1.Statistics fundamentals

- ✓ Probability distributions
- ✓ Population parameters and Sample statistics
- ✓ Central Limit Theorem
- ✓ Student’s t-distribution
- ✓ Confidence intervals for the mean
- ✓ Hypothesis testing

Probability distributions

Distributions

- Put measurements in bins → you get a histogram

Example: human height (cm)

Distributions

- Put measurements in bins → you get a histogram

Example: human height (cm)

Low probability to measure less than 155 cm or more than 185 cm

Smaller bins →more precise estimate of the distribution

Most measurements are between 155 and 185.
→ High probability

Distributions

- Curve to approximate the histogram:

  Low number of measurements (time or money are limiting!):
  The approximate curve, based on the mean and standard deviation of the data we were able to collect, is usually good enough.

Not for all bins measurements
→ use curve to estimate probability

Distributions

- Histogram and Curve are probability distributions:

They show probabilities of how measurements are distributed

Measurements are less likely in these regions

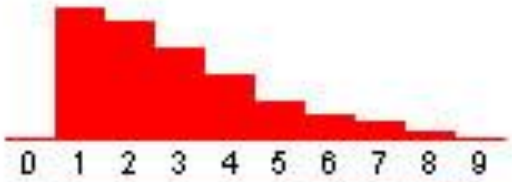
Measurements are likely in this region

Probability of humans being taller than 185 cm
(using histogram)
= number of humans taller than 185 cm / total number of humans
=0.10

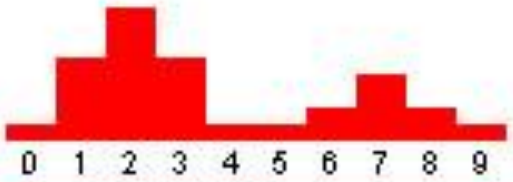
(using curve)
=area under the curve for all measurements above 185 cm / total area under the curve
=0.10 / 1
=0.10

Distribution shapes

Symmetric, unimodal, bell-shaped

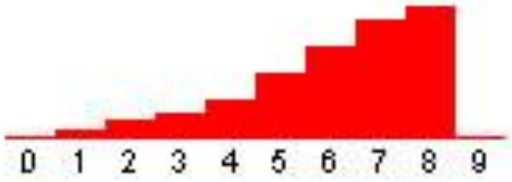


Skewed right



Non-symmetric, bimodal

Uniform



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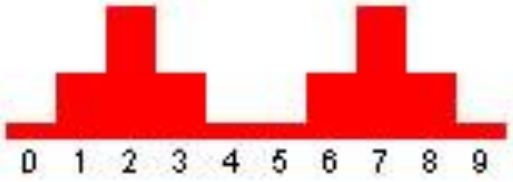


Symmetric, bimodal

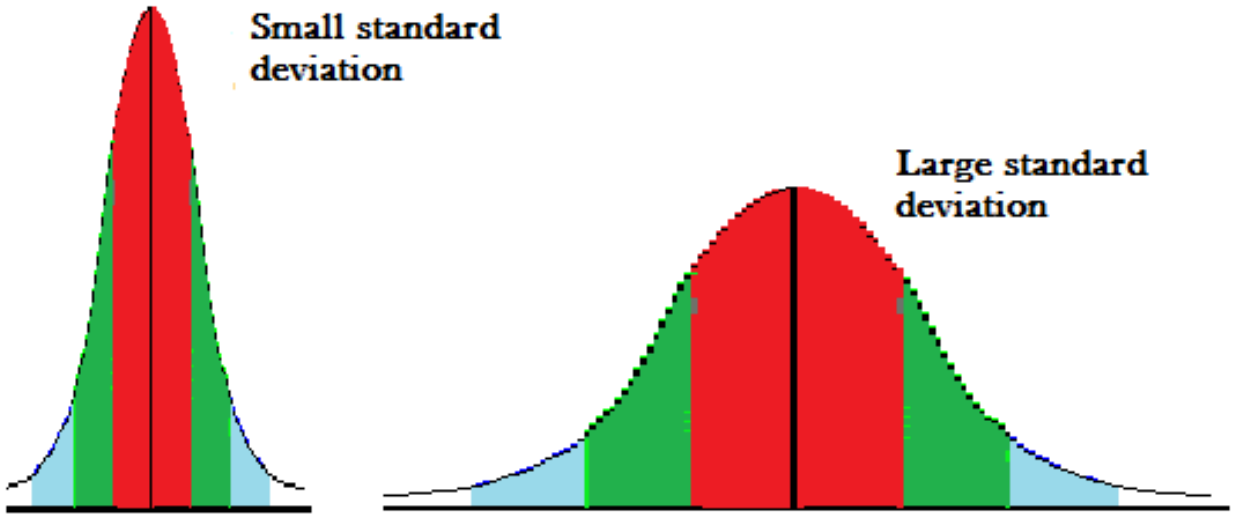
Among all distributions, the normal distribution is the most common in nature.
Why?.....The **CENTRAL LIMIT THEOREM!**

Normal distribution

- = Gaussian
- = Bell shaped curve
- Centered around the average value
- The width is defined by the standard deviation (SD)
- 95% of the measurements fall between +/- 2 SD around the mean
- Very common in nature.

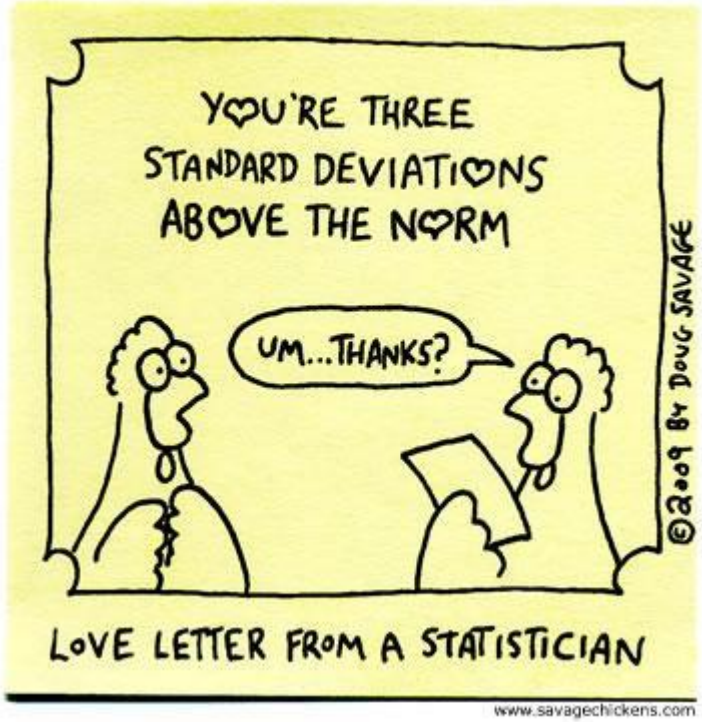
  Reason = « Central Limit Theorem » *(see later!)*

Normal distribution



Distance from the Mean	Percentage of Values Falling Within Distance
$\mu \pm 1\sigma$	68
$\mu \pm 2\sigma$	95
$\mu \pm 3\sigma$	99.7

Savage Chickens by Doug Savage



www.savagechickens.com

Normal distribution

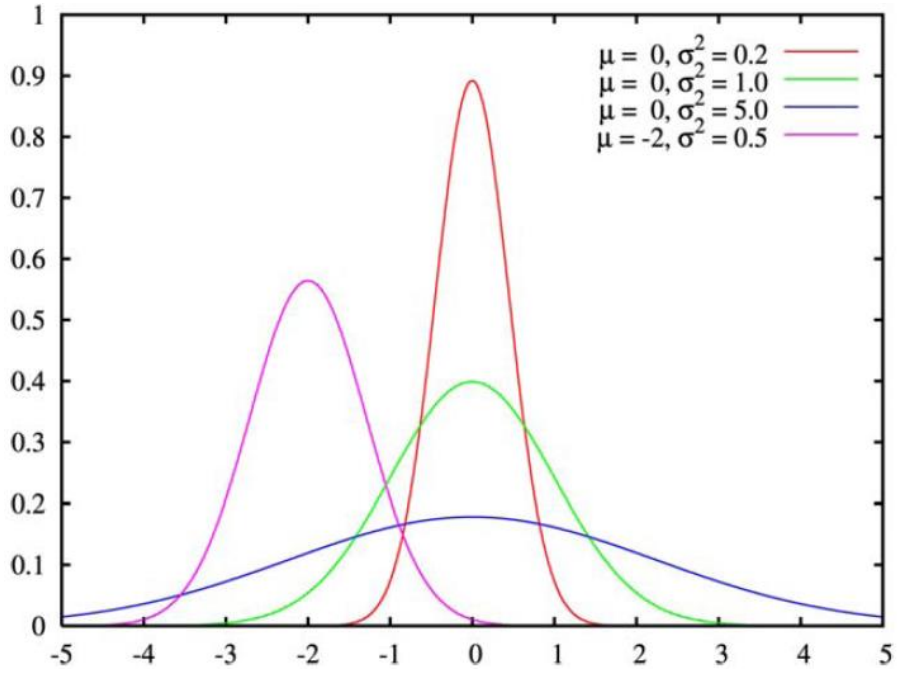
The width of the curve (SD) determines how tall it is:

- High probability to measure a baby within +/- 3 cm of the mean (95 %)
- Low probability to measure a man within +/- 3 cm of the mean *(because there are much more options for a man! → high SD*

Normal distribution

- Symmetric around μ

- **Defined by μ and σ^2**
- If we know that a variable has a normal distribution, and we know these parameters, then we know the probability of getting any particular value for the variable.



- The area under the curve = probability
- Total area under the curve = 1

Population parameters

- Imagine: you had the tools, time and money to measure the number of mRNA transcripts of gene X in ALL cells of the liver (240 000 000 000 cells) = POPULATION

This (almost) NEVER happens!!

Population parameters

- (If the histogram looks like this,) we can fit a normal distribution to the data, with
  - population mean = 20
  - population SD = 10

Population parameters

Population parameters

- (Almost) ALWAYS: we don't have these tools/time/money!!
- We estimate the population parameters using a relatively small number of measurements (= sample).

Population parameters

Instead of just describing the measurements of 5 cells (out of 240 000 000 000), we use them to estimate the population parameters (exp. 1)

New measurements in future experiments (exp. 2) will come from the same population!

We want to know the population parameters to ensure that the results drawn from our experiment are reproducible.

Mean

- In order to fit a normal curve to a histogram, we need to calculate mean and variance or standard deviation (SD) = Population parameters.
- Center normal curve over population mean
- $\overline{x} \neq \mu$ but with larger sample, $\overline{x}$ gets closer to μ

Population:
Measurements
of ALL liver cells

Sample:
Measurements
of 5 liver cells

Variance and SD

$\sigma^2 =$ Population variance $= \frac{\sum(x-\mu)^2}{N} = 100$

$\sigma^2 =$ average of the square differences between the data and μ

But the units for σ^2, are mRNA²

→ Cannot plot σ^2 on X-axis

To solve this problem: take the square root :

$\sigma =$ Population Standard Deviation $= \sqrt{\frac{\sum(x-\mu)^2}{N}} = \sqrt{100} = 10$

Population:
Measurements
of ALL liver cells

Variance and SD

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Population:
Measurements
of ALL liver cells

Variance and SD

But we almost never have population data!

So we almost never calculate μ, σ^2, and σ!

Instead, we estimate μ, σ^2, and σ from a relatively small sample.

$$s^2 = \text{Estimated Population variance} = \frac{\sum(x - \overline{x})^2}{n - 1} = 105.7$$

$$s = \text{Estimated Population Standard deviation} = \sqrt{\frac{\sum(x - \overline{x})^2}{n - 1}} = 10.3$$

Dividing by $n - 1$ instead of n, compensates for the fact that we are calculating differences from the sample mean instead of the population mean. Otherwise, we would consistently underestimate the variance around the population mean.

Estimated Probability Distribution, based on estimated population parameters, based on 5 observations

Population probability distribution

$$\sqrt{\frac{\sum(x - \overline{x})^2}{n}} = 9.2$$

Population parameters

- Problem: at each repetition of an experiment, we get different estimates of the population parameters and all these estimates are different from the true population values!

Population parameters

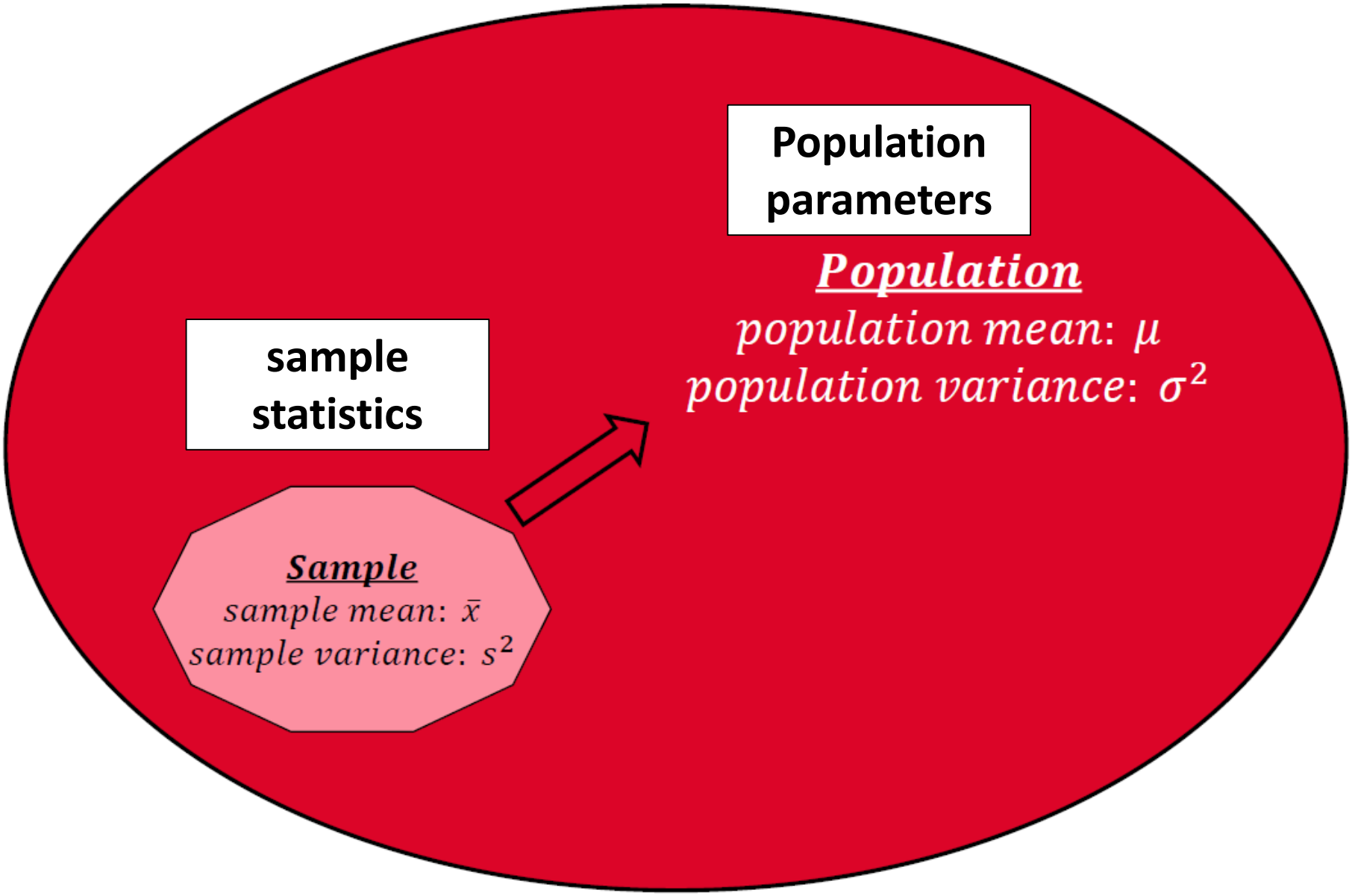
- The more data we have, the more confidence we can have in the accuracy of the estimates
- GOAL of statistics: quantifying how much confidence we can have in estimated population parameters

→calculate p-values and confidence intervals

→Tell if estimated population parameters of two experiments are significantly different

If estimated population parameters of two experiments are not significantly different, the measurements of the two experiments are samples of the same population

- Descriptive Statistics: summarize the sample data as means, variances, ranges, etc.
- Inferential Statistics: use the sample statistics to estimate the parameters of the population (confidence interval)


Population parameters
Population
population mean: μ
population variance: σ^2
sample statistics
Sample
sample mean: $\bar{x}$
sample variance: s^2

Sample Statistics to Estimate Population Parameters:

If simple random sampling (every observation has the same chance of being selected) is used to select n from N, then:

- Sample estimates are **unbiased estimates of their counterparts** (e.g., sample mean estimates the population mean), meaning that over all possible samples the sample statistics, averaged, would equal the population statistic.
- A particular sample value (e.g., sample mean) is called a "**point estimate**" – do not necessarily equal the population parameter for a given sample.
- Can calculate an interval where the true population parameter is likely to be, with a certain probability. This is a **Confidence Interval,** and can be obtained for any population parameter, IF the distribution of the sample statistic is known.

Parameters for populations
(→using Greek letters!)

MEASURES OF CENTRAL TENDENCY

1. Mean -- μ

e.g. for *N=5*

Y1=24; Y2=13; Y3=19, Y4=26, Y5=11

μ=18.6

2. Standard Deviation σ and Variance σ^2

$$\sigma^2 = \sum_{i=1}^{N} (y_i - \mu)^2 \Big/ N$$

$$\sigma = \sqrt{\sigma^2}$$

Statistics from the sample

(= estimates of the population parameters!)

1. Mean -- $\overline{y}$ e.g. for *n=3 and y1=5; y2=6; y3=7 ,* $\overline{y}$*= 6*
2. Standard Deviation *s* and Variance s^2 (often called "mean square")

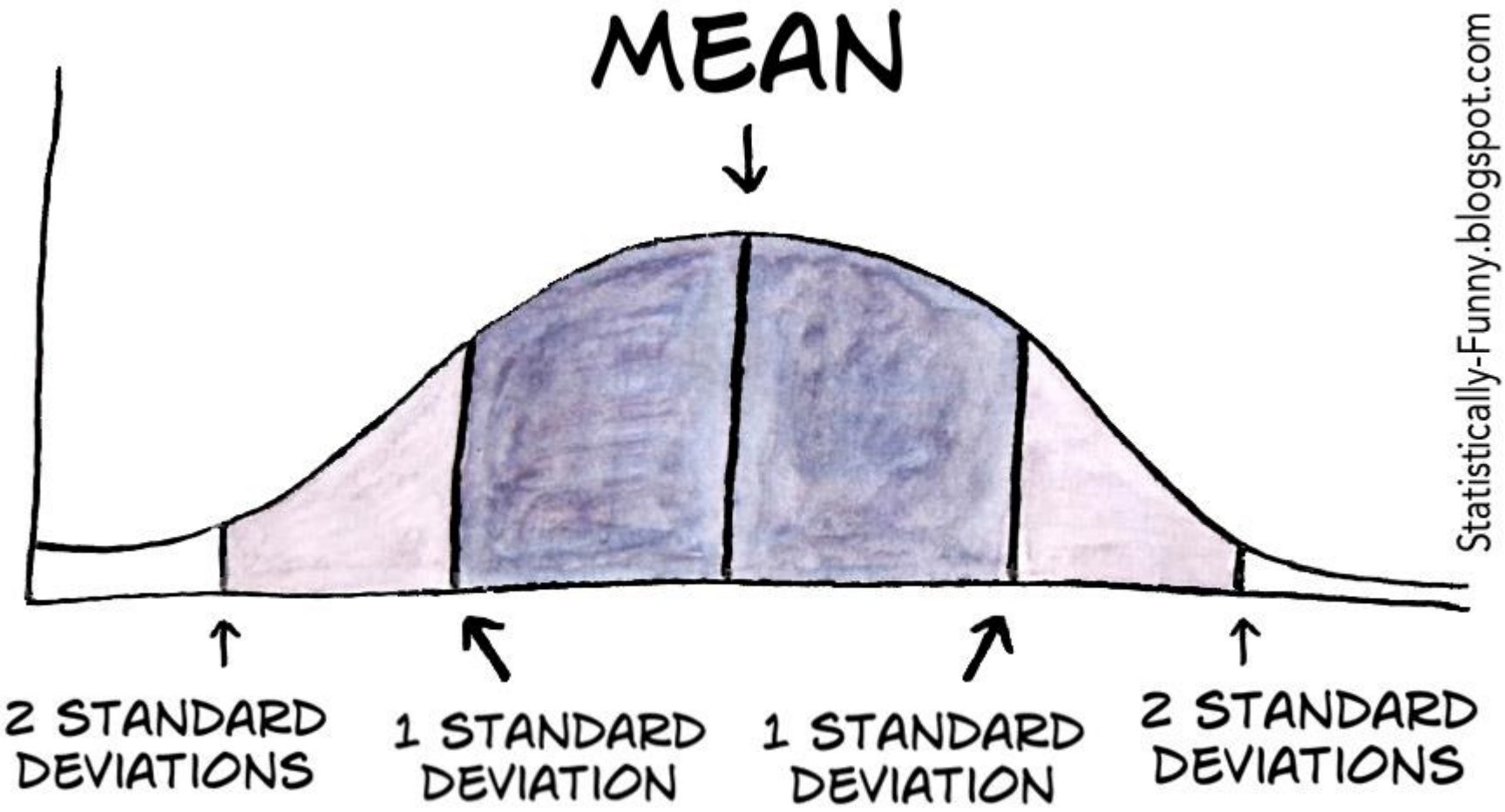
$$s^2 = \sum_{i=1}^{n} (y_i - \bar{y})^2 \Big/ (n-1)$$

$$s = \sqrt{s^2}$$

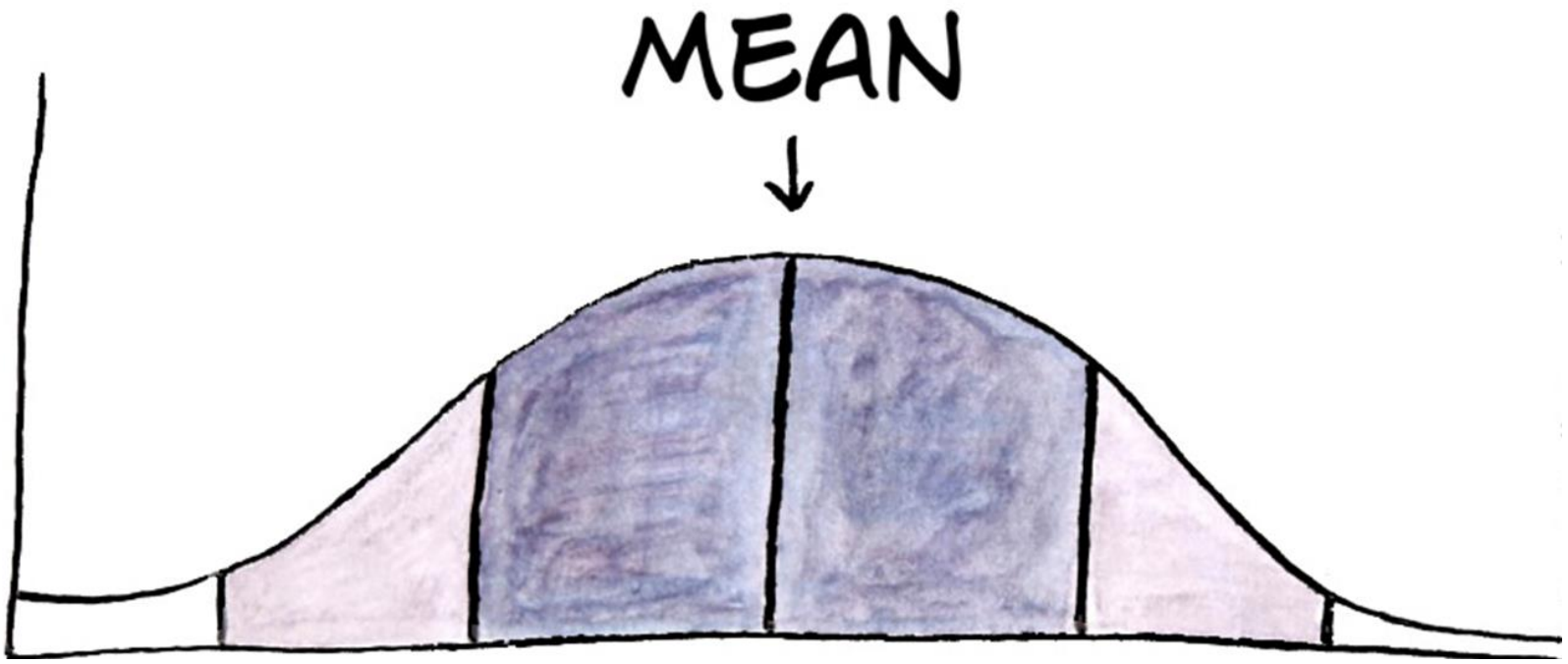
The fact that the sample mean is used instead of population mean makes the sum of squares of deviations smaller. You adjust for this by dividing by n-1 so that the sample variance would be an unbiased estimator of the population variance

A **rough estimate** of the standard deviation is

$$s \approx \frac{\text{range}}{4}$$



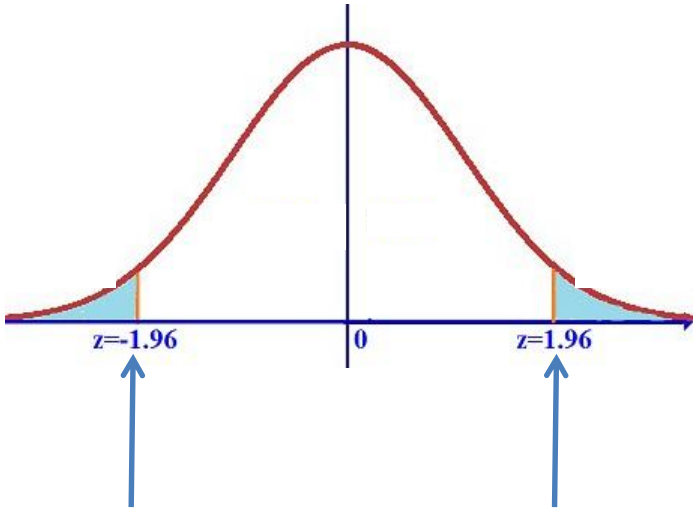
Percentiles



percentile

The n^{th} **percentile** of an observation variable is the value that cuts off the first *n* percent of the data values when it is sorted in ascending order.

(**quantile** is expressed in fractions *vs.* **percentile** is expressed in pct)



2.5 % of the data is smaller than this value
-1.96 is the 2.5th percentile

97.5 % of the data is smaller than this value
1.96 = 97.5th percentile

Normal distribution R functions

#random generation

rnorm(n, mean = 0, sd = 1)

```
> rnorm(5, mean = 0, sd = 1)
[1] -1.3986100  0.3028934 -0.9172586 -0.7261859 -1.6761790
```

#give quantile value based on probability

qnorm(p, mean = 0, sd = 1)

```
> qnorm(0.05/2)
[1] -1.959964
```

#give probability based on quantile value

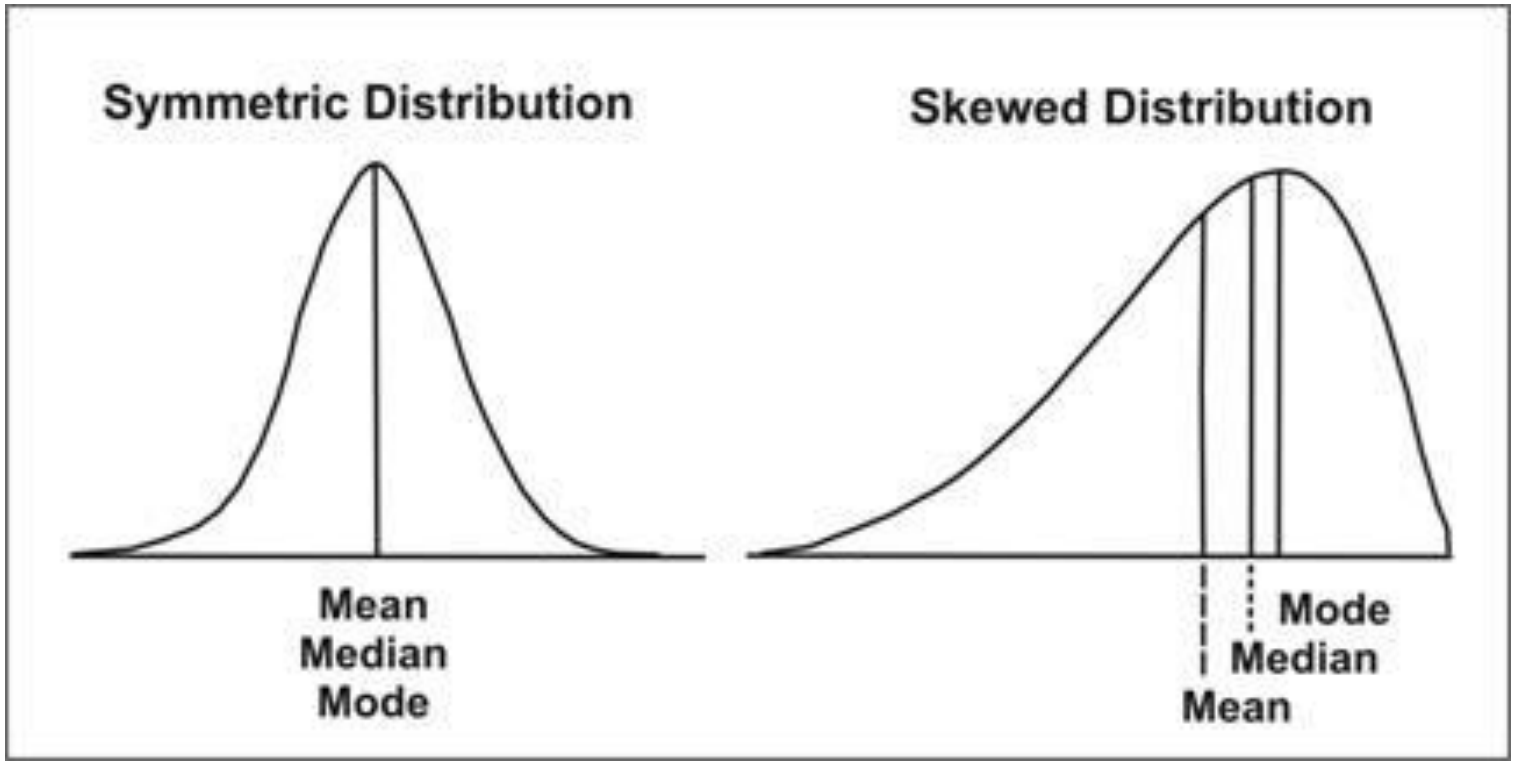
pnorm (q, mean = 0, sd = 1)

```
> pnorm (-1.96, mean = 0, sd = 1)
[1] 0.0249979
```

Median -- value which divides the distribution (50% of N observations are above and 50% are below)

= 50th percentile

Unaffected by extremely large and extremely small values.



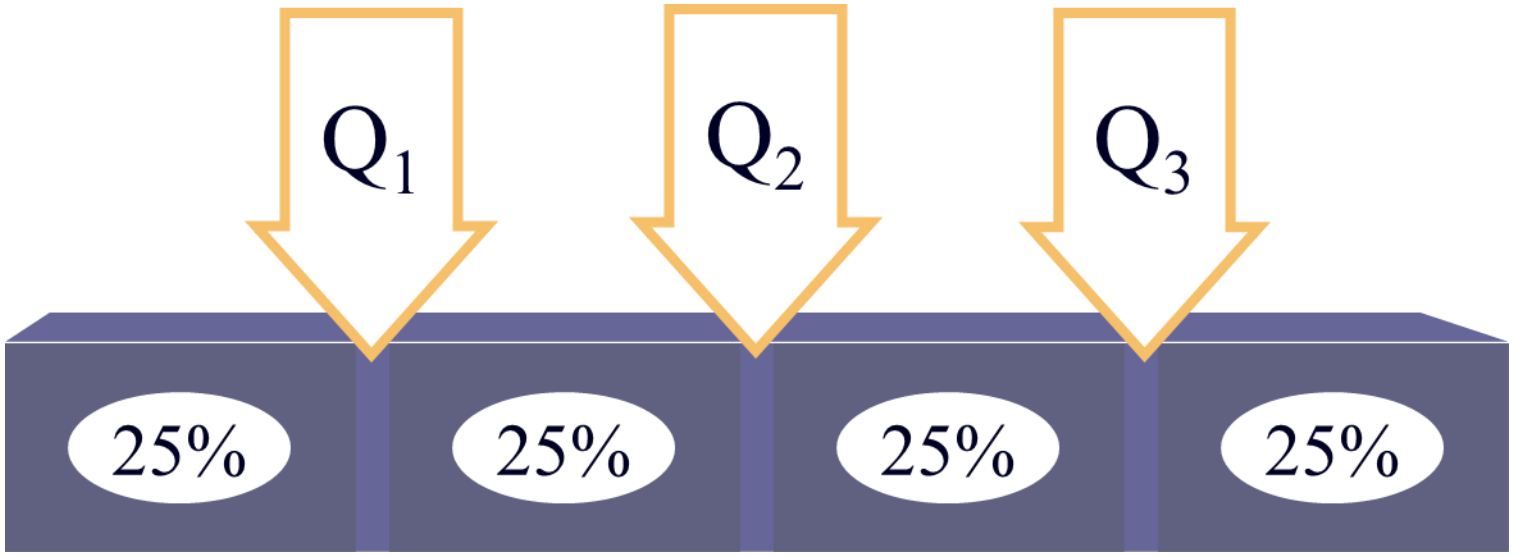
Median: Computational Procedure

- First Procedure
  - Arrange observations in an ordered array.
  - If number of terms is odd, the median is the middle term of the ordered array.
  - If number of terms is even, the median is the average of the middle two terms.

- Second Procedure
  - The median's position in an ordered array is given by (n+1)/2.

