# [IGP 484] Quantitative Biology: Data Analysis for Life Scientists

Dr. Katie Evans

🕒 Tu/Th 1:30-3:00, Hughes Auditorium

💻 github.com/katiesevans/IGP_biostatistics

biostats-484

🕒 Tu/Th 1:30-3:00, Hughes Auditorium*

💻 github.com/katiesevans/IGP_biostatistics

- Weekly homework assignments (40%)
- Class participation (5%)
- Midterm exam (15%)
- Final exam (15%)
- Final project (25%)

***9/23 and 11/11 — Class will meet in Daniel Hale Williams, McGaw 2-320***

🕒 Tu/Th 1:30-3:00, Hughes Auditorium

💻 github.com/katiesevans/IGP_biostatistics

- **Homework assignments**
  - Must be completed using R
  - Make sure to show ALL your work for credit
  - Submitted electronically as PDF
  - Due Tuesdays @ 5pm*

- **Final project**
  - Choose a dataset (rotation, internet, old publication…)
  - Perform a statistical analysis
  - Write up a report with conclusions
  - *More to come in second half of class, but start thinking about ideas!*

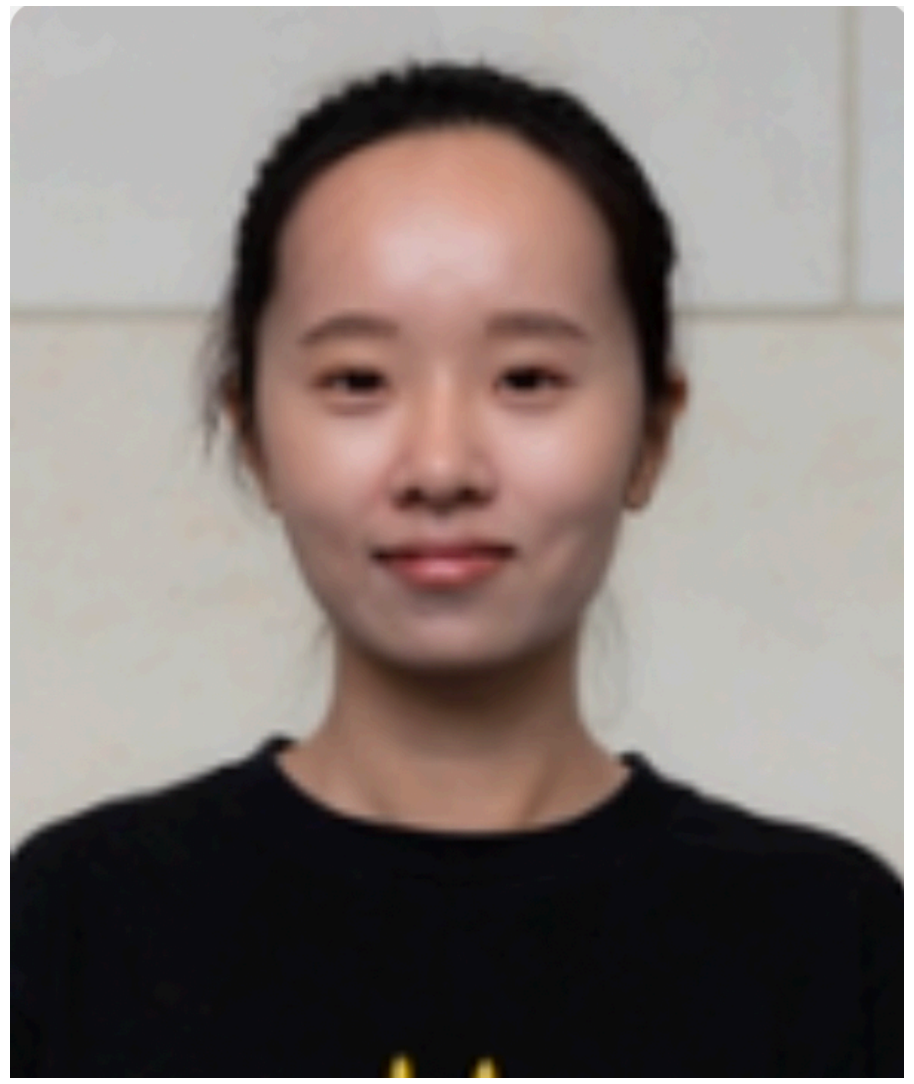
**Unless stated otherwise*

# Meet the class TA's!

**Saya**

**Jiexi**


**Sam**



**Yidan**

🕒 **TA office hours:** Tuesday 3-4 (TBD); Friday 1:30-2:30 (Zoom)

*(Or by appointment)*

Stats intro

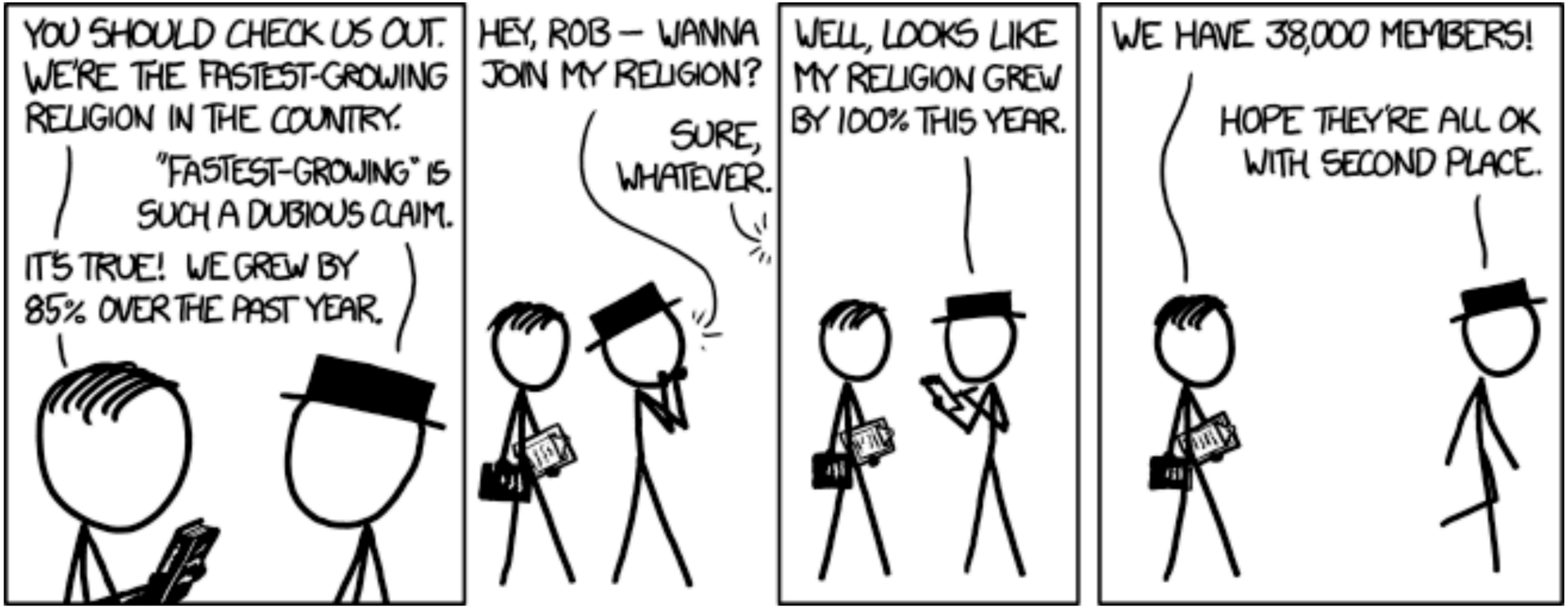
Hypothesis testing

| Date | Class | Lecture | Topics | Textbook Sections |
|---|---|---|---|---|
| September 21, 2021 | Lecture | Lecture 1: Introduction | Class intro, what is "statistics"?, displaying and summarizing data, getting started with R | 1.1-1.3, 2.1-2.7 |
| September 23, 2021 | Lecture | Lecture 2: Probability | notation, independence, conditional probability | 3.1-3.3 |
| September 28, 2021 | Lecture | Lecture 3: Probability (part 2) | conditional probability, Bayes theorem, practical implications | 3.3-3.5 |
| September 30, 2021 | Lecture | Lecture 4: Distributions | binomial and normal | 3.6, 4.1-4.3 |
| October 5, 2021 | Practicum | Practicum 1: Learning R | Data tidying with tidyverse, plotting with ggplot2, thinking like a data scientist, Rmarkdown | NA |
| October 7, 2021 | Lecture | Lecture 5: Distributions (part 2) | Central Limit Theorem, sampling | 5.1-5.4 |
| October 12, 2021 | Lecture | Lecture 6: Estimation, testing, and p-values | estimation, testing, p-values | 4.4, 6.1-6.5 |
| October 14, 2021 | Lecture | Lecture 7: One-sample t-tests | estimating and testing means | 6.6-6.7, 7.2-7.6, 7.8 |
| October 19, 2021 | Lecture | Lecture 8: Two-sample comparisons | unpaired t-tests, paired t-tests, power | 7.2-7.6, 8.2-8.3, 7.7 |
| October 21, 2021 | Lecture | Lecture 9: Nonparametric alternatives | permutation, Wilcoxin/Mann-Whitney, signed rank | 7.1, 7.10, 8.4-8.5 |
| October 26, 2021 | Review | Q&A: Project discussion and Midterm review | Bring your questions! | Ch. 1-8 |
| October 28, 2021 | Exam | Midterm exam | NA | NA |

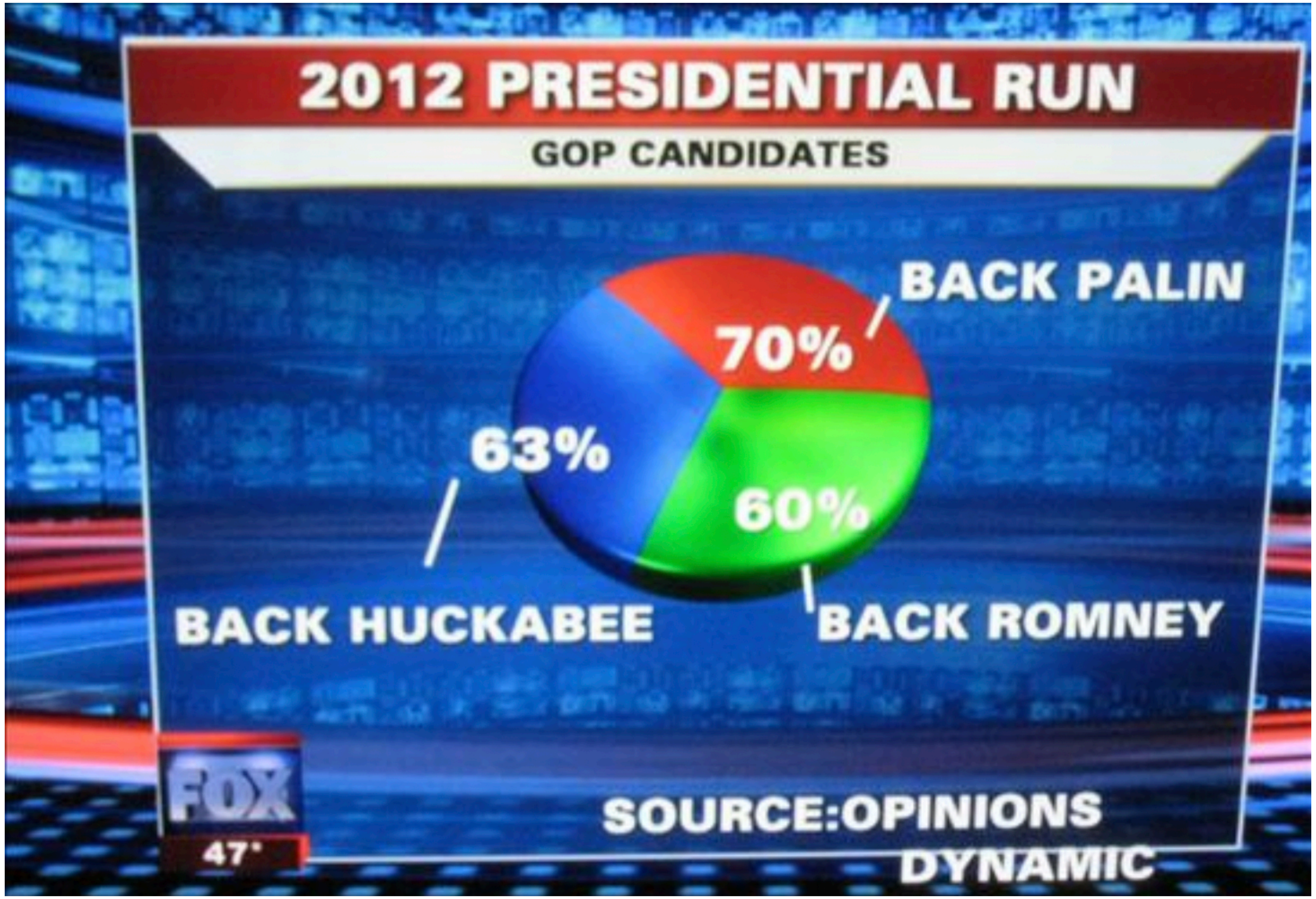
## Exploring Statistical Methods

| | | | | |
|---|---|---|---|---|
| November 2, 2021 | Lecture | Lecture 10: Multiple hypotheses | Urn models, "enrichment", Fischer's exact test | 10.4 |
| November 4, 2021 | | Practicum 2: Analyzing gene expression data with R | NA | NA |
| November 9, 2021 | Lecture | Lecture 11: Categorical data | contingency tables, chi-squared tests, relative risks and odds ratio | 9.1-9.2, 9.4, 10.1-10.3, 10.5-10.6, 10.9-10.10 |
| November 11, 2021 | Lecture | Lecture 12: Relationships in data | independence, covariance, and correlation | 12.1-12.2 |
| November 16, 2021 | Lecture | Lecture 13: Regression models | linear assumptions, interpretation, limitations, transformations | 12.4-12.6 |
| November 18, 2021 | Lecture | Lecture 14: Models with categorical covariates | indicator/"dummy" variables | 11.1-11.5 |
| November 23, 2021 | Lecture | Lecture 15: ANOVA | one-way ANOVA, two-way ANOVA | 11.7-11.8 |
| November 25, 2021 | | No class: Thanksgiving! | NA | NA |
| November 30, 2021 | Practicum | Practicum 3: Model fitting in R | NA | NA |
| December 2, 2021 | Review | Q&A: "Overflow" topics and final review | Cumulative! | NA |
| December 7, 2021 | Exam | Final Exam | Cumulative! | NA |

# Misleading statistics

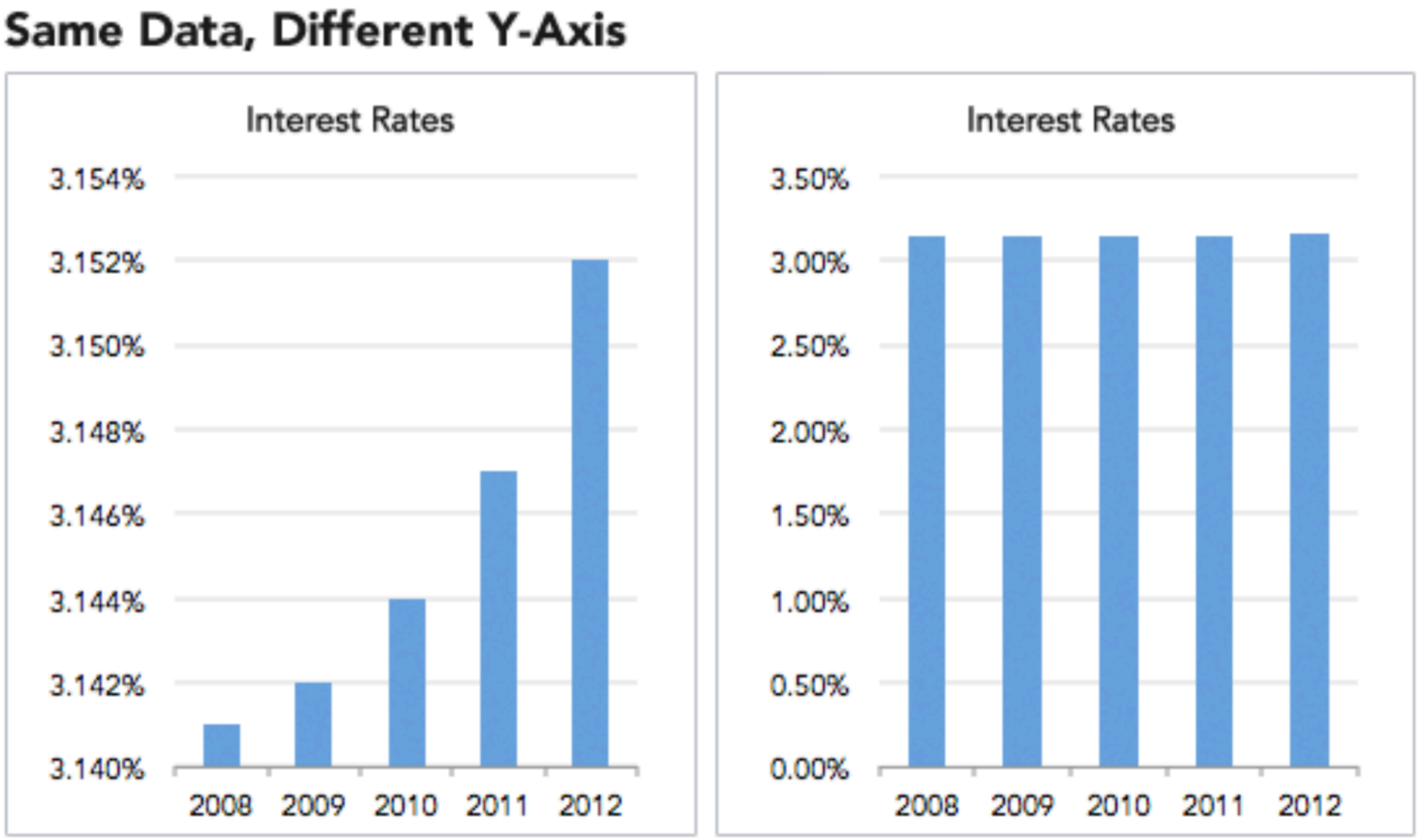


# Misleading statistics




https://www.statisticshowto.com/probability-and-statistics/descriptive-statistics/misleading-graphs/

# Misleading statistics



# Misleading statistics

# Reproducible research

The New York Times

*For Big-Data Scientists, 'Janitor Work' Is Key Hurdle to Insights*

By STEVE LOHR AUG. 17, 2014

Monica Rogati, Jawbone's vice president for data science, with Brian Wilt, a senior data scientist.
Peter DaSilva for The New York Times

FORTUNE

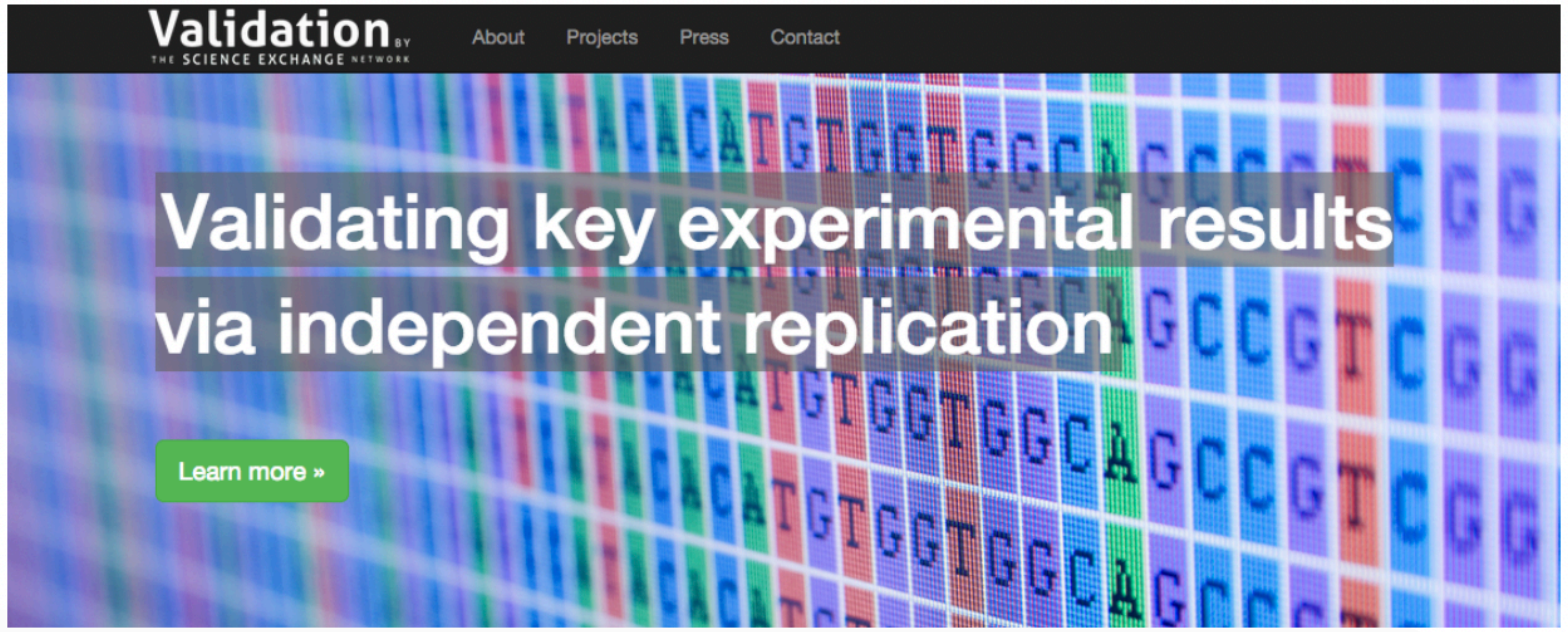
Big data's dirty problem

by Verne Kopytoff @vkopytoff JUNE 30, 2014, 10:58 AM EDT

PHYS.ORG

**Science is in a reproducibility crisis: How do we resolve it?**

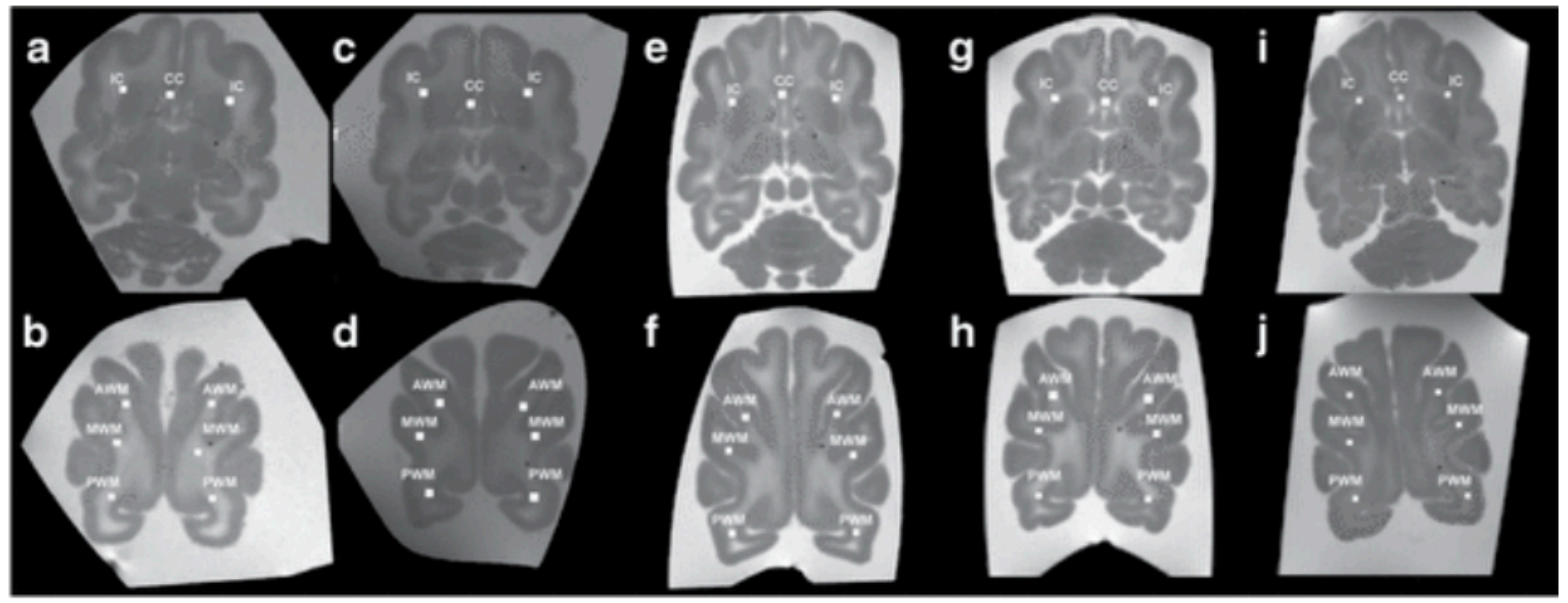
Sep 20, 2013 by Fiona Fidler & Ascelin Gordon, The Conversation



