msleep['sleep_total'], 0.5)
```

```
10.1
```

*0.5 quantile = median*

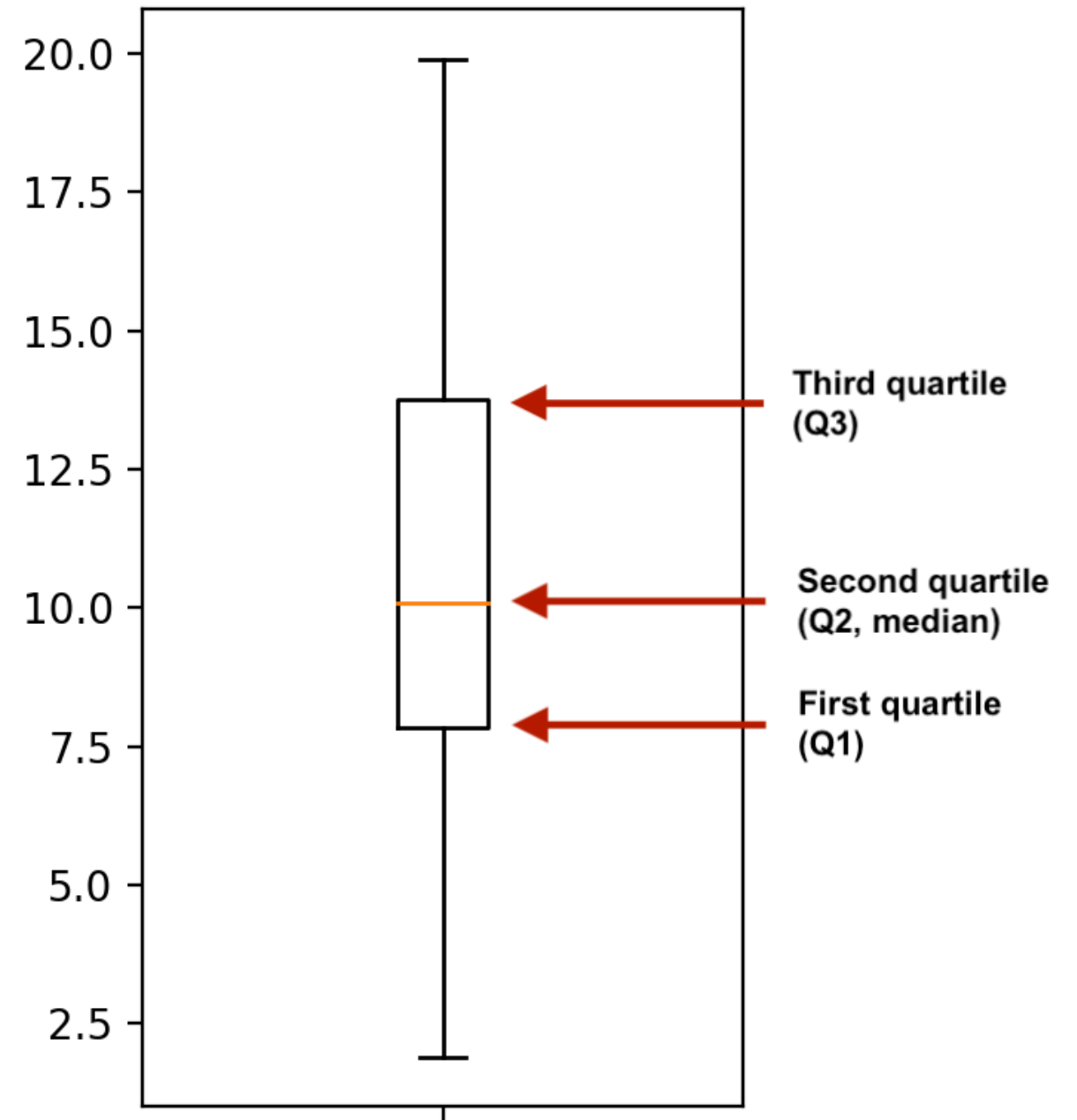
***Quartiles:***

```
np.quantile(msleep['sleep_total'], [0, 0.25, 0.5, 0.75, 1])
```

```
array([ 1.9 ,  7.85, 10.1 , 13.75, 19.9 ])
```

# Boxplots use quartiles

```
import matplotlib.pyplot as plt
plt.boxplot(msleep['sleep_total'])
plt.show()
```



# Quantiles using np.linspace()

```
np.quantile(msleep['sleep_total'], [0, 0.2, 0.4, 0.6, 0.8, 1])
```

```
array([ 1.9 ,  6.24,  9.48, 11.14, 14.4 , 19.9 ])
```

```
np.linspace(start, stop, num)
```

```
np.quantile(msleep['sleep_total'], np.linspace(0, 1, 5))
```

```
array([ 1.9 ,  7.85, 10.1 , 13.75, 19.9 ])
```



# Interquartile range (IQR)

*Height of the box in a boxplot*

```
np.quantile(msleep['sleep_total'], 0.75) - np.quantile(msleep['sleep_total'], 0.25)
```

```
5.9
```

```
from scipy.stats import iqr  
iqr(msleep['sleep_total'])
```

```
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:

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

# Finding outliers

```
from scipy.stats import iqr
iqr = iqr(msleep['bodywt'])
lower_threshold = np.quantile(msleep['bodywt'], 0.25) - 1.5 * iqr
upper_threshold = np.quantile(msleep['bodywt'], 0.75) + 1.5 * iqr
```

```
msleep[(msleep['bodywt'] < lower_threshold) | (msleep['bodywt'] > upper_threshold)]
```

```
      name  vore  sleep_total  bodywt
4      Cow  herbi           4.0  600.000
20  Asian elephant  herbi           3.9 2547.000
22      Horse  herbi           2.9  521.000
...
```

# All in one go

```
msleep['bodywt'].describe()
```

```
count      83.000000  
mean      166.136349  
std       786.839732  
min         0.005000  
25%        0.174000  
50%        1.670000  
75%       41.750000  
max      6654.000000  
Name: bodywt, dtype: float64
```