	DISCRETE VARIABLES		CONTINUOUS VARIABLES	
Provides:	**Nominal**	**Ordinal**	**Interval**	**Ratio**
The "order" of values is known		✔	✔	✔
"Counts," aka "Frequency of Distribution"	✔	✔	✔	✔
Mode	✔	✔	✔	✔
Median		✔	✔	✔
Mean			✔	✔
Can quantify the difference between each value			✔	✔
Can add or subtract values			✔	✔
Can multiple and divide values				✔
Has "true zero"				✔

Quartiles



Quartiles, *continued*

- Q_1 is equal to the 25th percentile
- Q_2 is located at 50th percentile and equals the median
- Q_3 is equal to the 75th percentile

Quartile values are not necessarily members of the data set

Quartiles: Example

- Ordered array: 106, 109, 114, 116, 121, 122, 125, 129

- Q_1: $i = \frac{25}{100}(8) = 2 \qquad Q_1 = \frac{109+114}{2} = 111.5$

- Q_2: $i = \frac{50}{100}(8) = 4 \qquad Q_2 = \frac{116+121}{2} = 118.5$

- Q_3: $i = \frac{75}{100}(8) = 6 \qquad Q_3 = \frac{122+125}{2} = 123.5$

R functions for sample statistics

summary()

max(), min(), range()
mean(), median()
var(),
quantile(), IQR()
➔these functions work on vectors and full matrices

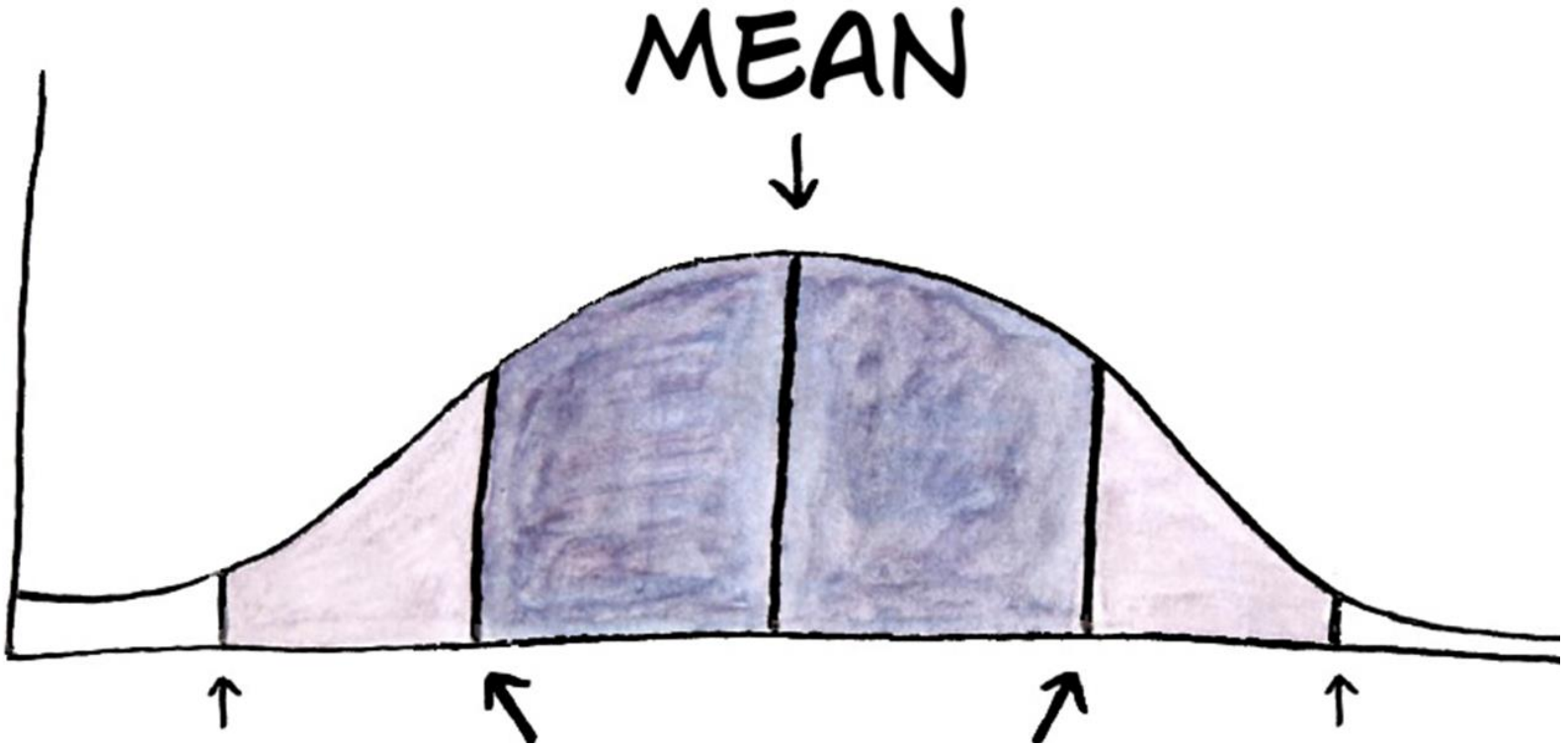
Exercise: In the "ufc_processed" dataset,

- what are the mean, median, standard deviation, minimum, maximum, and interquartile range of the diameter (in centimeter)?

script 1_confidenceinterval.R

Standardization

Z-score = number of standard deviations that a particular value is away from the mean



Z-score

- z-scores = standard score
- **Transformation to the z-score = standardization = scaling:**

  scale the values for y by subtracting the mean, and dividing by the standard deviation.

$$z_i = \frac{y_i - \mu}{\sigma}$$

→ z-score is the number of standard deviations that a particular value is away from the mean

→ Z-score follows the standard normal distribution N(0,1)

E.g., for mean = 20, and standard deviation of 2 and y = 10,

Z = -5 (an extreme value)

Figure 7. List of putatively structurally characterized metabolites with a different abundance in inflorescence stems of *ccr1-6 ProSNBE:CCR1* plants as compared with the wild type or *ccr1-6* mutants. Eighty-two compounds were characterized, of which the abundance was significantly different between *ccr1-6 ProSNBE:CCR1* and the wild type, on the one hand, and/or *ccr1-6 ProSNBE:CCR1* and *ccr1-6*, on the other hand. The differentially accumulating metabolites were classified into eight different groups (Fig. 6B). Each putatively structurally characterized metabolite has a unique number that represents (1) the group that the metabolite belongs to and (2) the ranking within this group. The metabolites are listed per metabolic class, and the dashed lines separate the different groups present in a specific metabolic class. The average peak intensities are represented by a heat map, ranging from low values represented in blue to high values represented in red (wild type, n = 8; *ccr1-6*, n = 6; and *ccr1-6 ProSNBE:CCR1*, n = 13).

THIS IS WRONG!

43519

43352

517
9

Different colors but same value

The blue value is higher than the red value

Plant Physiology; De Meester et al., 2017

- Normal distribution for $\mu=0$ and $\sigma^2=1$

= N(0,1)

= **standard normal distribution**

= **Z-distribution**

- Probability tables for $\mu = 0$ and $\sigma^2 = 1$, are often called **z-tables**.

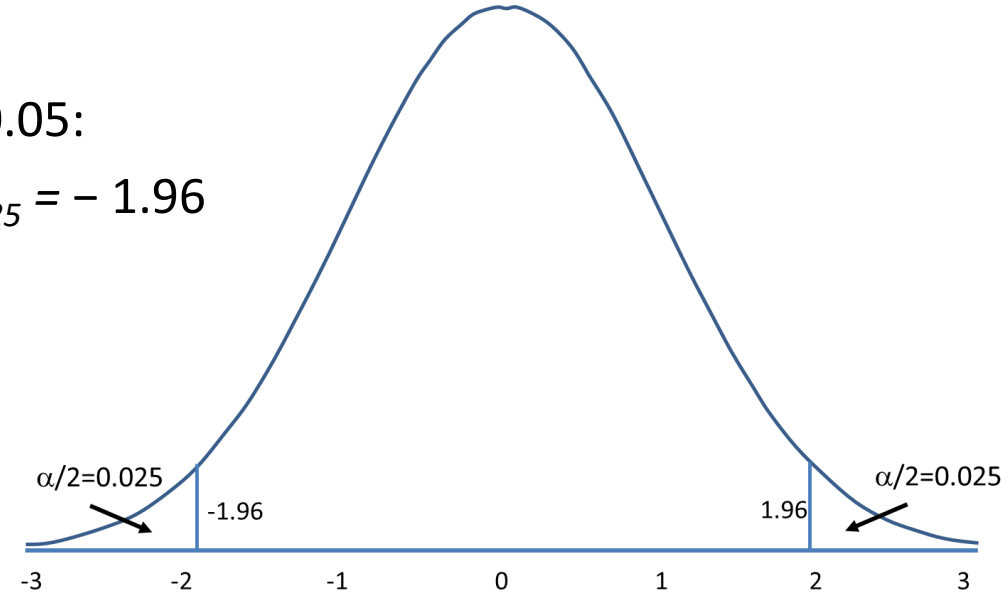
- Example:

  P(-1.96 < z < 1.96) = 0.95

  Notation:

  For **significance level α** = 0.05:

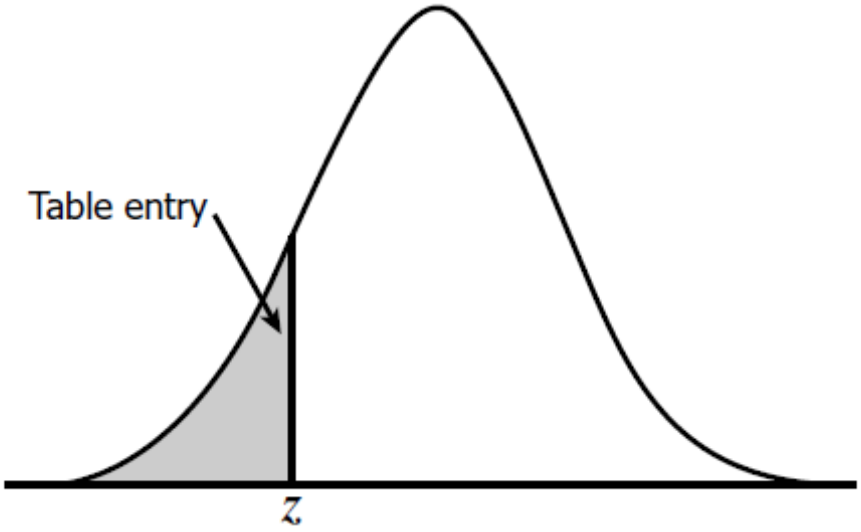
  Critical z-value = $z_{\alpha/2} = z_{0.025} = -1.96$

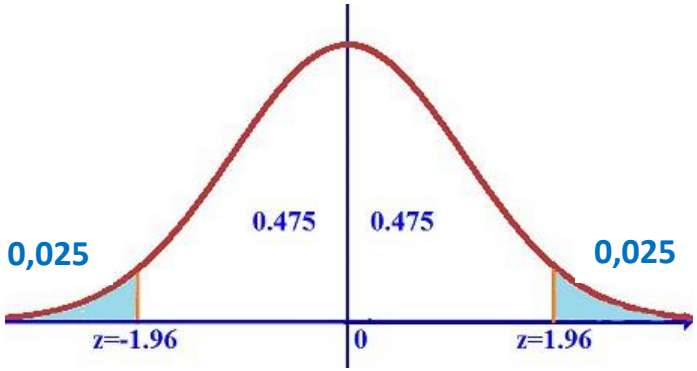


Using the Z-table to find the critical z-value at **significance level α**=0.05:

The z-table gives areas = probabilities

Look up the z-value corresponding to α/2 = 0.025 in the table: 1.96!





Example

- **Problem**

  Assume that the test scores of a college entrance exam fits a normal distribution. Furthermore, the mean test score is 72, and the standard deviation is 15.2. What is the percentage of students scoring 84 or more in the exam?

- **Problem**

  normal distribution; mean = 72; sd = 15.2

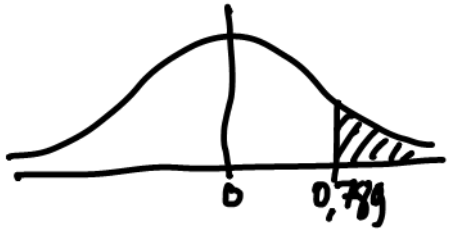
  percentage above 84?

- **Solution using Probability tables**

  We transform the value to the corresponding z-value

  z = (84-72)/15.2 = 0.789

  We draw the z-distribution (standard normal) and determine which area we are looking for

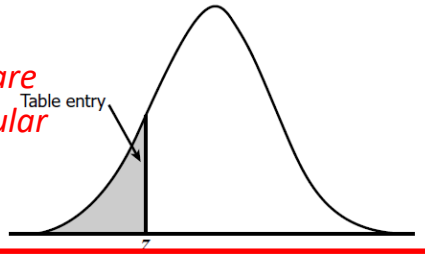


$P = 0.5 - P_{z0.789}$

We look up the P-value for z = 0.789 in the table

P = 0.2148

Check which probability values are given in this particular table!



Answer

The percentage of students scoring 84 or more in the college entrance exam is 21.5%.

- **Problem**

  normal distribution; mean = 72; sd = 15.2

  percentage above 84?

- **Solution using R**

  the function

  pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)

  gives the probability to be under (lower.tail) or above (lower.tail = FALSE) a certain percentile (**q**uantile) value.

  We don't need to transform to z-value: we can specify the mean and sd.

  Here we are looking for the percentage of students scoring higher than 84, we are interested in the *upper tail* of the normal distribution.

```
> pnorm(84, mean=72, sd=15.2, lower.tail=FALSE)
[1] 0.21492
```

- **Answer**

  The percentage of students scoring 84 or more in the college entrance exam is 21.5%.

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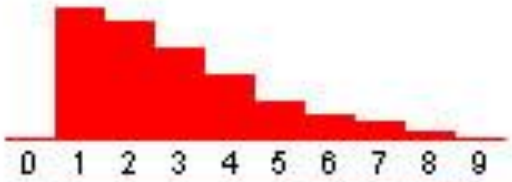
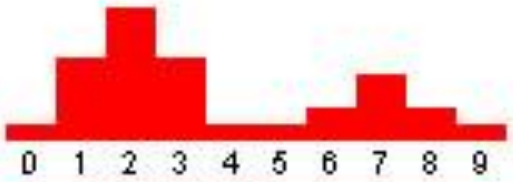
The Central Limit Theorem

Distribution shapes

Symmetric, unimodal, bell-shaped

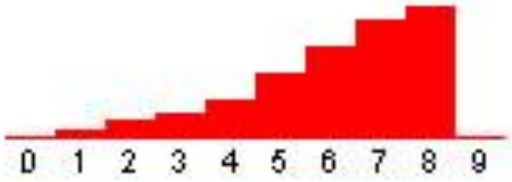


Skewed right



Non-symmetric, bimodal

Uniform



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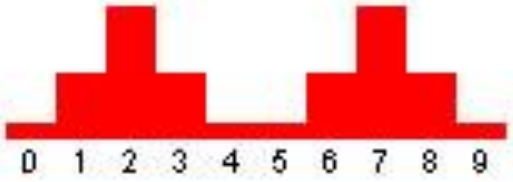
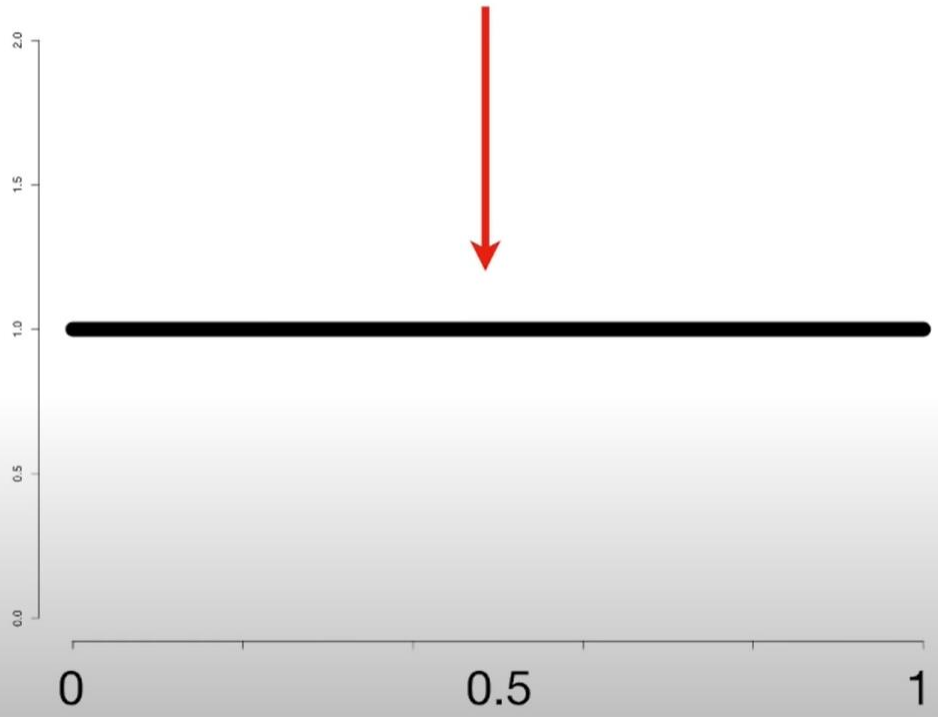


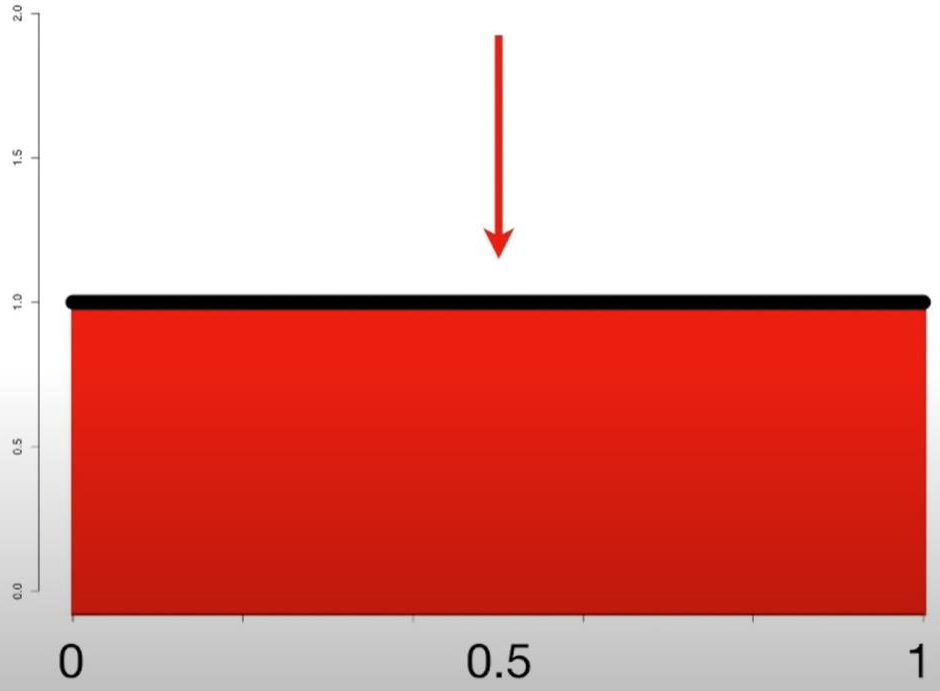
Symmetric, bimodal

Among all distributions, the normal distribution is the most common in nature.
Why?.....The **CENTRAL LIMIT THEOREM!**

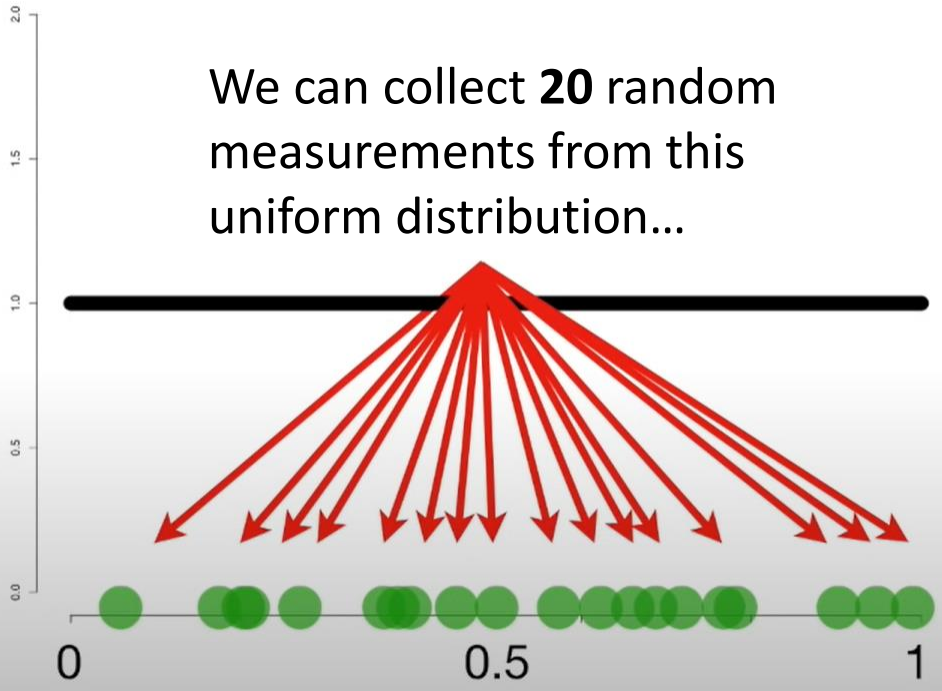
So let's start with a Uniform Distribution.



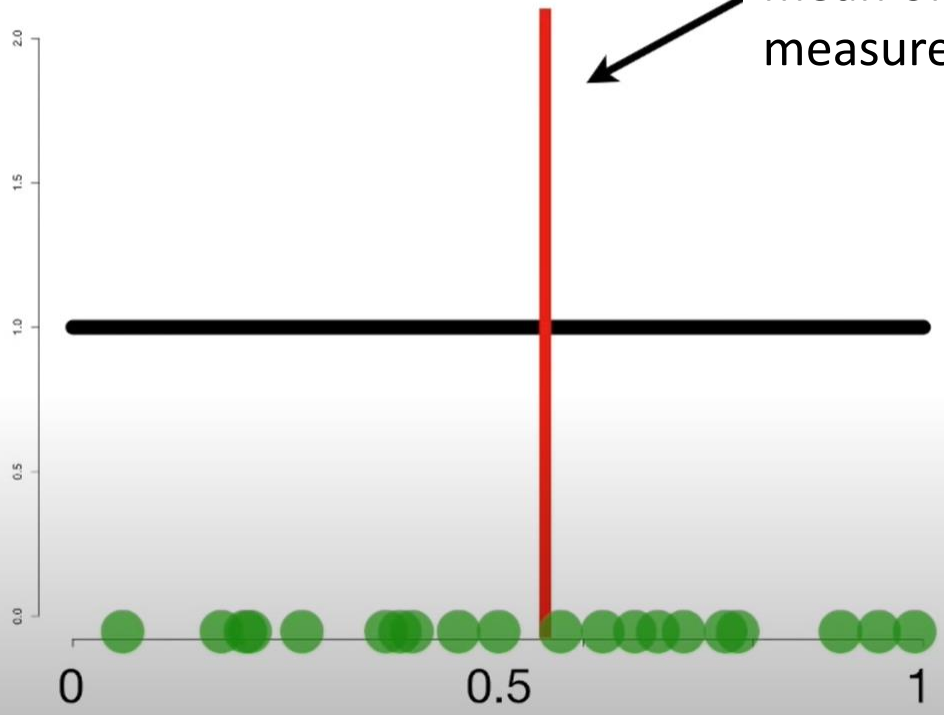
The probabilities are all equal,
and thus, are “uniform”.



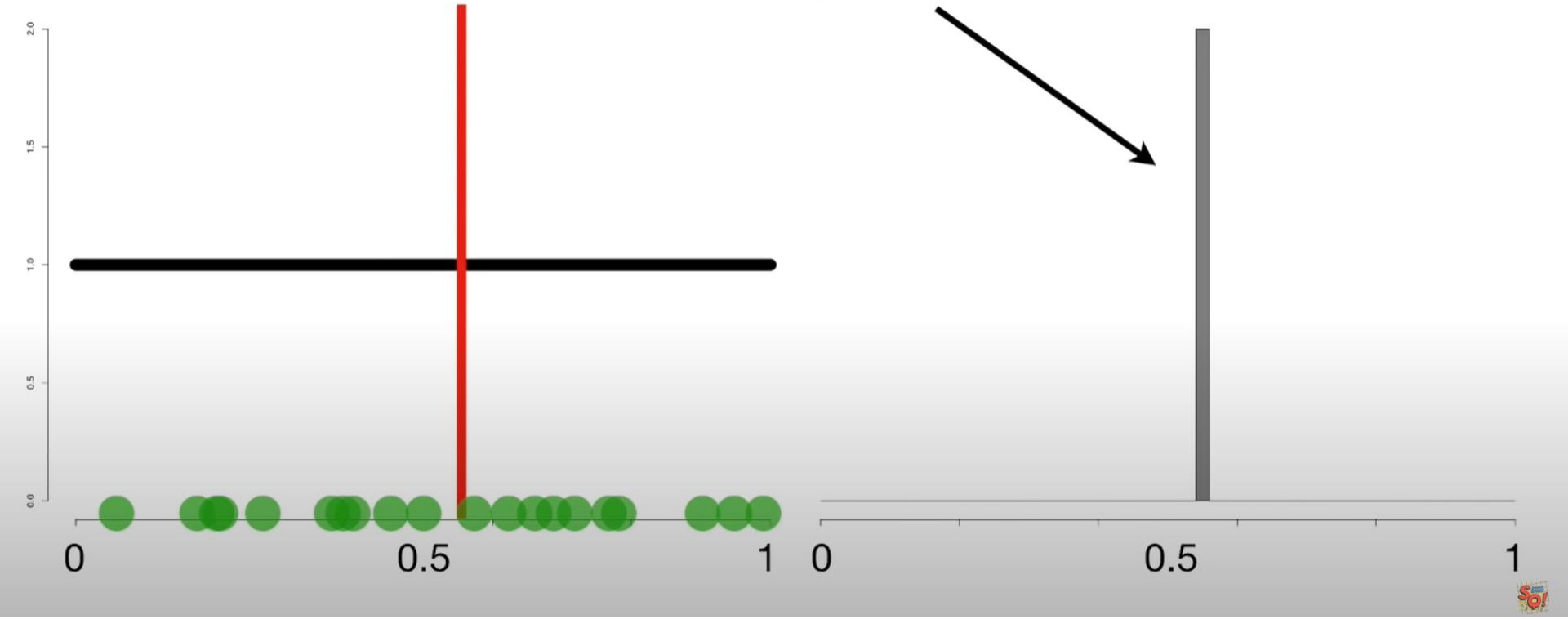
We can collect **20** random measurements from this uniform distribution…



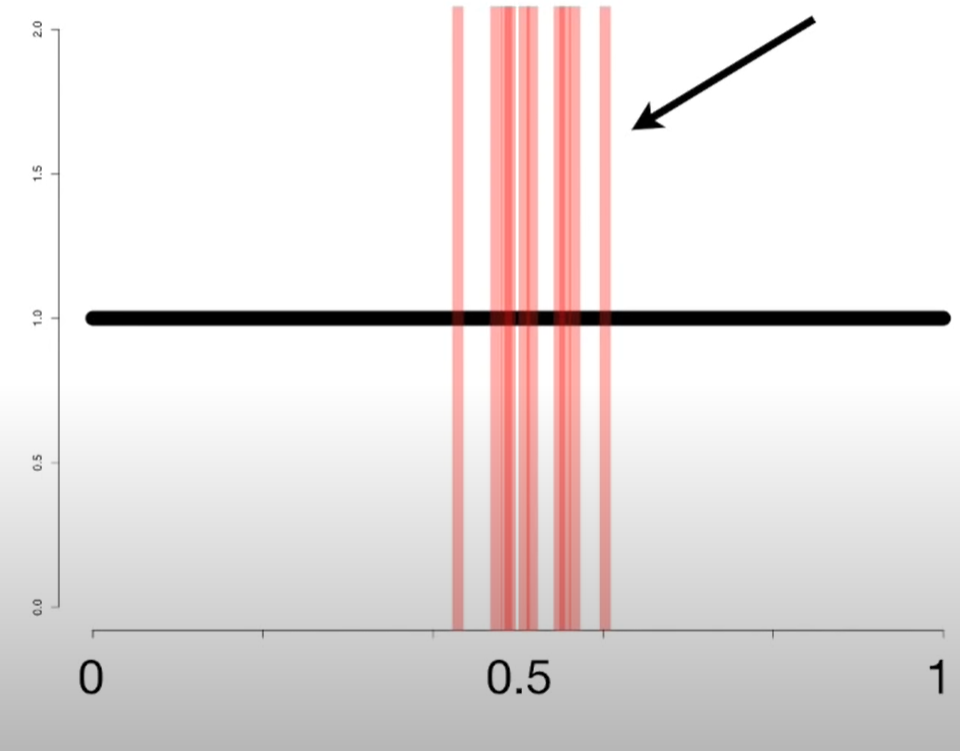
…and then calculate the mean of the measurements.

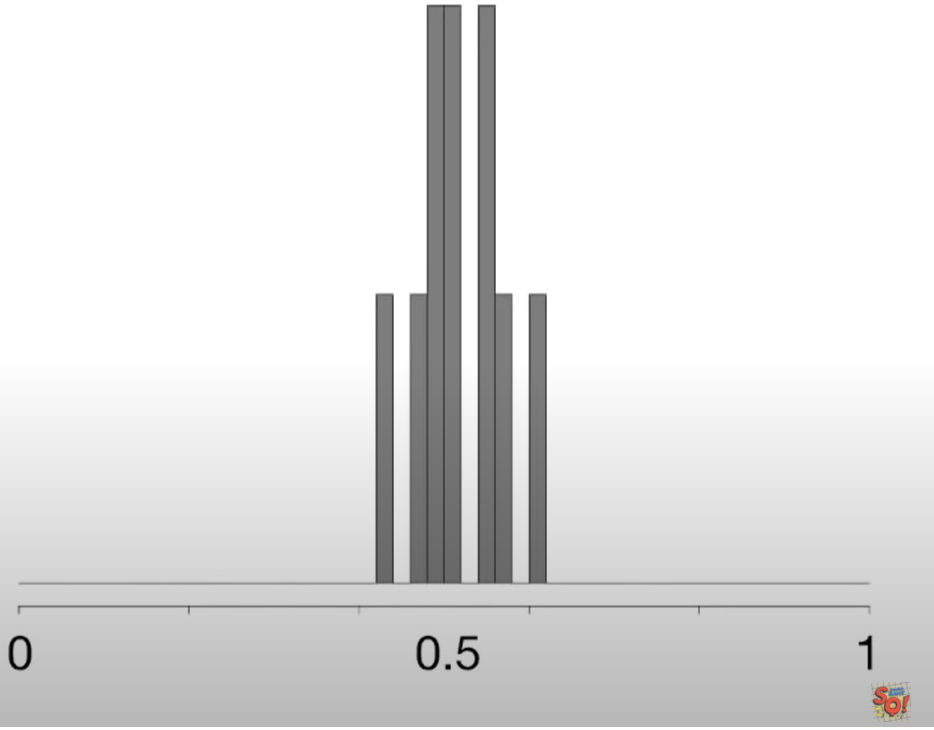


On the right, we can draw a histogram of the mean value.

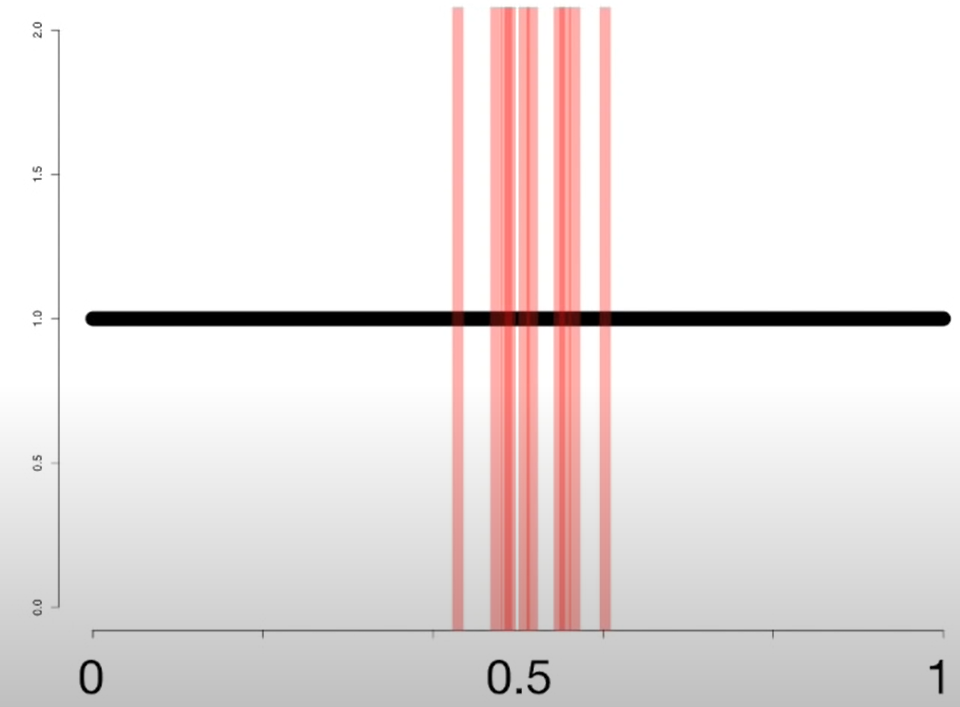


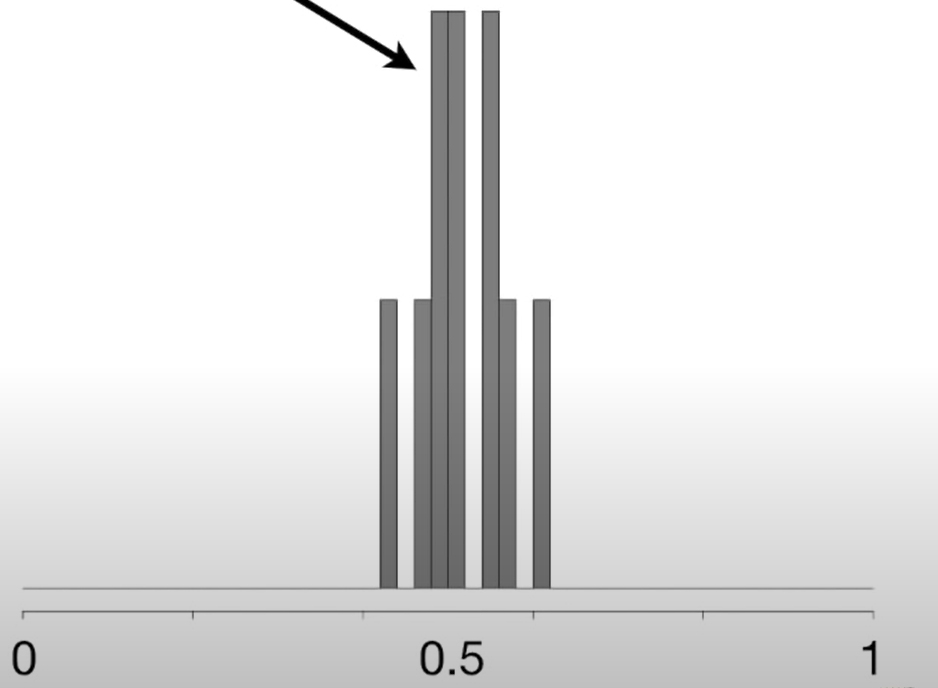
If we collect 10 more samples of **20** measurements from this uniform distribution…



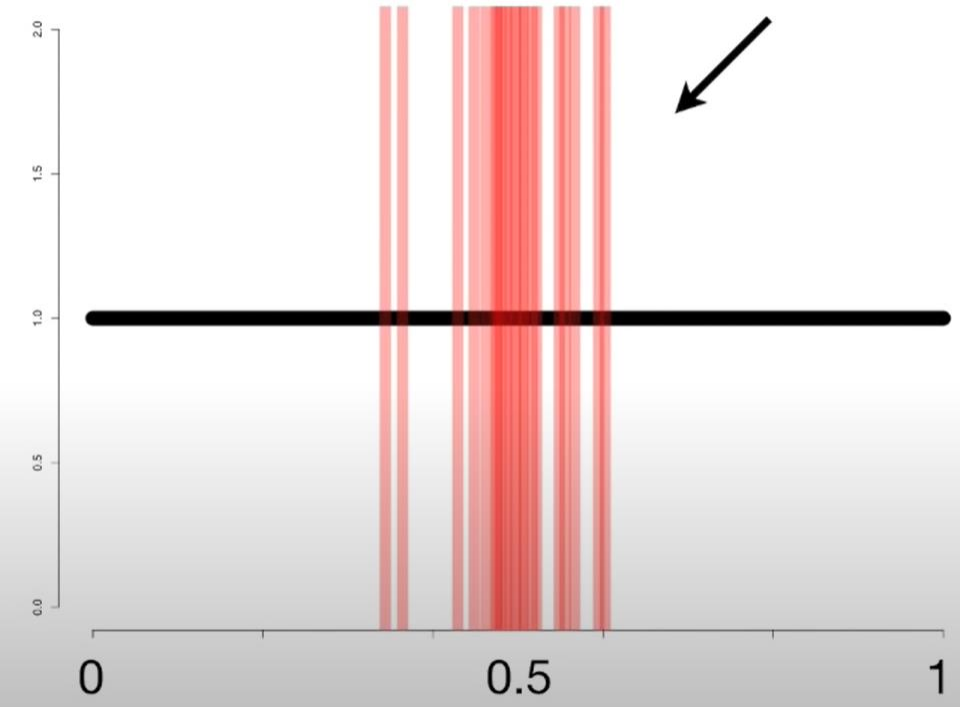


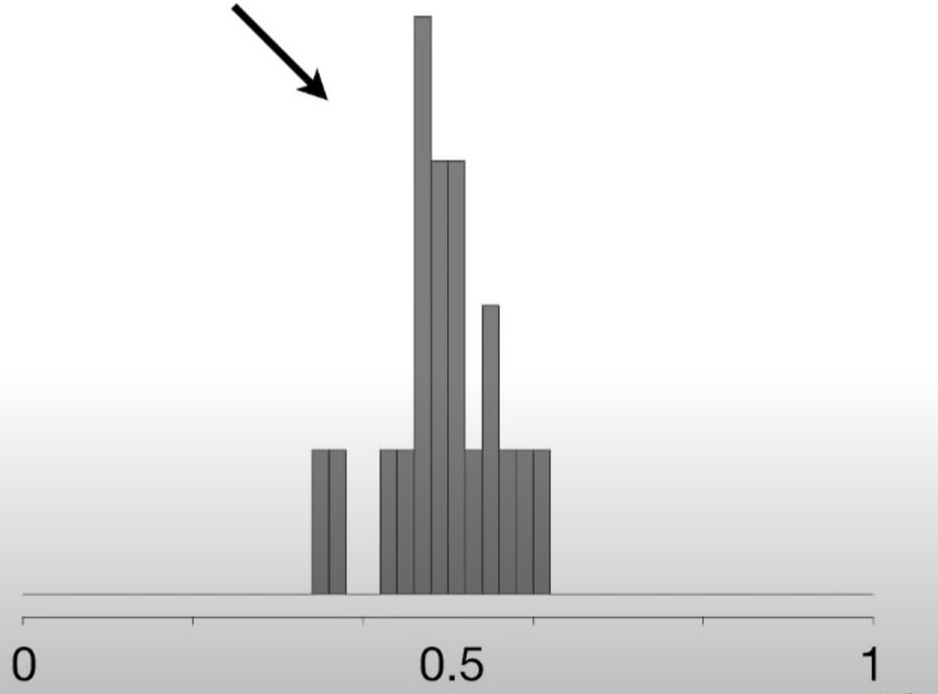
…the histogram starts to look at little more interesting.