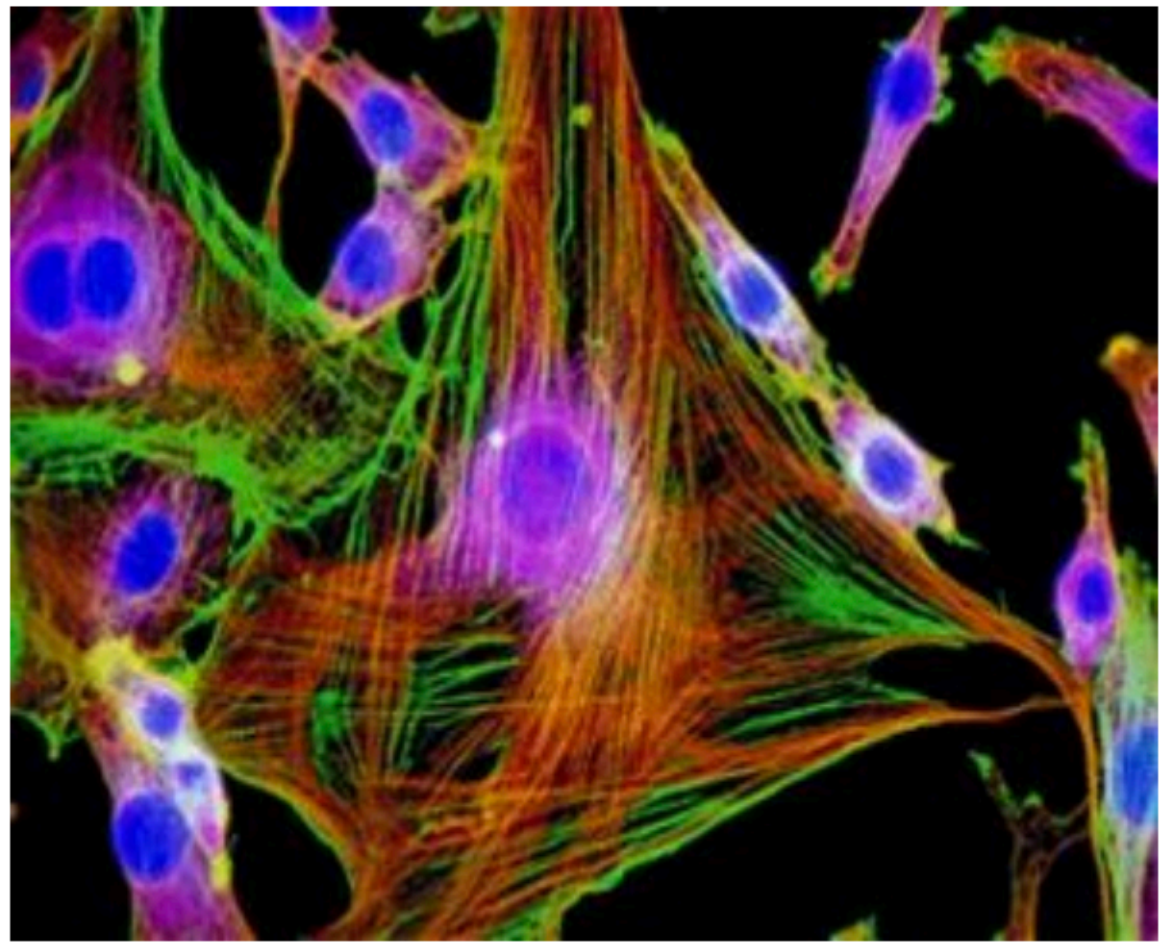

Reproducibility initiatives will invite increased scrutiny into data cleaning methods.

Cr: Erik Andersen

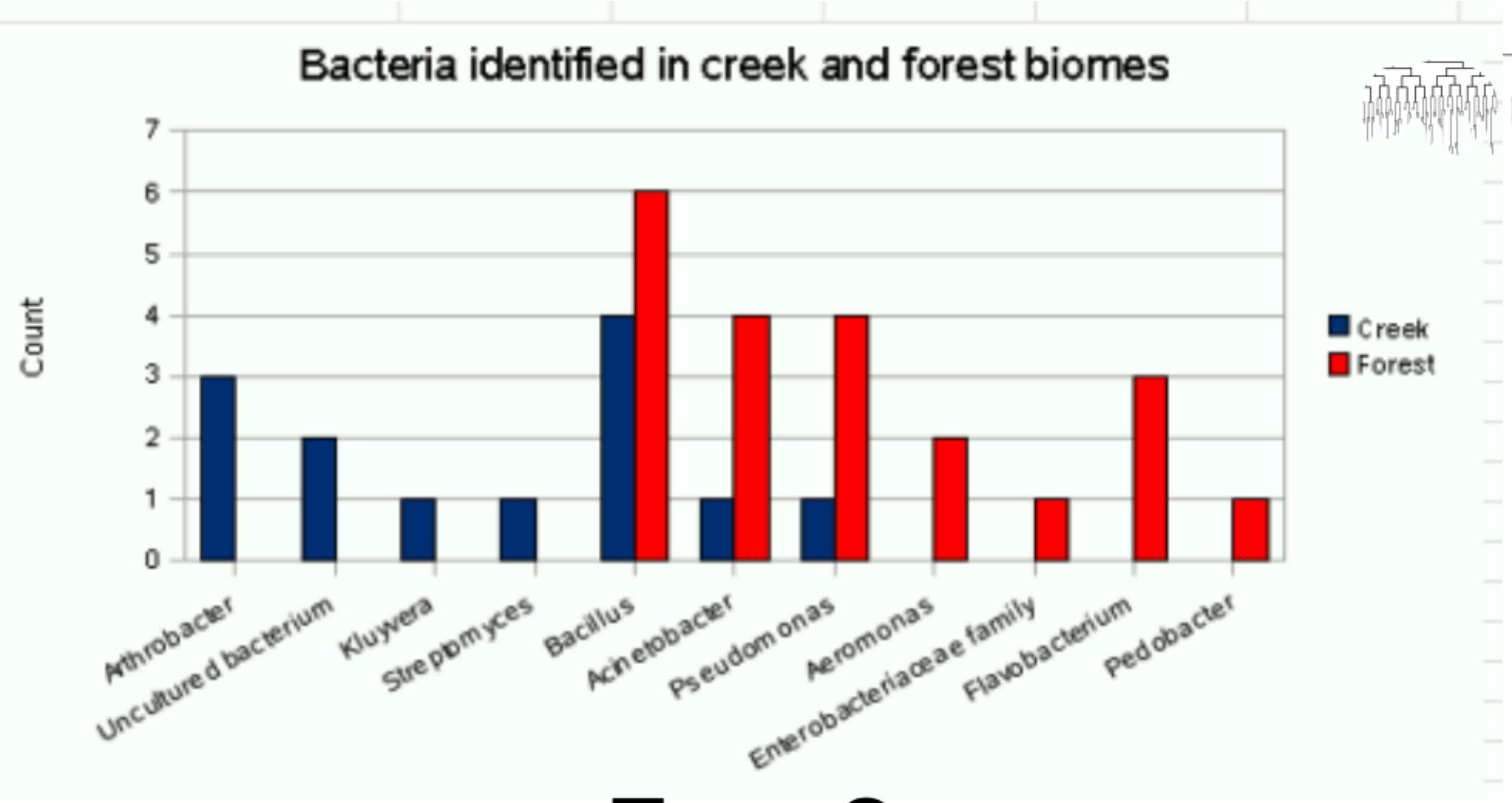
# Reproducible research



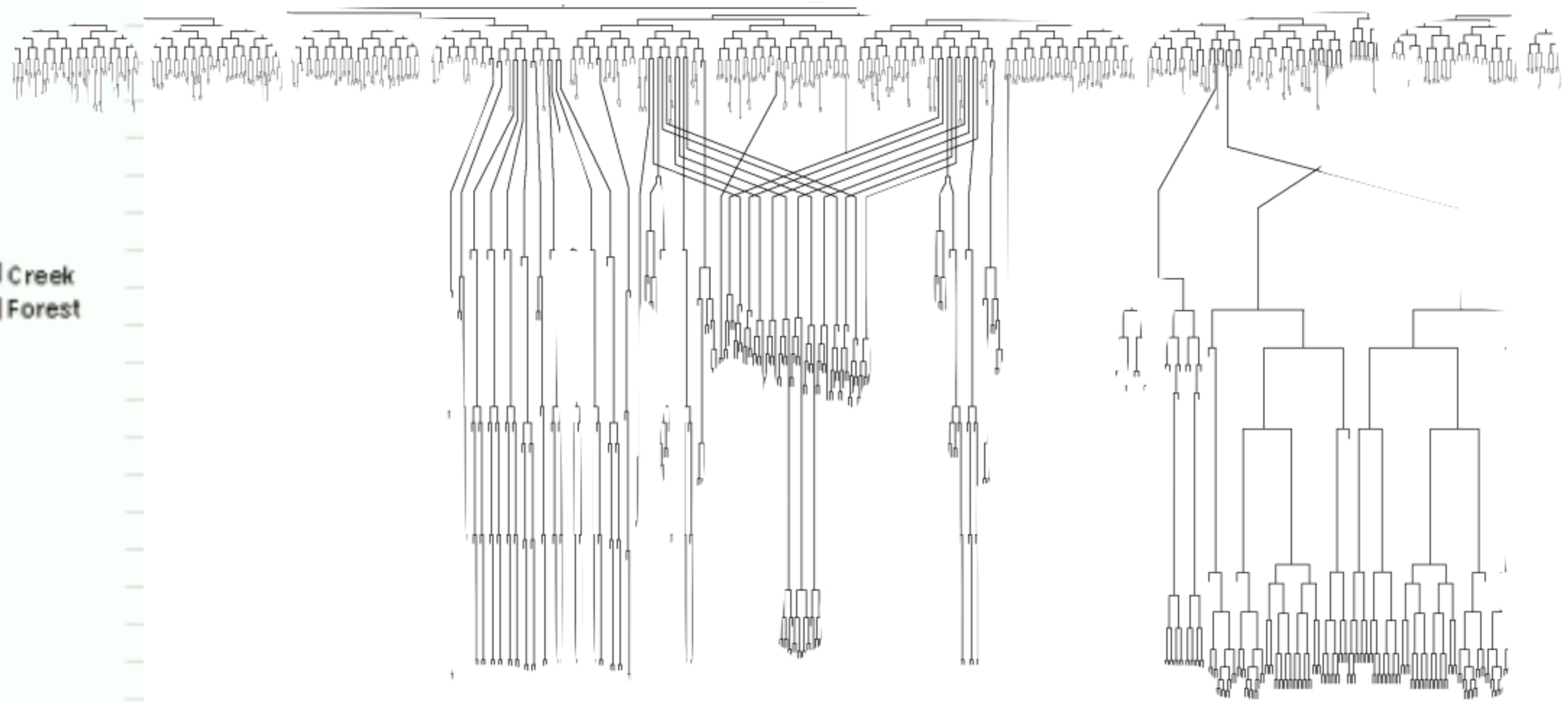

**Reproducibility?**



**Sampling?**



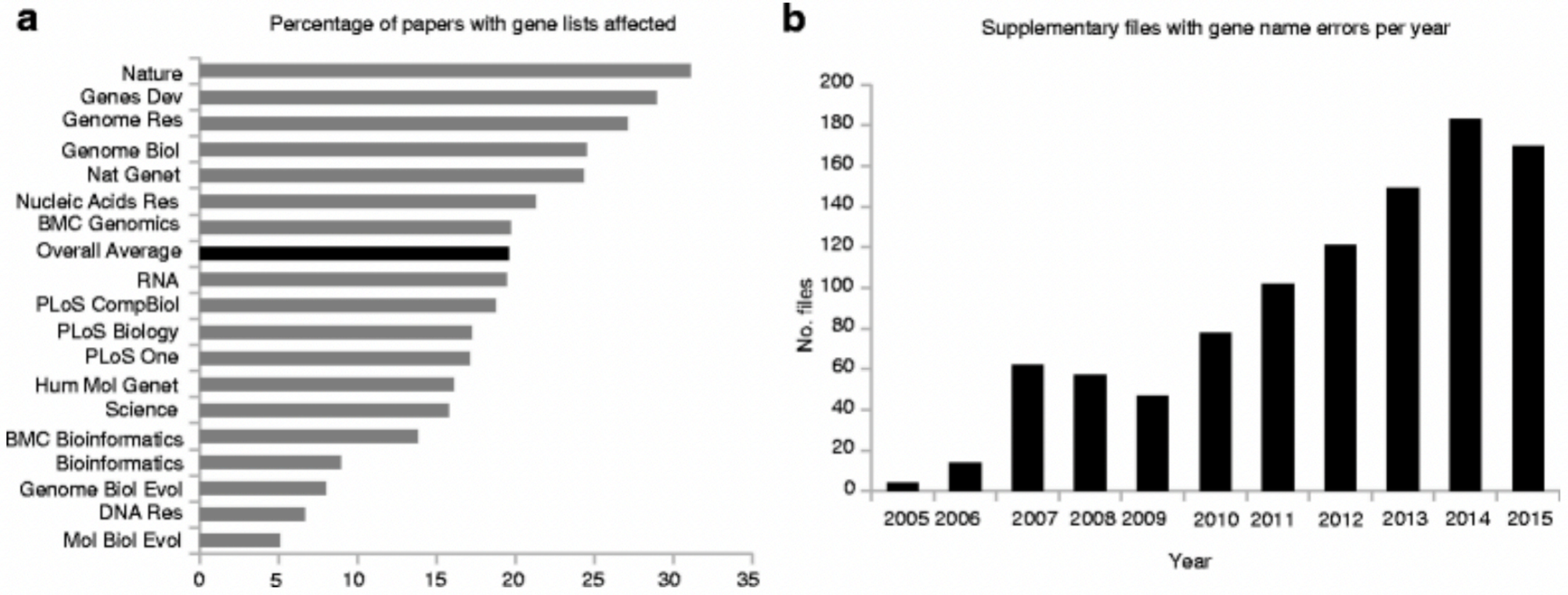

**Error?**



**Automation?**

Cr: Erik Andersen

# Reproducible research




Ziemann et al. Genome Biology (2016) 17:177

# What I hope you learn from this class:

- Biology is becoming more and more **quantitative**, so data analysis, reproducible research, and proper statistics skills are more important than ever

- Excel is great for some things, but data analysis should be **scripted** (in R or another language) in a way that any person could take your raw data and reproduce the figures in your manuscript

- Statistics can be slimy! (1) you must be **cautious and critical** when reviewing others' statistics and (2) you must be **transparent and honest** when providing your own analysis

# Science, variability, and statistics

***Response of sheep to anthrax***

| Response | Vaccinated | Not vaccinated |
|---|---|---|
| Died of anthrax | 0 | 24 |
| Survived | 24 | 0 |
| **Total** | **24 (100%)** | **0 (0%)** |

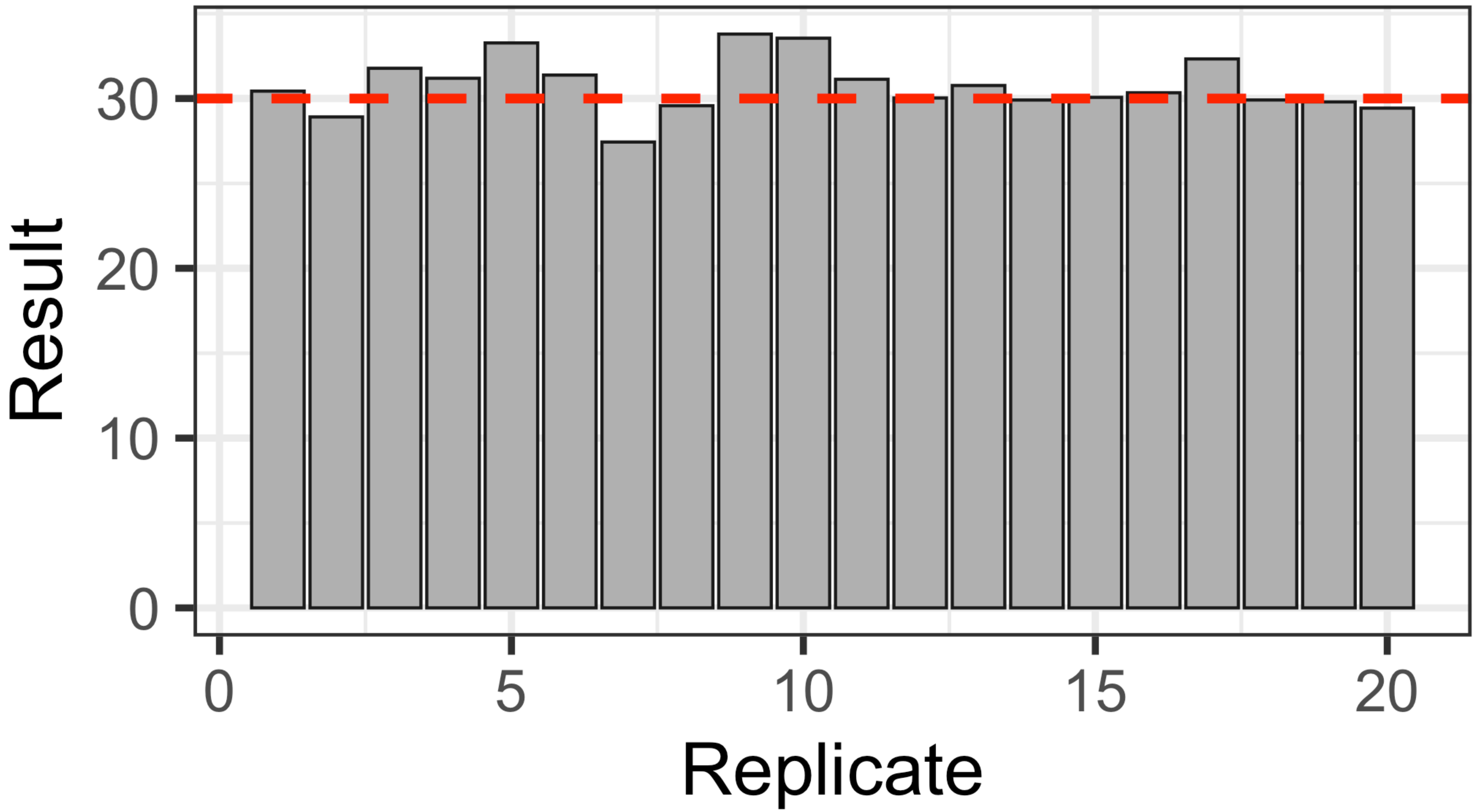
✔ ***Significant!***

***Incidence of liver tumors in mice***

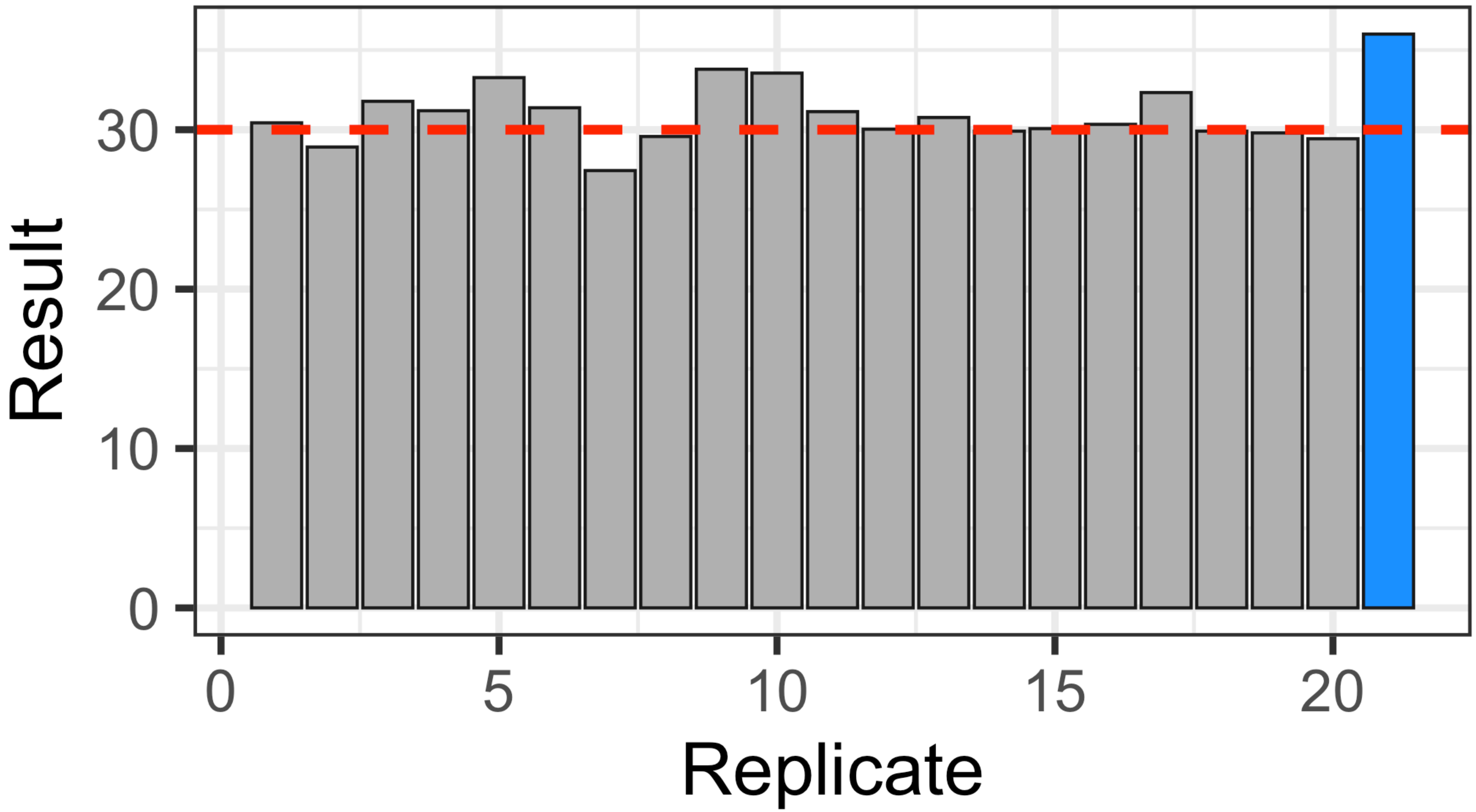
| Response | *E. coli* | Germ free |
|---|---|---|
| Liver tumors | 8 | 19 |
| No tumors | 5 | 30 |
| **Total** | **13 (62%)** | **49 (39%)** |