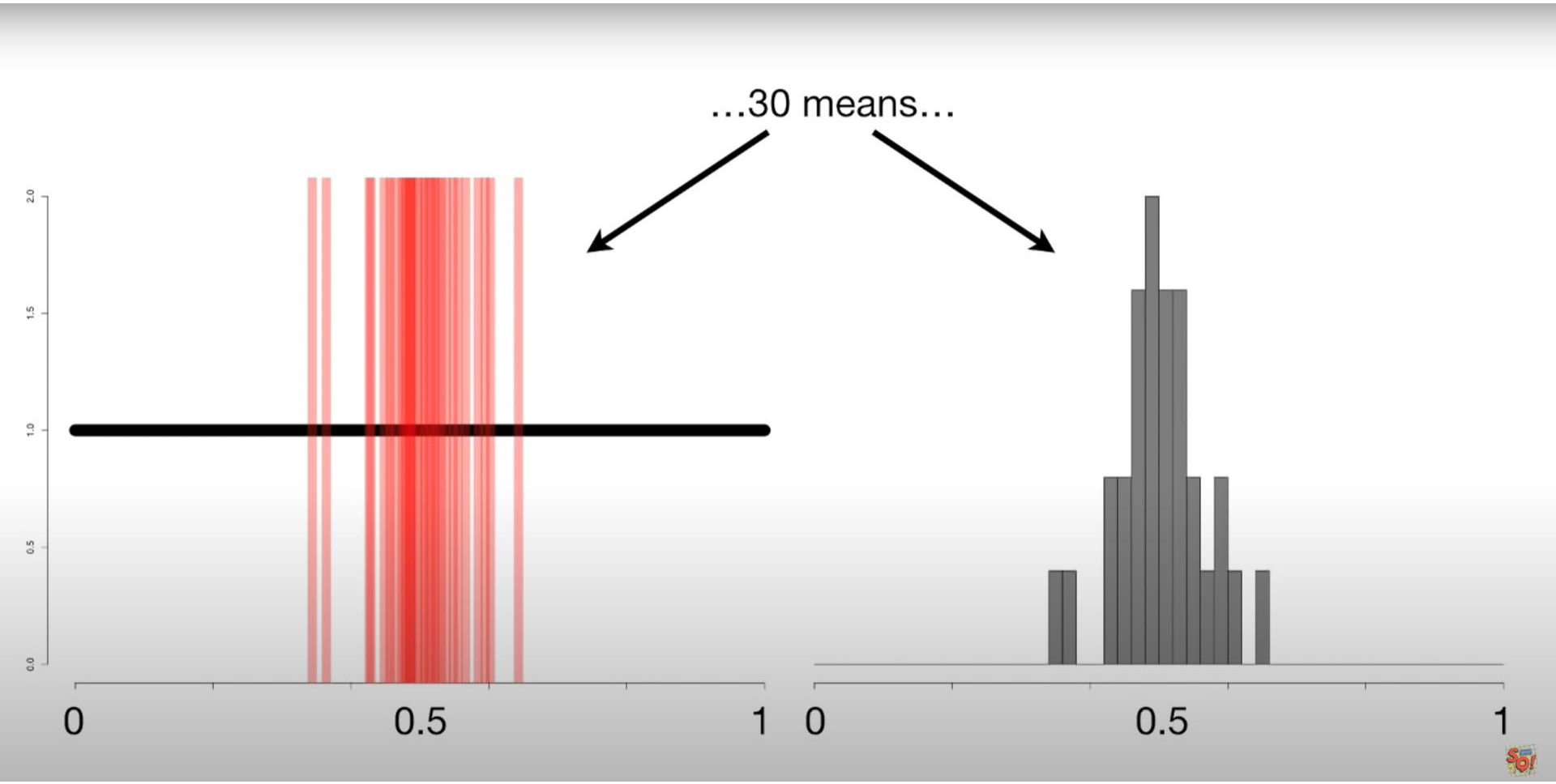


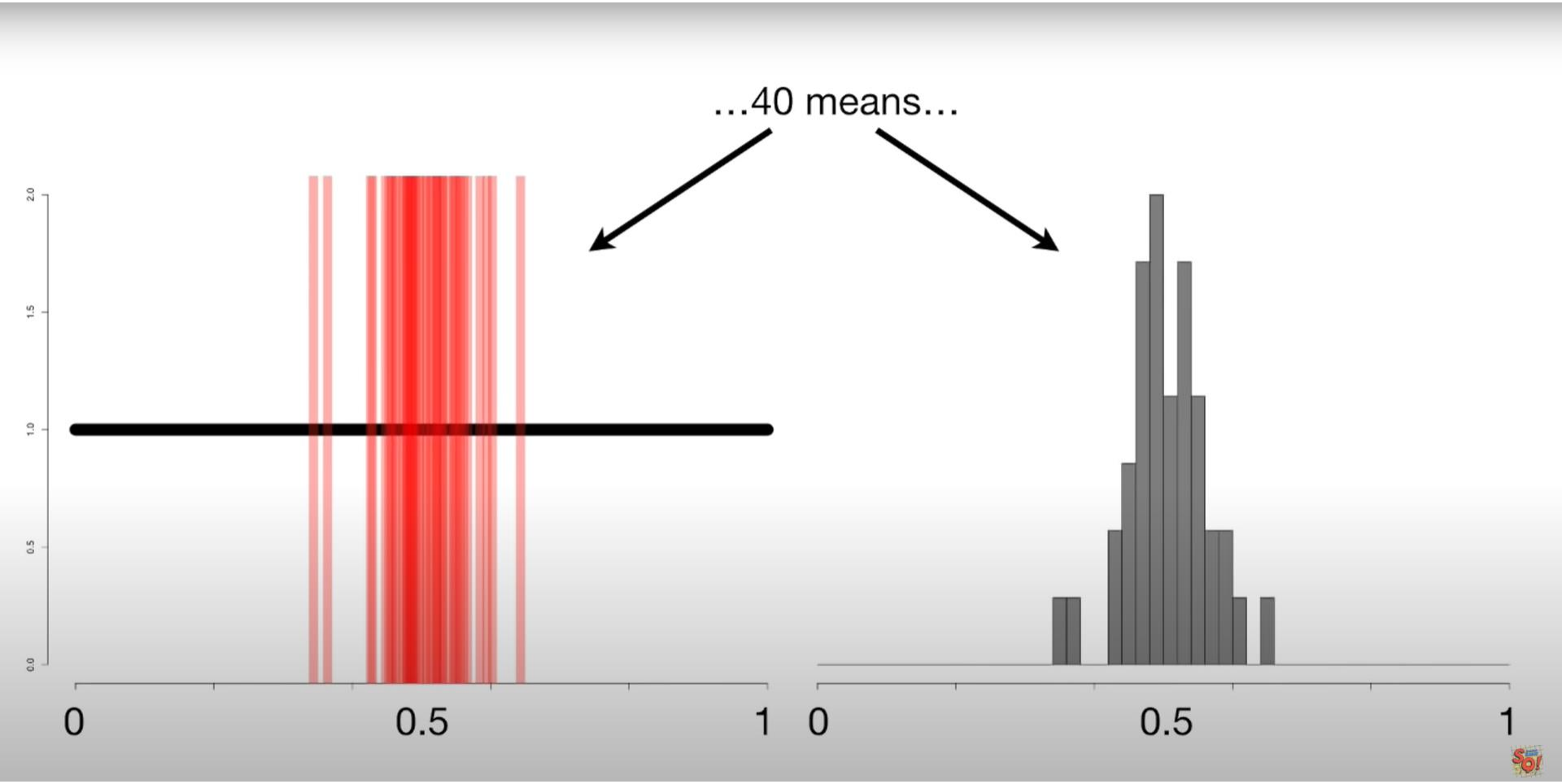


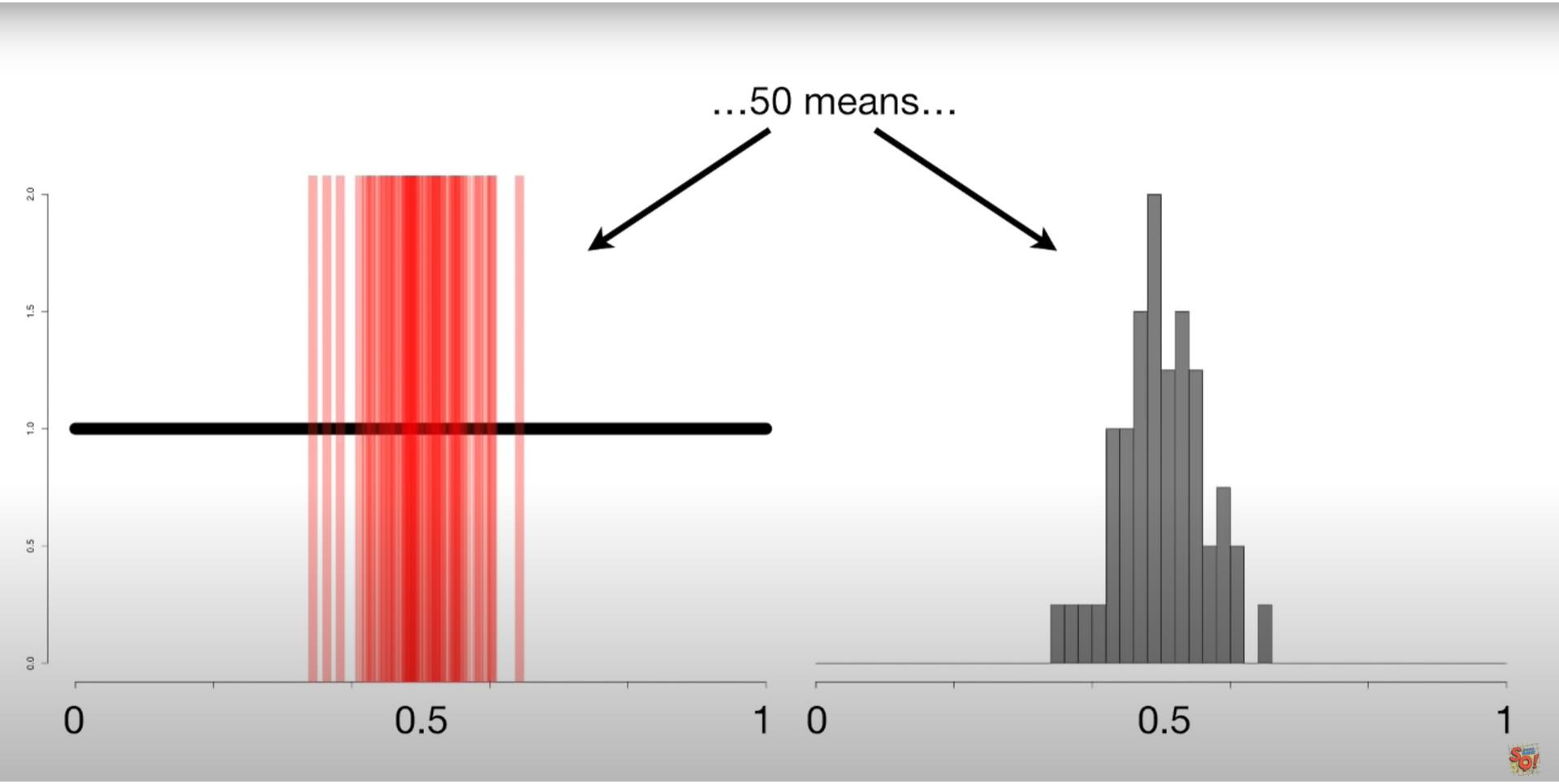
Here's the histogram after collecting 20 samples and calculating 20 means…

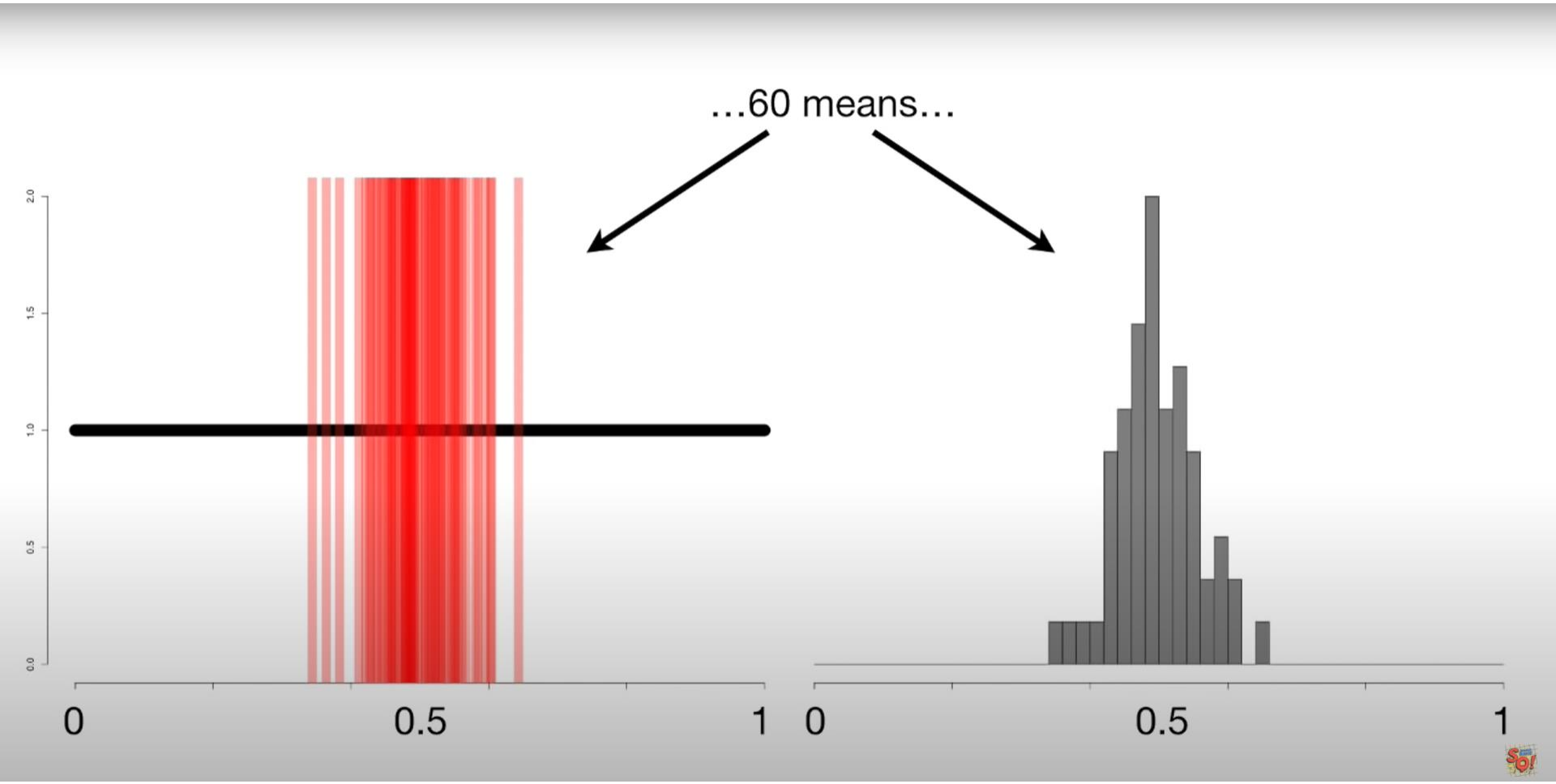


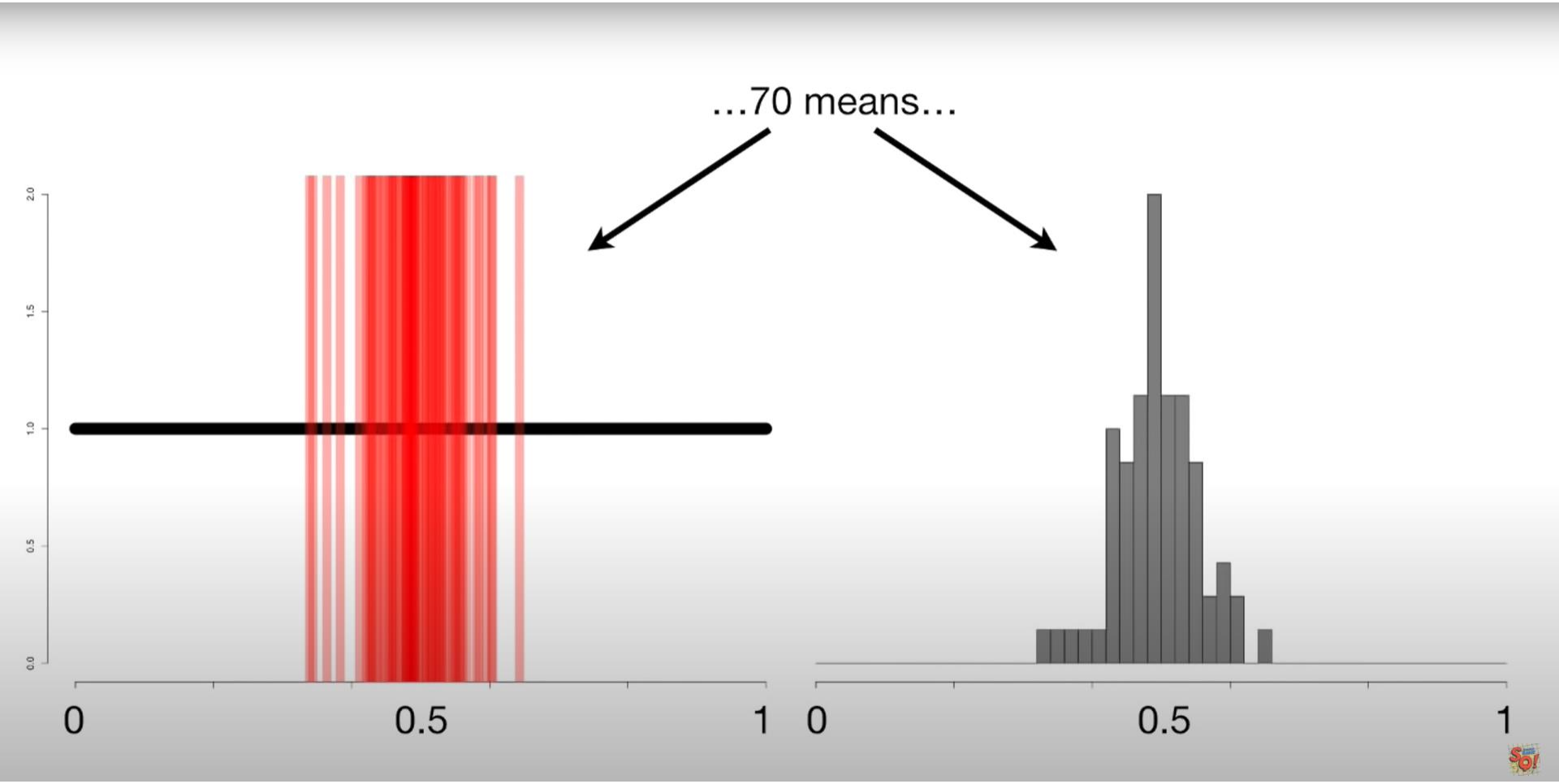


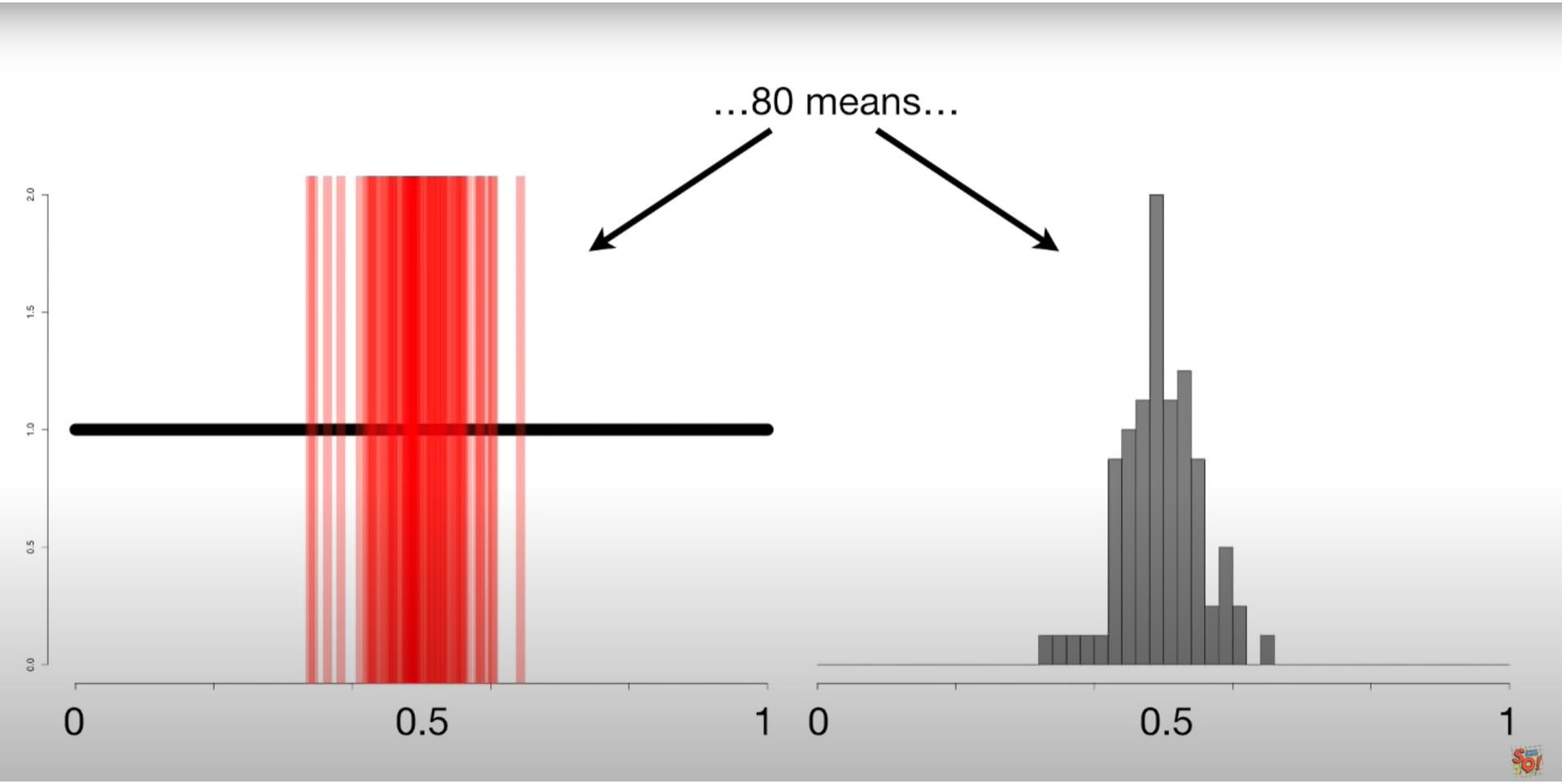

…30 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1

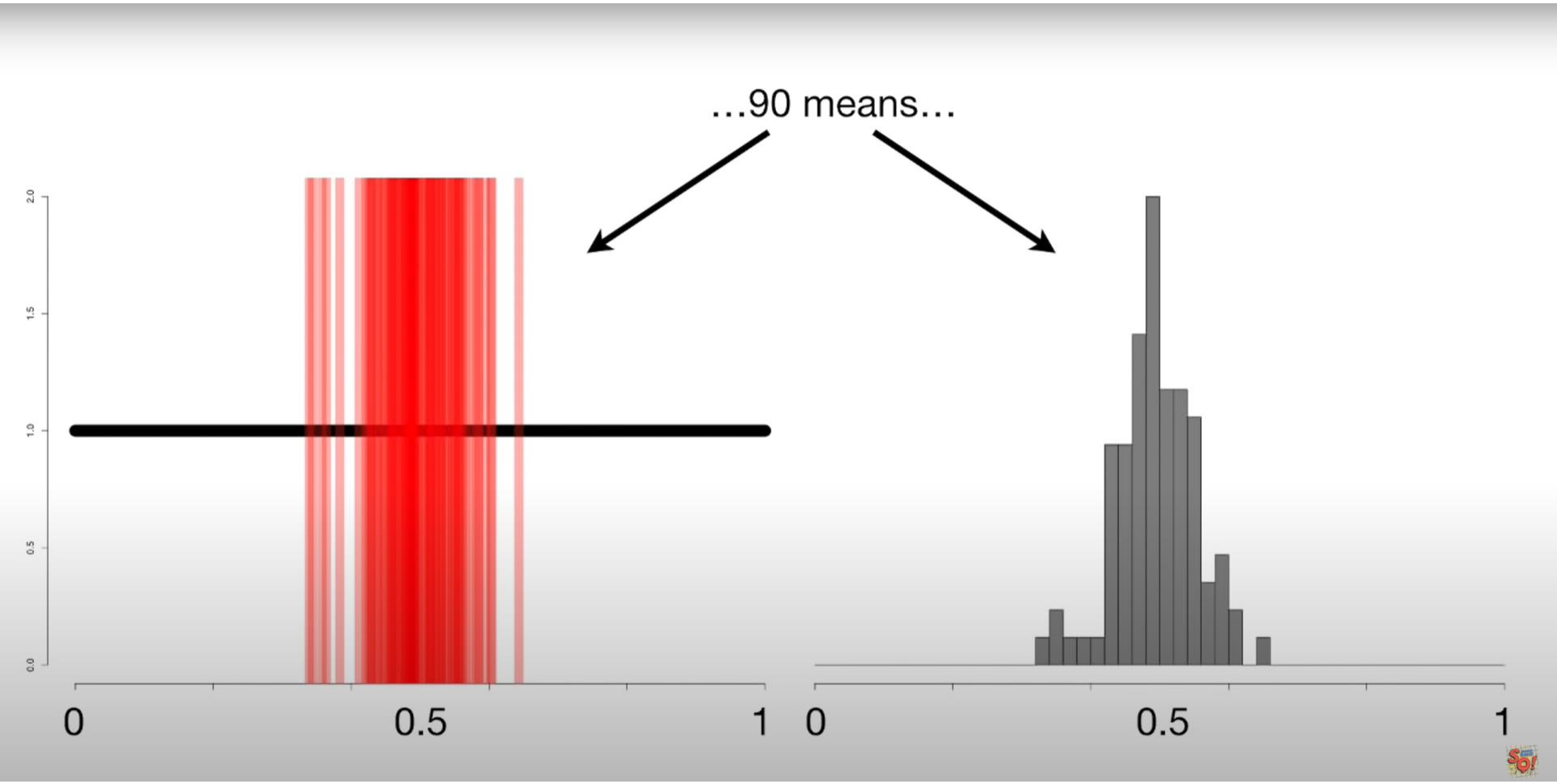

…40 means…
0.0
0.5
1.0
1.5
2.0
0
0.5
1
0
0.5
1

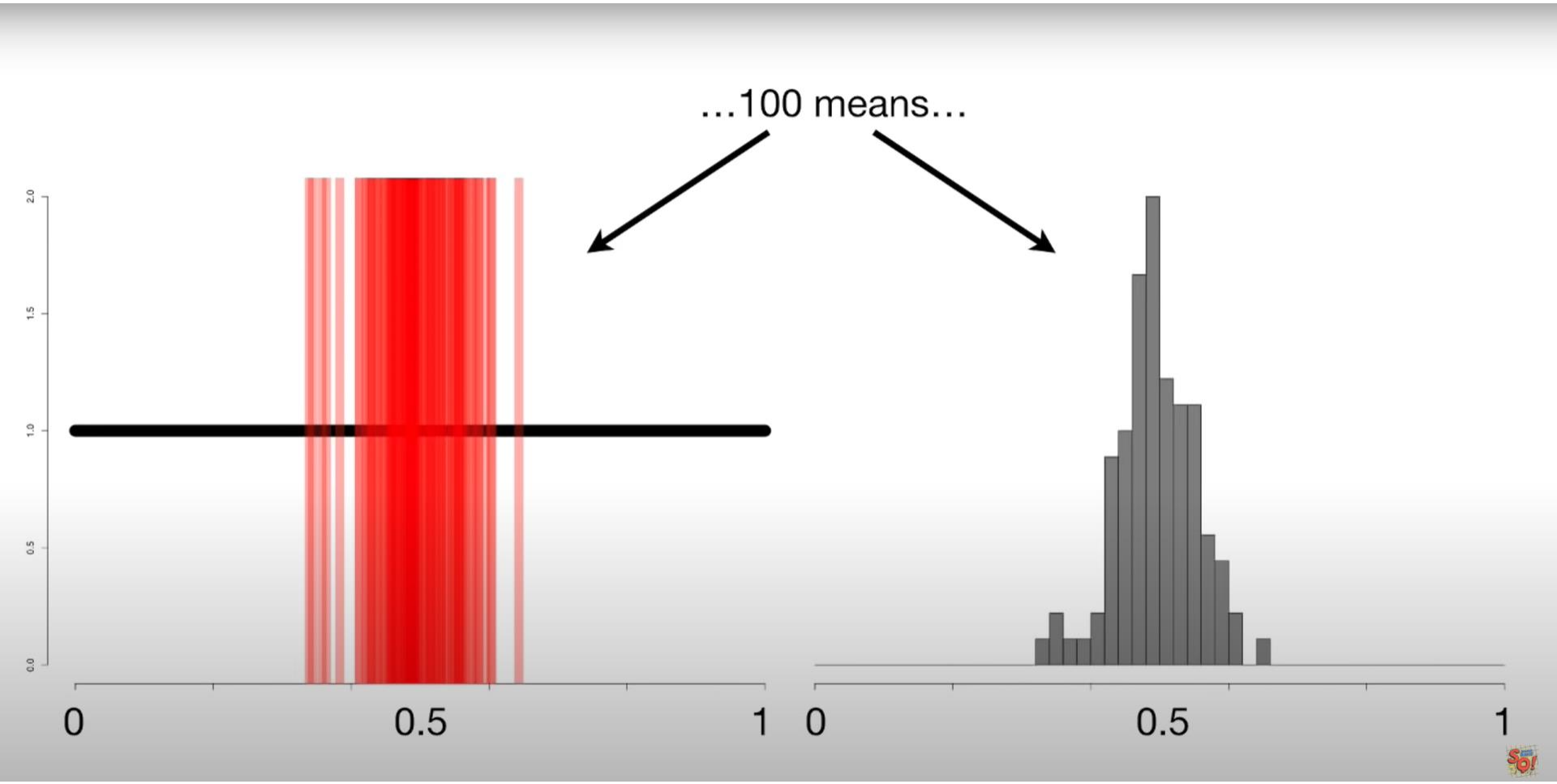

…50 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1


…60 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1

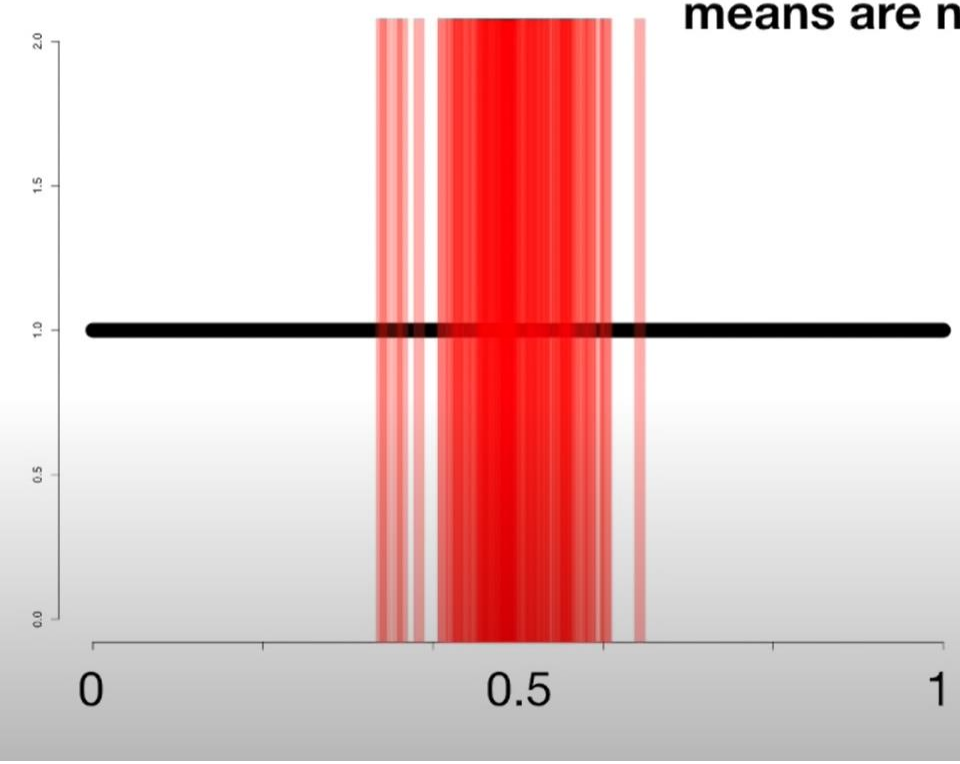

…70 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1

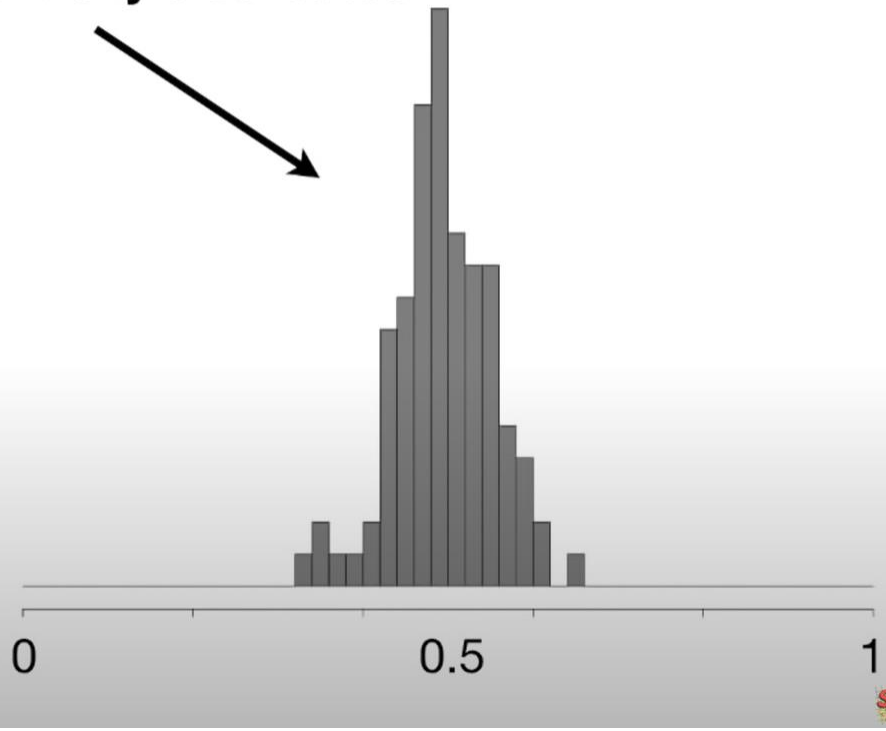

…80 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1


…90 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1

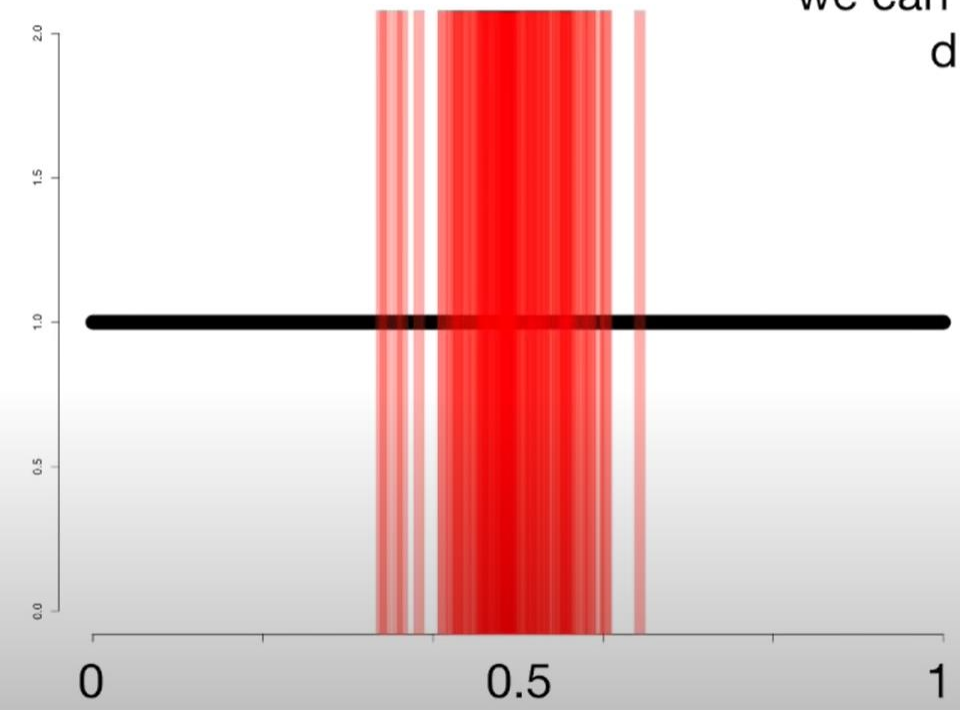

…100 means…
2.0
1.5
1.0
0.5
0.0
0
0.5
1
0
0.5
1

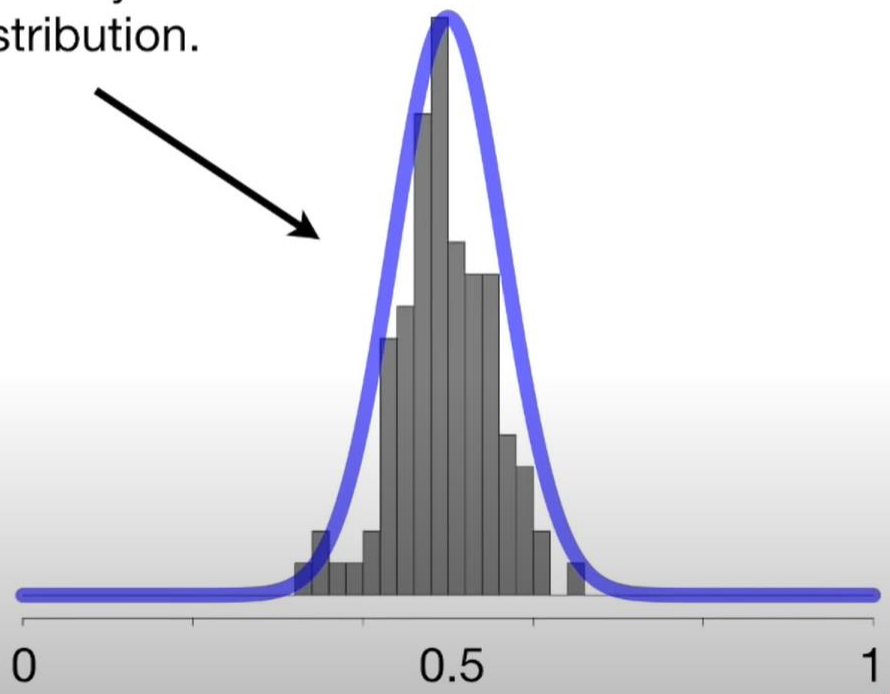
After adding 100 means to the histogram, it's pretty easy to see that these **means are normally distributed.**

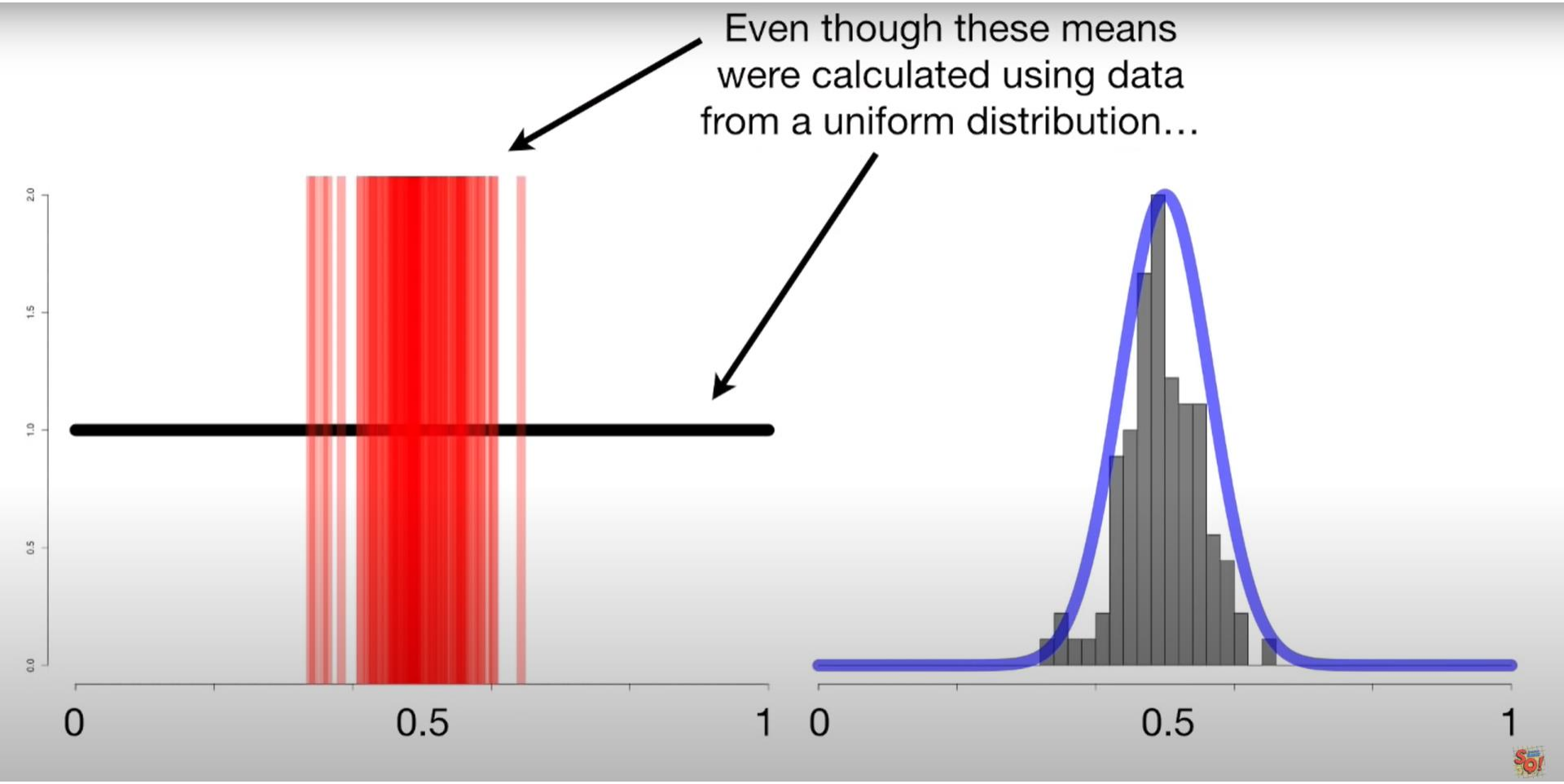




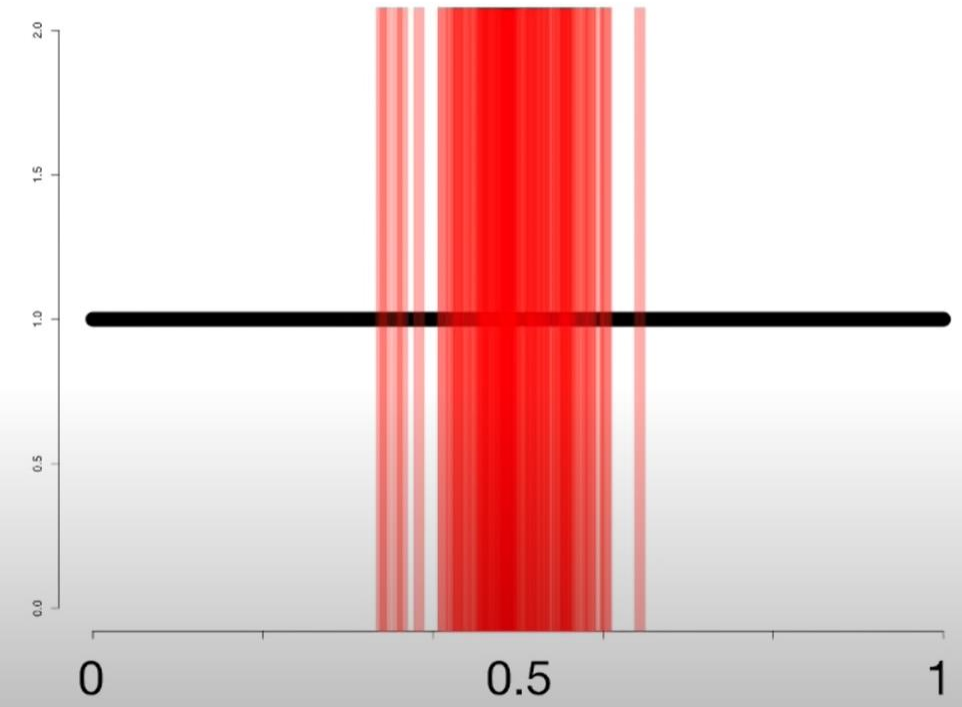
However, to make super easy to see that the **means are normally distributed**, we can overlay a normal distribution.

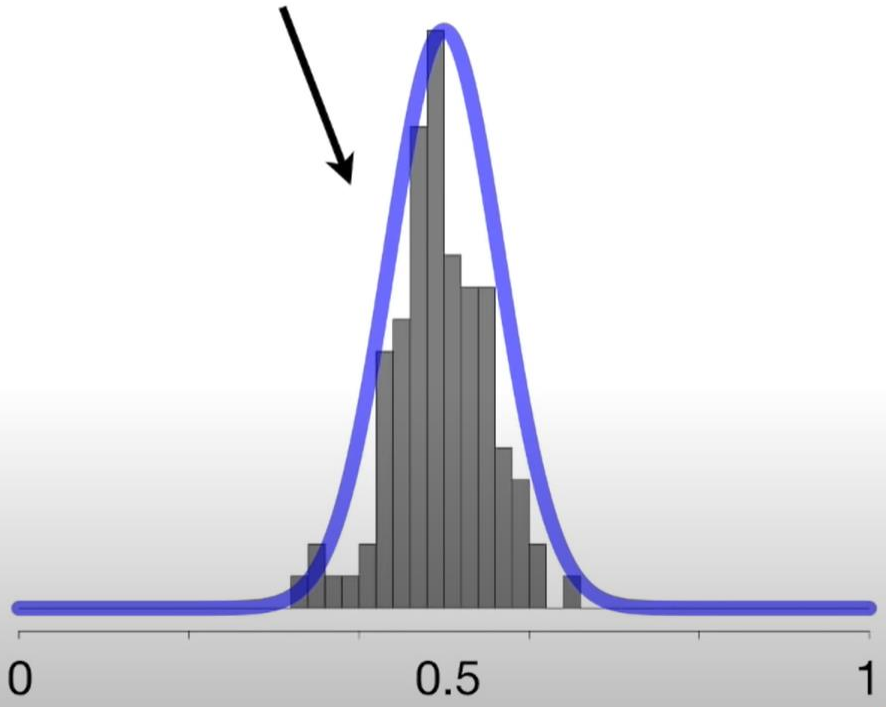




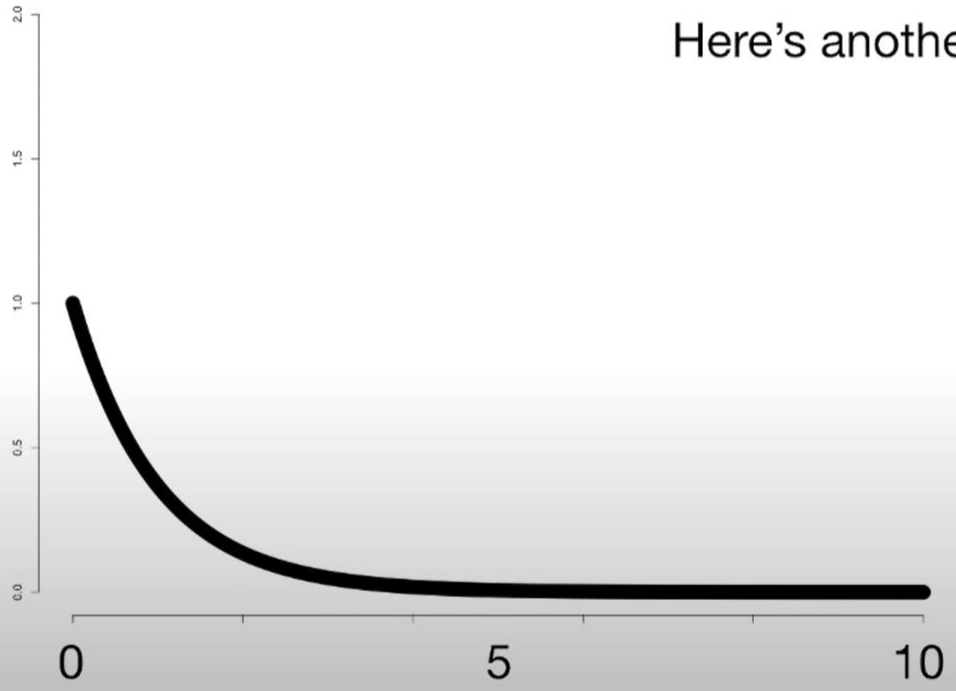

Even though these means were calculated using data from a uniform distribution…
0.0
0.5
1.0
1.5
2.0
0
0.5
1
0
0.5
1

…the means themselves are not uniformly distributed. Instead, the **means are normally distributed**.

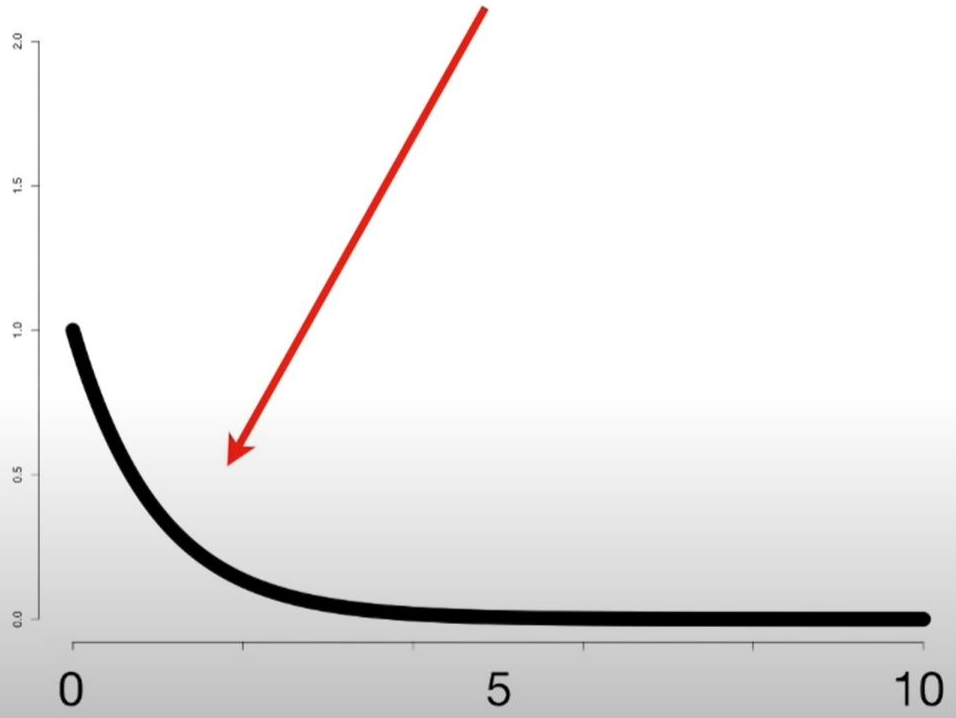




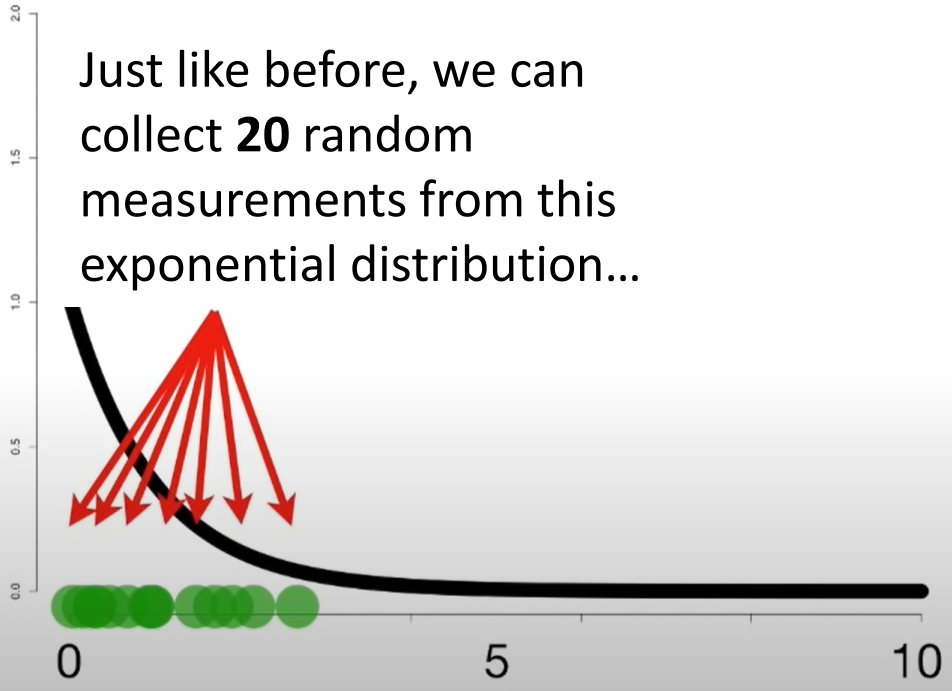
Here's another example…

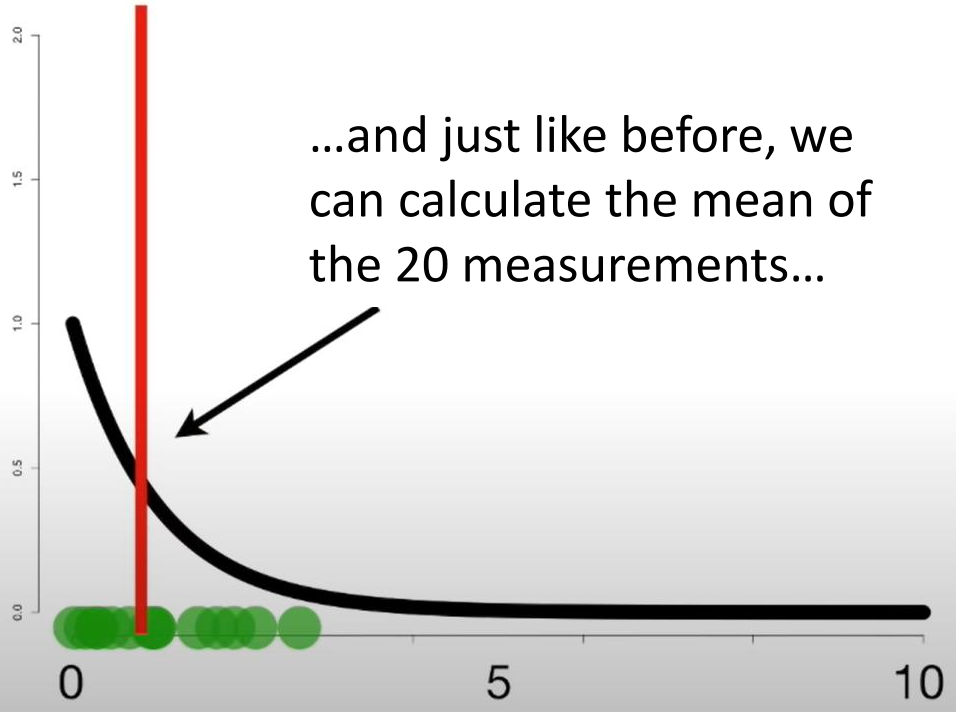


This time we'll start with an Exponential Distribution.



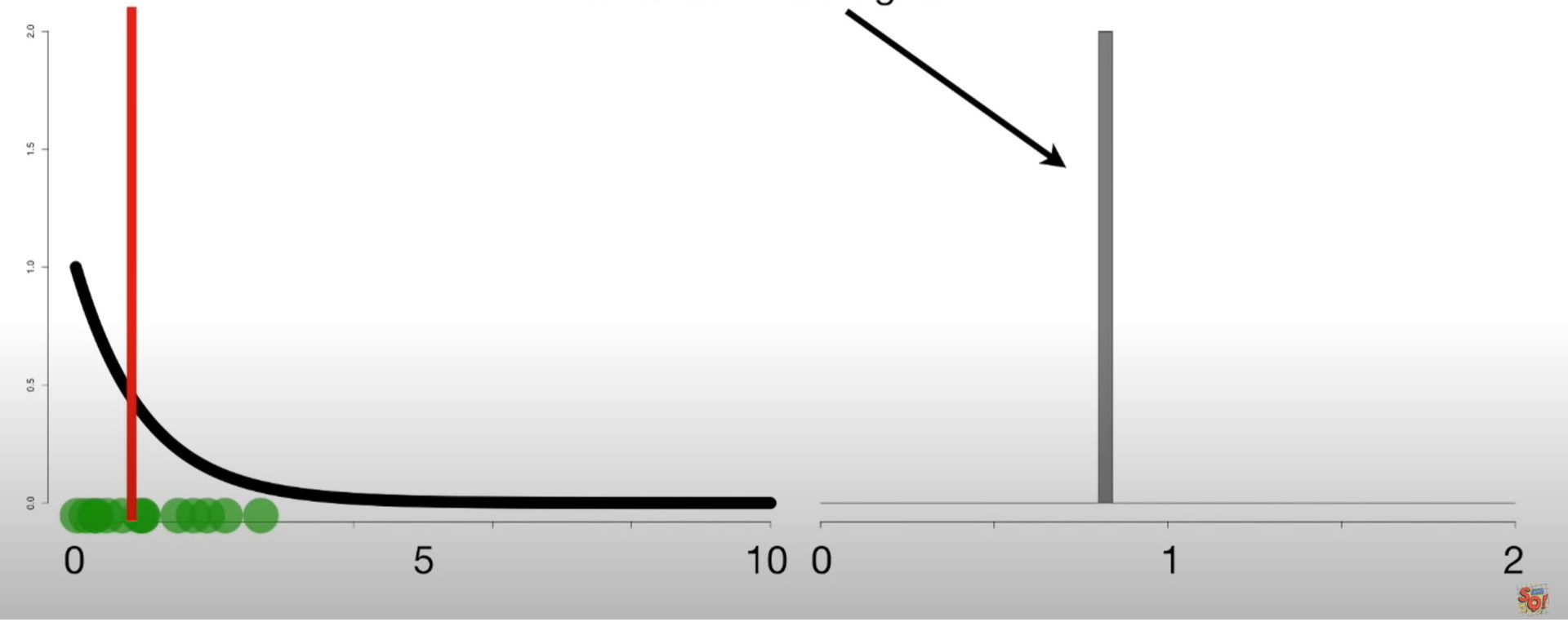
Just like before, we can collect **20** random measurements from this exponential distribution…



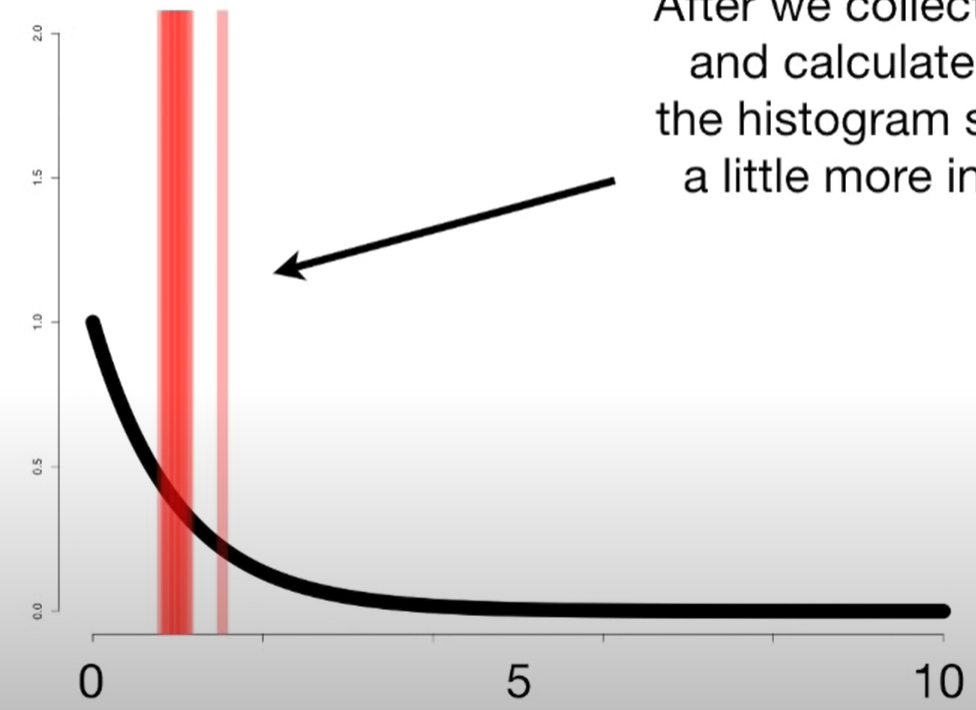


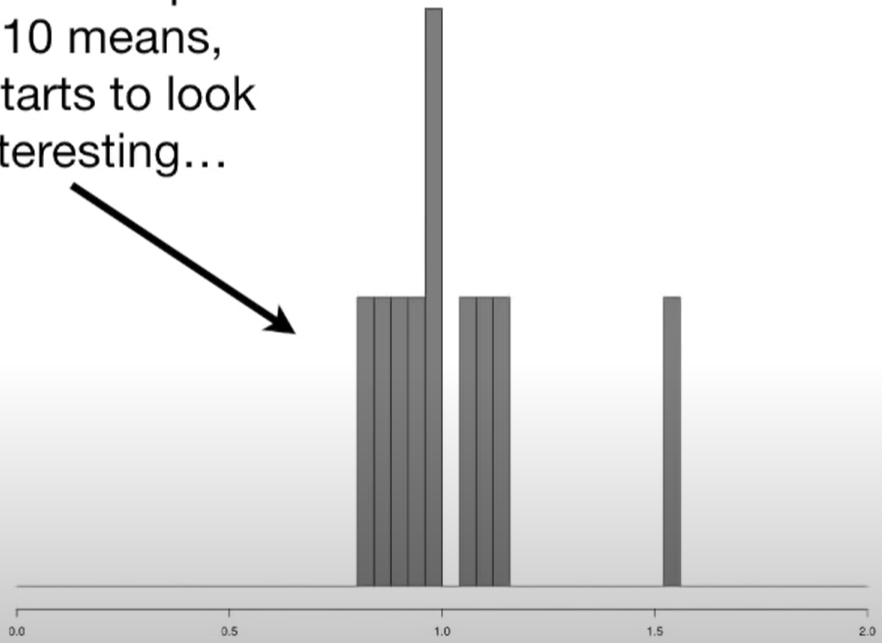
…and just like before, we can calculate the mean of the 20 measurements…

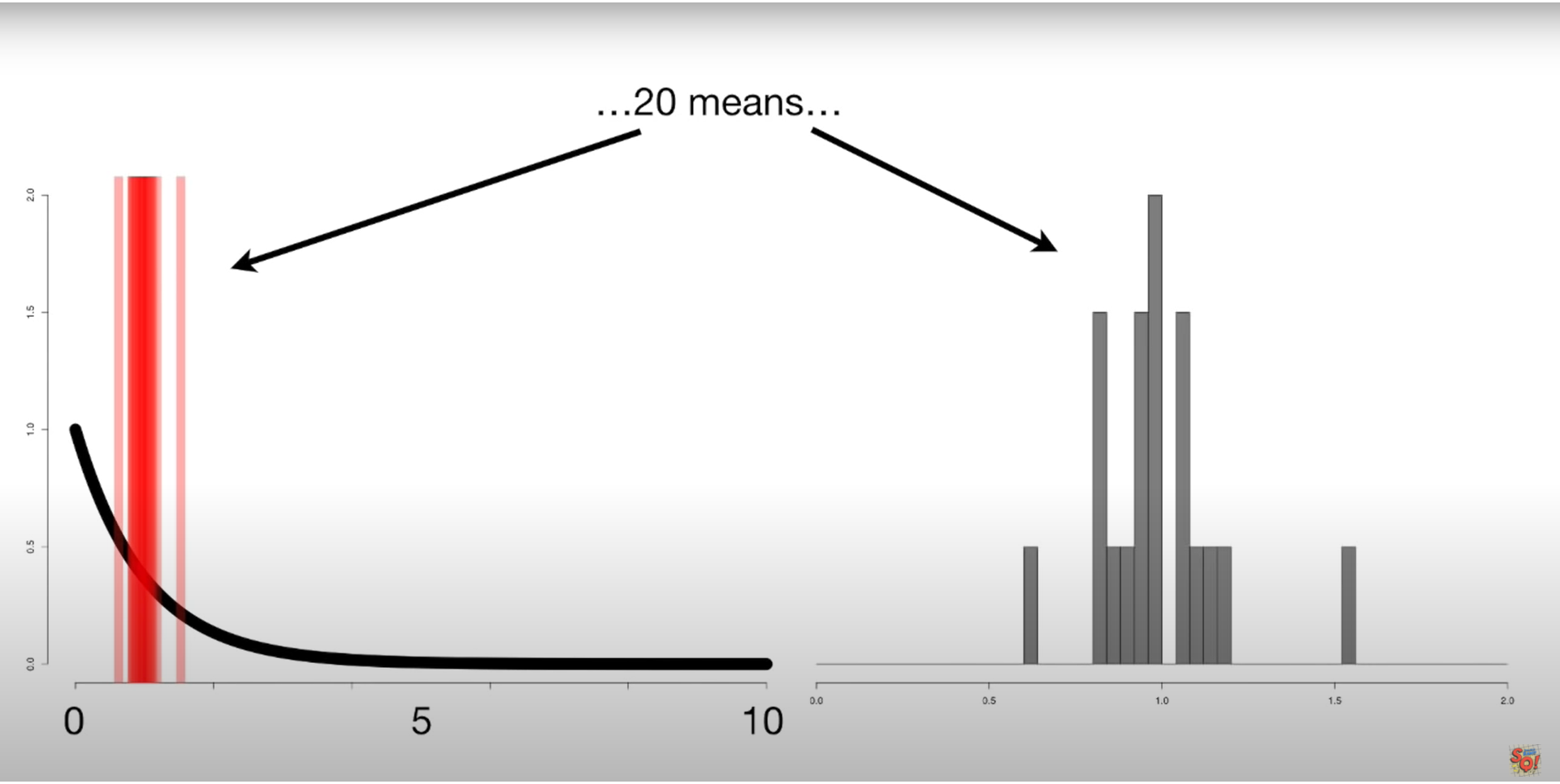
…and lastly, we can draw a histogram of that mean over here on the right.