***Significant?***

# Science, variability, and statistics



# Science, variability, and statistics



# Science, variability, and statistics

***Response of sheep to anthrax***

| Response | Vaccinated | Not vaccinated |
|---|---|---|
| Died of anthrax | 0 | 3 ~~24~~ |
| Survived | 3 ~~24~~ | 0 |
| **Total** | **3 ~~24~~ (100%)** | **0 (0%)** |

***Significant?***

***Incidence of liver tumors in mice***

| Response | *E. coli* | Germ free |
|---|---|---|
| Liver tumors | 8 | 19 |
| No tumors | 5 | 30 |
| **Total** | **13 (62%)** | **49 (39%)** |

***Significant?***

# Observational studies v. experiments

**Collecting data from subjects as an observer, not manipulating conditions**

Survey about smoking habits and health

Performing a GWA/disease risk analysis on individuals with different genotypes

**Collecting data in a controlled environment where researchers impose the conditions**

Clinical trial for a new drug treatment

Knocking out a gene and then testing growth/survival with and without the gene

# Controls: an essential part of any study

**Collecting data from subjects as an observer, not manipulating conditions**

(Smokers & non-smokers)
Survey about smoking habits and health

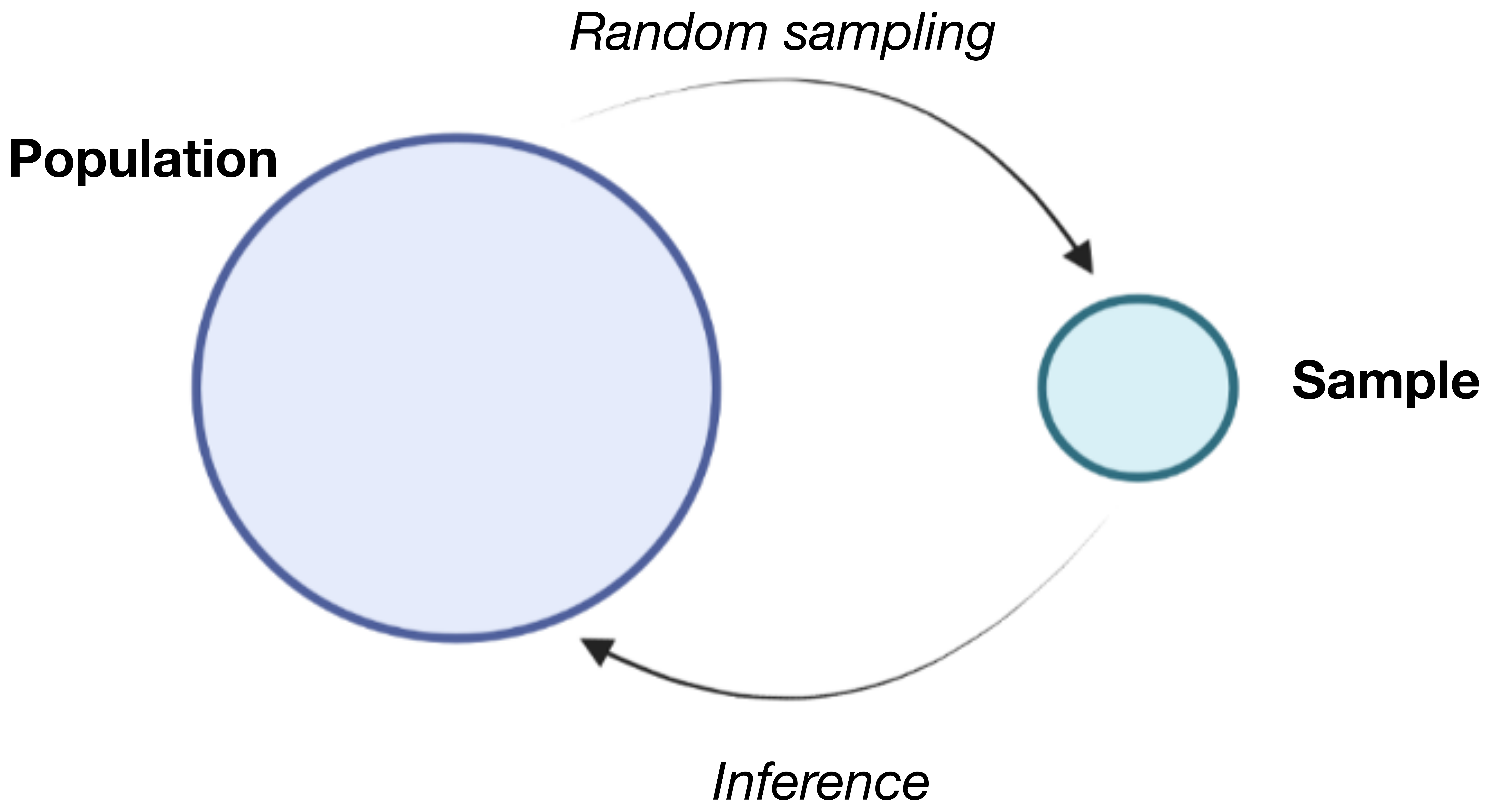
(Disease & non-disease)
Performing a GWA/disease risk analysis on individuals with different genotypes

**Collecting data in a controlled environment where researchers impose the conditions**

(Drug & placebo)
Clinical trial for a new drug treatment

(Knockout & wild-type)
Knocking out a gene and then testing growth/survival with and without the gene

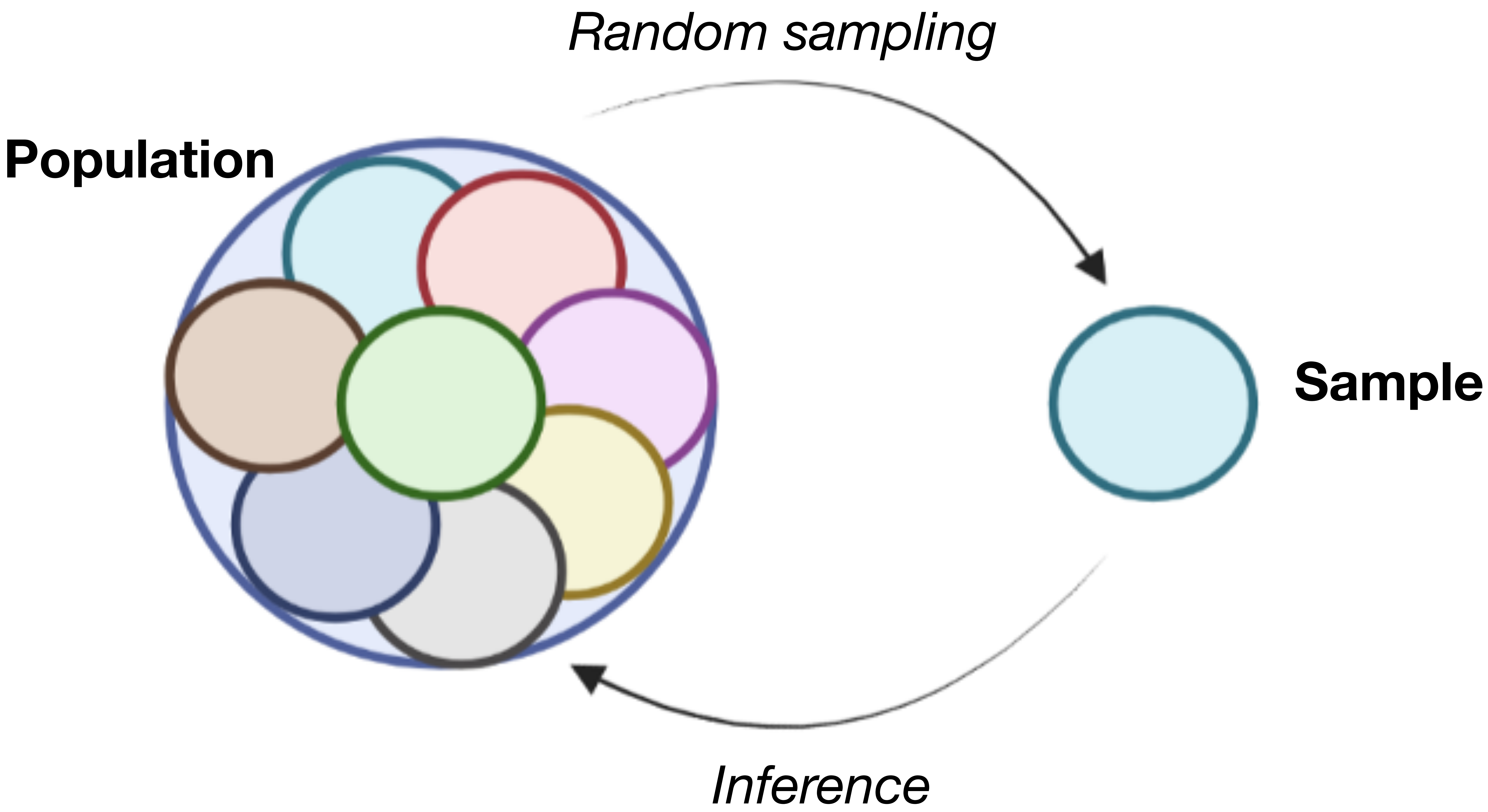
# Populations and sampling



# Simple random sample

- Every member of the population has the **same** chance of being included in the sample
- Members of the sample are chosen **independently** of each other
    - *Not dependent on which other members are chosen*
- How we gather our data has ***tremendous*** implications on our choice of analysis methods and validity of our studies
    - ***There is no replacement for good/clean data!!!***

# Populations and sampling



# Types of variables

## **Categorical**

Blood type (A, B, AB, O)

Fish sex (male, female)

Shape of pea (smooth, wrinkled)

Success in trial (Alive, dead)

## **Numeric**

Human height

Blood cholesterol of patient

Number of bacterial colonies

Length of DNA segment

# Types of variables

**Discrete**

## Categorical

Blood type (A, B, AB, O)

Fish sex (male, female)

Shape of pea (smooth, wrinkled)

Success in trial (Alive, dead)

**Continuous**

## Numeric

*Human height*

*Blood cholesterol of patient*

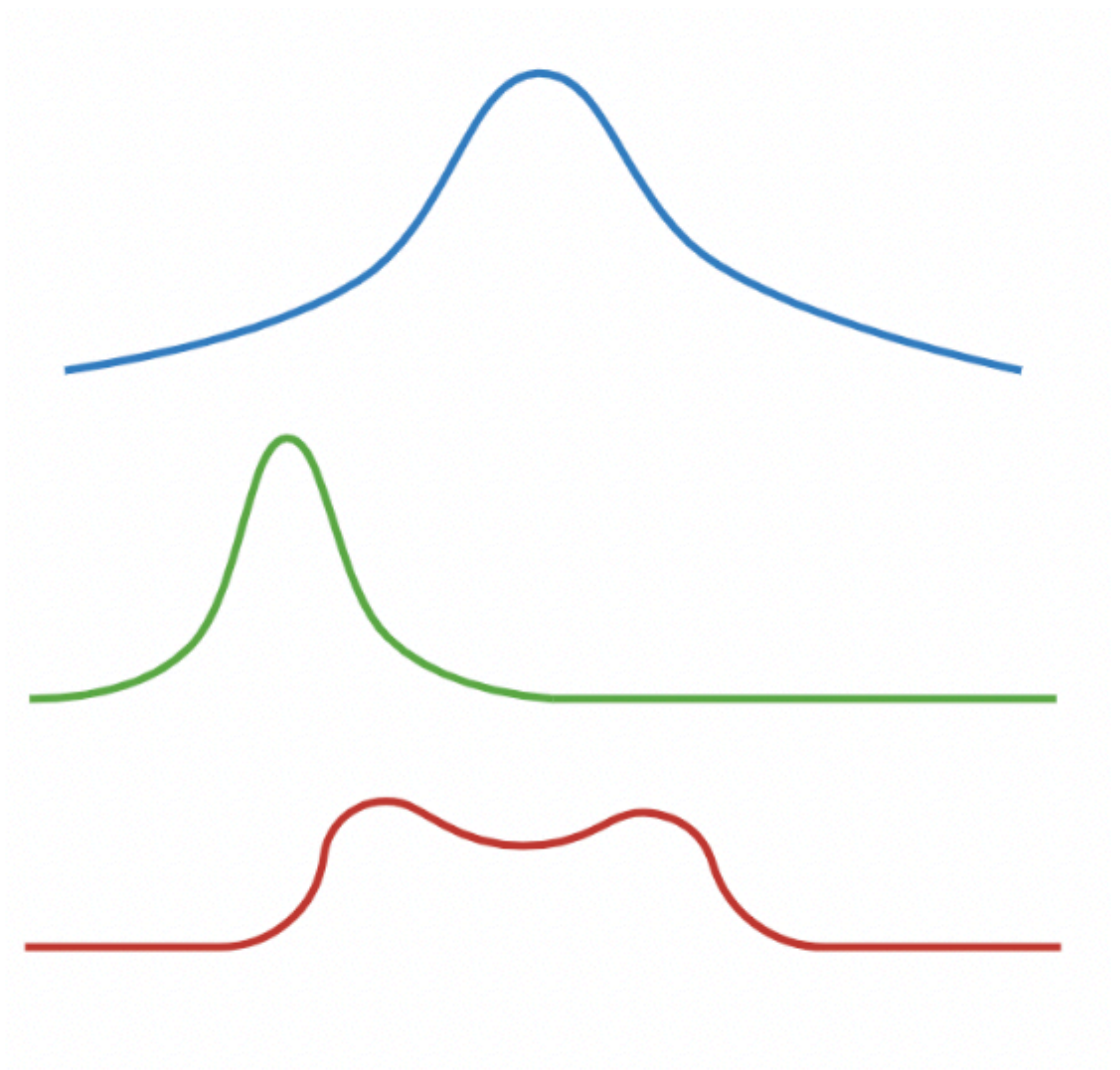
Number of bacterial colonies

Length of DNA segment

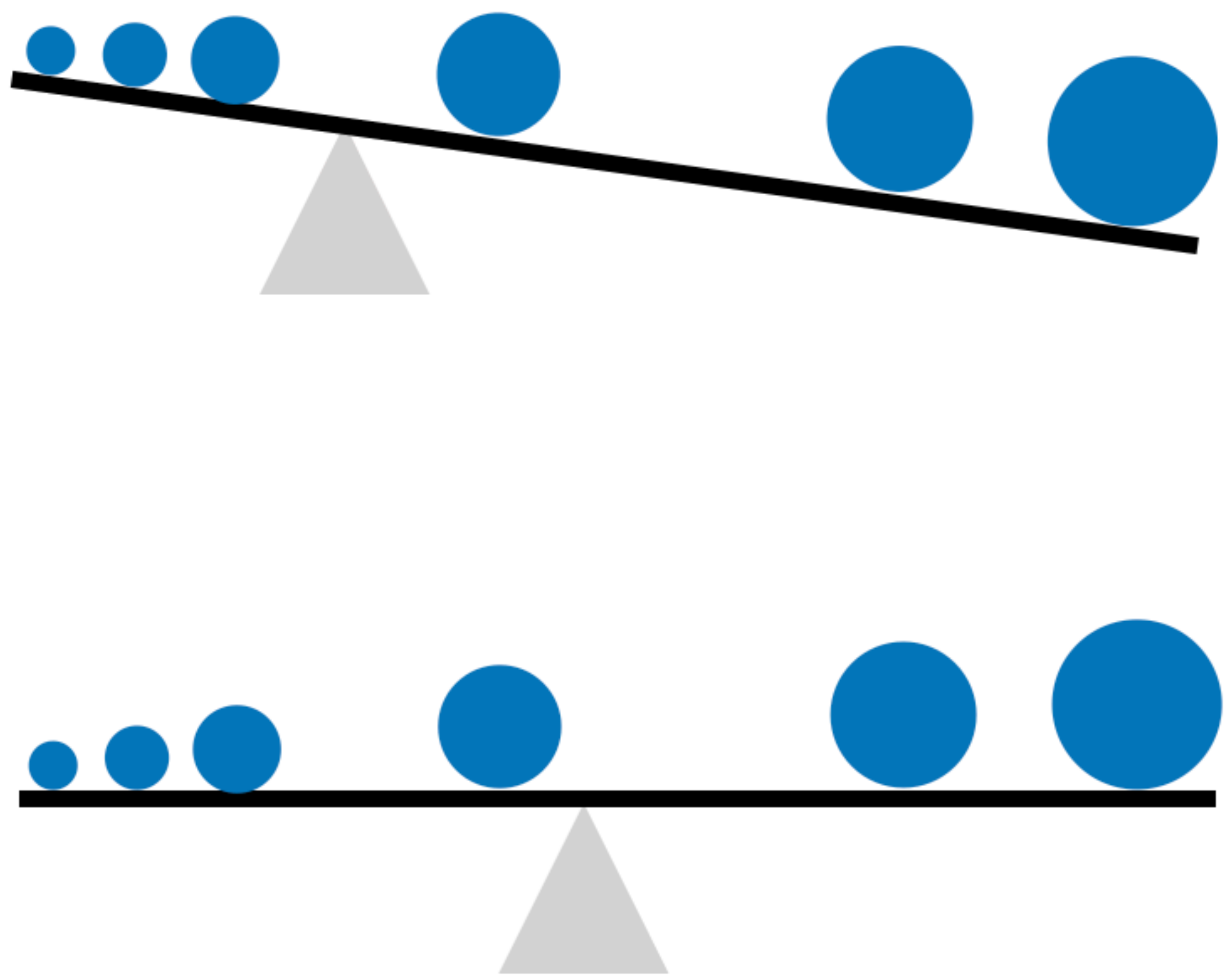
**Discrete**

# Data exploration and summarization

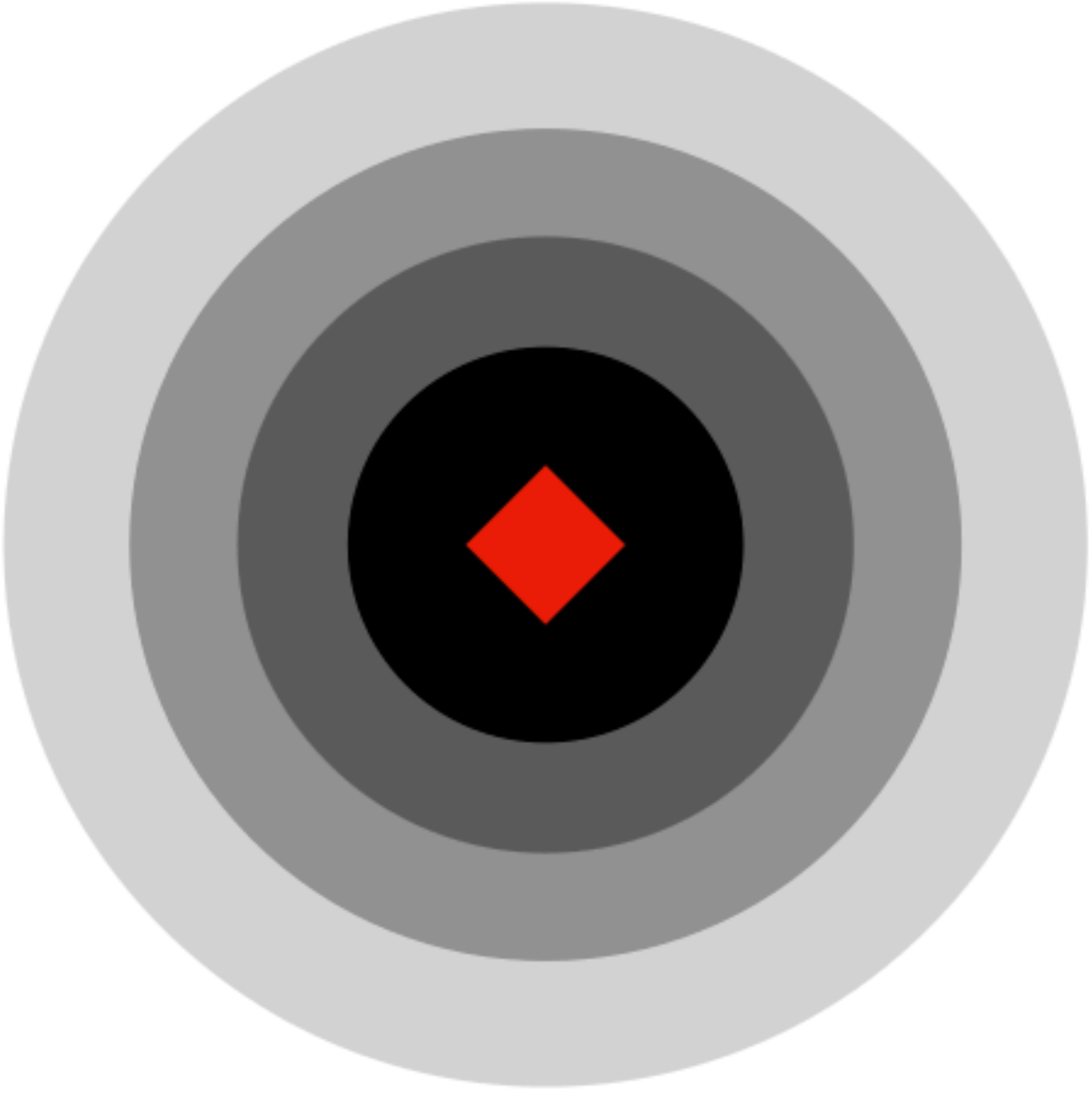
## Shape



## Center

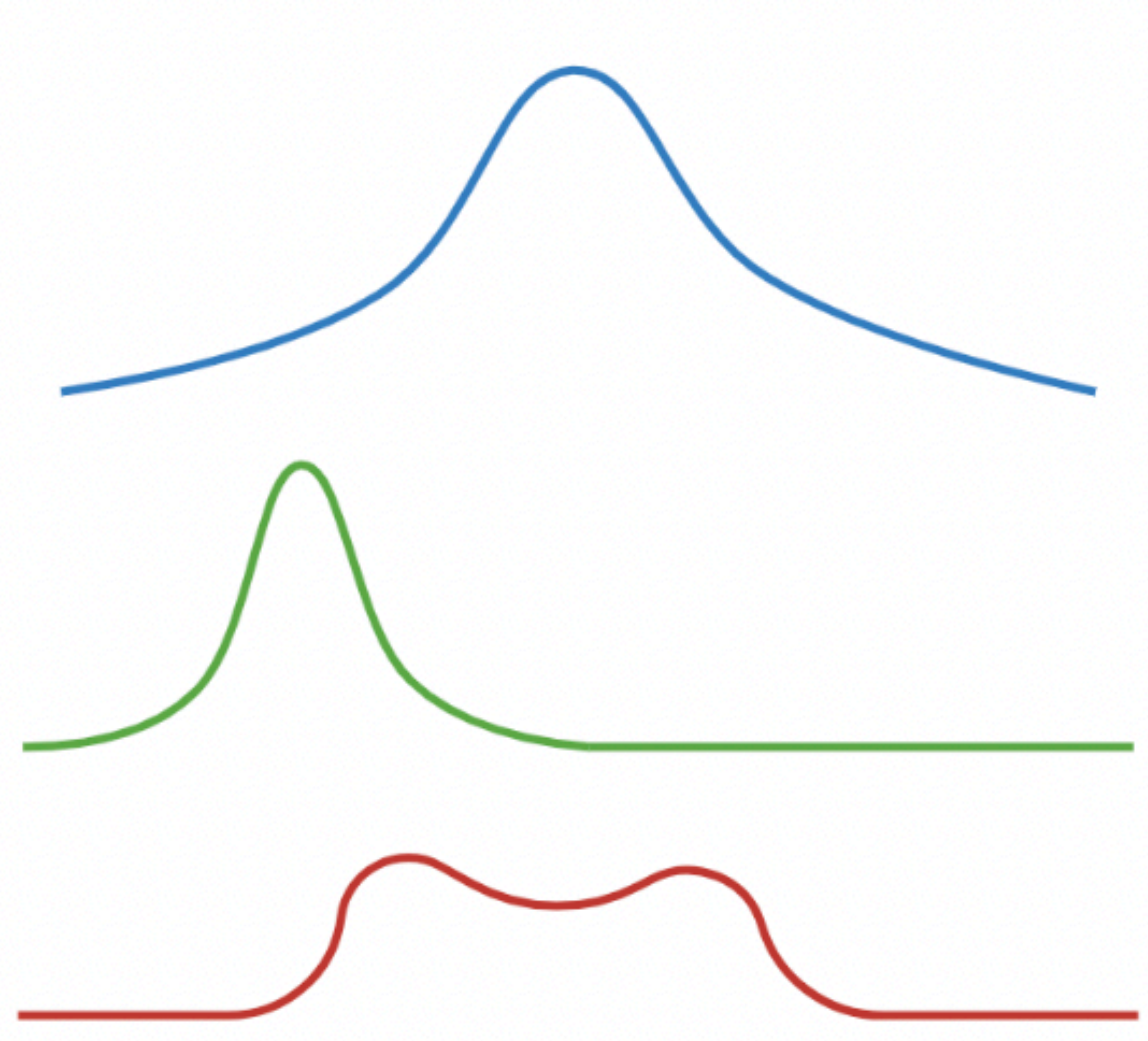


## Spread



# Data exploration and summarization

## Shape



## Center

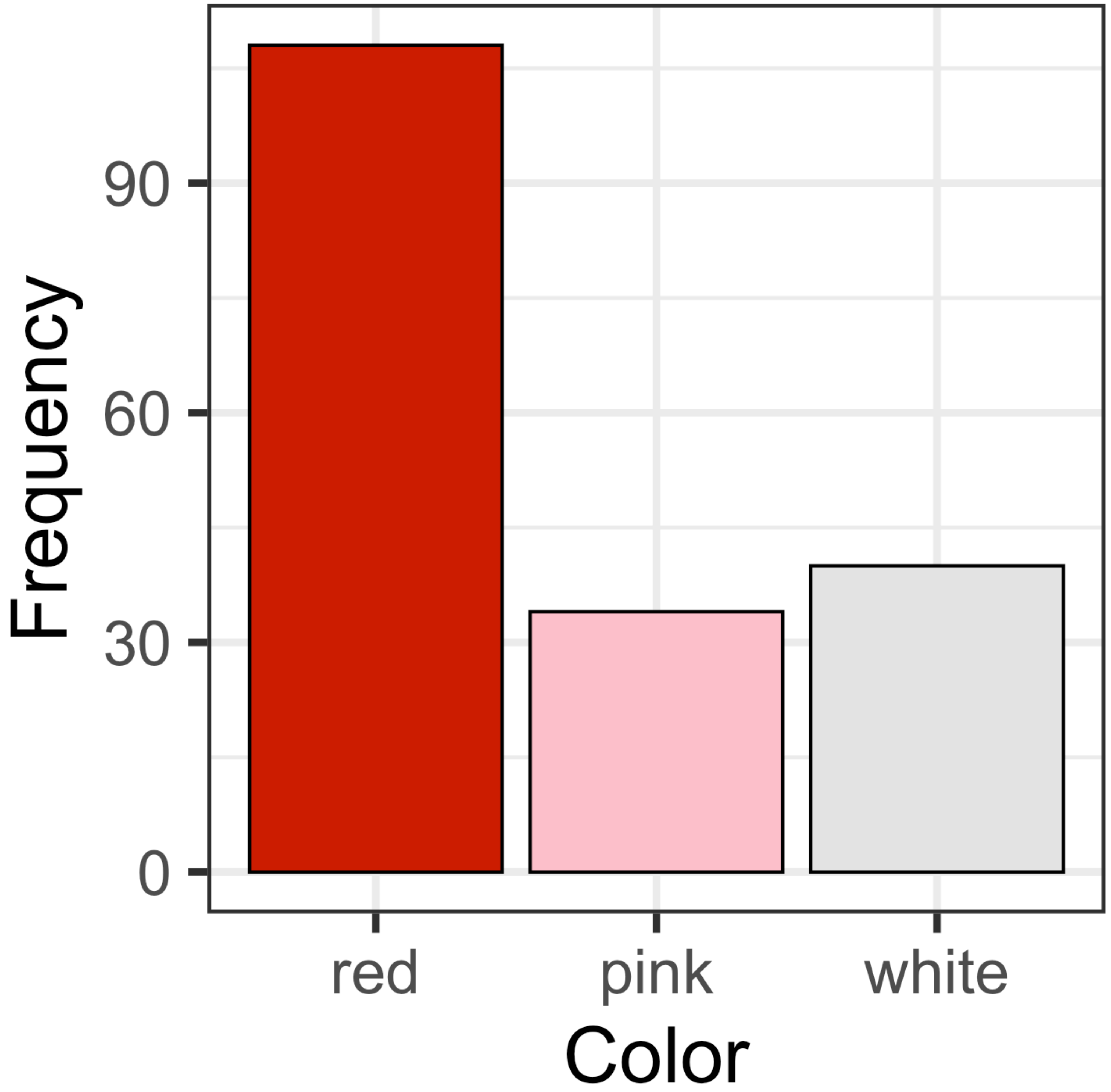


## Spread

# Visualizing frequency distributions

| Color | Frequency |
|---|---|
| Red | 108 |
| Pink | 34 |
| White | 40 |
| Total | 182 |

- Categorical data can be represented with a **bar chart**

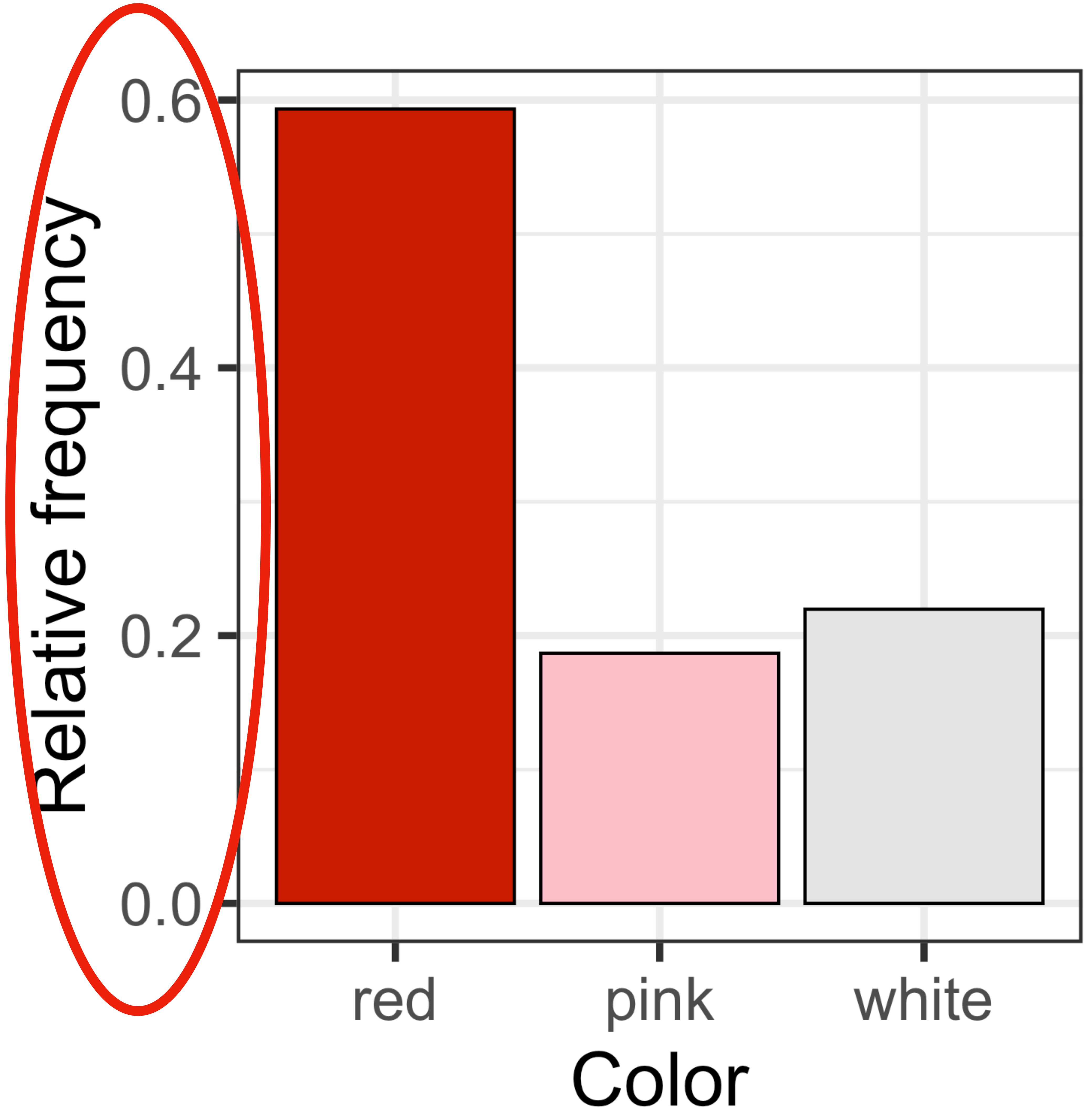


# Visualizing frequency distributions

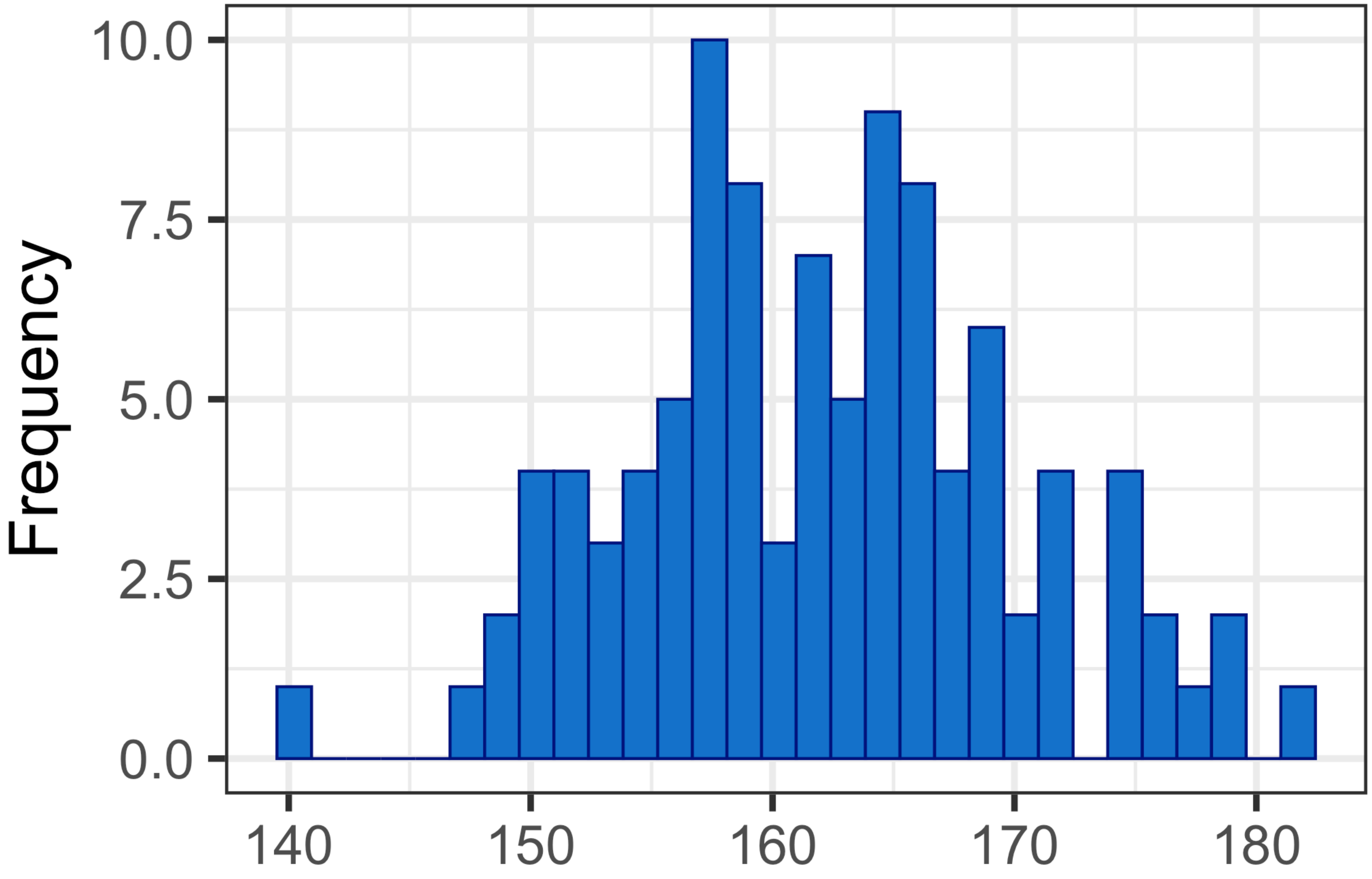
| Color | Frequency | Relative frequency | Percent frequency |
|---|---|---|---|
| **Red** | 108 | 0.59 | 59.34 |
| **Pink** | 34 | 0.19 | 18.68 |
| **White** | 40 | 0.22 | 21.98 |
| **Total** | **182** | **1** | **100** |

- Categorical data can be represented with a **bar chart**

- **Relative frequency** can be useful to compare datasets of different sizes



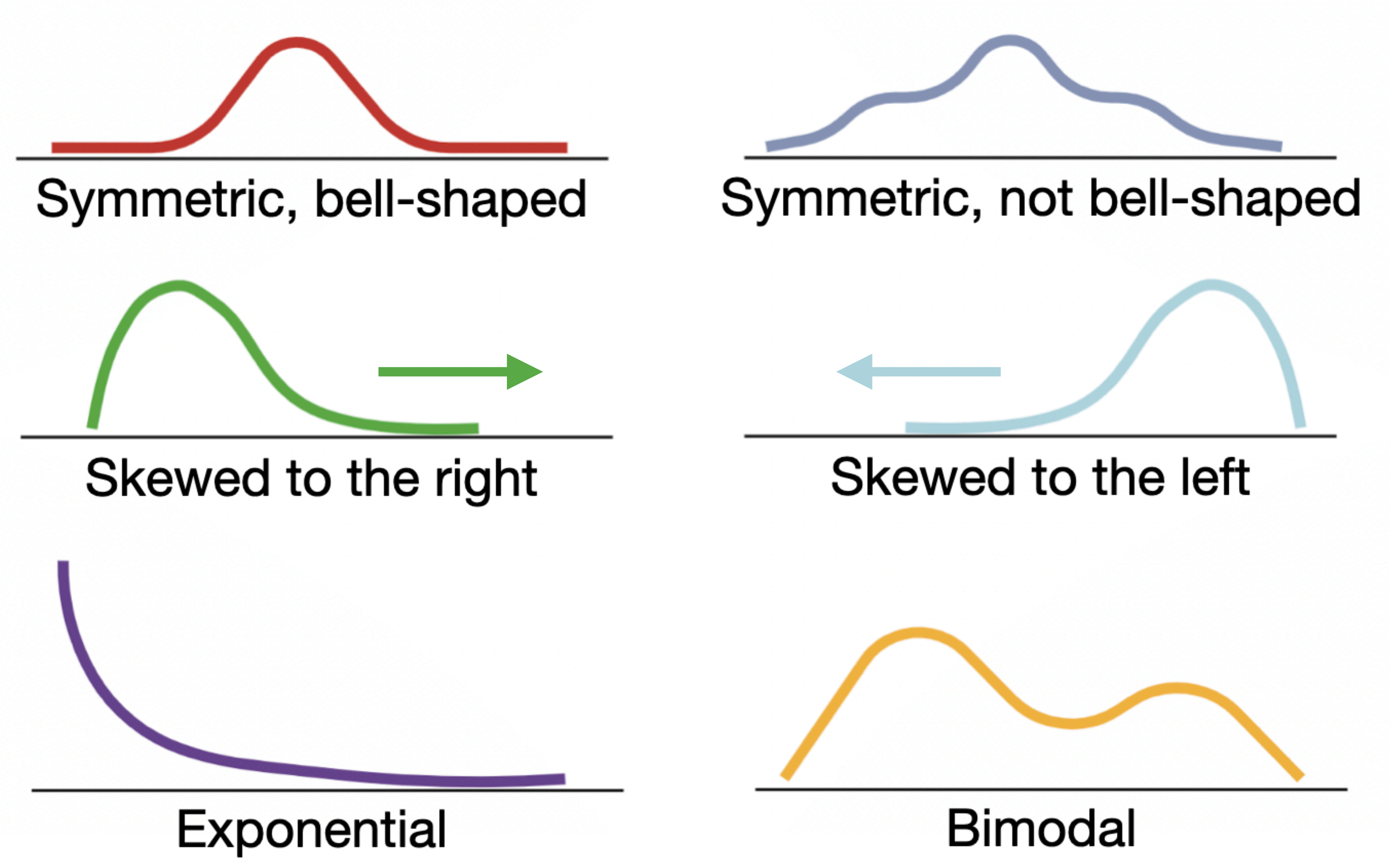
# Histograms show shape of numerical data