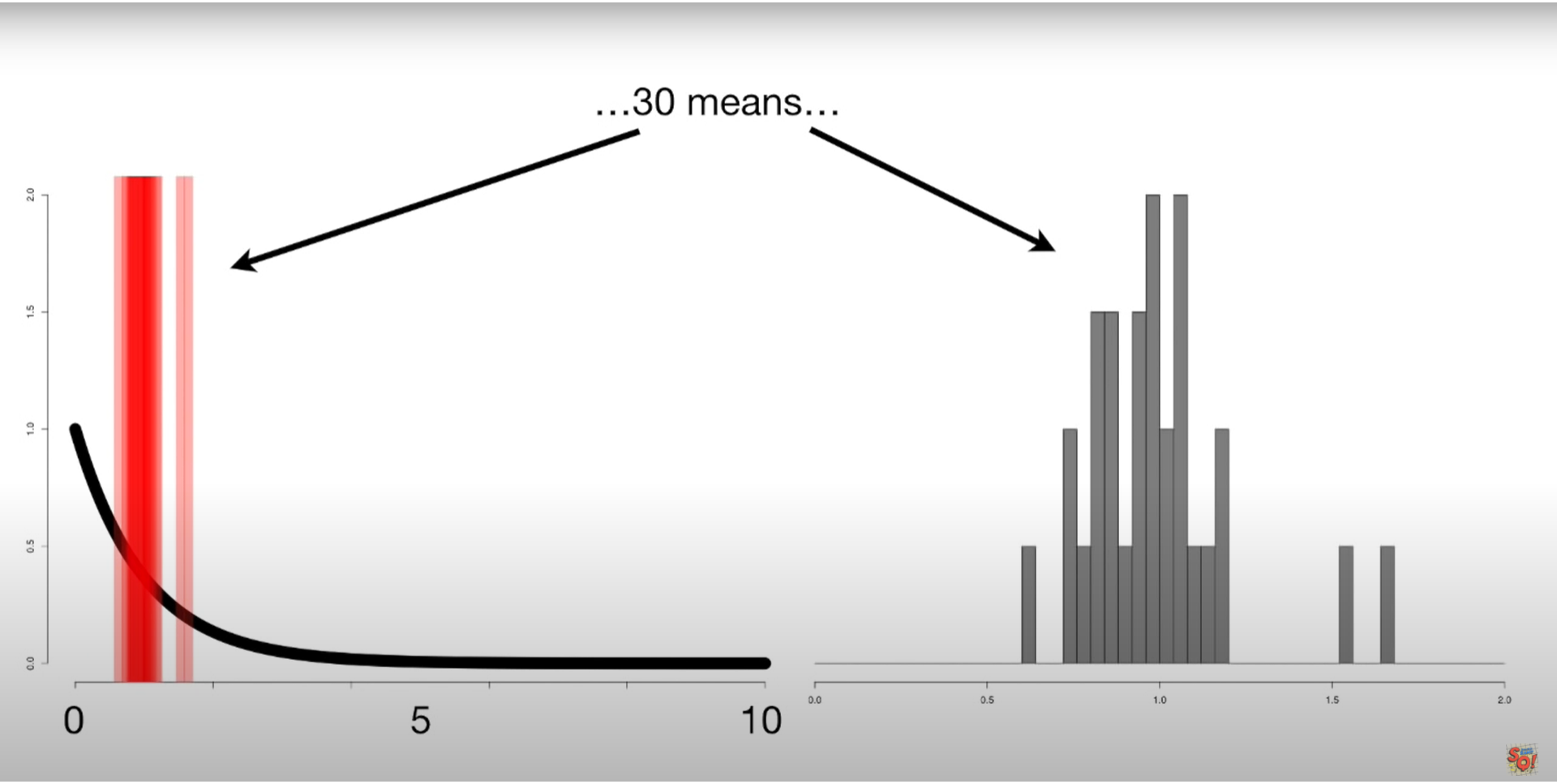


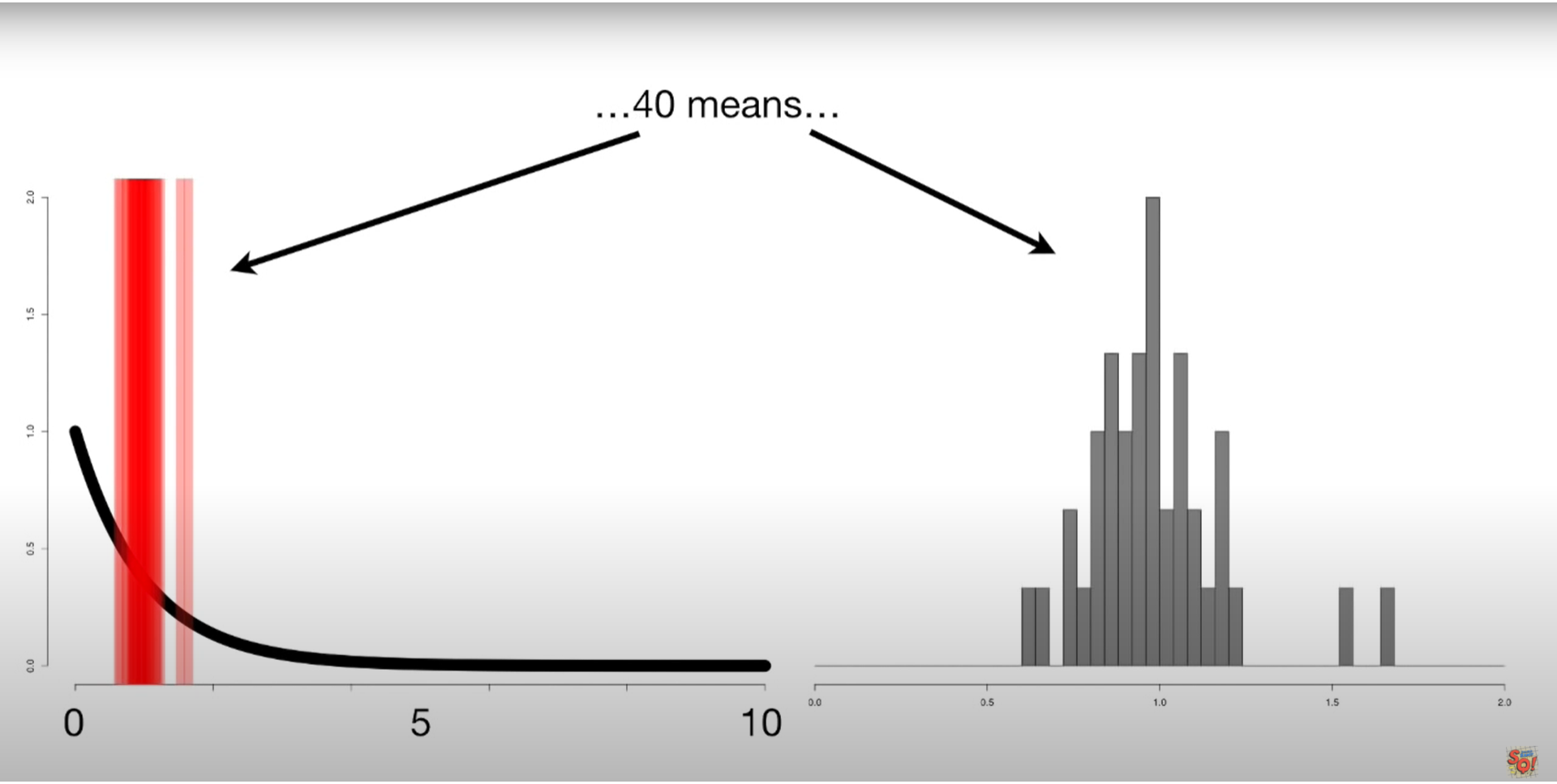
After we collect 10 samples and calculate 10 means, the histogram starts to look a little more interesting…