# Histograms show shape of numerical data

# Histograms show shape of numerical data

# Biological frequency distribution shapes

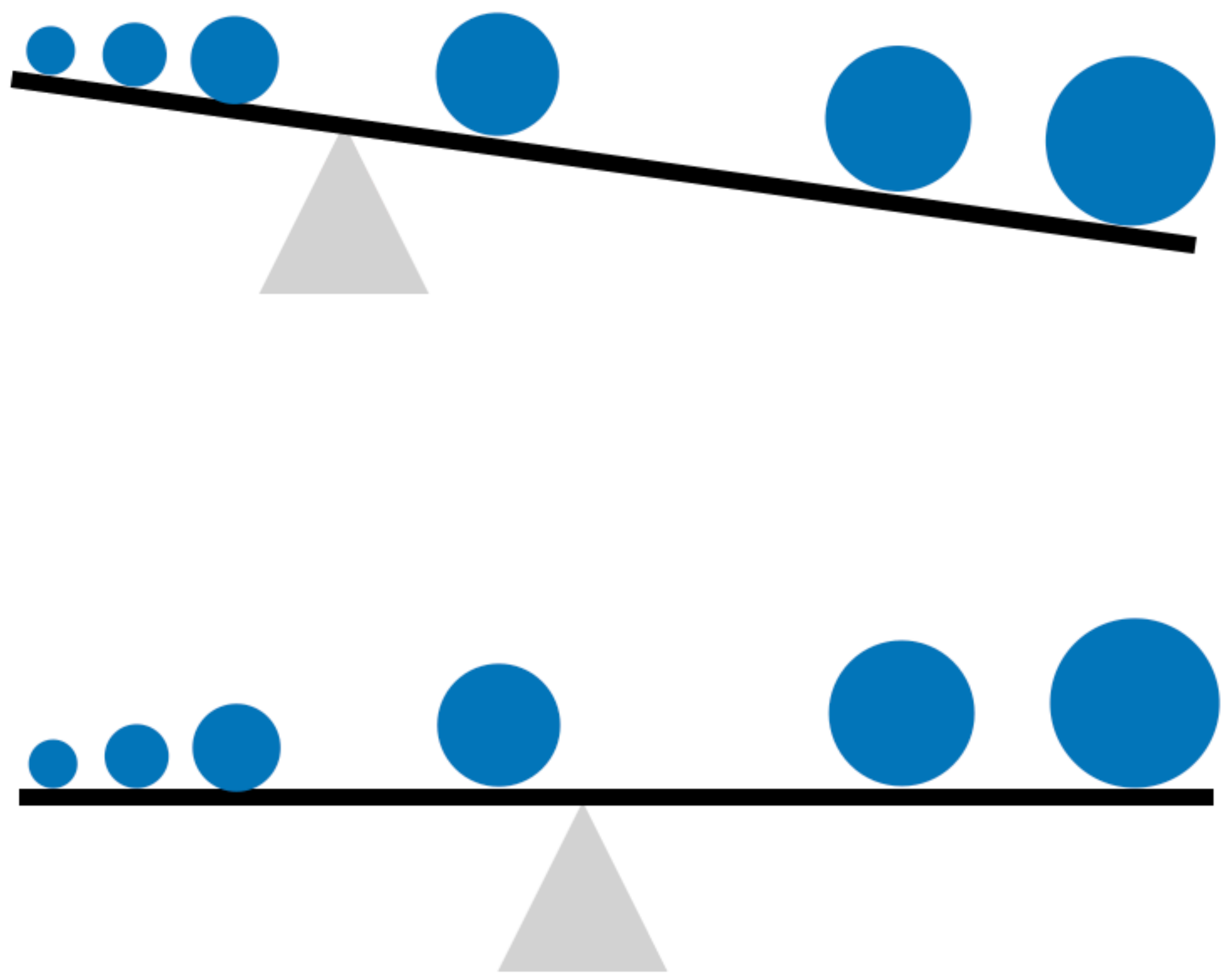


# Data exploration and summarization

## Shape



## Center



## Spread

# Measures of center: **median** vs. **mean**

4 3 6 9 12

4 20 1

15

# Measures of center: **median** vs. **mean**

$$\mathrm{sum}(1 \quad 3 \quad 4 \quad 4 \quad 6 \quad 9 \quad 12 \quad 15 \quad 20) \div 9 = 8.2$$

6.8

median

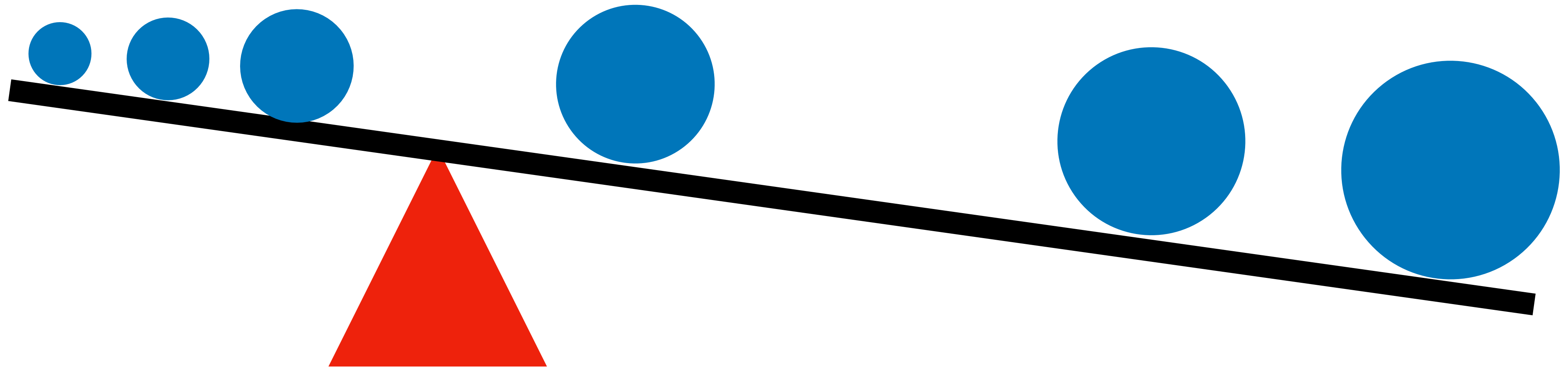
mean

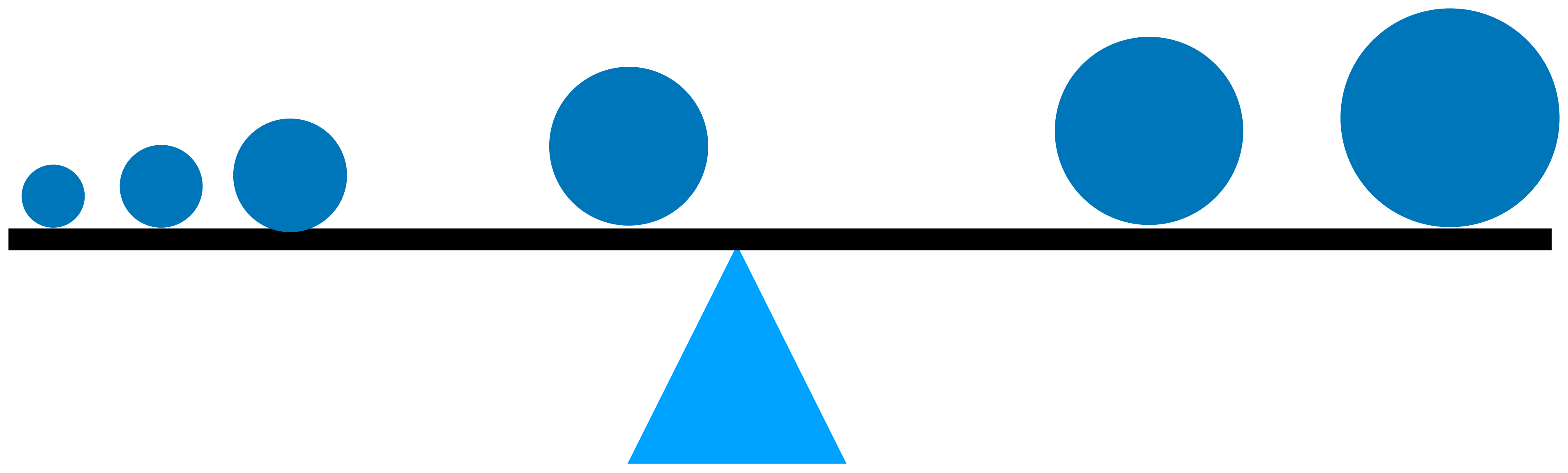
deviation

- Median is a more **robust** statistic
- `median(x)`

- Mean can be influenced by extremes
- `mean(x)`

# Measures of center: **median** vs. **mean**





- Median is a more **robust** statistic
- `median(x)`

- Mean can be influenced by extremes
- `mean(x)`

# Data exploration and summarization

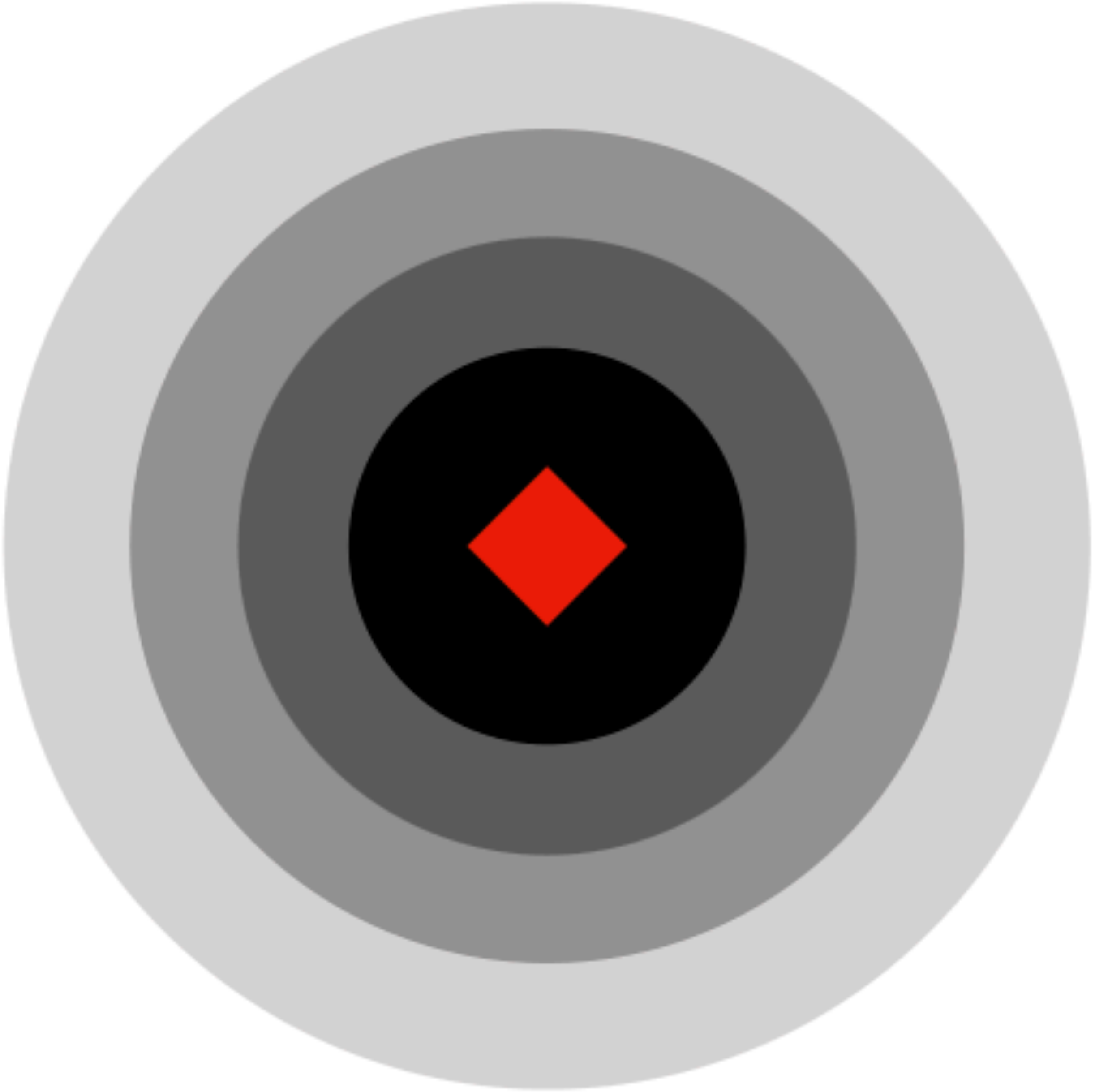
**Shape**



**Center**



**Spread**



# Measures of dispersion: **range** and **IQR**

| -10, 0, 10, 20, 30 | | 8, 9, 10, 11, 12 |
|---|---|---|
| **median:** 10 | ??? | **median:** 10 |
| **mean:** 10 | | **mean:** 10 |

# Measures of dispersion: **range** and **IQR**

-10, 0, 10, 20, 30

8, 9, 10, 11, 12

40 .............. **range** .............. 4

20 .............. **IQR** .............. 2

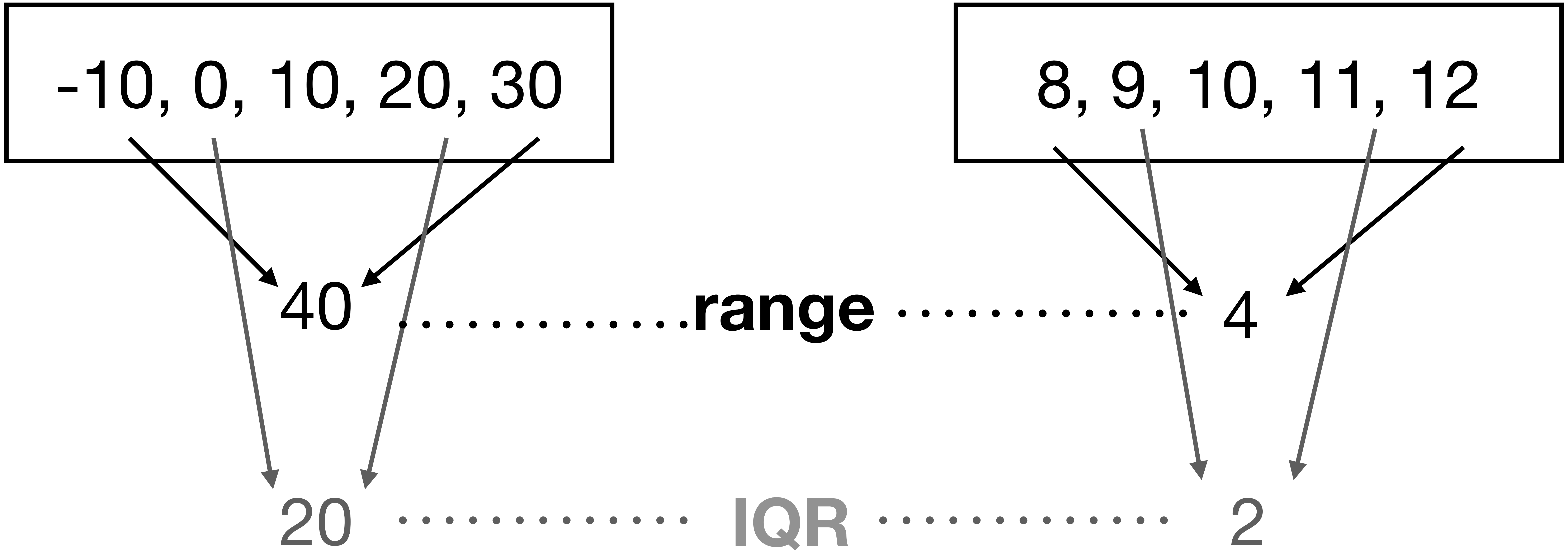
**median:** 10

**mean:** 10

**median:** 10

**mean:** 10

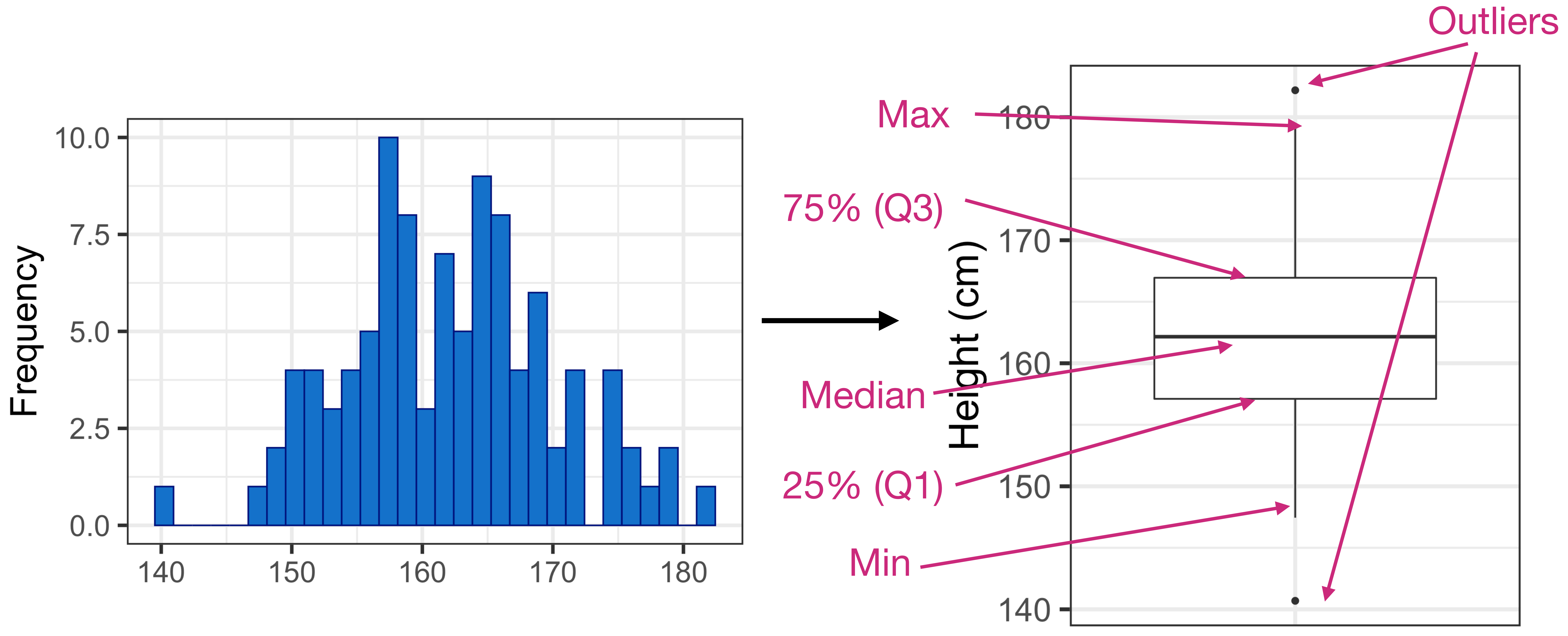
# Measures of dispersion: **range** and **IQR**



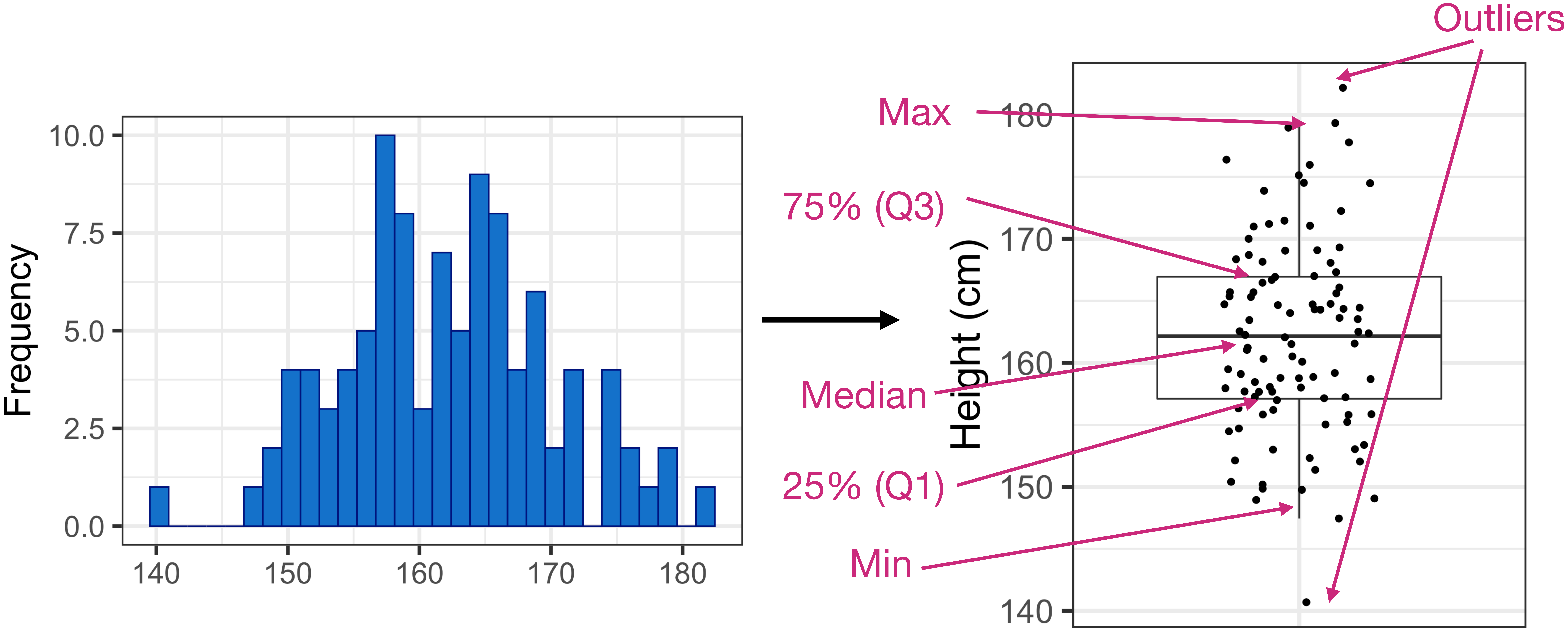

**> median:** 10 **> median:** 10

**mean:** 10 **mean:** 10

# Plotting distributions with boxplots



# Plotting distributions with boxplots



# Measures of dispersion: **standard deviation**

| -10, 0, 10, 20, 30 | 8, 9, 10, 11, 12 |
|---|---|

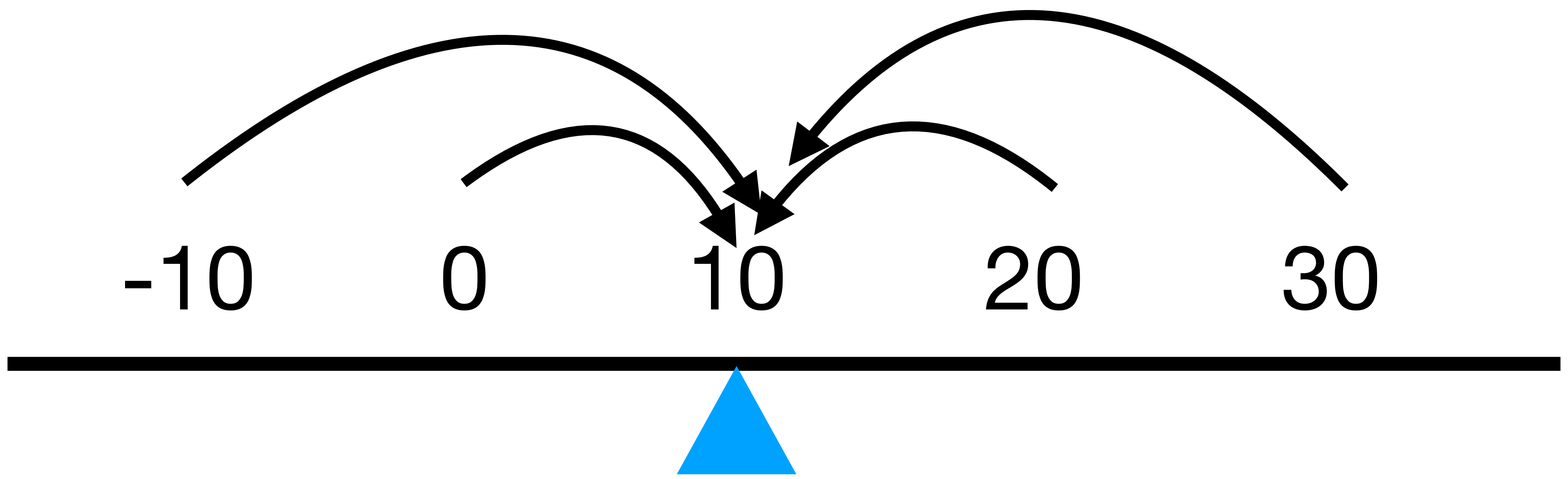
**Variance:** Mean of the squared deviations