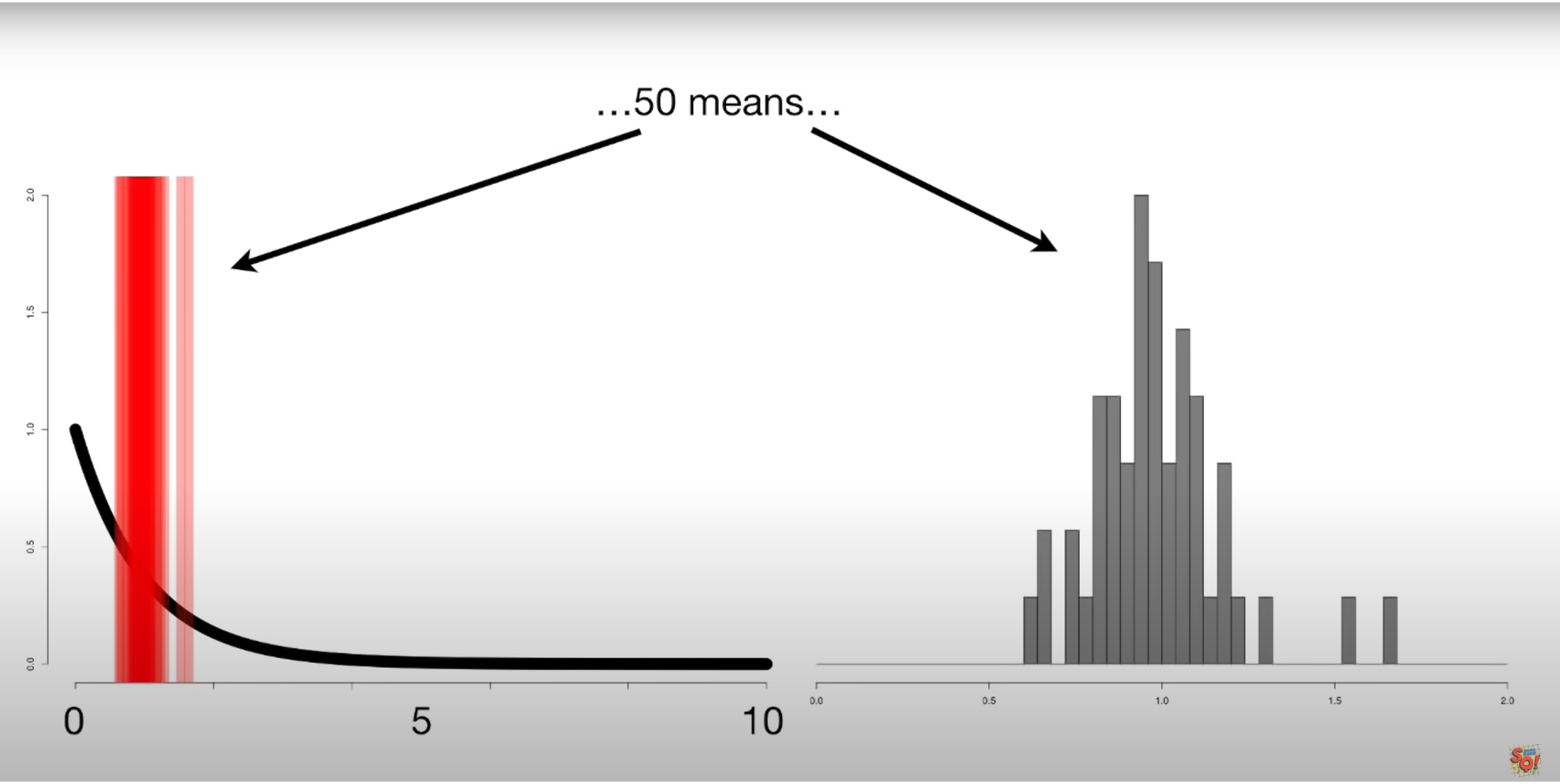


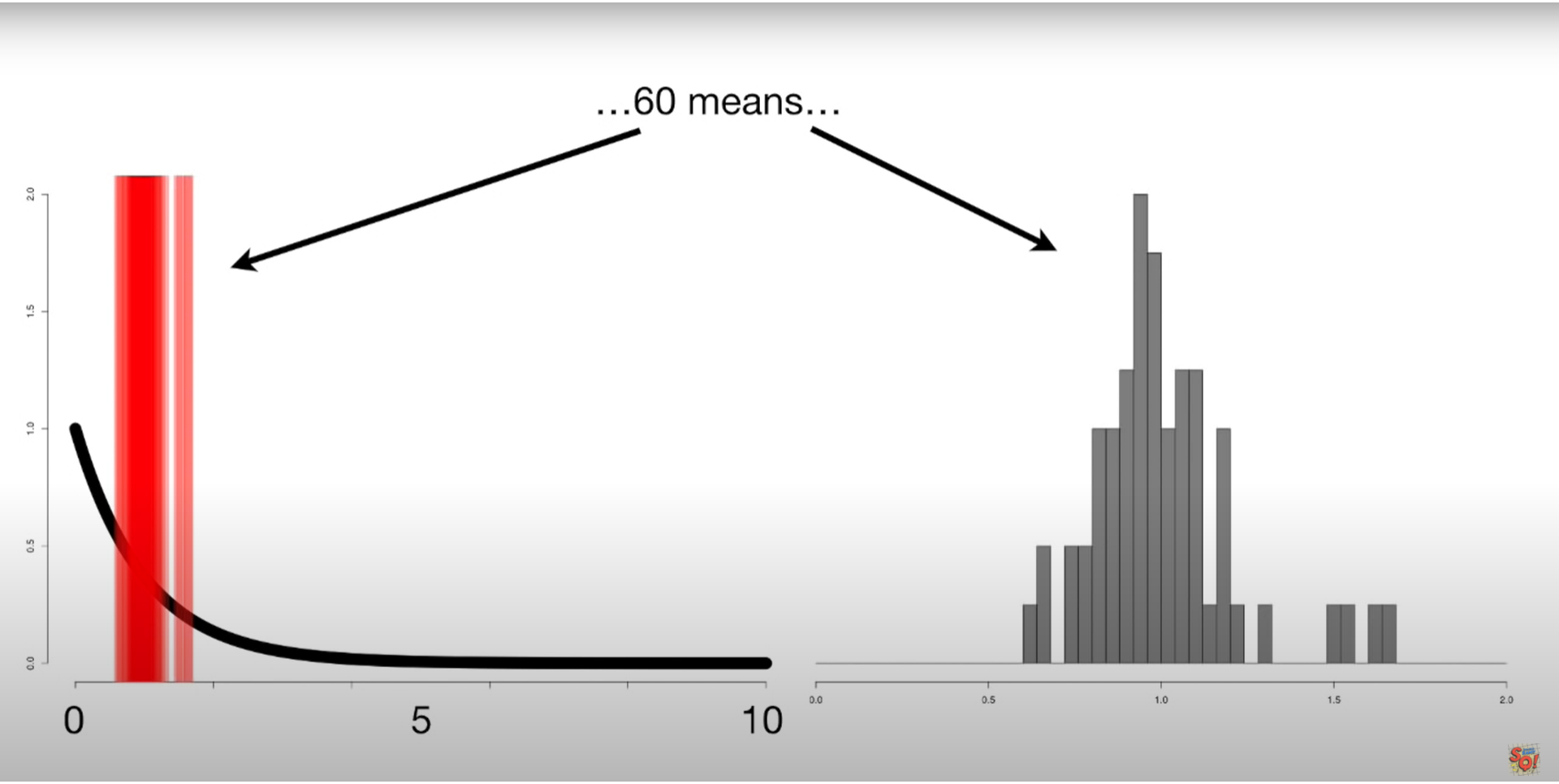


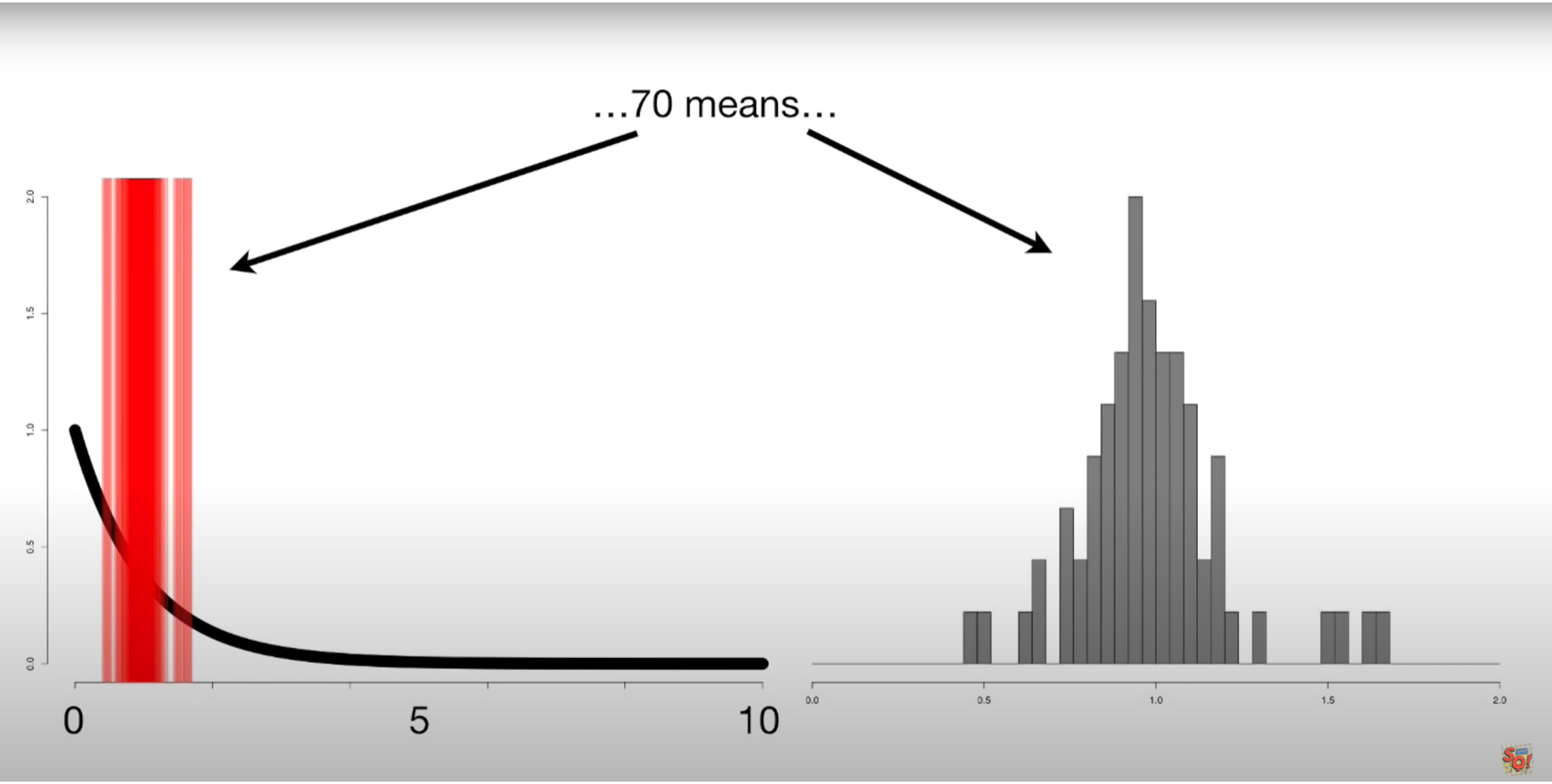

…20 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

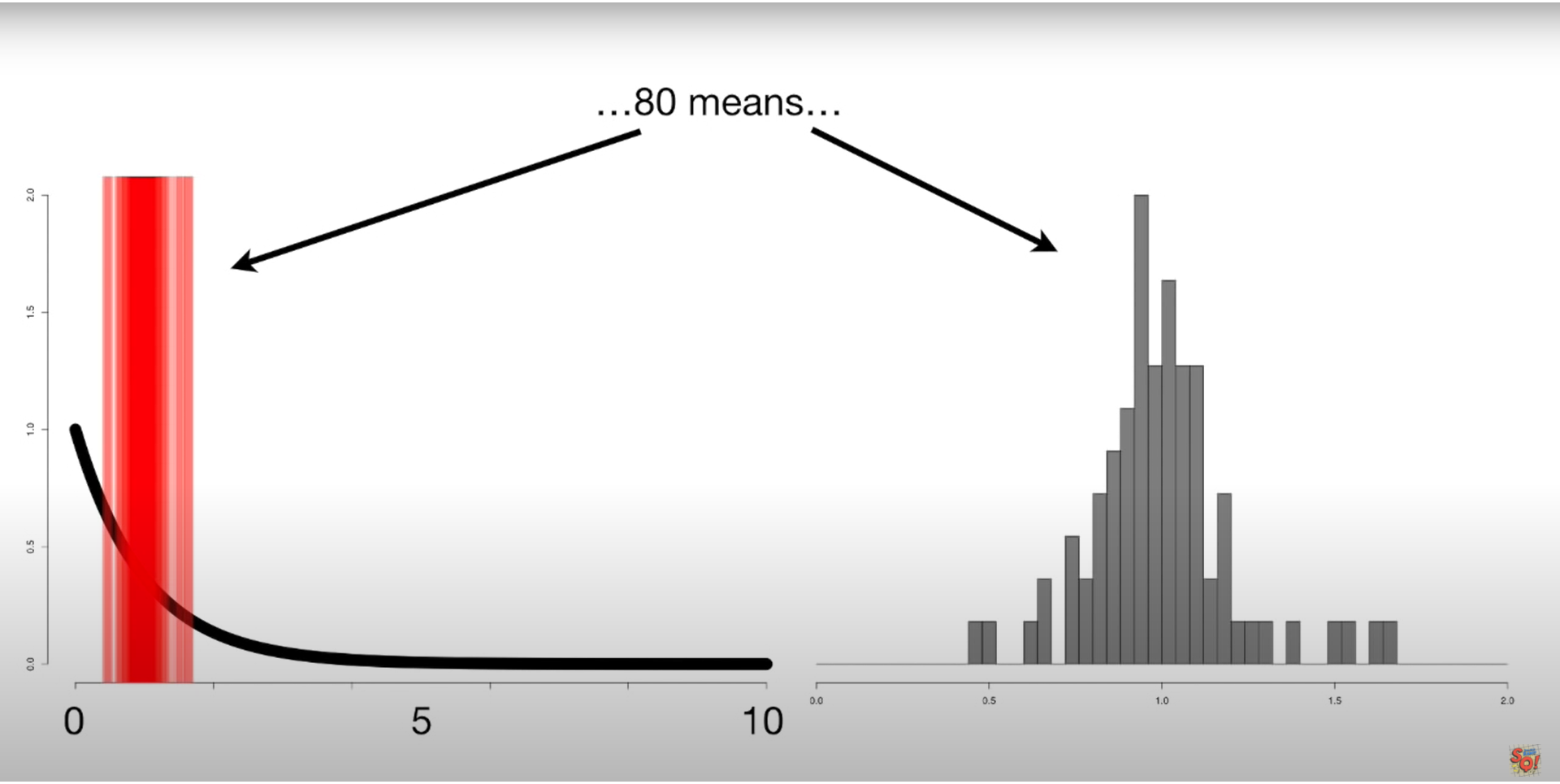

…30 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

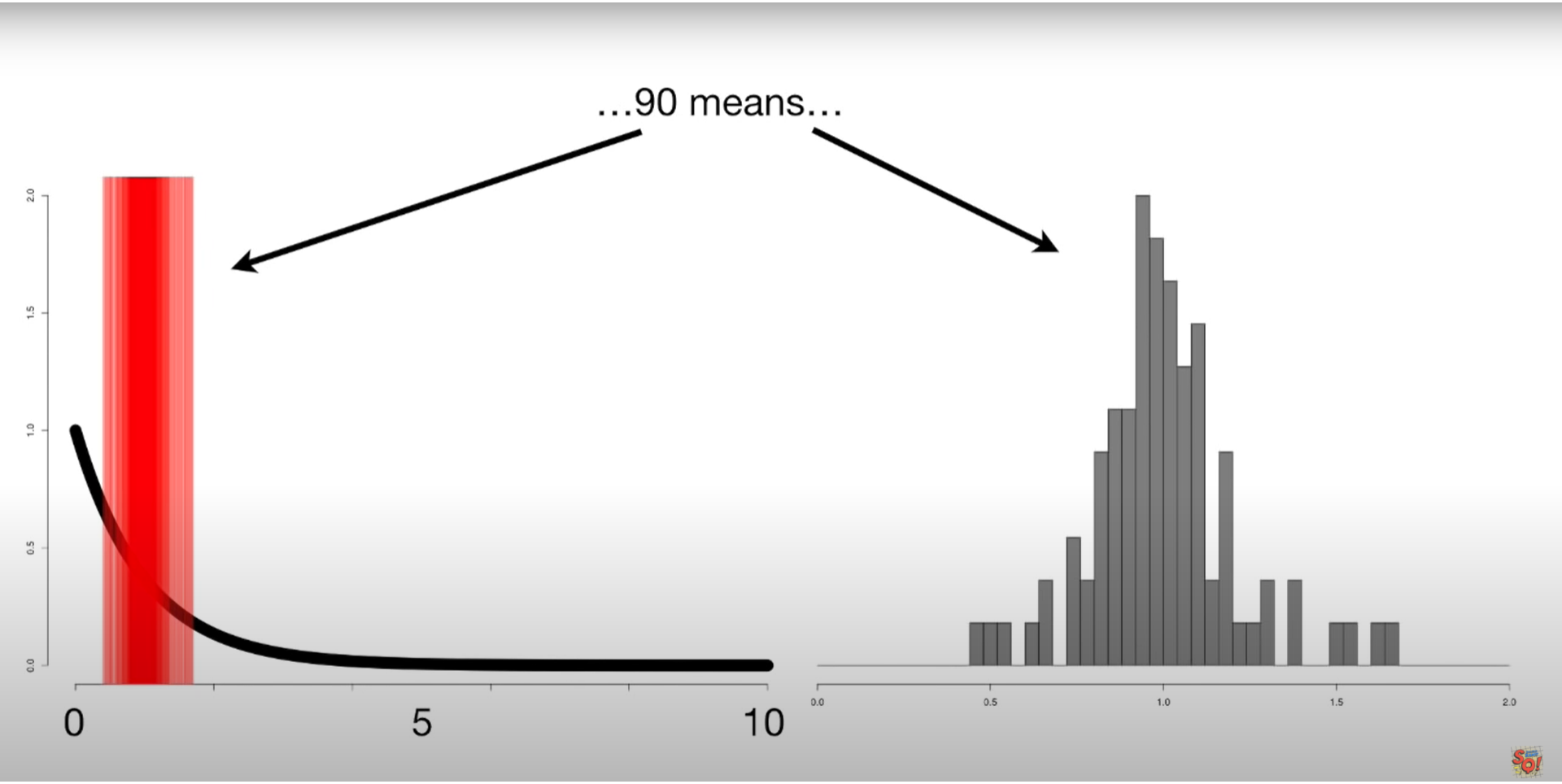

…40 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

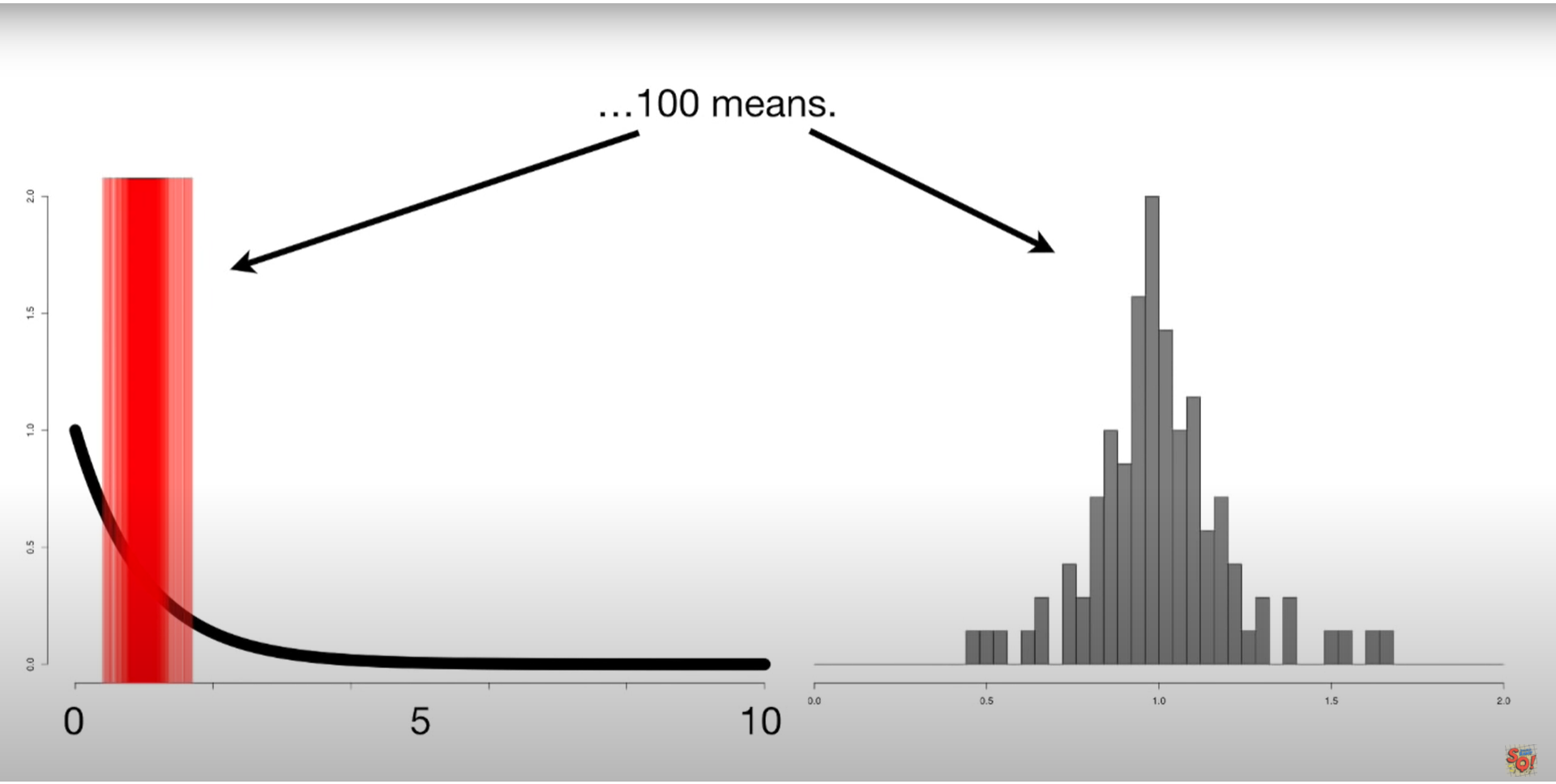

…50 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0


…60 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

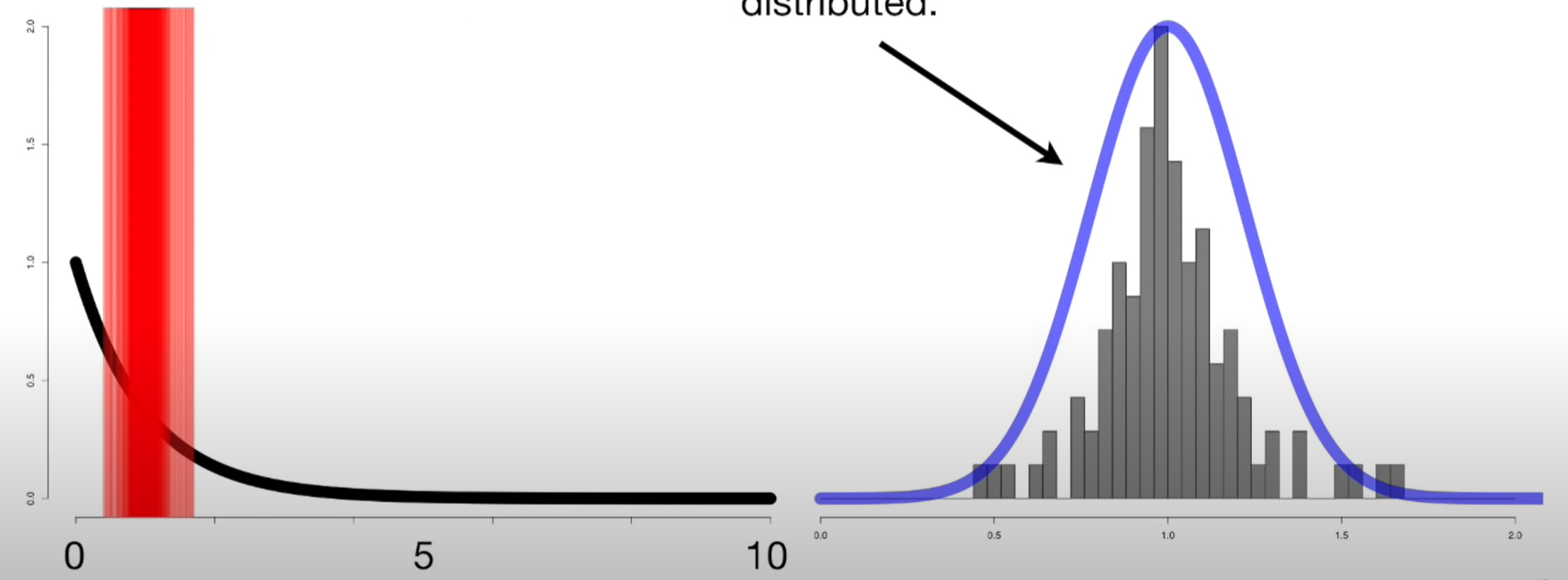

…70 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

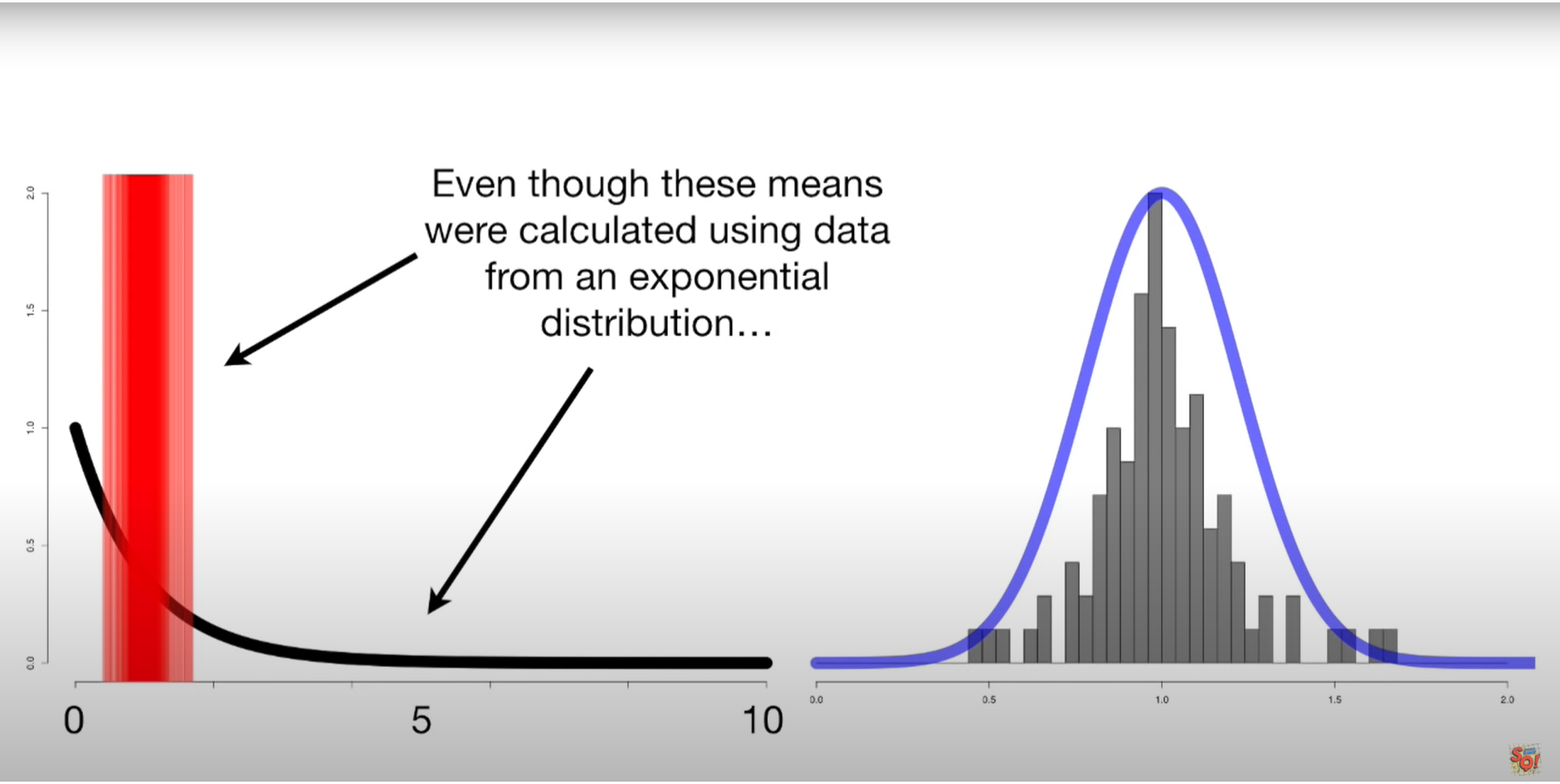

…80 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0


…90 means…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

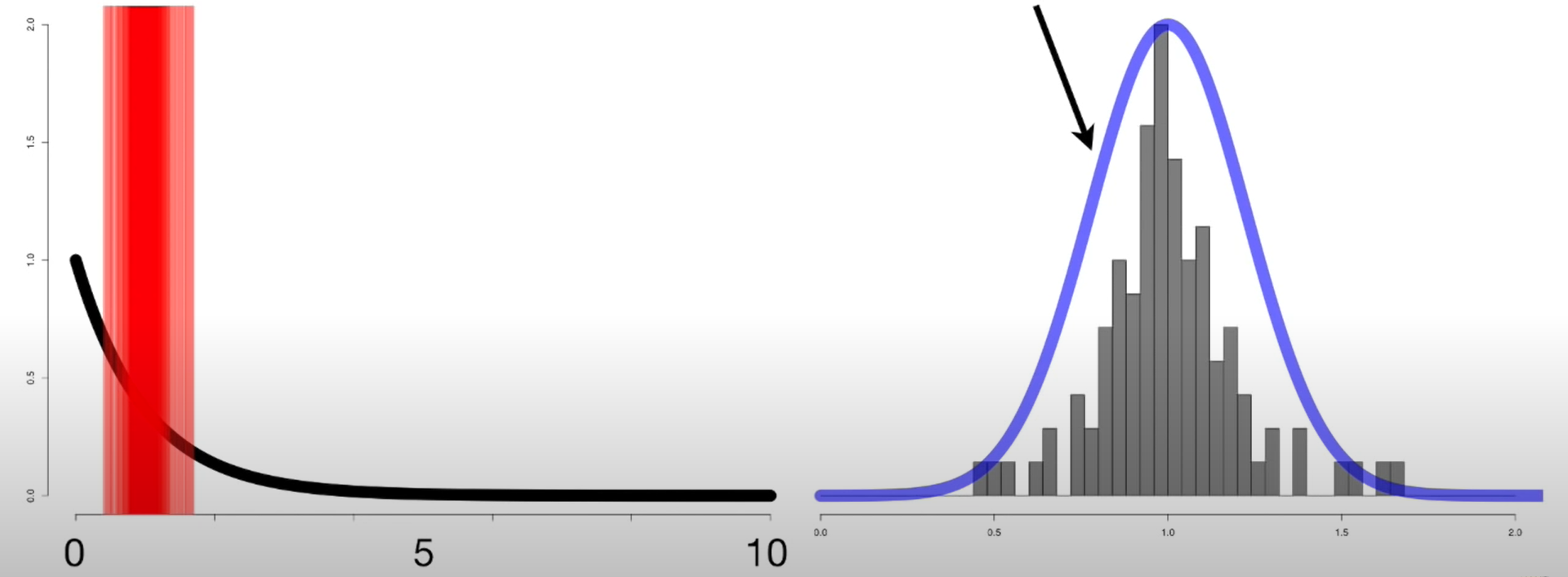

…100 means.
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

After adding 100 means to the histogram, we can see that they are normally distributed.

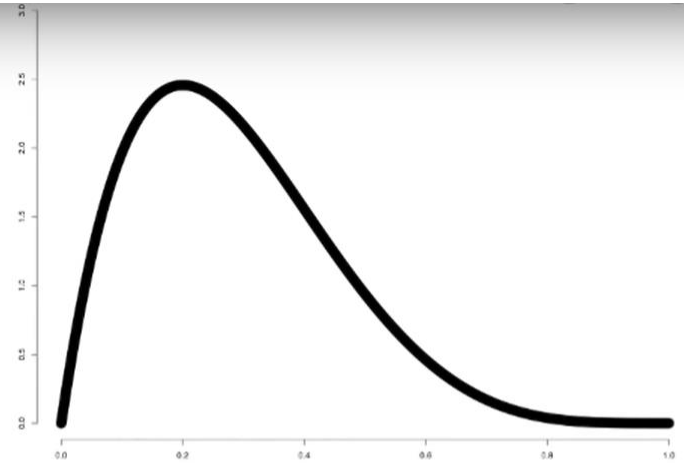


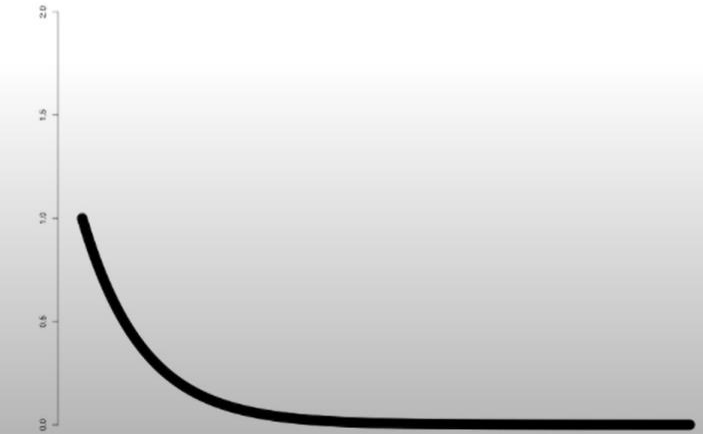

Even though these means were calculated using data from an exponential distribution…
0.0
0.5
1.0
1.5
2.0
0
5
10
0.0
0.5
1.0
1.5
2.0

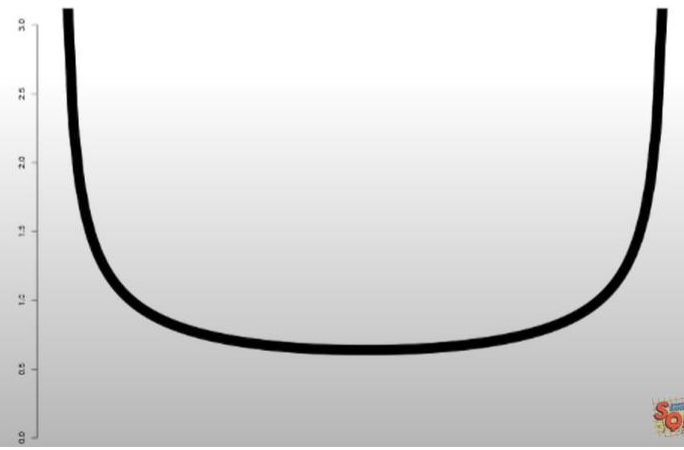
…the means themselves are not exponentially distributed. Instead, the **means are normally distributed**.

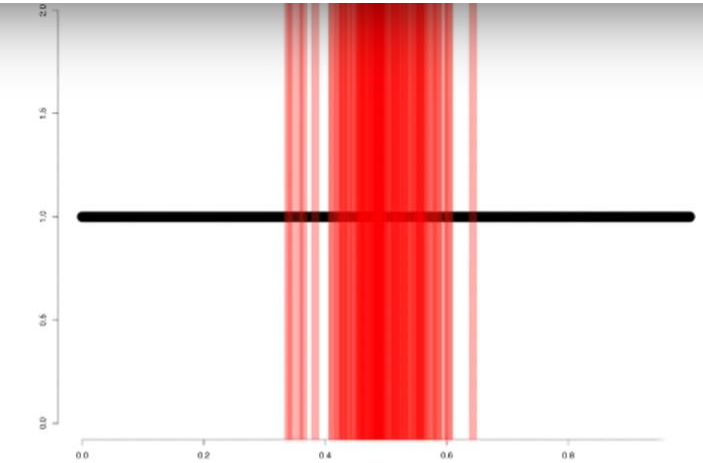


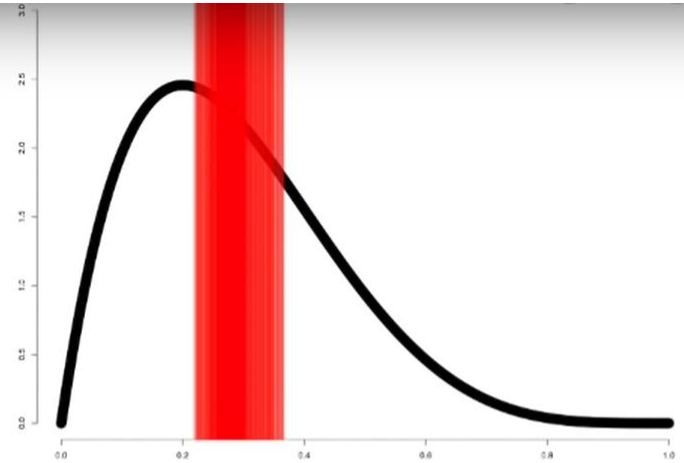
Well, it turns out that it doesn't matter what distribution you start with…



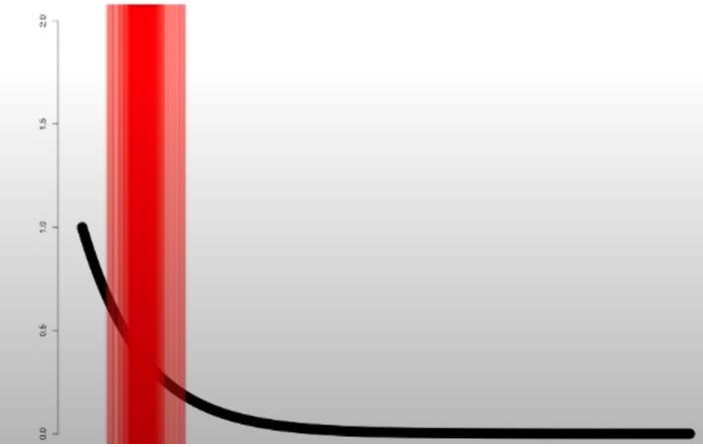


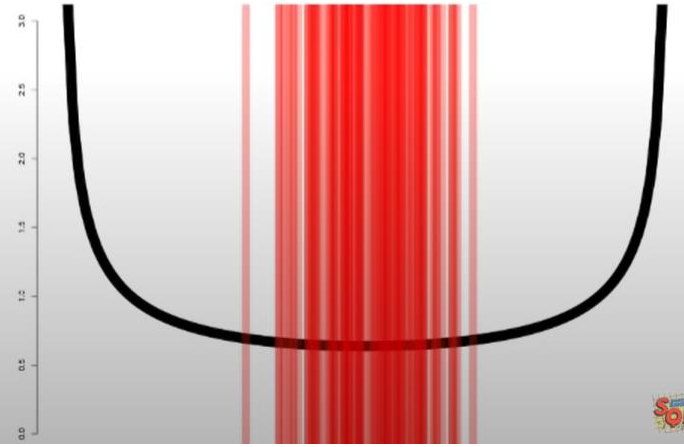


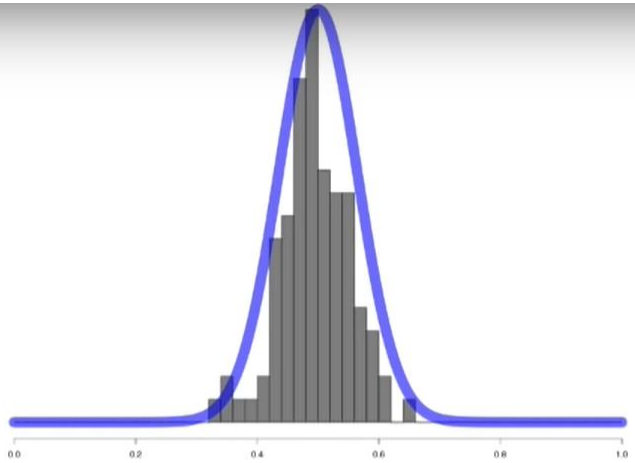


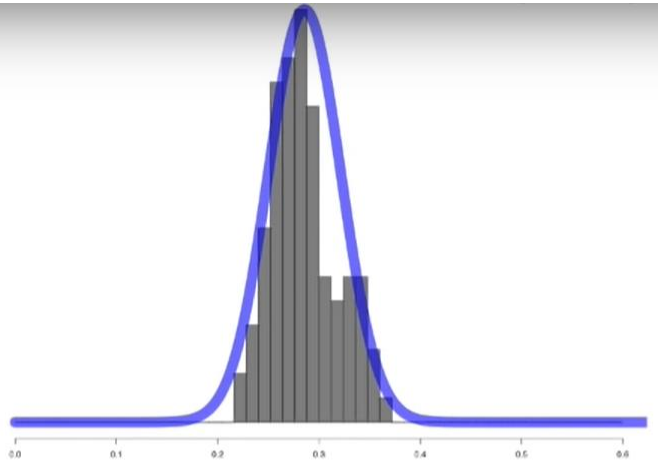


…if you collect samples from those distributions…

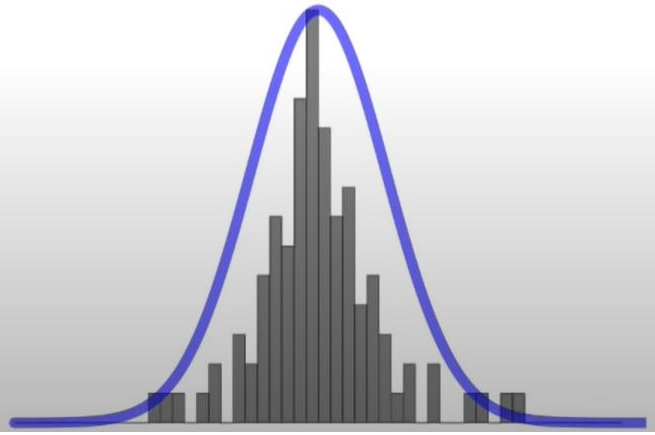


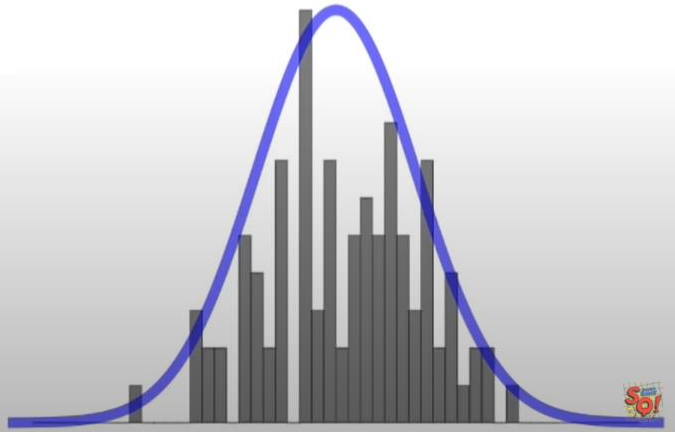


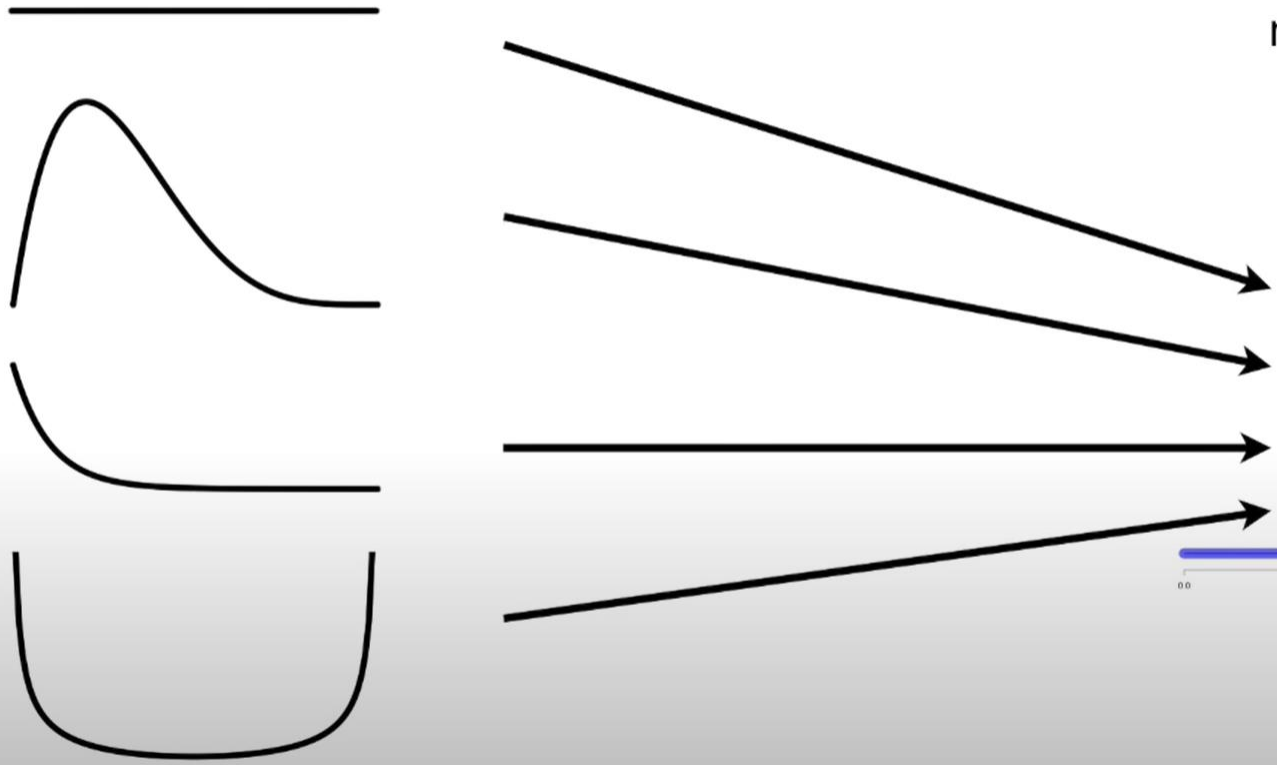




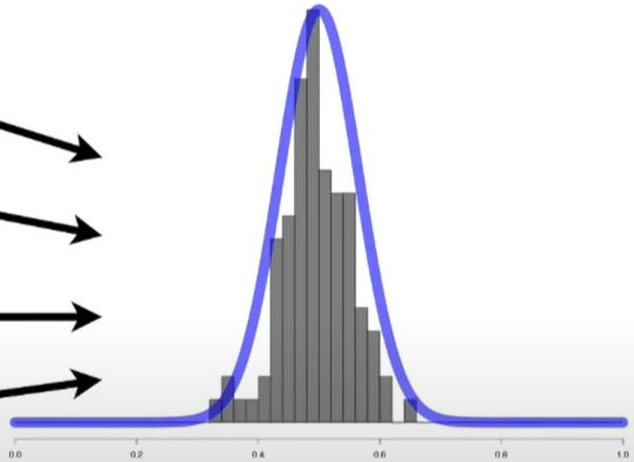
…then **the means will be normally distributed**.

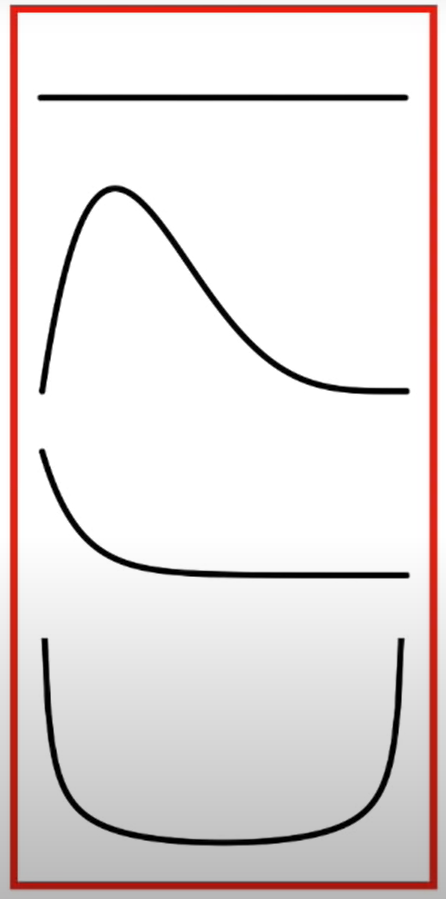




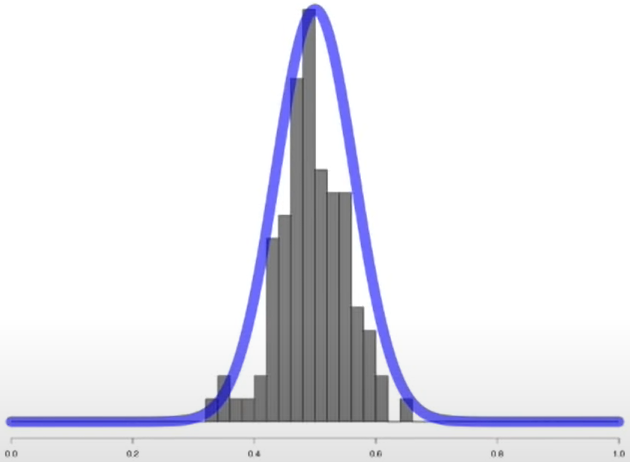


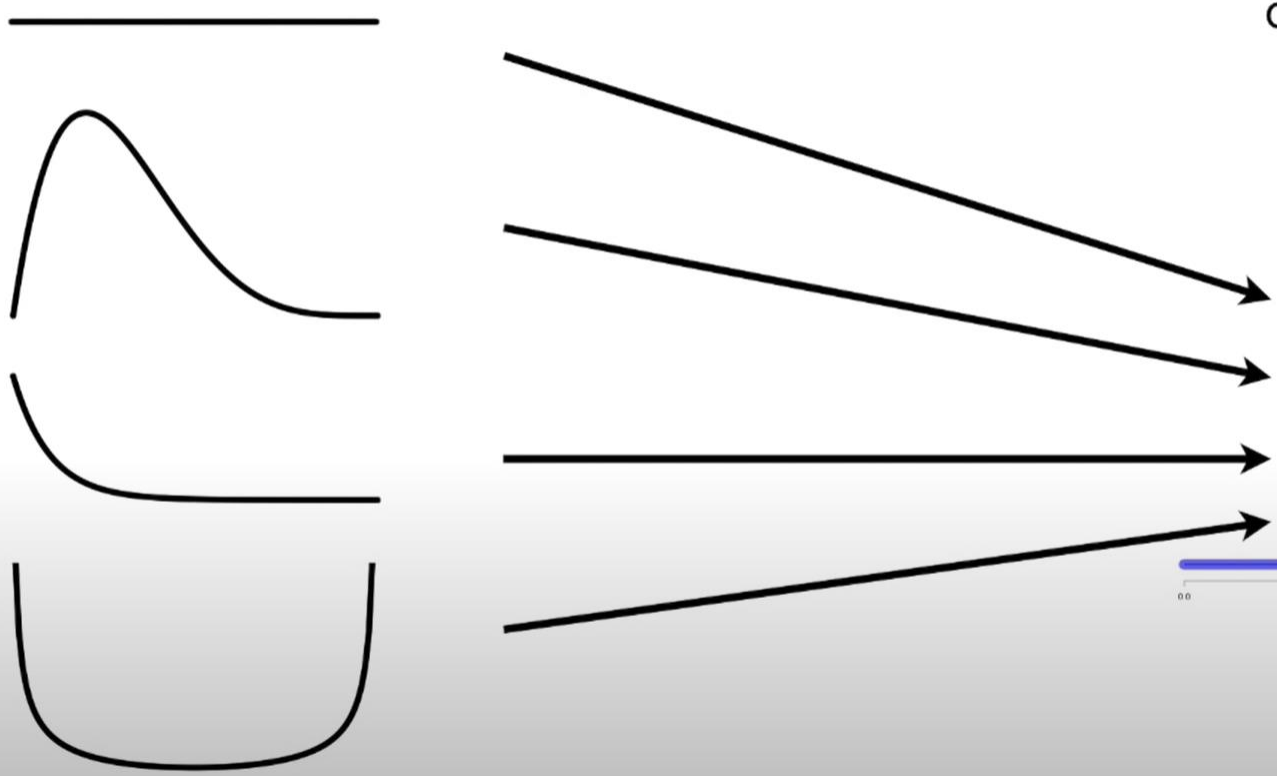
Because we know that the sample means are normally distributed…



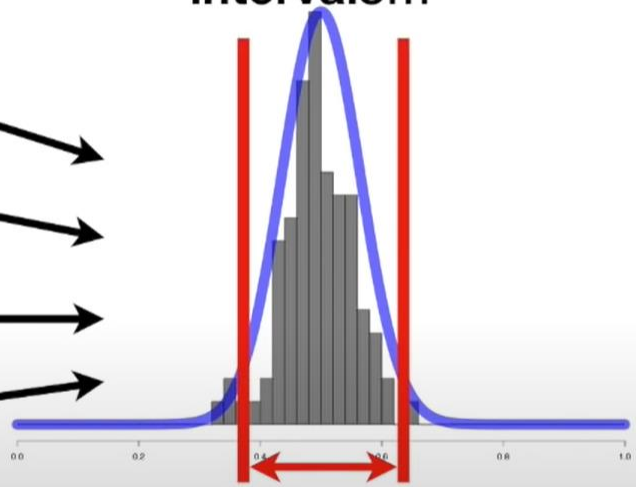


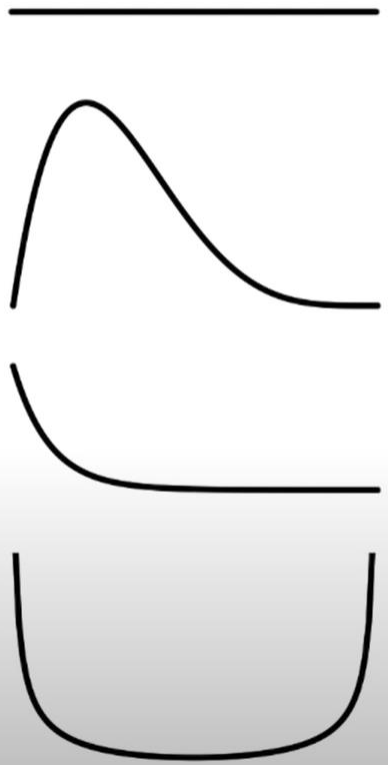
…we don't need to worry too much about the distribution that the samples came from.



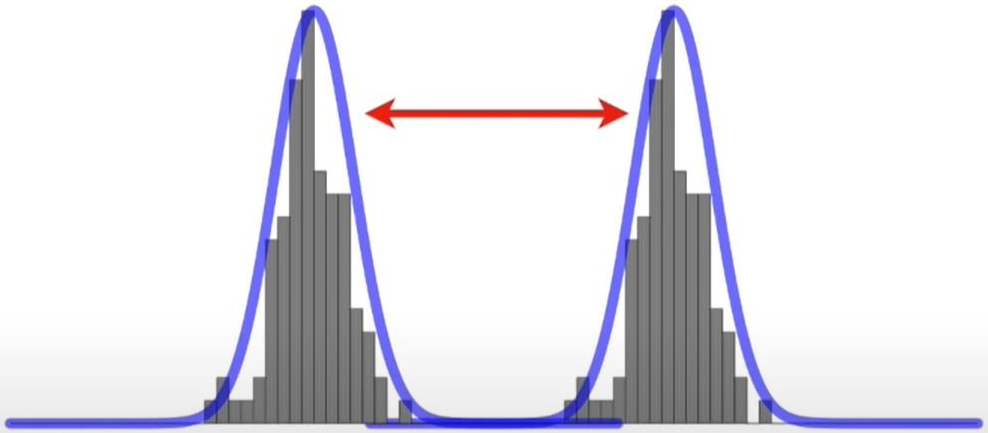


We can use the mean's normal distribution to make **confidence intervals**…

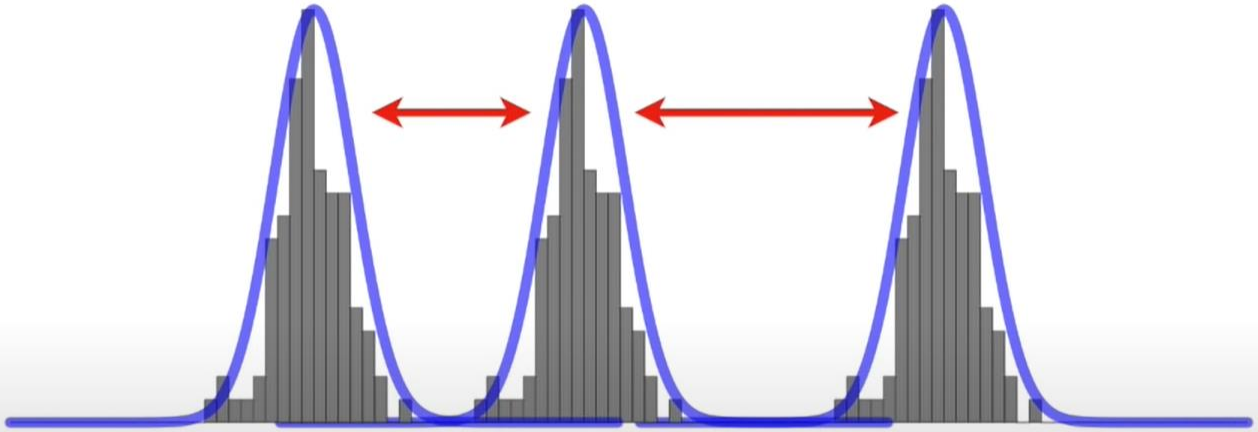


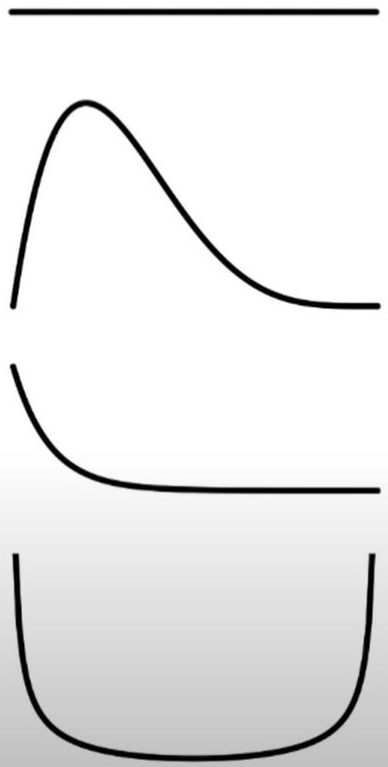


…do **t-tests**, where we ask if there is a difference between the means from two samples…

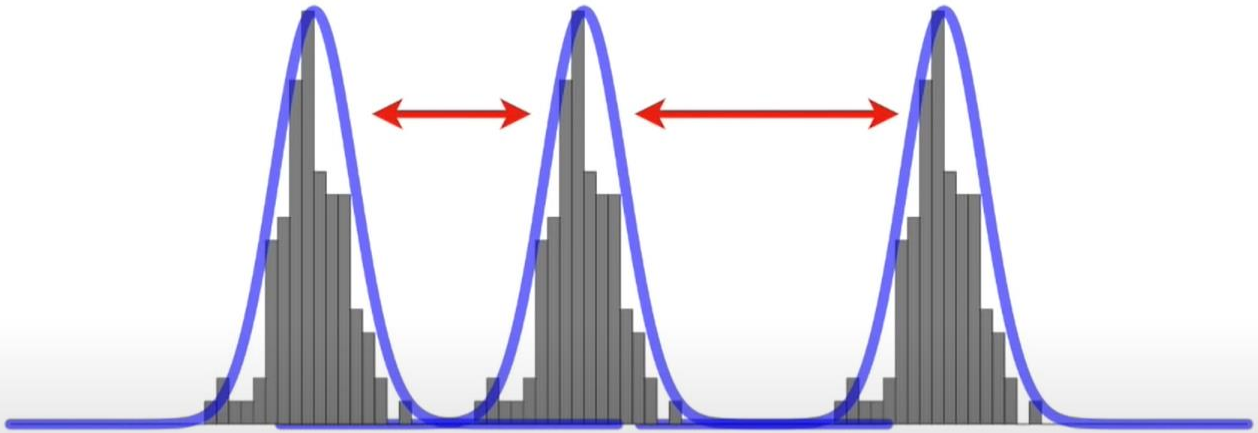


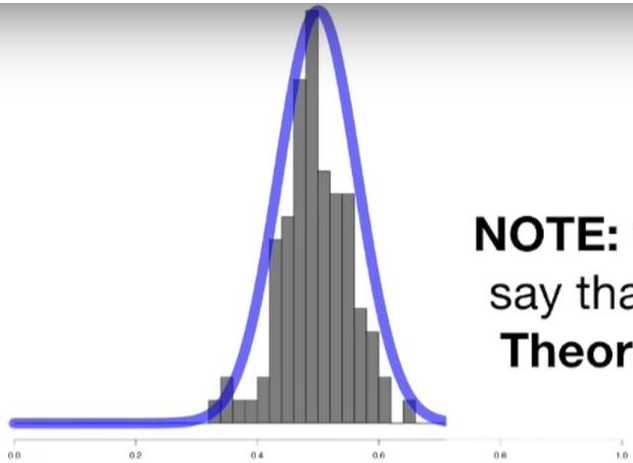
…and **ANOVA**, where we ask if there is a difference among the means from three or more samples…



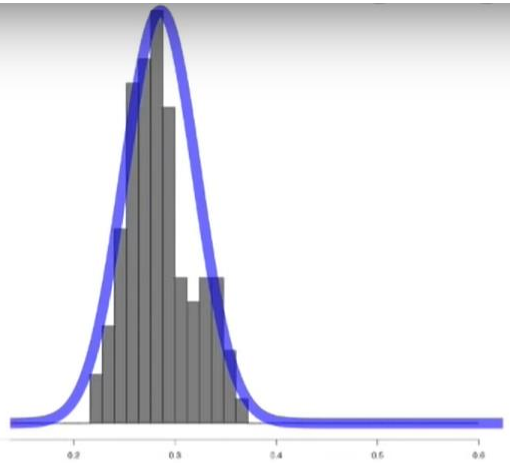


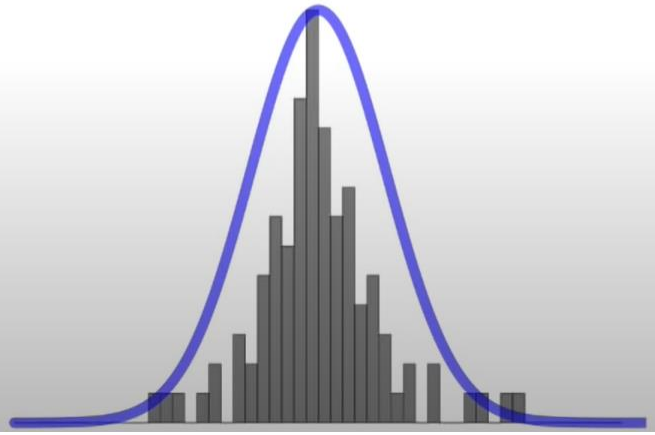
…and pretty much any statistical test
that uses the sample mean.

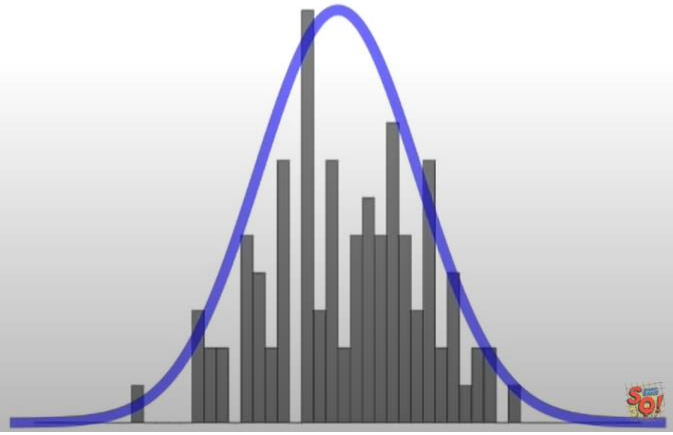


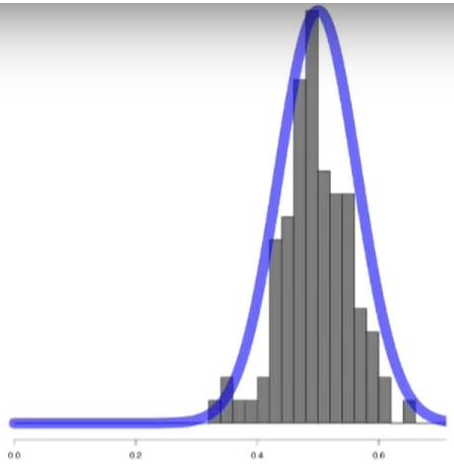


NOTE: Out there in the wild some folks say that in order for the **Central Limit Theorem** to be true, the sample size must be at least **30**.

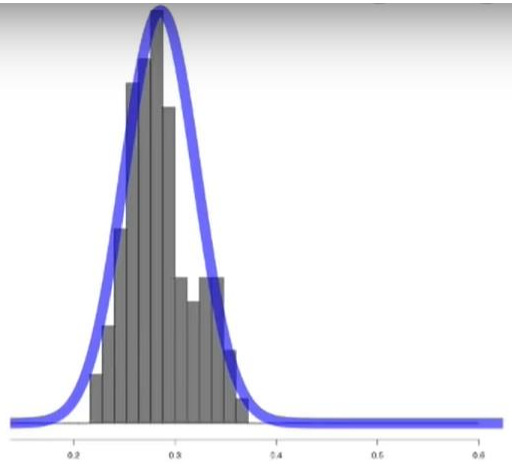




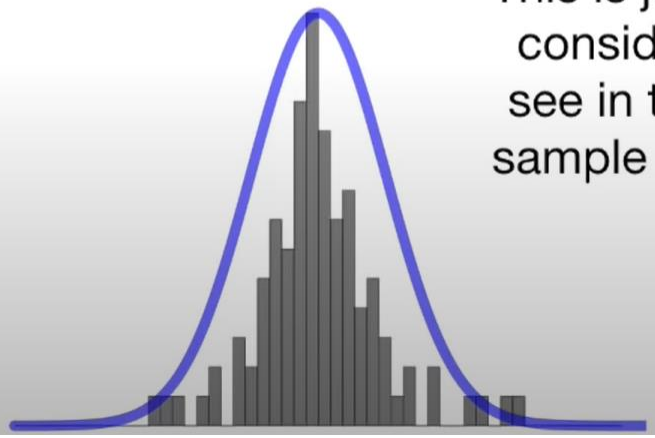


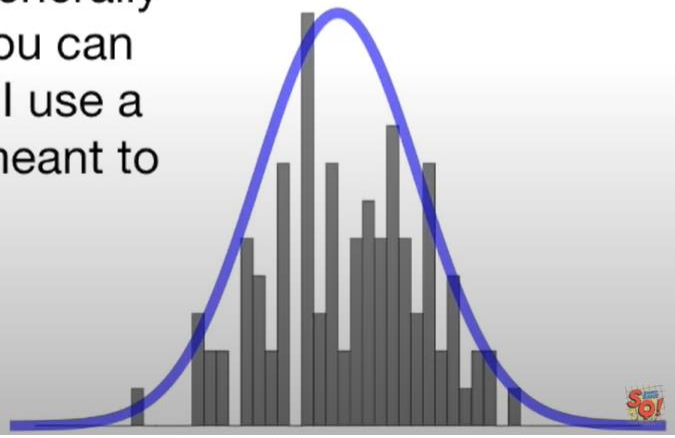


NOTE: Out there in the wild some folks say that in order for the **Central Limit Theorem** to be true, the sample size must be at least **30**.



This is just a rule of thumb and generally considered safe. However, as you can see in the examples here where I use a sample size of **20**, the rule was meant to be broken.





Central Limit Theorem

- As n increases, the distribution of **sample means** will approach a normal distribution.
- More generally, as n increases, the distribution of the **sums** of n measurements will approach a normal distribution.

If you multiply something that is normally distributed (ex. means) by a constant value, you end up with something that is normally distributed:

mean = [sum of 30 measurements]/30 **normally distributed**

mean x 30 = [**sum of 30 measurements**] **normally distributed**

- In nature, things are often the sum of lots of little things! (example: human height)

  → **Normal distribution is common**.

Central Limit Theorem

When the original variable is normally distributed

OR sample size ≥ 30,

the distribution of the means of **all** possible samples of size n will be normally distributed with

$$\mu_{\bar{X}} = \mu$$

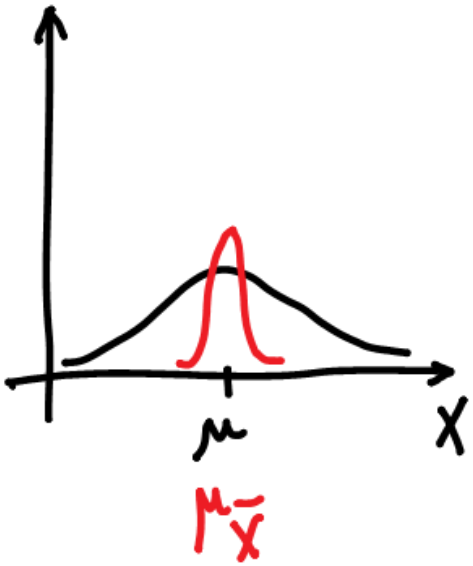
$$\sigma_{\bar{X}} = \frac{\sigma}{\sqrt{n}}$$

Standard Error of the Mean
= Standard Error

Statistics from the sample

(= estimates of the population parameters!)

Standard Deviation of the sample means (also called the **Standard Error**, short for Standard Error of the Mean) and it's square called the variance of the sample means are estimated by:



$$s_{\bar{y}}{}^2 = s^2/n$$

$$s_{\bar{y}} = \sqrt{s^2/n} = \frac{s}{\sqrt{n}}$$

Standard Error of the Mean
= Standard Error

Other standard errors…

- We can calculate the standard deviation of any other statistic (standard deviation, median, mode, percentiles…) that we calculate for multiple samples.

→ This is the « **standard error** of … » .

Central Limit Theorem

When the original variable is normally distributed

OR sample size ≥ 30,

the distribution of the means of **all** possible samples of size n will be normally distributed with

$$\mu_{\bar{X}} = \mu$$

$$\sigma_{\bar{X}} = \frac{\sigma}{\sqrt{n}}$$

Standard Error of the Mean
= Standard Error

$$Z = \frac{\bar{X} - \mu}{\sigma/\sqrt{n}} \text{ follows a standard normal distribution}$$

$$Z = \frac{\bar{X} - \mu}{\sigma/\sqrt{n}}$$ follows a standard normal distribution

The Student’s t-distribution

$$Z = \frac{\bar{X} - \mu}{\sigma/\sqrt{n}} \text{ follows a standard normal distribution}$$

- We will use this notion to construct a confidence interval for the population mean μ.
- But σ is a population parameter
  - →This value is unknown!
  - →We will use the sample standard deviation *s* to estimate it.

$$t = \frac{\bar{X} - \mu}{s/\sqrt{n}} \text{ follows a t distribution with n}-1 \text{ degrees of freedom}$$

- s is a statistic
  - →has a sample distribution; it will vary from sample to sample; t will be more variable than z
- The t-distribution looks like the Z-distribution but is wider: heavier tails and lower peak!
- The degrees of freedom of the t are related to the degrees of freedom of the sample variance s^2 (denominator = n-1)
- As the degrees of freedom increase (larger samples), the t-distribution looks more and more like the standard normal distribution (less variation in s!)

Common continuous distributions: t-distribution

- Looks like standard normal distribution:
- Symmetric about the mean (=0)
- BUT

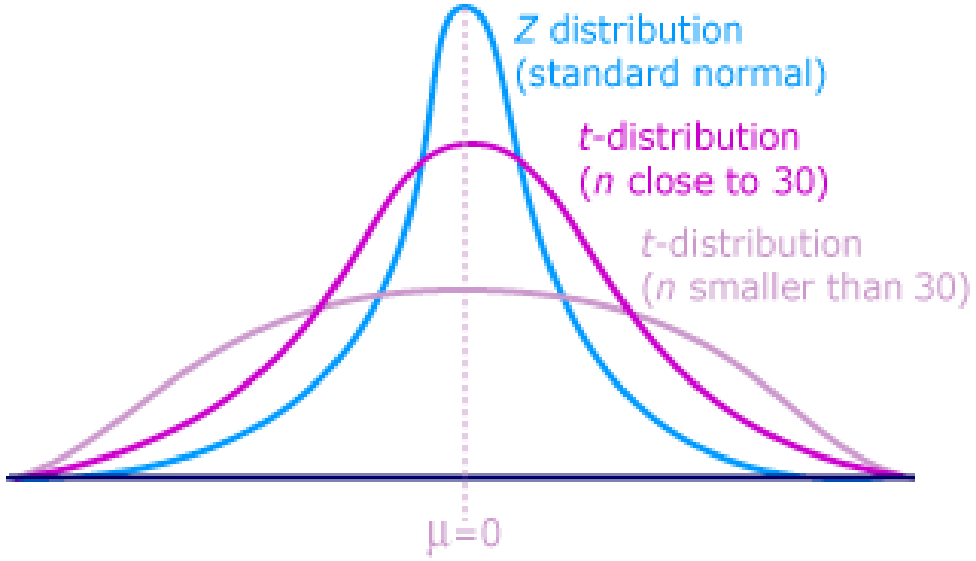
  t-distribution is a family of curves with $\sigma^2 > 1$
- σ^2 depends on the degrees of freedom (d.f)

  d.f. $\rightarrow +\infty$

  $\sigma^2 \rightarrow 1$

  t-distribution $\rightarrow$ standard normal distribution N(0,1)
- Used for a normally distributed variable whenever the variance of that variable is not known.

Common continuous distributions: t-distribution



t-distribution R functions

#random generation

rt(n, df)

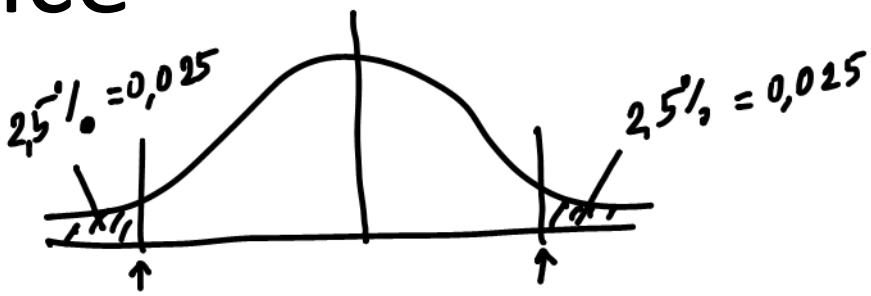
#give quantile value based on probability

qt(p, df)

#give probability based on quantile value

pt (q, df)

Exercice



- **Problem**

  Find the 2.5th and 97.5th percentiles of the t-distribution with 5 degrees of freedom.

- **Solution using Probability tables**

  We are looking for t-values based on area's

  In the table we need the d.f. , alpha, and to know whether we look at one or two tails.

  Draw the t-distribution and the 2.5th and 97.5th percentiles

  - we have two tails
  - alpha is 5% (=0.05) divided over two tails
  - 5 d.f.

  Correspondingly, in the table we find: t = 2.571

- **Answer**

  The 2.5th and 97.5th percentiles of the Student t distribution with 5 degrees of freedom are -2.571 and 2.571 respectively.

Exercice

- **Problem**

  Find the 2.5th and 97.5th percentiles of the t-distribution with 5 degrees of freedom.

- **Solution using R**

  We are looking for t-values (quantiles, percentiles) based on area's (probabilities)

  We apply the quantile function qt of the Student t distribution

  qt(p, df, ncp, lower.tail = TRUE, log.p = FALSE)

  > qt(c(.025, .975), df=5) # 5 degrees of freedom
  [1] -2.5706 2.5706

- **Answer**

  The 2.5th and 97.5th percentiles of the Student t distribution with 5 degrees of freedom are -2.5706 and 2.5706 respectively.

T-distribution, example

$t_{n-1,\ 1-\alpha/2}$:

- *n-1 is the degrees of* freedom
- we are looking for the 1−α/2 percentile

For example, for n = 5 and α = 0.05, we are looking for t with 4 degrees of freedom and the 0.975 percentile.

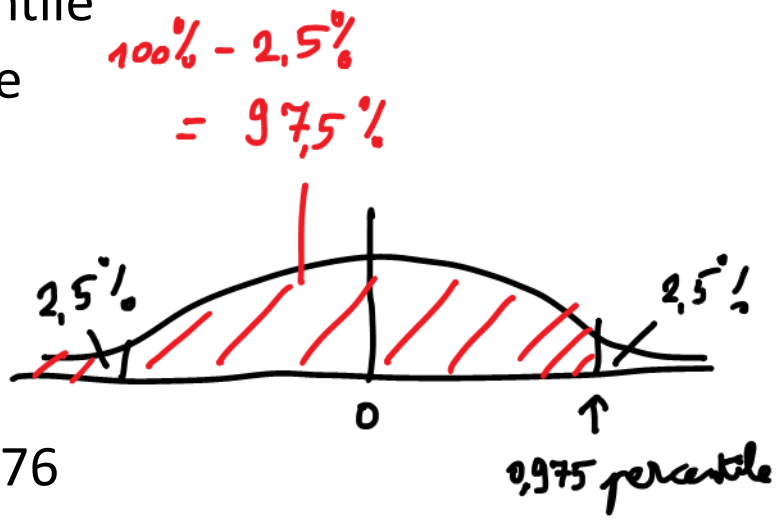


Table:

two tails; alpha = 0.05; d.f. = 4 ➔ t=2.776

Using R:

```
> qt(0.975, 4)
[1] 2.776445
```

Confidence intervals for the mean

Confidence intervals for the mean

- Collect data and get point estimates:
  - The sample mean $\bar{y}$ *to estimate the* population mean μ .
  - The sample variance, s^2 *to estimate* the population variance σ^2

- Can calculate interval estimates of each point estimate e.g. 95% confidence interval for the true mean
  - *If* $\bar{y}$ is normally distributed

    this is:
    - If the *y's are normally distributed OR*
    - The sample size is large enough that the Central Limit Theorem holds -- $\bar{y}$ *will be* normally distributed

A. Original variable normally distributed and **σ known *OR* sample size ≥30**

- Distribution of the means is normal distribution
- Mean of sample means = population mean

$$\mu_{\bar{X}} = \mu$$

- Standard deviation of sample means (SE)

$$\sigma_{\bar{X}} = \frac{\sigma}{\sqrt{n}}$$

- In the case sample size ≥30, s can substitute σ

A. Original variable normally distributed and **σ known (*OR* sample size ≥30)***

- Sample mean lays a number of standard deviations away from the mean (population mean)
- That number is the z-value (follows standard normal distribution N(0,1)
- With 1- α percent certainty, the mean of the sample lays z standard errors away from the population mean μ (value of z depends on alpha)

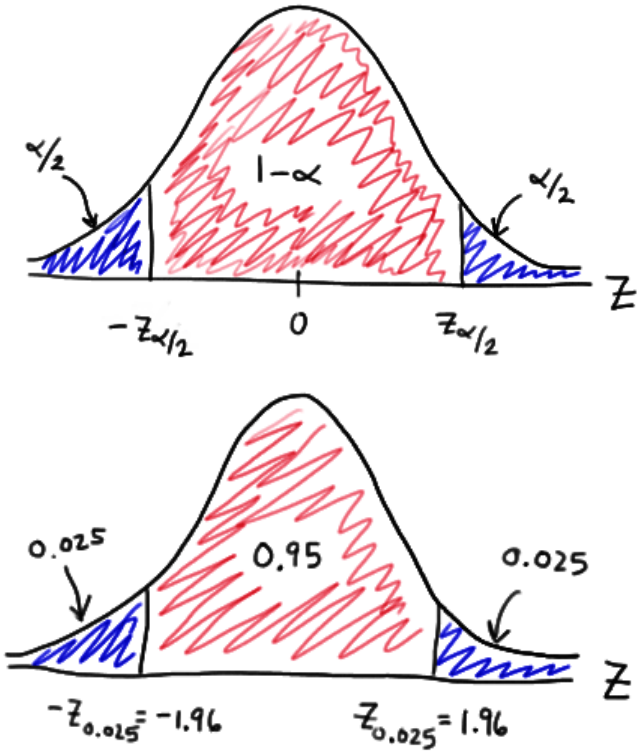
$$\mu - z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right) < \overline{X} < \mu + z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right)$$

*depends on the points of view of the statistician

- Based on standard normal distribution:
- Confidence interval for a specific α:
- For α = 0.05

⇔ 95% confidence interval

The values are, with 95% confidence, how many standard deviations away from the mean? → critical z-value



- Look up 100(1- α/2) percentile
  - = 97.5th percentile
  - = denoted $z_{\alpha/2}$
  - = z value for P= (0.95/2)
  - = z value for P= (0.475)
  - =1.96

A. Original variable normally distributed and **σ known (*OR* sample size ≥30)***

- interval for the true mean of the population for a specific alpha (level of significance):

$$\overline{X} - z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right) < \mu < \overline{X} + z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right)$$

- Intuitively: z values are actually the number of standard deviations that a value is away from the mean
- → for α = 0.05, 95% probability that real population mean is less than two standard errors away of $\overline{X}$
- **Margin of Error:** $z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right)$

*depends on the points of view of the statistician

B. Original variable normally distributed but **σ is unknown (and n < 30)***

- You can use the standard deviation of the sample in place of the standard deviation of the population BUT with another distribution: "**t-distribution**"

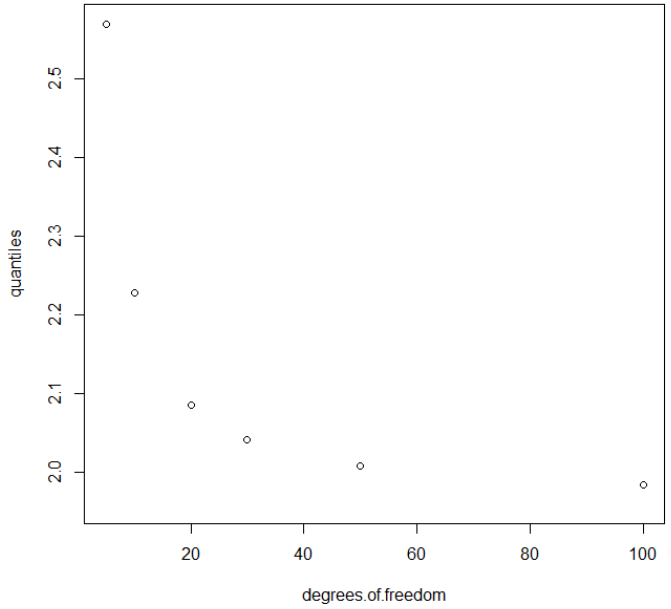
- interval for the true mean of the population for a specific alpha (level of significance):

$$\overline{X} - t_{\alpha/2}\left(\frac{s}{\sqrt{n}}\right) < \mu < \overline{X} + t_{\alpha/2}\left(\frac{s}{\sqrt{n}}\right)$$

*depends on the points of view of the statistician

Create your own point of view: calculate the $t_{.025}$ values (for 95% confidence intervals)

n	df	$t_{.025}$
6	5	
11	10	
21	20	
31	30	
51	50	
101	100	
∞	∞	$= z_{.025}$

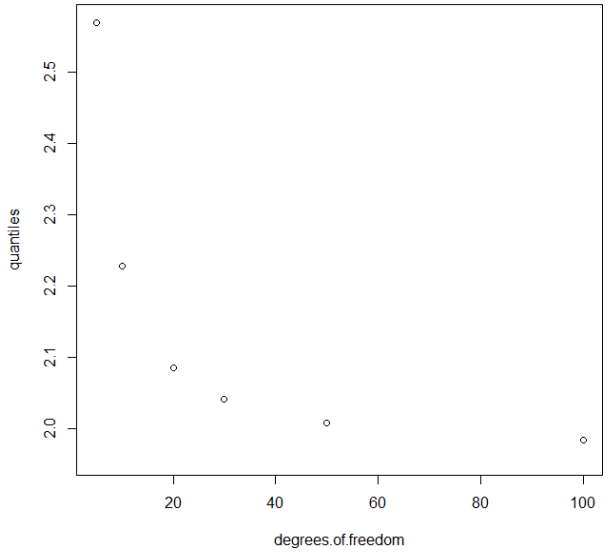



```
> degrees.of.freedom <- c(5,10,20,30,50,100,Inf)
> quantiles <- qt(p=0.025,df=degrees.of.freedom,lower.tail=FALSE)
>  quantiles
[1] 2.570582 2.228139 2.085963 2.042272 2.008559 1.983972 1.959964
> plot(degrees.of.freedom,quantiles)
```

$= z_{.025}$

Create your own point of view: calculate the $t_{.025}$ values (for 95% confidence intervals)

n	df	$t_{.025}$
6	5	
11	10	
21	20	
31	30	
51	50	
101	100	
∞	∞	



If the samples are very small:

- ➔ the population mean μ is, with 95% confidence, in an interval of which the limits are MORE than two standard errors away from the mean.
- ➔ Our prediction of where the population mean should be is LESS PRECISE: a larger 95% confidence interval.
- ➔ The less data we have, the less confidence we can have in the accuracy of the estimates
- ➔ If we use the z-value, we underestimate the margin of error!

Example

- In the data set survey of the package “MASS”, the survey is performed on a sample of the student population. We will look at the student height data
- For convenience, we first filter out missing values in survey$Height with the na.omit function, and save it in height.response.

```
> library(MASS)                 # load the MASS package
> height.response <- na.omit(survey$Height)
```

script 1_confidenceinterval.R

Example

- **Problem 1**

  Assume the population standard deviation σ of the student height in survey is 9.48. Find the best point estimate of the population mean and the margin of error and interval estimate at 95% confidence level.

- **Problem 2: the real world!**

  Without assuming the population standard deviation of the student height in survey, find the margin of error and interval estimate at 95% confidence level.

script 1_confidenceinterval.R

Exercise 1

- Find the 95% confidence interval of the population mean of all numeric data in “ufc_processed.csv”

script TADE_exercise_1.R

Hypothesis testing

Hypothesis Tests:

- Can hypothesize what the true value of any population parameter might be, and state this as **null hypothesis (H0:)**
- We also state an **alternate hypothesis (H1: or Ha:)** that it is a) not equal to this value; b) greater than this value; or c) less than this value
- Collect **sample data** to test this hypothesis
- From the sample data, we calculate a sample statistic as a **point estimate of this population parameter and an estimated variance of the sample statistic**.
- We calculate a **"test-statistic"** using the sample estimates
- **Under H0, this test-statistic will follow a known distribution**.
- If the test-statistic is very unusual, compared to the tabular values for the known distribution, then the H0 is very unlikely and we conclude H1

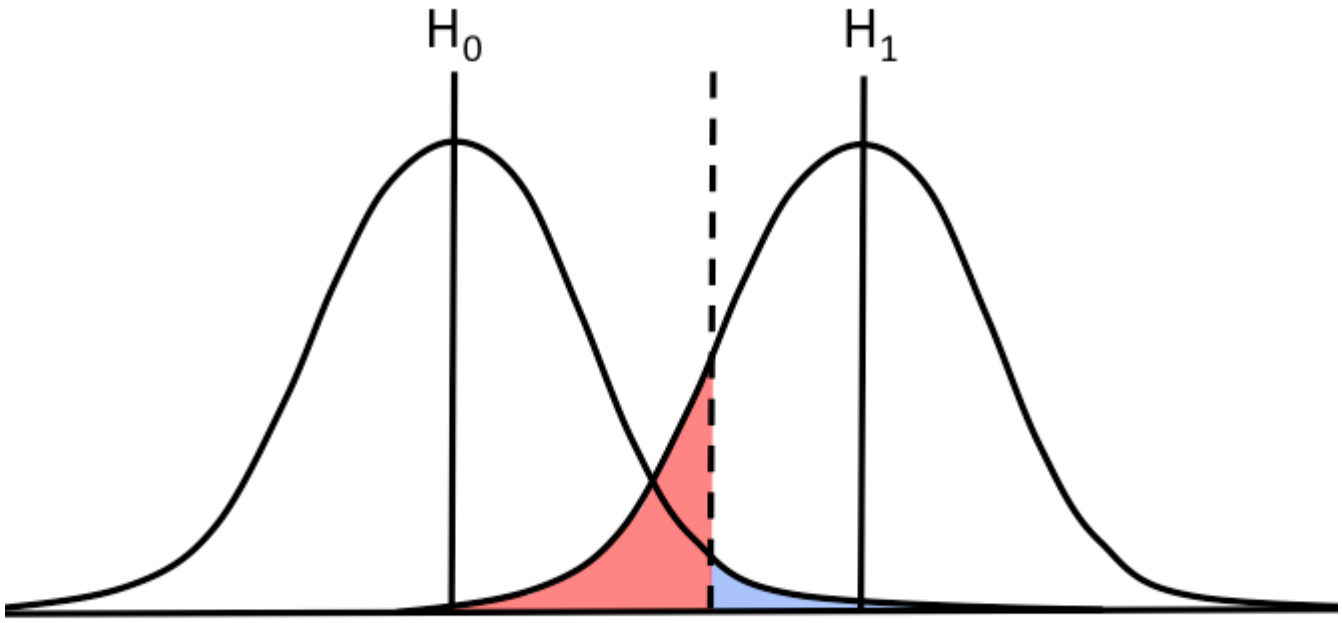
Errors of hypothesis testing

	H0 True	H0 False
Accept	1-α	β (Type II error)
Reject	α (Type I error)	1-β

- **Type I Error**: Reject H0 when it was true.
  Probability of this happening is α

- **Type II Error**: Accept H0 when it is false.
  Probability of this happening is β

- **Power of the test**: Reject H0 when it is false.
  Probability of this is 1-β


H_0
H_1
β
α
Type II error
Type I error

- **Level of significance**

  = maximum probability of committing a type I error

  = alpha

  Chosen by the researcher before the statistical test is conducted
- **P-value**

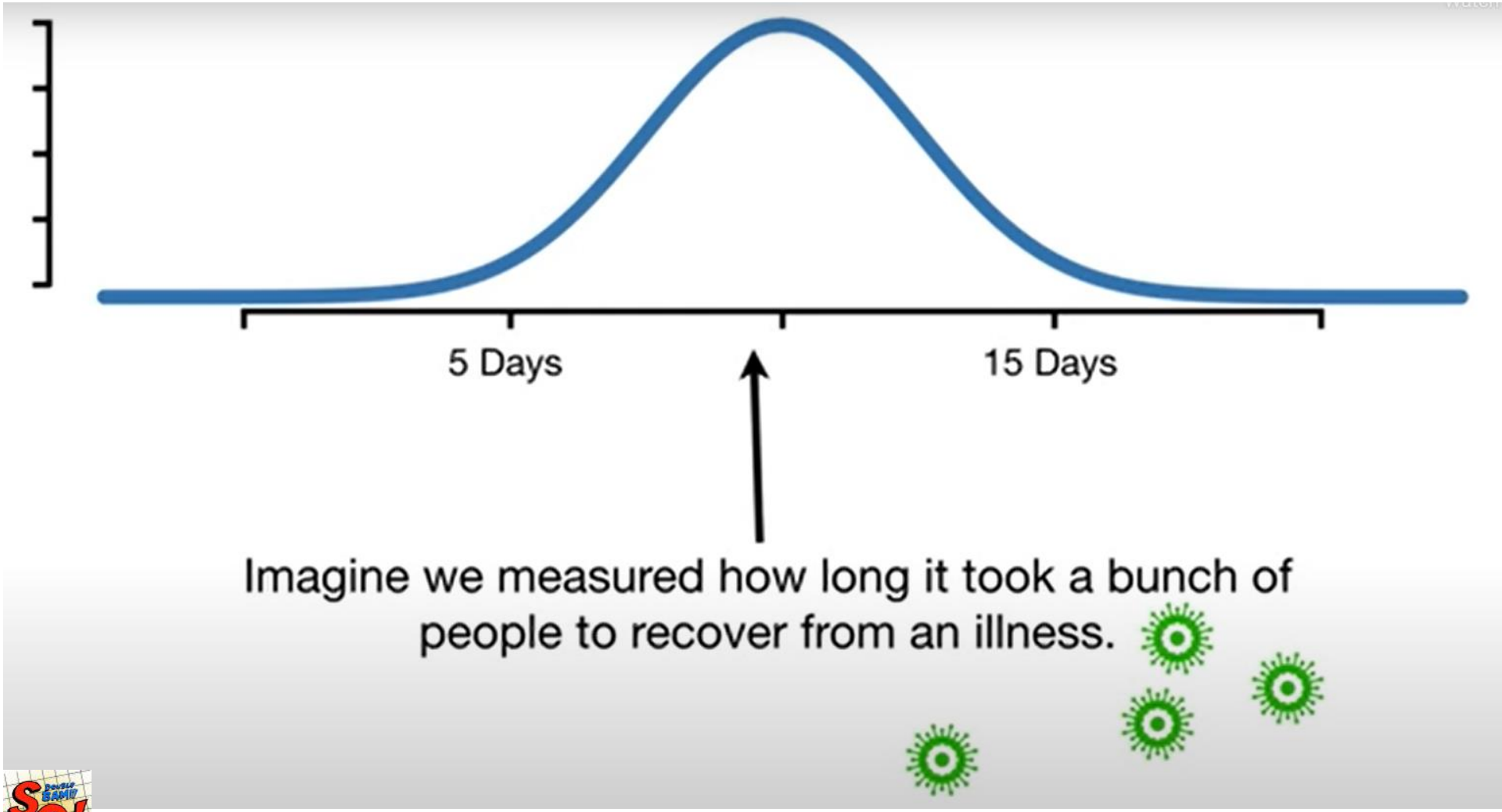
  = Probability of getting a sample statistic or a more extreme statistic in the direction of the alternative hypothesis *when the null hypothesis is true*

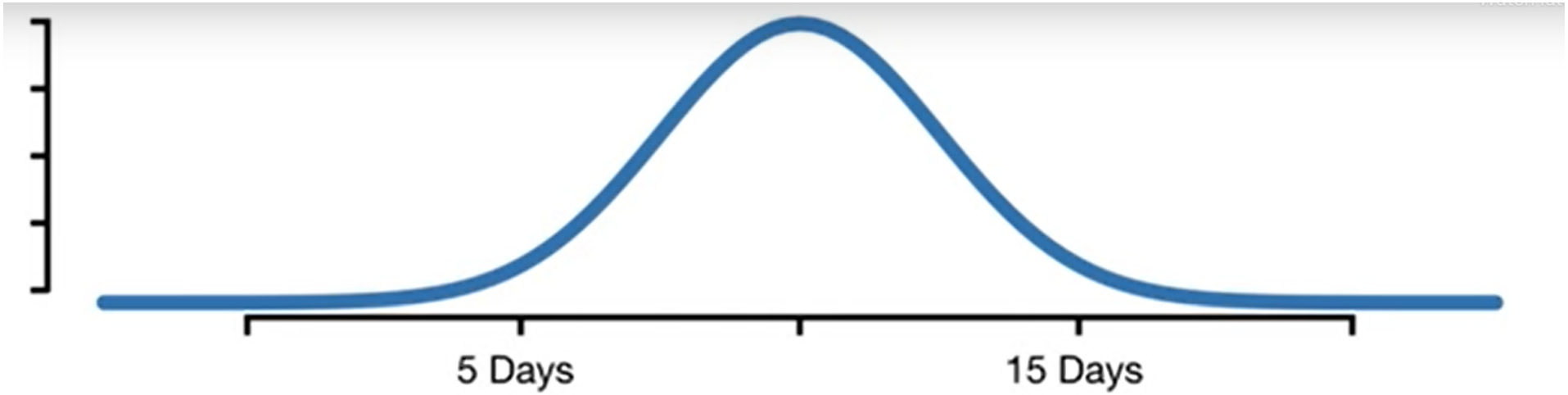
  Computed after sample statistic is found