**Standard deviation:** square root of the variance

| | |
|---|---|
| **median:** 10 | **median:** 10 |
| **> mean:** 10 | **> mean:** 10 |

# Measures of dispersion: **standard deviation**

| -10, 0, 10, 20, 30 | **mean:** 10 | 8, 9, 10, 11, 12 |
|---|---|---|
| -20, -10, 0, 10, 20 | **deviations** | -2, -1, 0, 1, 2 |




**Variance:** Mean of the squared deviations

# Measures of dispersion: **standard deviation**

| | | |
|---|---|---|
| -10, 0, 10, 20, 30 | **mean:** 10 | 8, 9, 10, 11, 12 |
| -20, -10, 0, 10, 20 | **deviations** | -2, -1, 0, 1, 2 |
| **Mean:** 400, 100, 0, 100, 400 | **deviations$^2$** | **Mean:** 4, 1, 0, 1, 4 |
| 200 | **variance** | 2 |

**Variance:** Mean of the squared deviations

# Measures of dispersion: **standard deviation**

| | | |
|---|---|---|
| -10, 0, 10, 20, 30 | **mean:** 10 | 8, 9, 10, 11, 12 |
| -20, -10, 0, 10, 20 | **deviations** | -2, -1, 0, 1, 2 |
| 400, 100, 0, 100, 400 | **deviations$^2$** | 4, 1, 0, 1, 4 |
| 200 | **variance** | 2 |
| 14.1 | **standard deviation** | 1.41 |

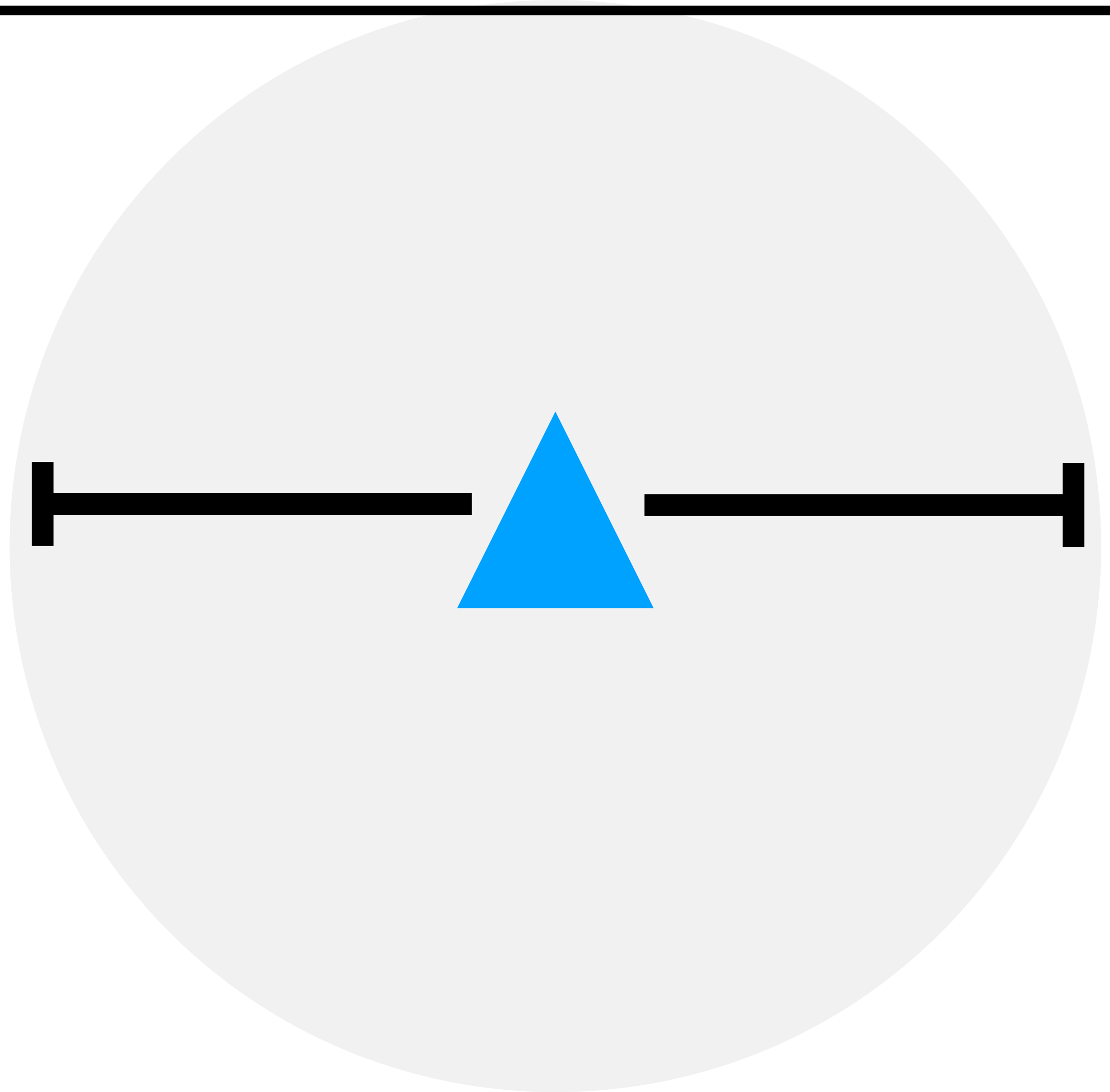
**Standard deviation:** square root of the variance

# Measures of dispersion: **standard deviation**

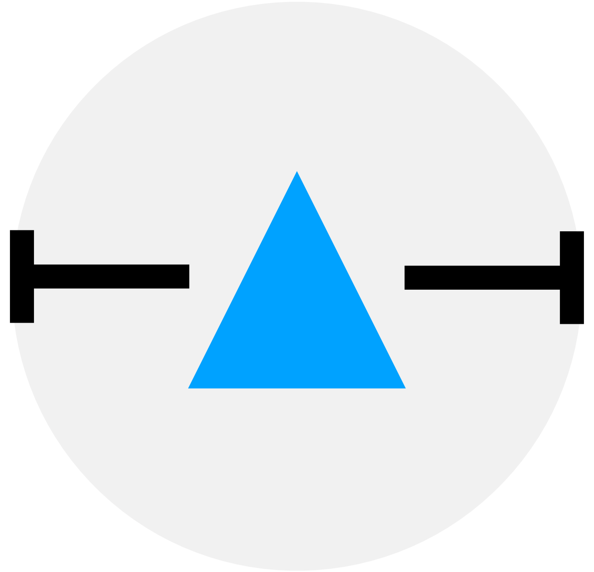
-10, 0, 10, 20, 30

**mean:** 10

8, 9, 10, 11, 12



*“typical distance of the observations from their mean”*



14.1

**standard deviation**

1.41

**Standard deviation:** square root of the variance

# Measures of dispersion: **standard deviation**

```
> var(x)
> sd(x)
```

$$\sigma = \underbrace{\sqrt{\frac{\sum \left(x_i - \mu\right)^2}{N}}}_{\text{Standard deviation}}$$

deviations: $x_i - \mu$

Squared deviations: $(x_i - \mu)^2$

variance: $\frac{\sum (x_i - \mu)^2}{N}$

Standard deviation

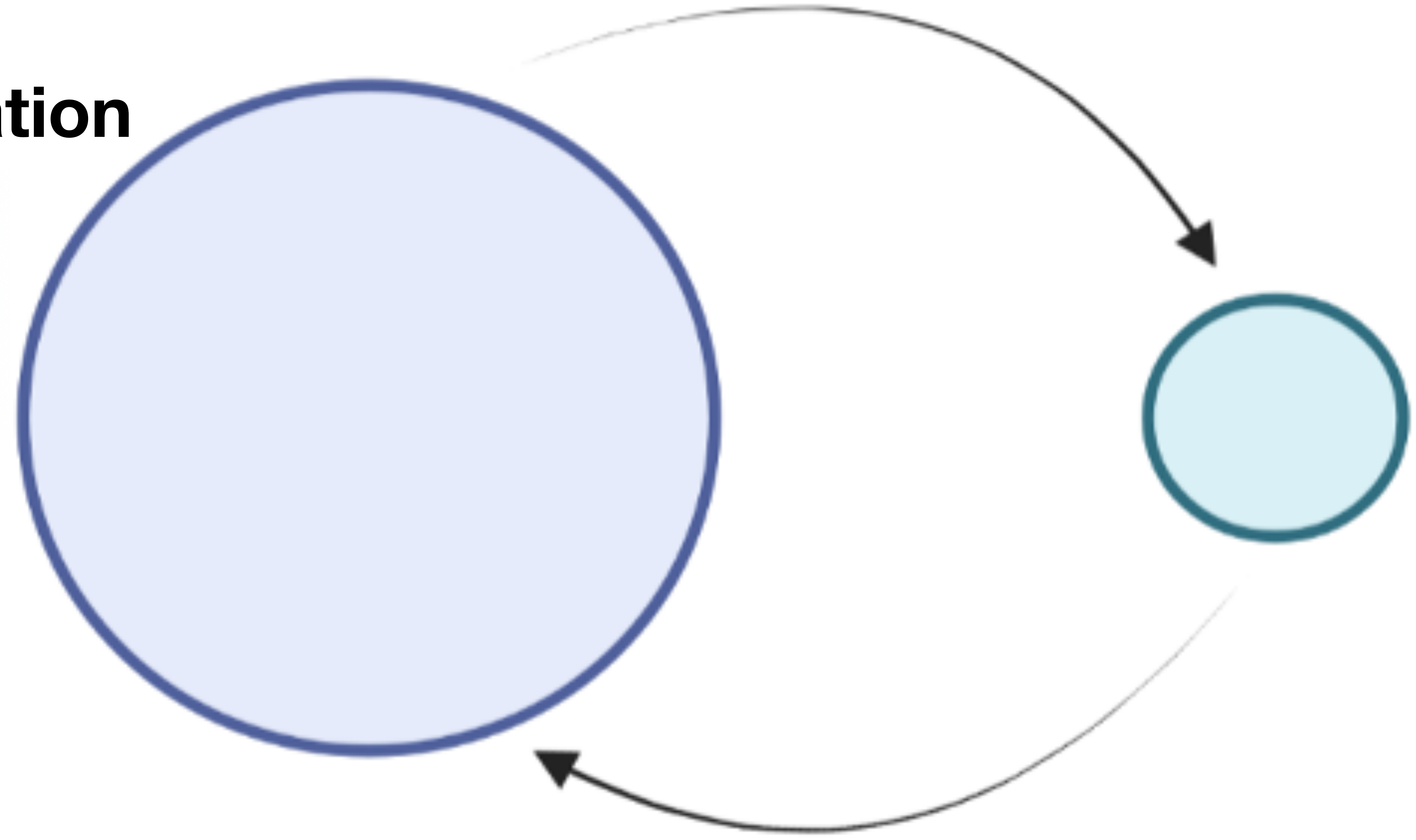
$\sigma$: population standard deviation

$x_i$: observed values

**N:** Size of population

$\mu$ : population mean

# Similar, but different, equations describe a population vs. a sample




$$\sigma = \sqrt{\frac{\sum (x_i - \mu)^2}{N}}$$

$$s = \sqrt{\frac{\sum_{i=1}^{N} (x_i - \overline{x})^2}{N - 1}}$$

# Measures of dispersion: **standard deviation**

```
> var(x)
> sd(x)
```

$$s = \sqrt{\frac{\sum_{i=1}^{N}(x_i - \overline{x})^2}{N-1}}$$

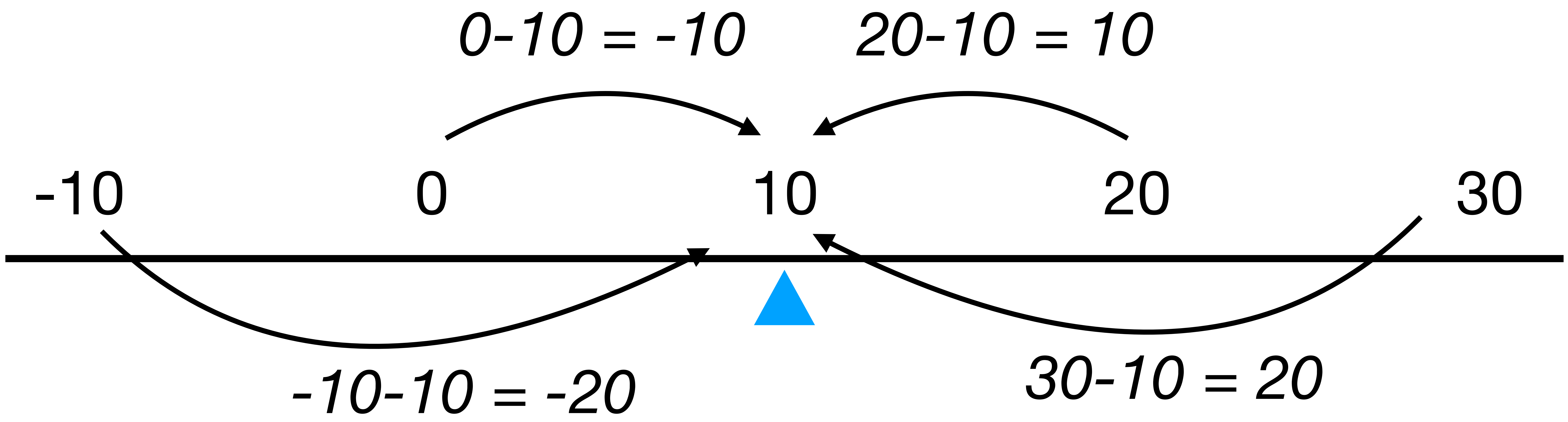
**s:** sample standard deviation

**N:** number of observations

$x_i$ : observed values

$\bar{x}$ : mean value of samples

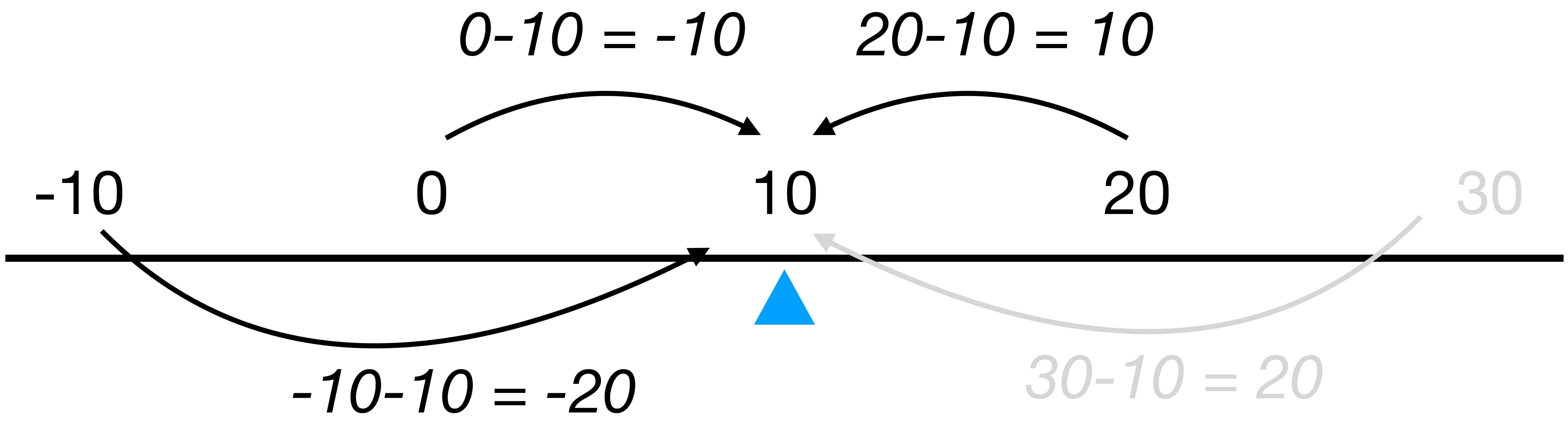
# N-1: **degrees of freedom** explained




$$(-20) + (-10) + (10) + (20) = 0$$

**Sum of deviations is always zero!**

# N-1: **degrees of freedom** explained

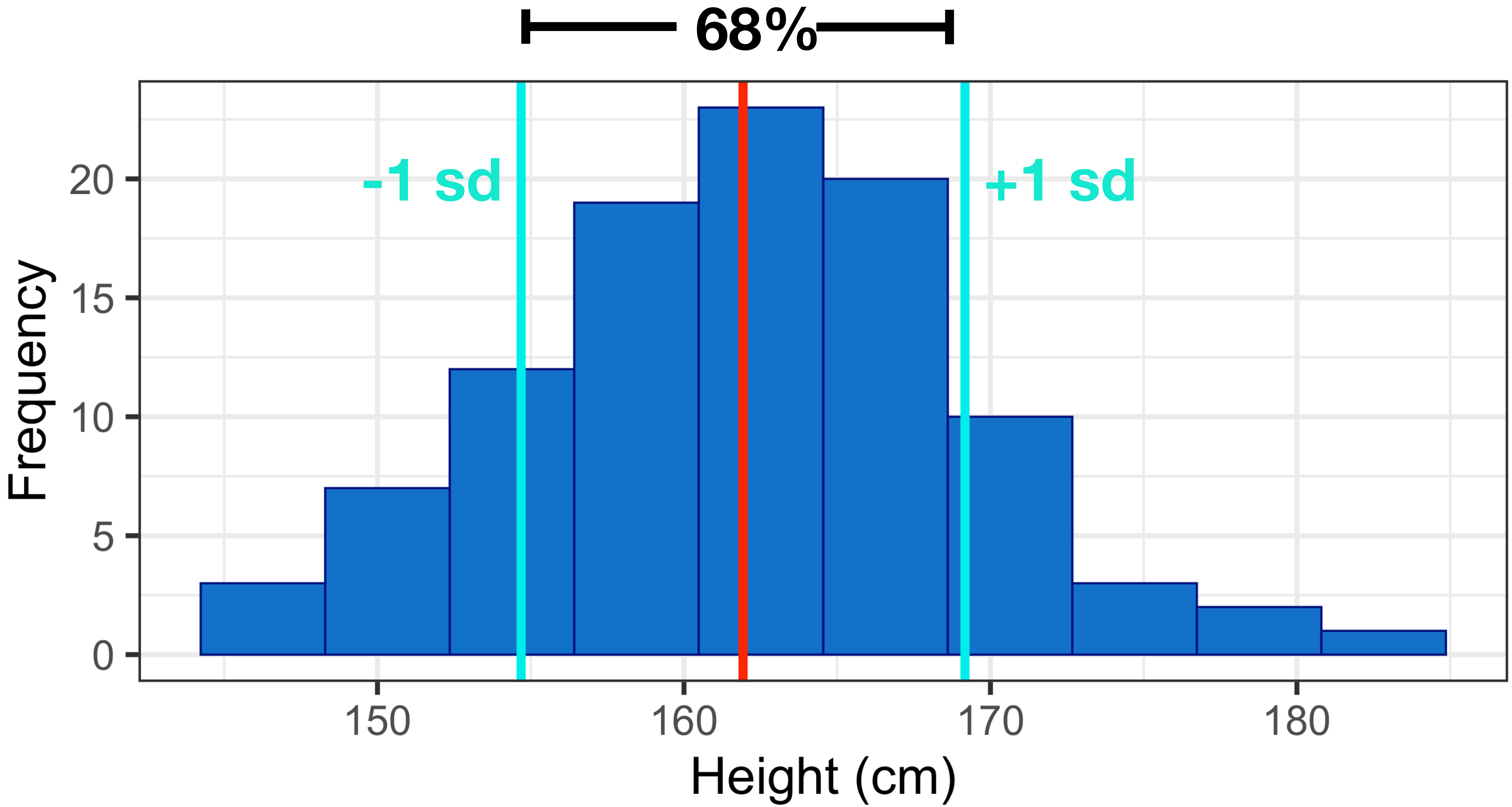



Has to be +20 from mean…

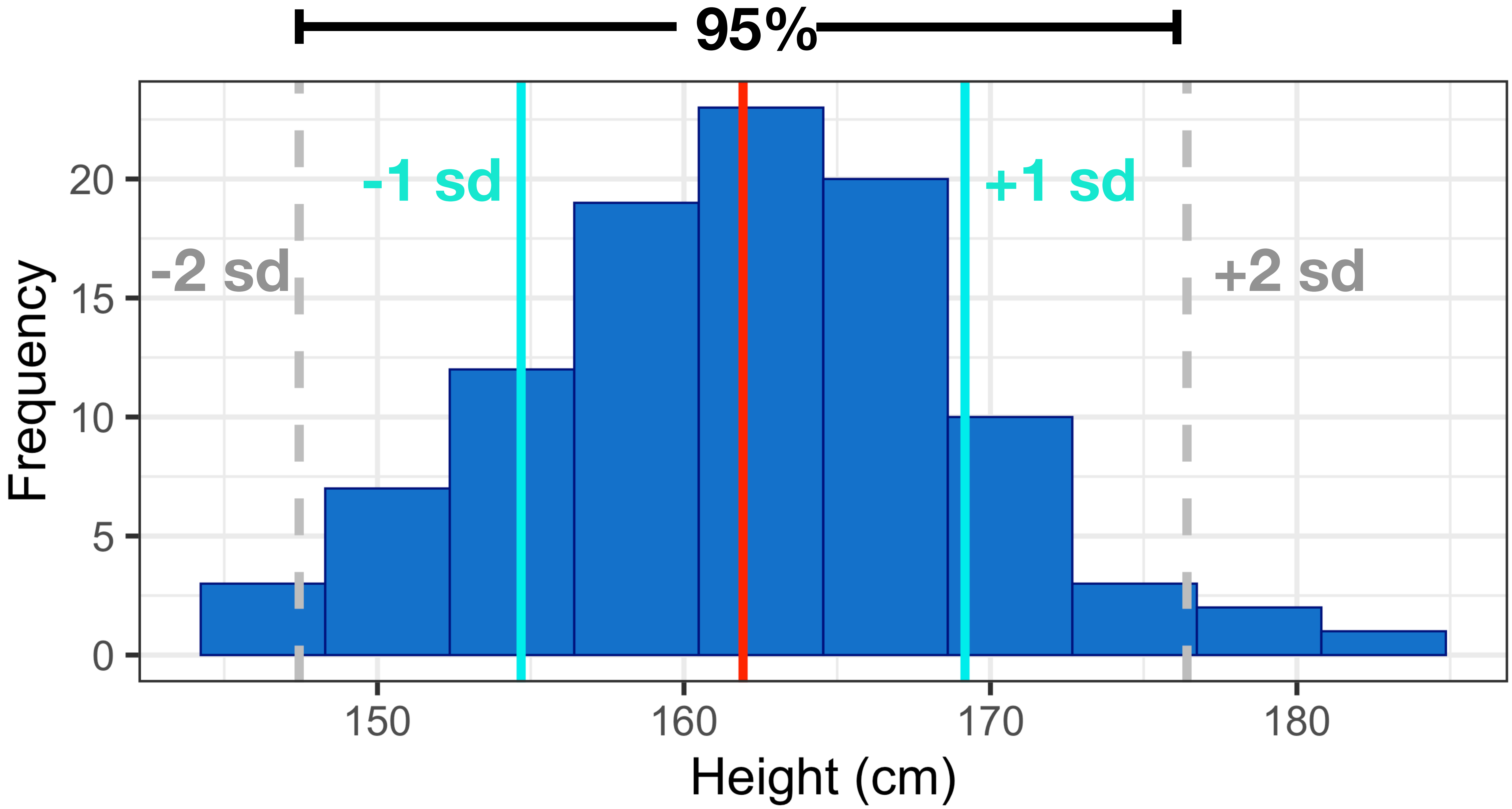
$$(-20) + (-10) + (10) + X = 0$$

**Sum of deviations is always zero!**

# Measures of dispersion: **standard deviation**



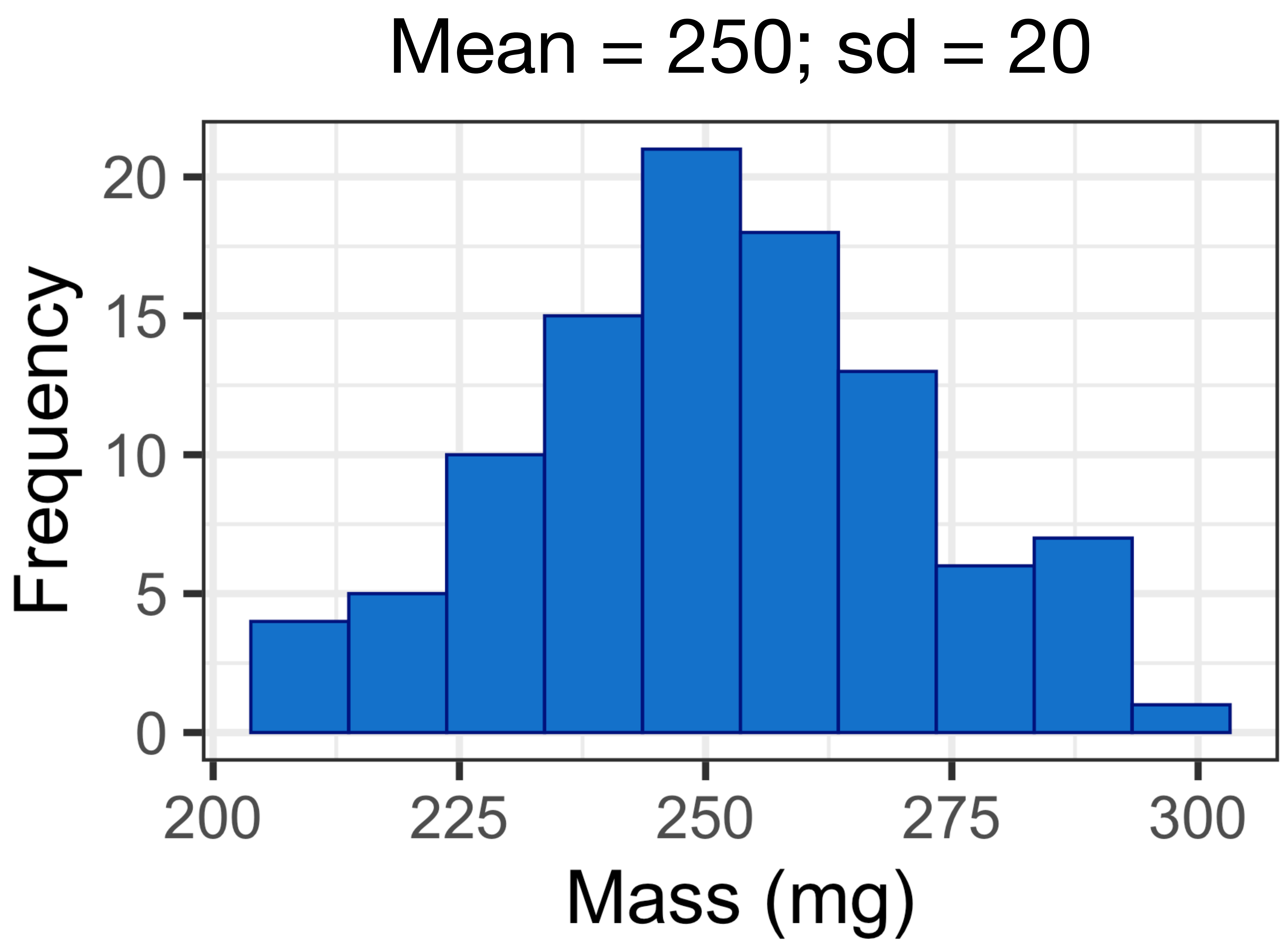
# Measures of dispersion: **standard deviation**



# Linear transformation of variables

**Suppose you collected data in milligrams but need to convert to grams.**

```
new_data = (1/1000) * old_data
```

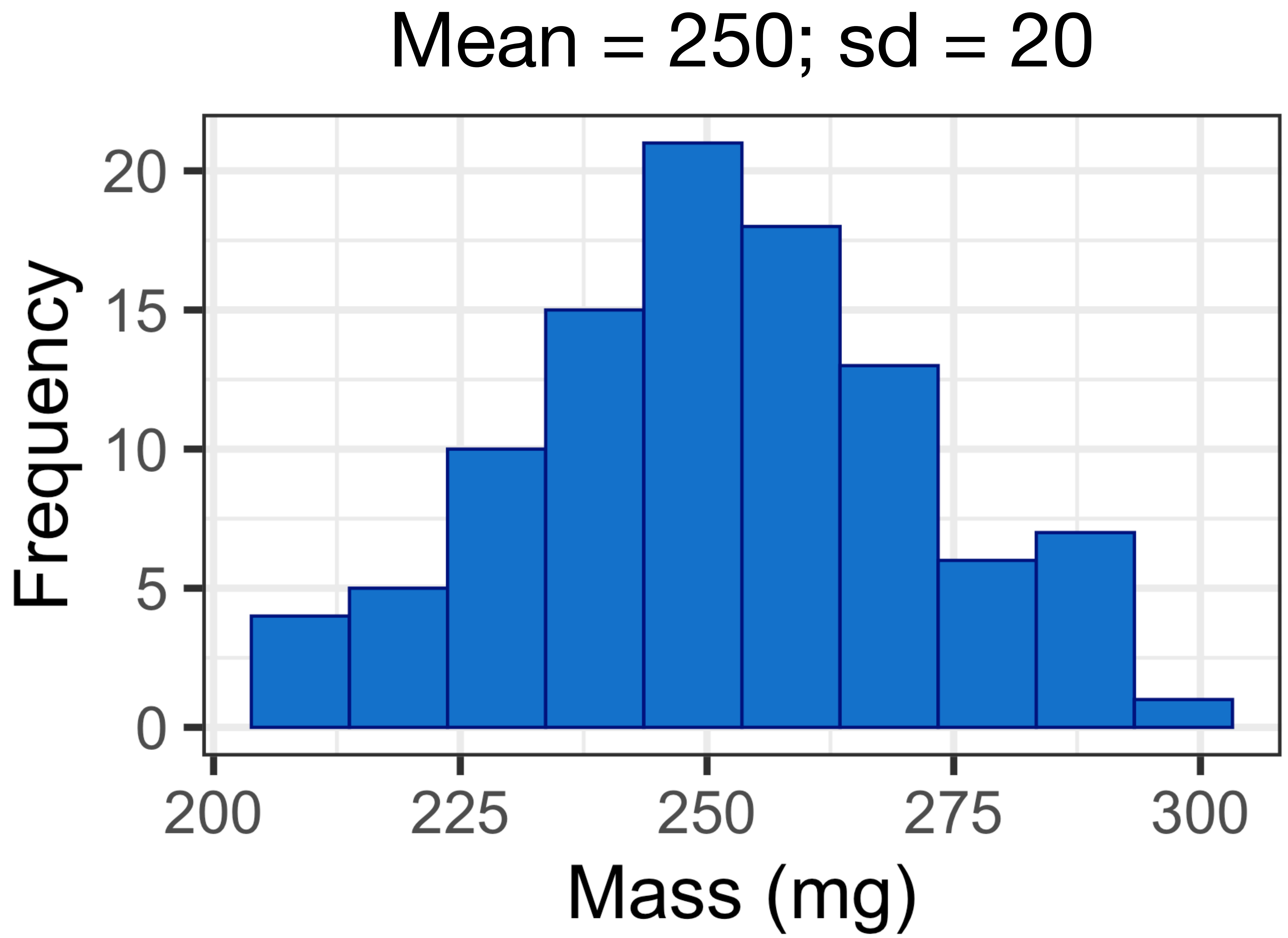


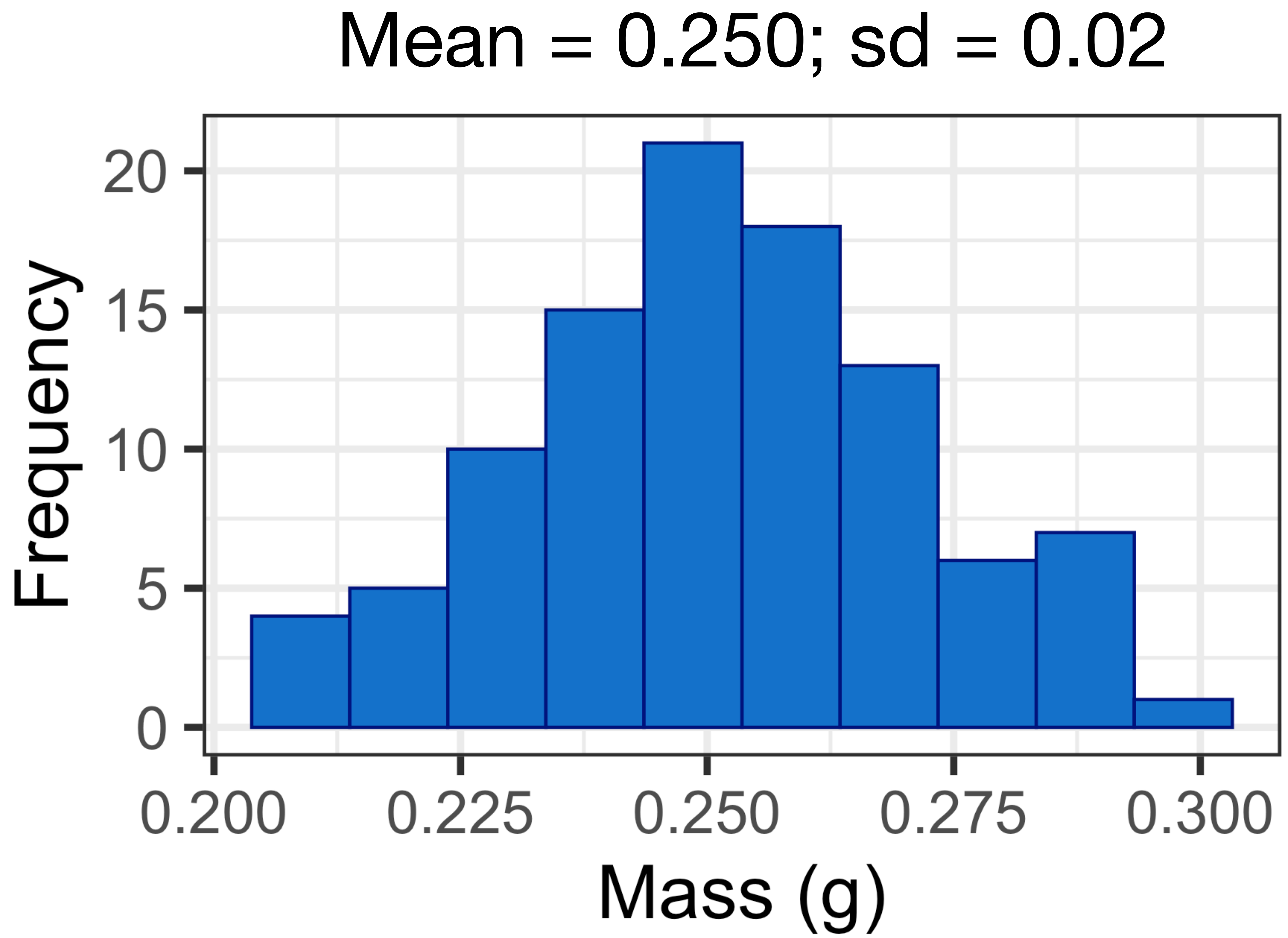
# Linear transformation of variables

**Suppose you collected data in milligrams but need to convert to grams.**

```
new_data = (1/1000) * old_data
```

**Mean & SD scale**

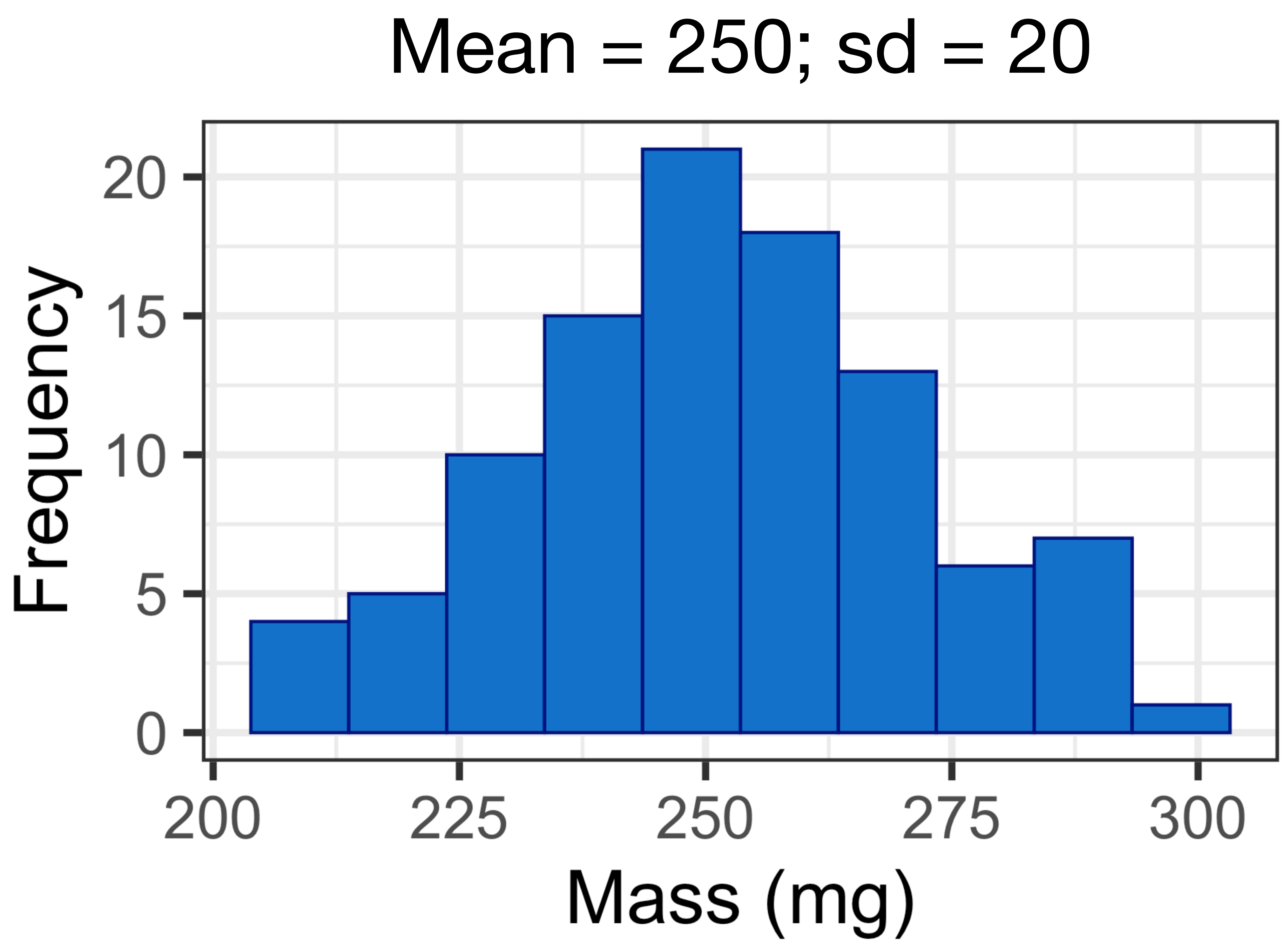


# Linear transformation of variables

**Suppose your scale is off by 50 mg…**

```
new_data = old_data + 50
```

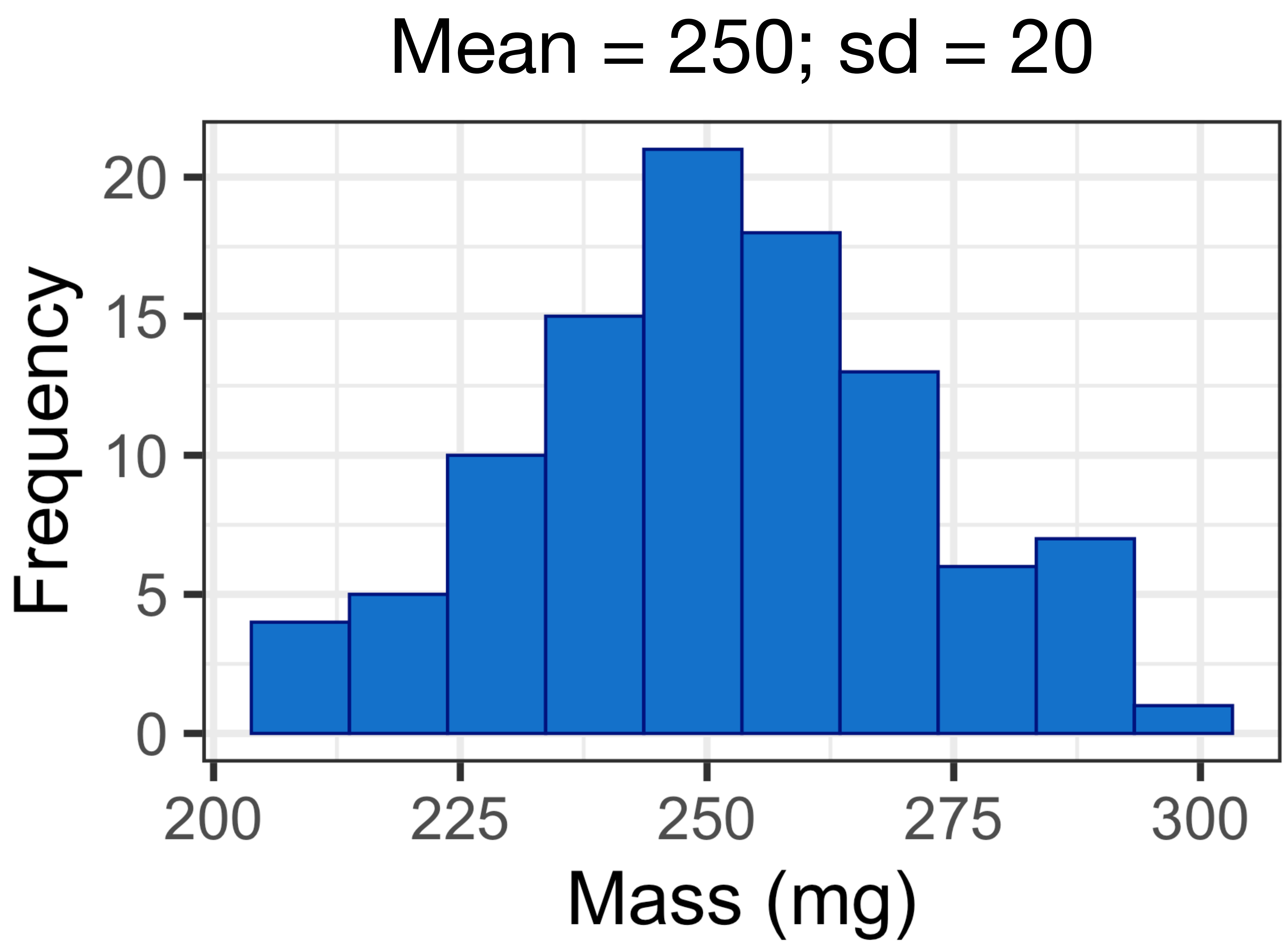


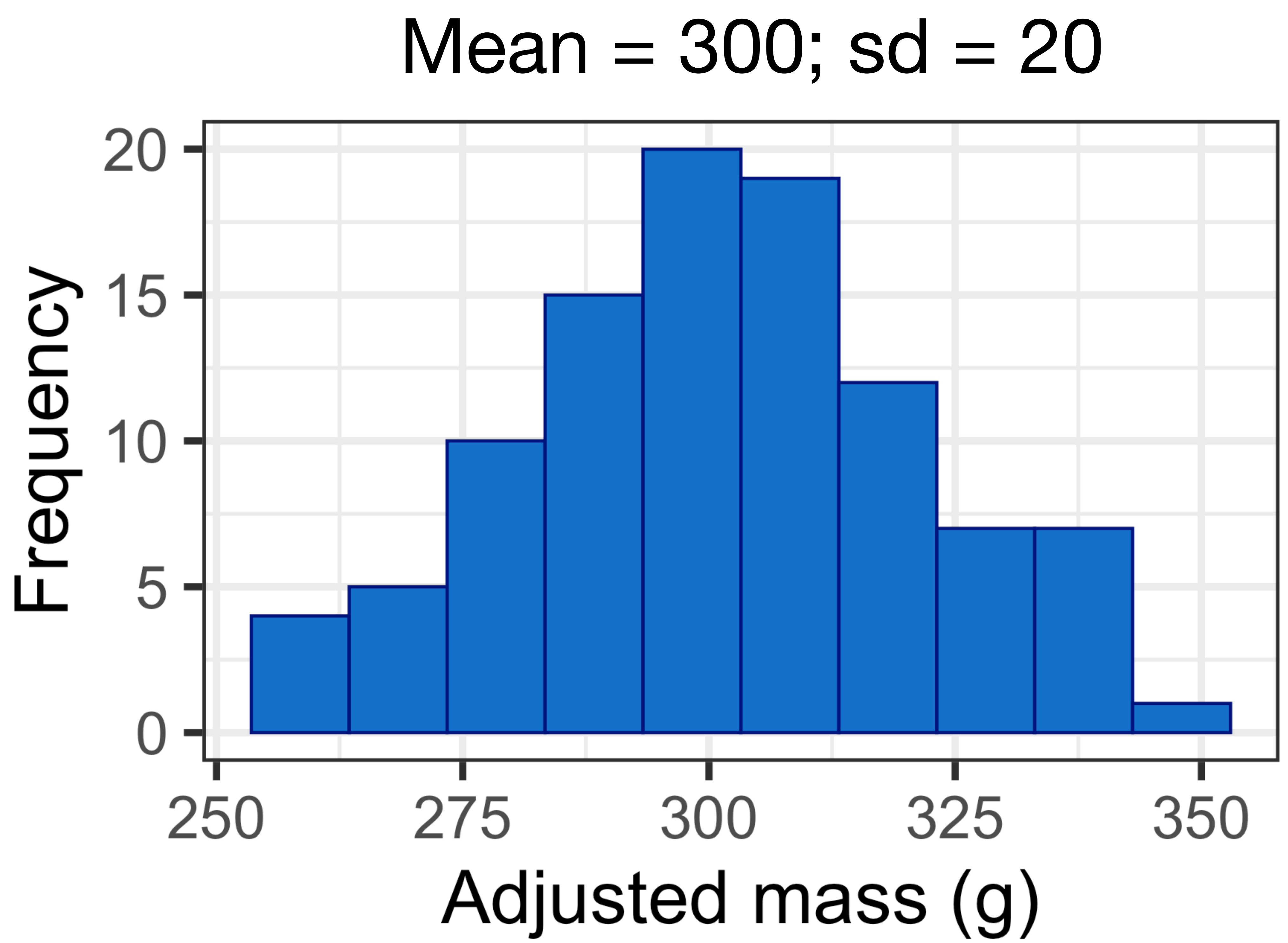
# Linear transformation of variables

**Suppose your scale is off by 50 mg…**

```
new_data = old_data + 50
```

**Mean scales, SD not**



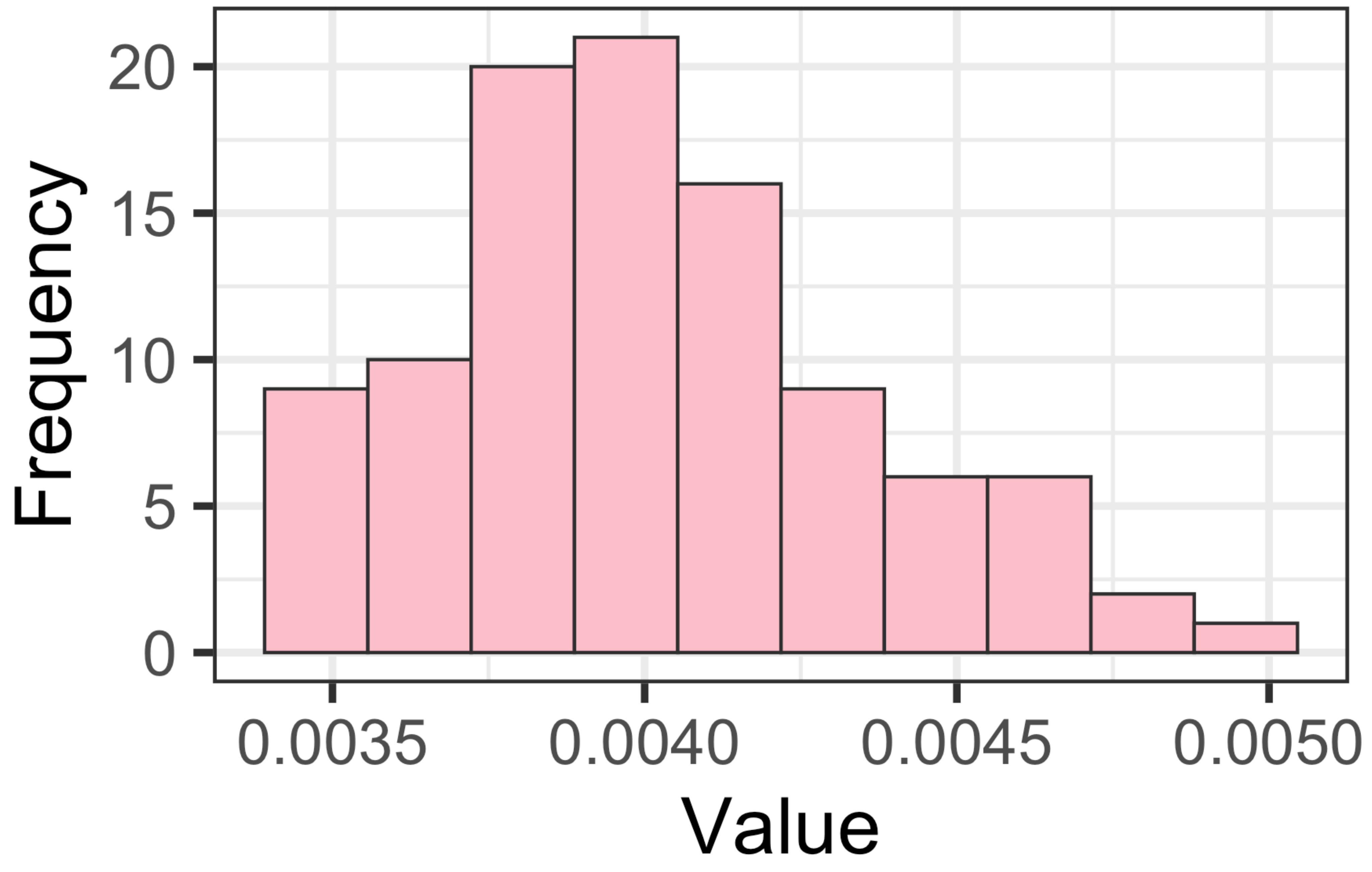



# Non-linear transformation of variables

**Suppose your data has a strong right skew…**

```
new_data = log(old_data)
```

Mean = 0.004; sd = 0.0003



# Non-linear transformation of variables

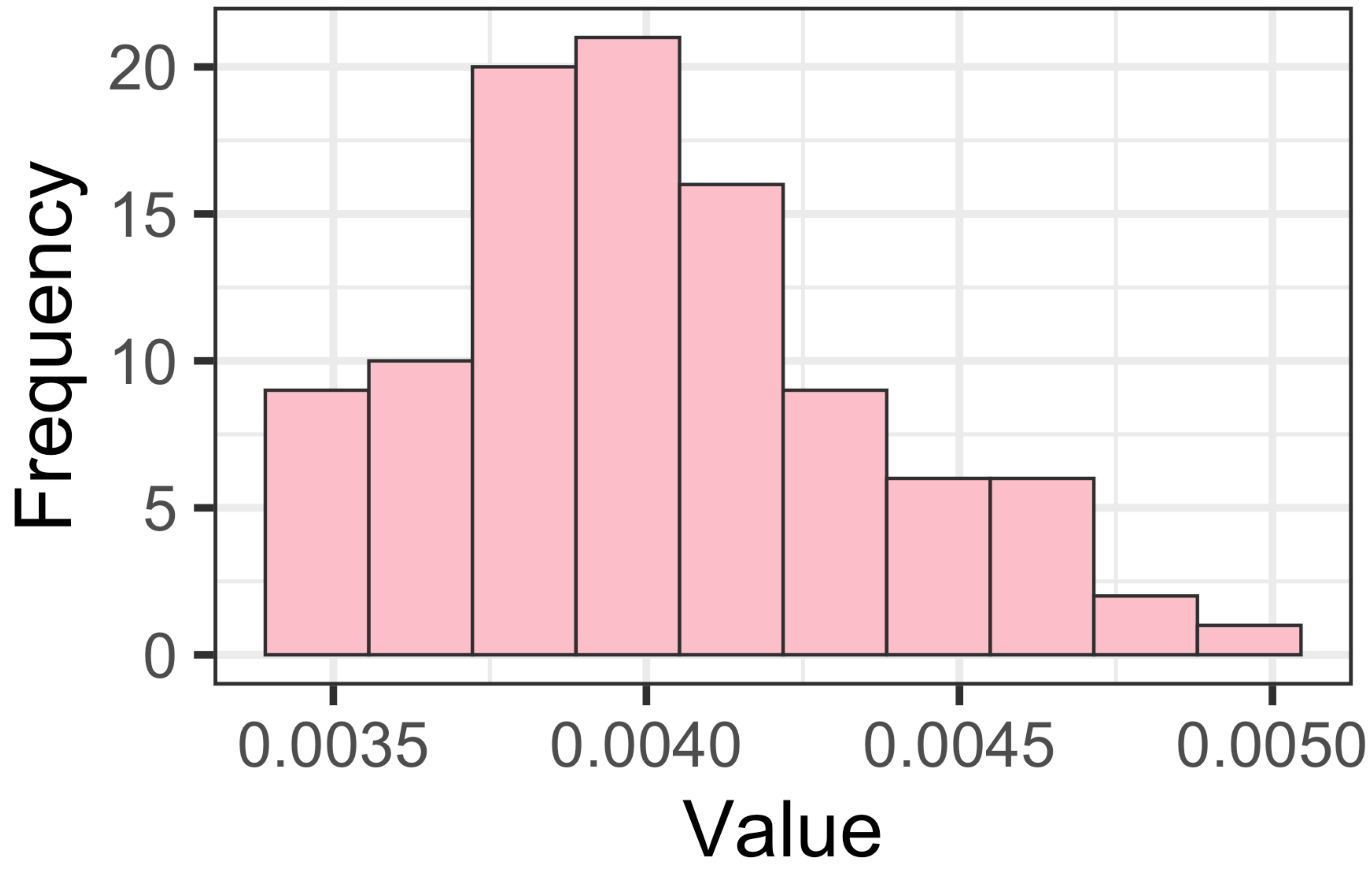
- $Y' = \sqrt{Y}$
- $Y' = \log(Y)$
- $Y' = 1/Y$
- $Y' = Y^2$

**Suppose your data has a strong right skew…**

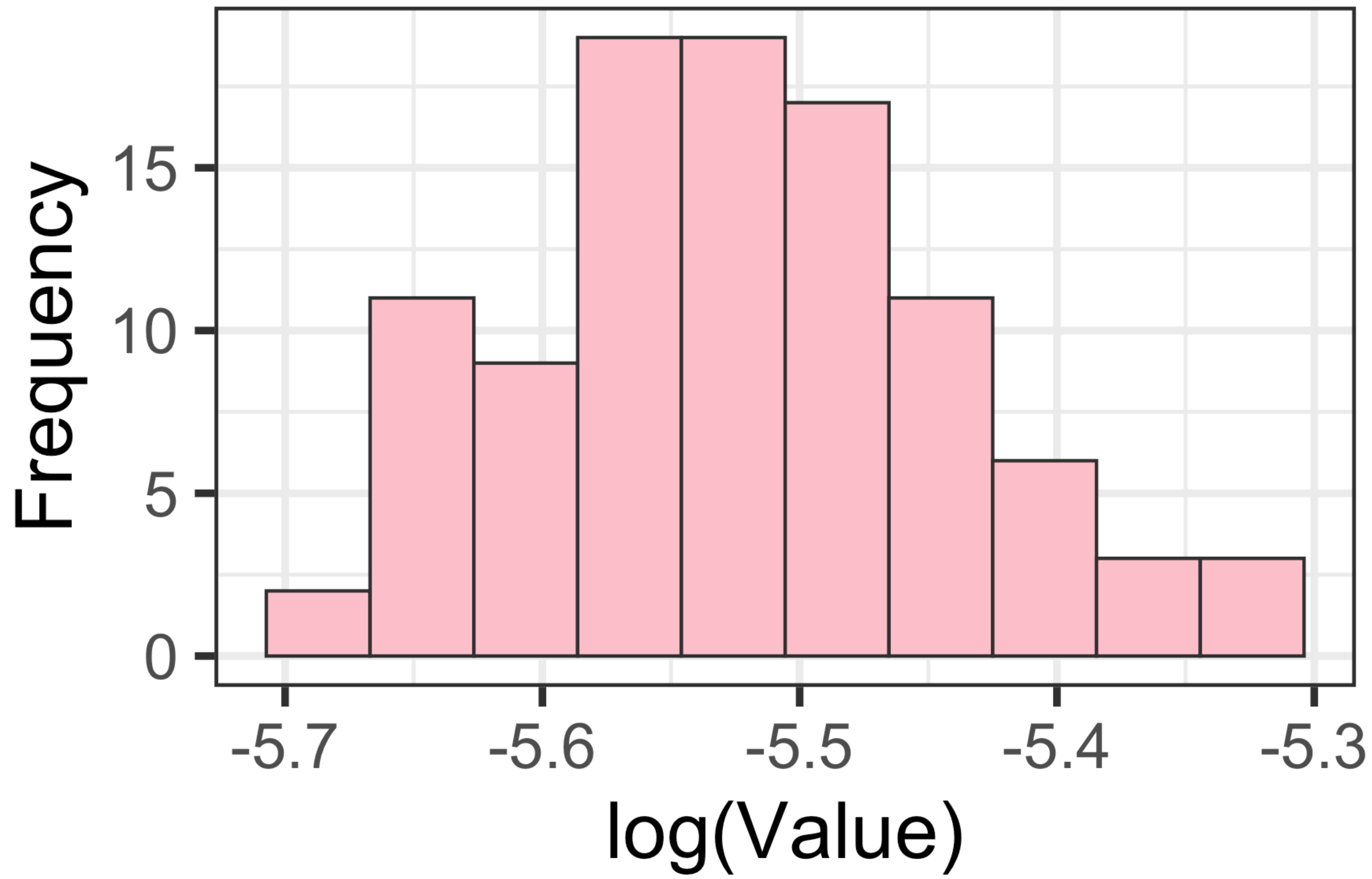
```
new_data = log(old_data)
```

**Mean and SD scale non-linearly**

Mean = 0.004; sd = 0.0003




Mean = -5.5; sd = 0.08

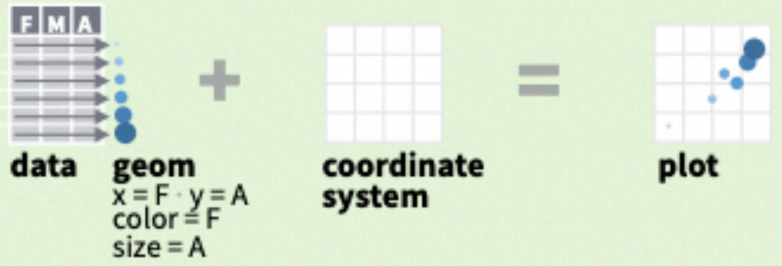


# Data Visualization with ggplot2 : : CHEAT SHEET

## Basics

**ggplot2** is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and geoms—visual marks that represent data points.


To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.




Complete the template below to build a graph.

```
ggplot (data = <DATA> ) +
  <GEOM_FUNCTION> (mapping = aes( <MAPPINGS> ),
  stat = <STAT> , position = <POSITION> ) +
  <COORDINATE_FUNCTION> +
  <FACET_FUNCTION> +
  <SCALE_FUNCTION> +
  <THEME_FUNCTION>
```

required — Not required, sensible defaults supplied

**ggplot**(data = mpg, **aes**(x = cty, y = hwy)) Begins a plot that you finish by adding layers to. Add one geom function per layer.

aesthetic mappings · data · geom

**qplot**(x = cty, y = hwy, data = mpg, geom = "point") Creates a complete plot with given data, geom, and mappings. Supplies many useful defaults.

**last_plot()** Returns the last plot

**ggsave("plot.png", width = 5, height = 5)** Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

## Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

### GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

**a + geom_blank()**
(Useful for expanding limits)

**b + geom_curve**(aes(yend = lat + 1, xend=long+1,curvature=z)) - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

**a + geom_path**(lineend="butt", linejoin="round", linemitre=1)
x, y, alpha, color, group, linetype, size

**a + geom_polygon**(aes(group = group))
x, y, alpha, color, fill, group, linetype, size

**b + geom_rect**(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)) - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

**a + geom_ribbon**(aes(ymin=unemploy - 900, ymax=unemploy + 900)) - x, ymax, ymin, alpha, color, fill, group, linetype, size

### LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

**b + geom_abline**(aes(intercept=0, slope=1))
**b + geom_hline**(aes(yintercept = lat))
**b + geom_vline**(aes(xintercept = long))

**b + geom_segment**(aes(yend=lat+1, xend=long+1))
**b + geom_spoke**(aes(angle = 1:1155, radius = 1))

### ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

**c + geom_area(stat = "bin")**
x, y, alpha, color, fill, linetype, size

**c + geom_density**(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

**c + geom_dotplot()**
x, y, alpha, color, fill

**c + geom_freqpoly()** x, y, alpha, color, group, linetype, size

**c + geom_histogram**(binwidth = 5) x, y, alpha, color, fill, linetype, size, weight

**c2 + geom_qq**(aes(sample = hwy)) x, y, alpha, color, fill, linetype, size, weight

### discrete

d <- ggplot(mpg, aes(fl))

**d + geom_bar()**
x, alpha, color, fill, linetype, size, weight

### TWO VARIABLES

#### continuous x , continuous y

e <- ggplot(mpg, aes(cty, hwy))

**e + geom_label**(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE) x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

**e + geom_jitter**(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

**e + geom_point()**, x, y, alpha, color, fill, shape, size, stroke

**e + geom_quantile()**, x, y, alpha, color, group, linetype, size, weight

**e + geom_rug**(sides = "bl"), x, y, alpha, color, linetype, size

**e + geom_smooth**(method = lm), x, y, alpha, color, fill, group, linetype, size, weight

**e + geom_text**(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE), x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

#### discrete x , continuous y

f <- ggplot(mpg, aes(class, hwy))

**f + geom_col()**, x, y, alpha, color, fill, group, linetype, size

**f + geom_boxplot()**, x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

**f + geom_dotplot**(binaxis = "y", stackdir = "center"), x, y, alpha, color, fill, group

**f + geom_violin**(scale = "area"), x, y, alpha, color, fill, group, linetype, size, weight

#### discrete x , discrete y

g <- ggplot(diamonds, aes(cut, color))

**g + geom_count()**, x, y, alpha, color, fill, shape, size, stroke

#### continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

**h + geom_bin2d**(binwidth = c(0.25, 500))
x, y, alpha, color, fill, linetype, size, weight

**h + geom_density2d()**
x, y, alpha, colour, group, linetype, size

**h + geom_hex()**
x, y, alpha, colour, fill, size

#### continuous function

i <- ggplot(economics, aes(date, unemploy))

**i + geom_area()**
x, y, alpha, color, fill, linetype, size

**i + geom_line()**
x, y, alpha, color, group, linetype, size

**i + geom_step(direction = "hv")**
x, y, alpha, color, group, linetype, size

#### visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

**j + geom_crossbar**(fatten = 2)
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

**j + geom_errorbar()**, x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

**j + geom_linerange()**
x, ymin, ymax, alpha, color, group, linetype, size

**j + geom_pointrange()**
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

#### maps

data <- data.frame(murder = USArrests$Murder,
state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

**k + geom_map**(aes(map_id = state), map = map)
**+ expand_limits**(x = map$long, y = map$lat),
map_id, alpha, color, fill, linetype, size

### THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2))l <- ggplot(seals, aes(long, lat))

**l + geom_contour(aes(z = z))**
x, y, z, alpha, colour, group, linetype, size, weight

**l + geom_raster**(aes(fill = z), hjust=0.5, vjust=0.5, interpolate=FALSE)
x, y, alpha, fill

**l + geom_tile**(aes(fill = z)), x, y, alpha, color, fill, linetype, size, width

# {swirl}

Learn R, in R.

swirl teaches you R programming and data science interactively, at your own pace, and right in the R console!

```
1: R Programming: The basics of programming in R
```

# Ice cream analysis

The data were collected on 200 high school students and are scores on various tests, including a video game and a puzzle. The outcome measure in this analysis is the student's favorite flavor of ice cream – vanilla, chocolate or strawberry- from which we are going to see what relationships exists with video game scores (**video**), puzzle scores (**puzzle**) and gender (**female**).

| Variable name | Variable | Data type |
|---|---|---|
| **Id** | Identity of the student | Nominal |
| **female** | Gender (0: Male, 1:Female) | Binary |
| **ice_cream** | Favorite Flavor (1: Vanilla, 2: Chocolate, 3: Strawberry) | Nominal |
| **video** | Score on the video game | Scale/Continuous |
| **puzzle** | Score on the puzzle | Scale/Continuous |

REMEMBER: ROOM CHANGE

Thursday we will be in **Daniel Hale Williams, McGaw 2-320**

*Tuesday we will be back in Hughes Audiorium, Lurie 1-133*

**And don't forget to please take the pre-course survey (link on GitHub)**