- P-value ≤ α ⇔ reject H0
- P-value > α ⇔ accept H0

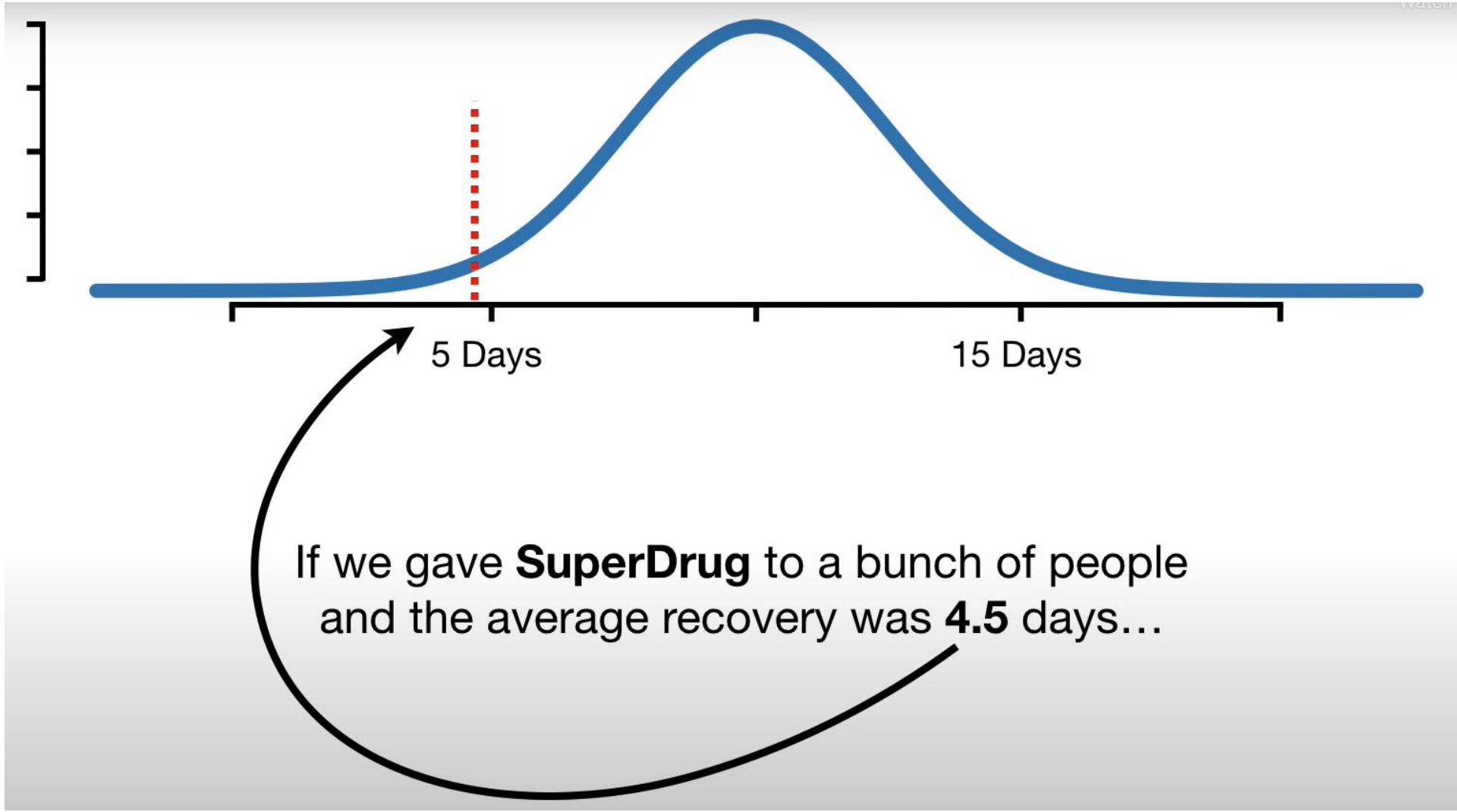
Same for one-tailed and two-tailed tests

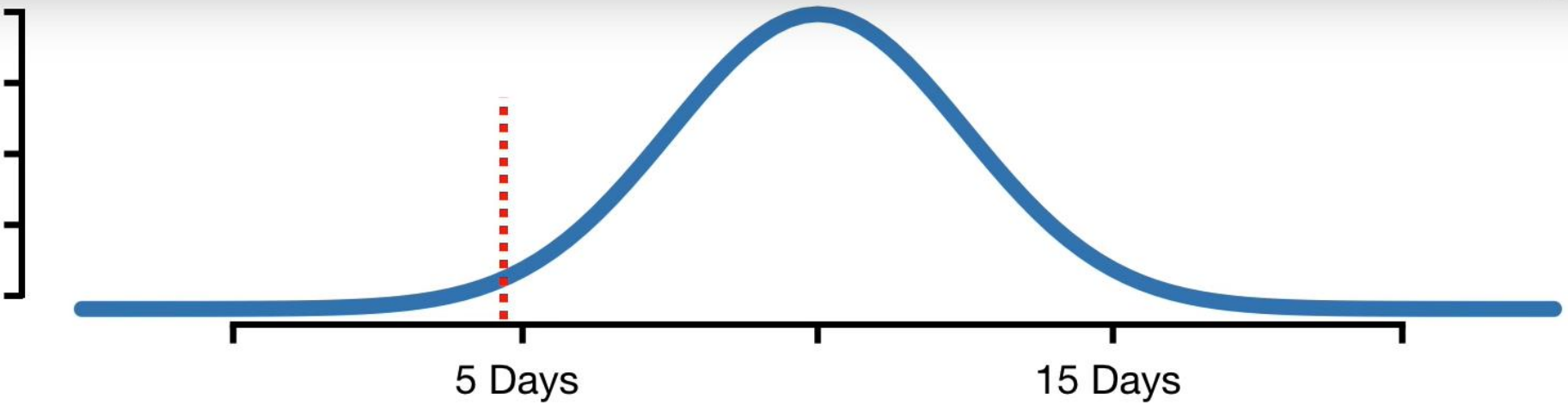
One- or two-tailed tests?



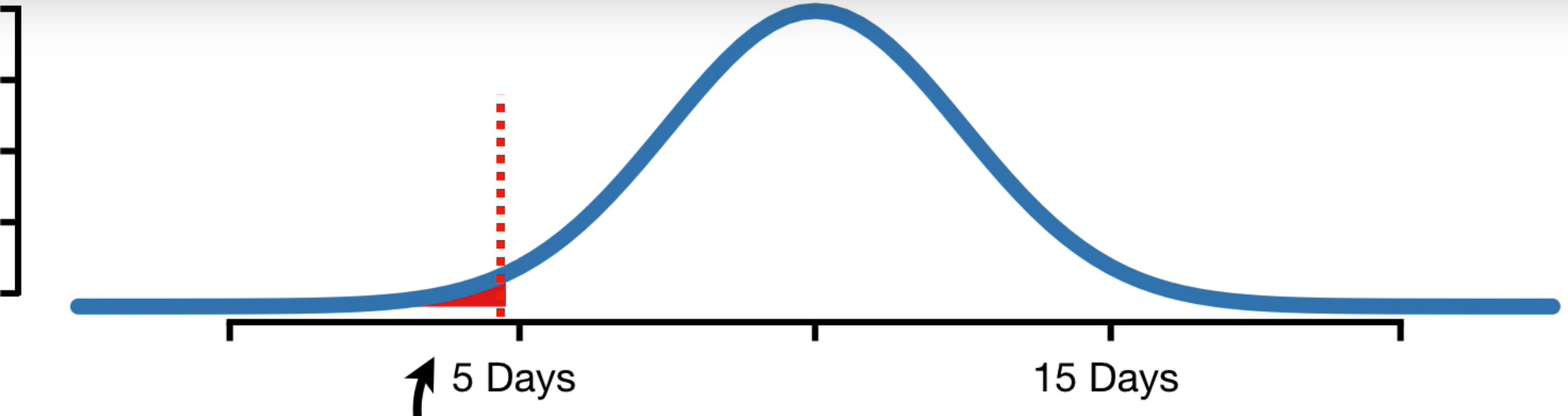


Now imagine we created a new drug, **SuperDrug**, and wanted to see if it helped people recover in fewer days.


5 Days
15 Days
If we gave **SuperDrug** to a bunch of people
and the average recovery was **4.5** days…

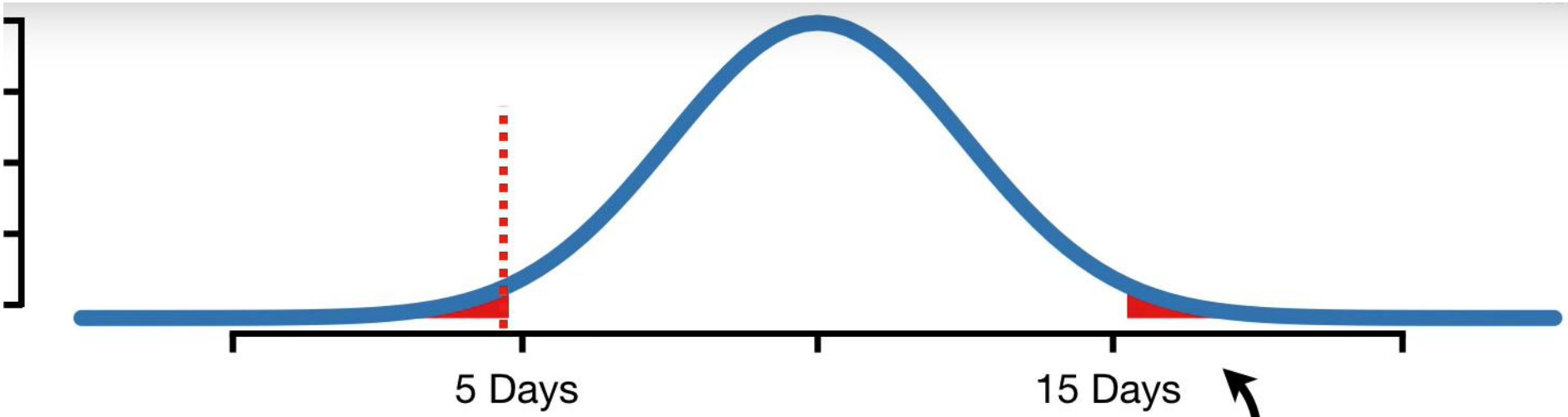


…then a **Two-Sided p-value**, like the ones we've been computing all along, would be…



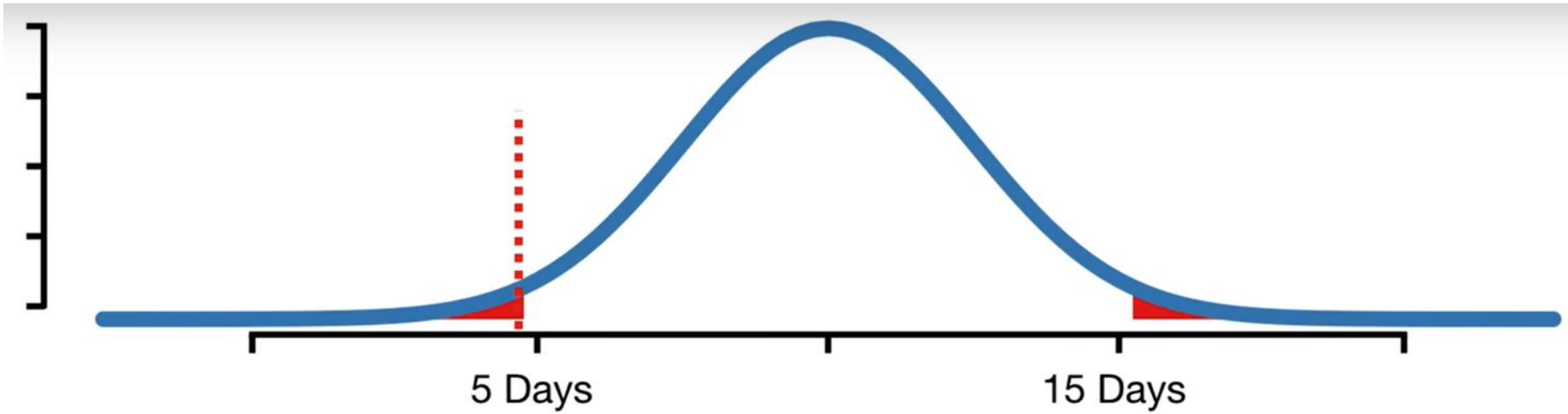
…the sum of *this* area under the curve, **0.016**…

Two-Sided p-value for **4.5** days = 0.016



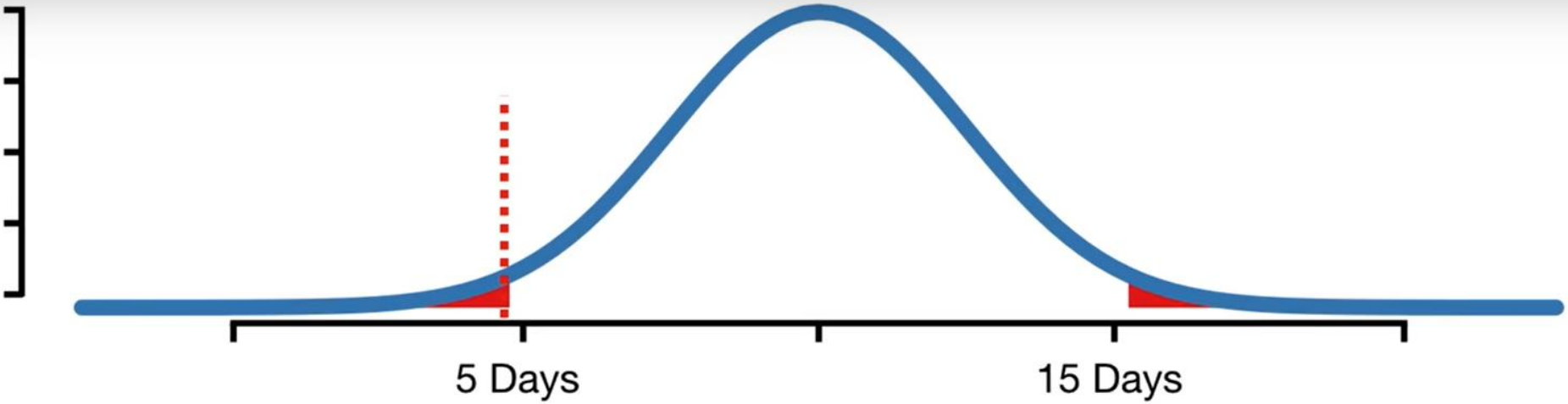
…plus *this* area under the curve, **0.016**…

Two-Sided p-value for **4.5** days = 0.016 + 0.016



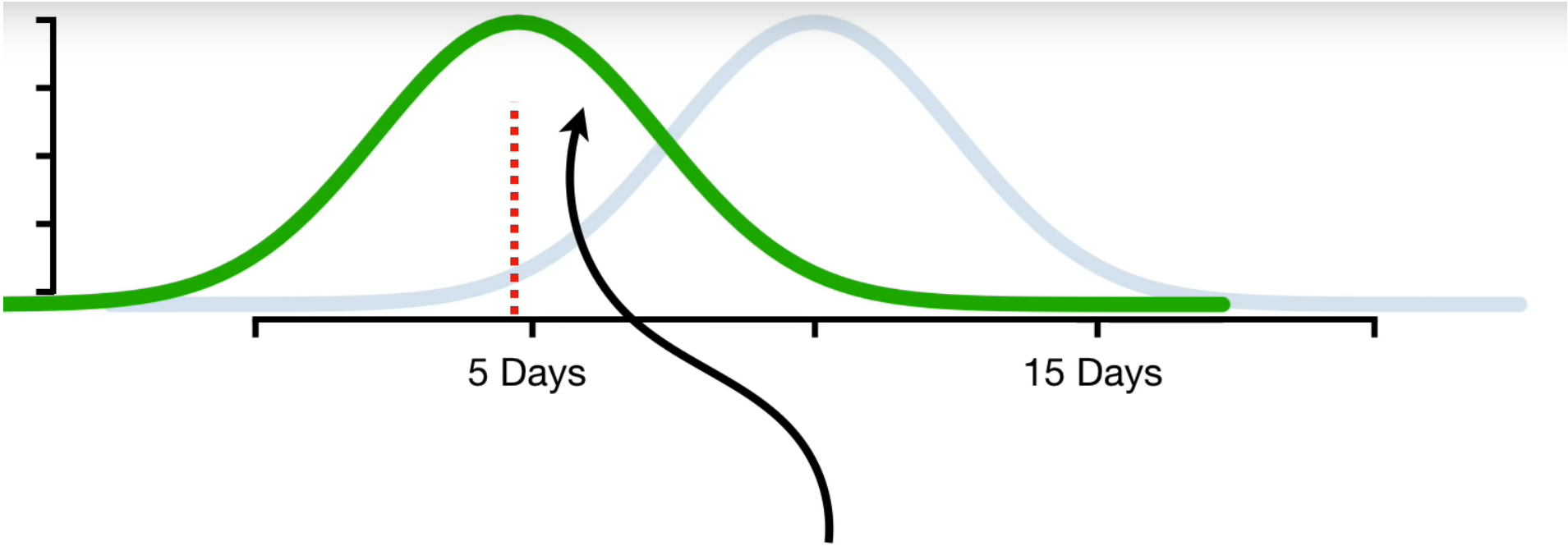
…and the total is **0.03**.

Two-Sided p-value for **4.5** days = 0.016 + 0.016 = 0.03



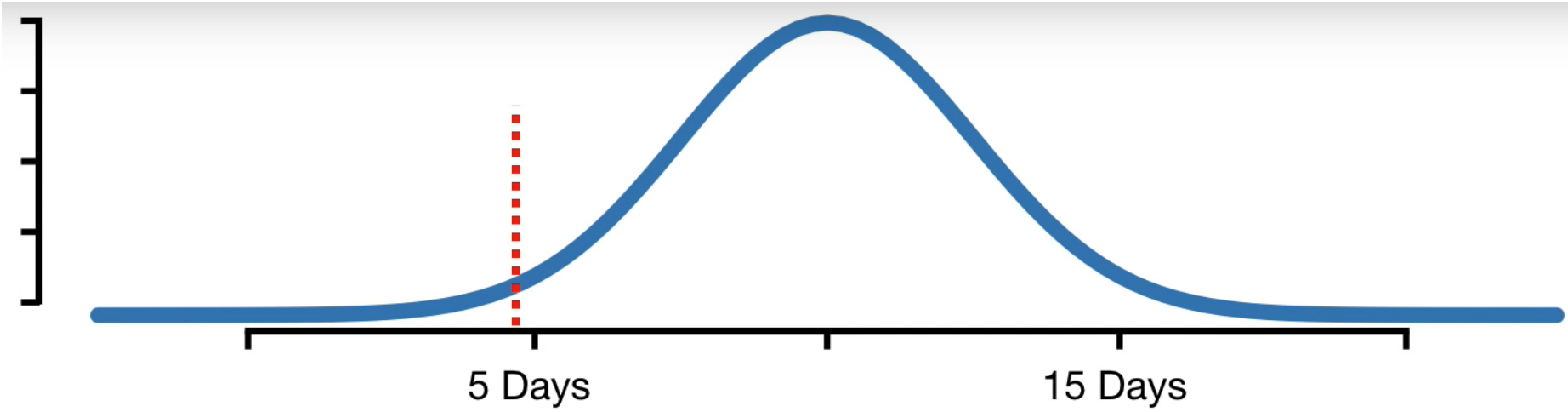
And since **0.03 < 0.05**, the **Two-Sided p-value** tells us that, given this distribution of recovery times, **SuperDrug** did something unusual.

Two-Sided p-value for **4.5** days = 0.016 + 0.016 = 0.03

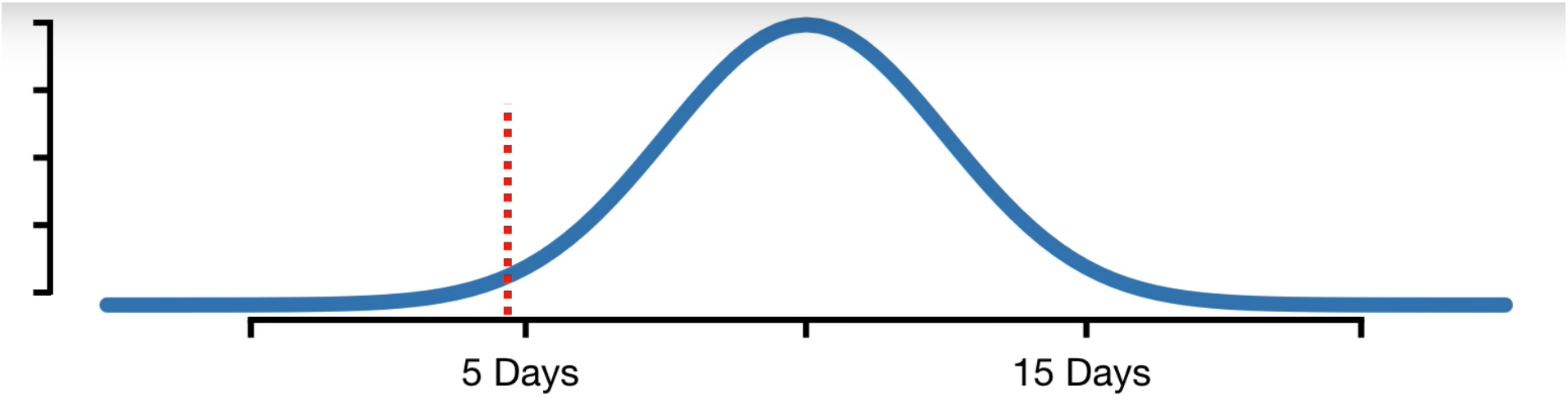


…and that suggests that some other distribution does a better job explaining the data.

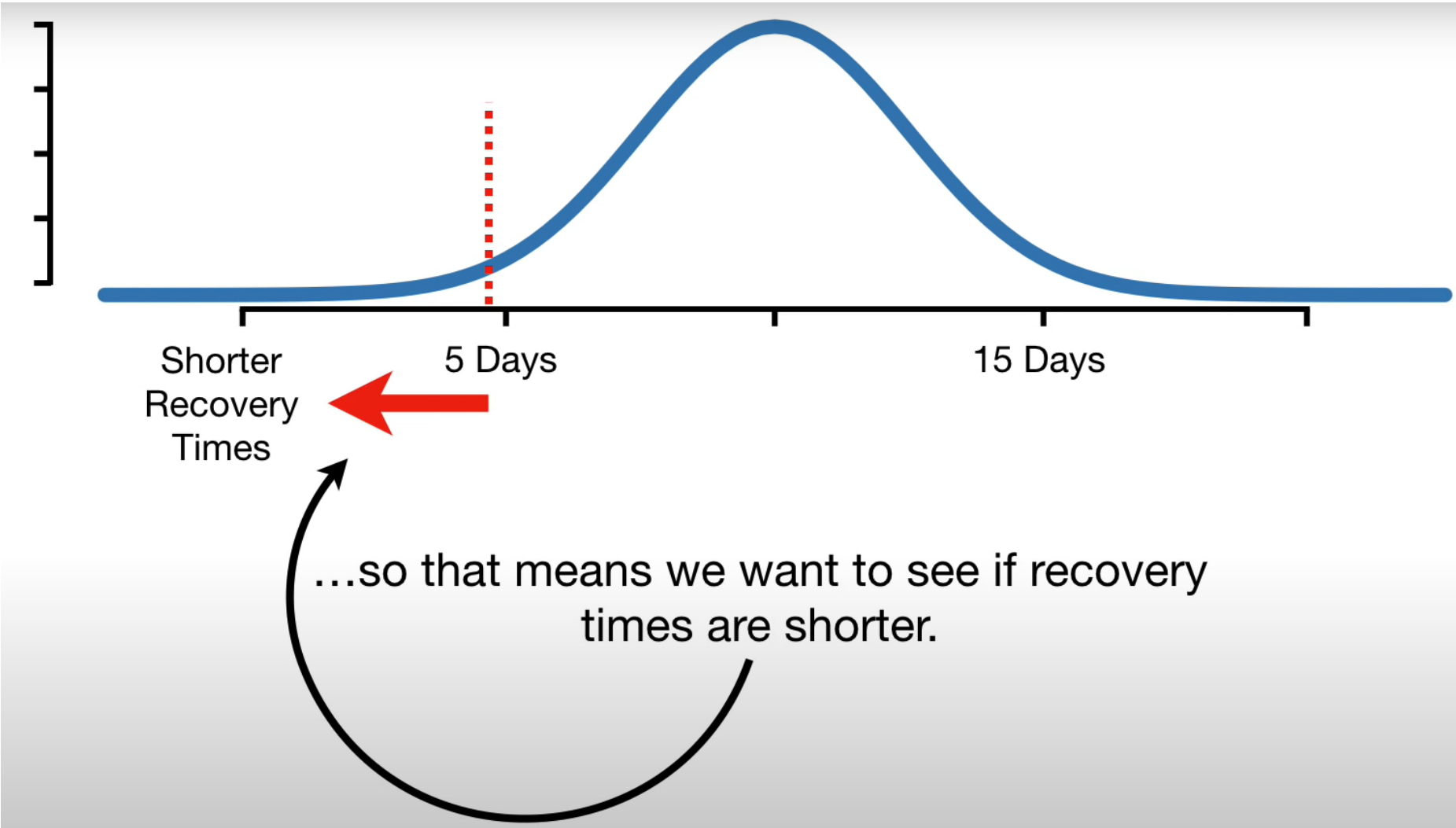
Two-Sided p-value for **4.5** days = 0.016 + 0.016 = 0.03

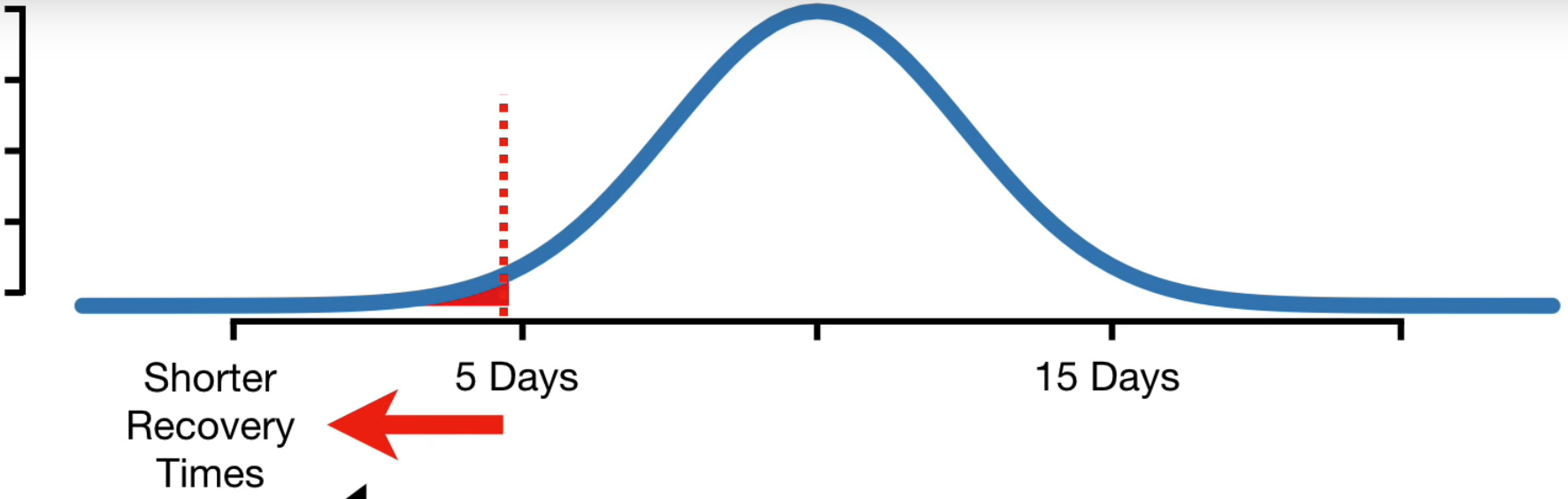


For a **One-Sided p-value**, the first thing we do is decide which direction we want to see change in.

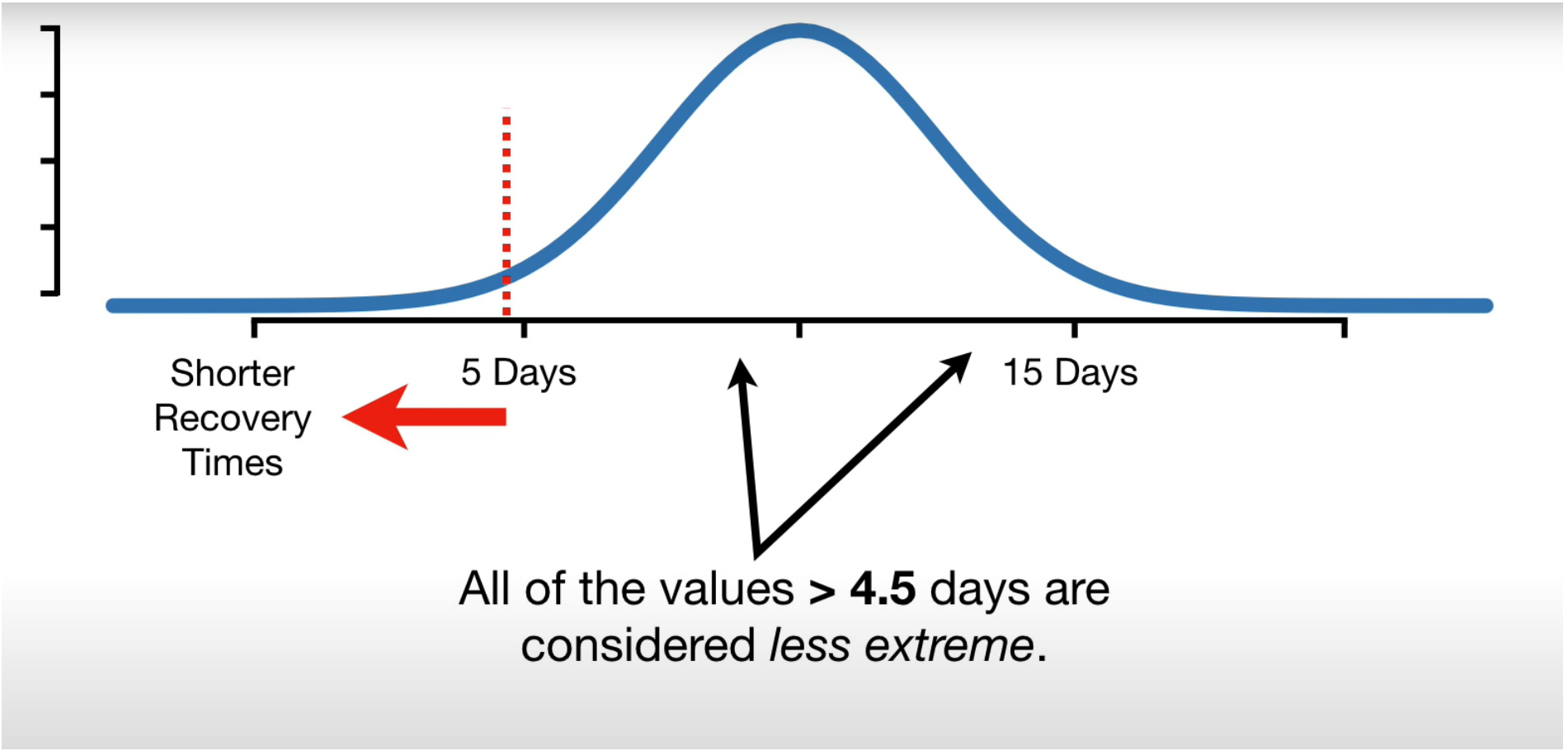


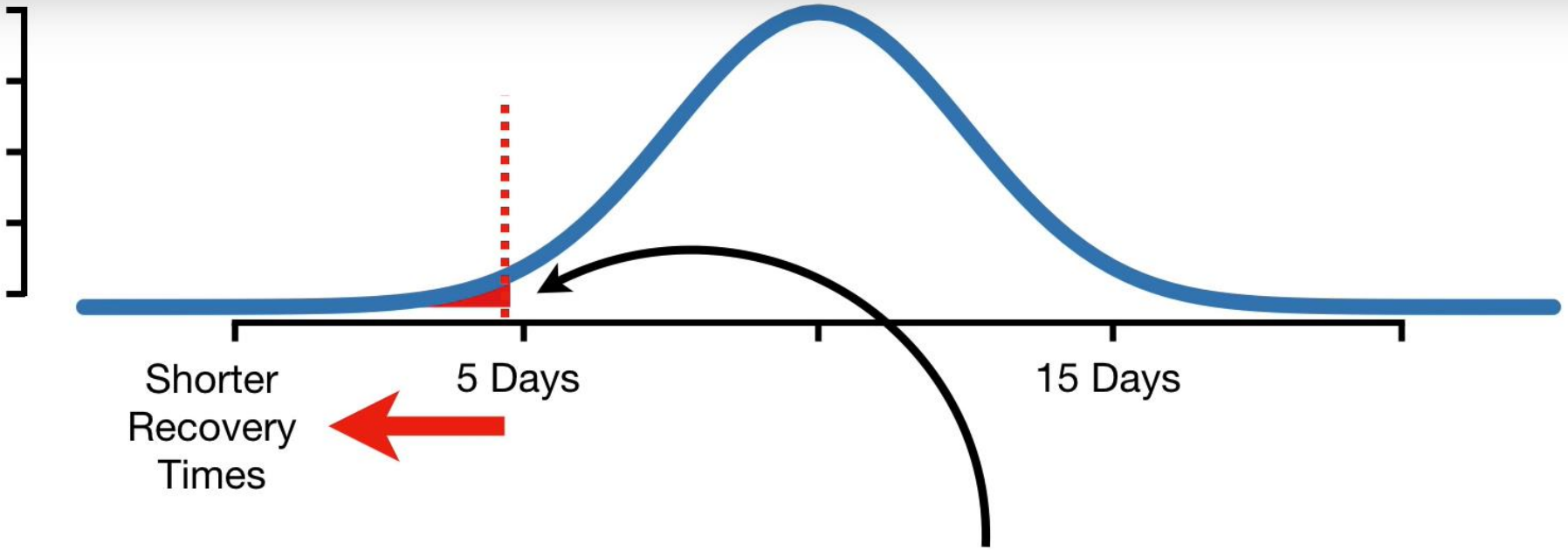
In this case, we'd like **SuperDrug** to shorten the time it takes to recover from the illness…


Shorter
Recovery
Times
5 Days
15 Days
…so that means we want to see if recovery
times are shorter.



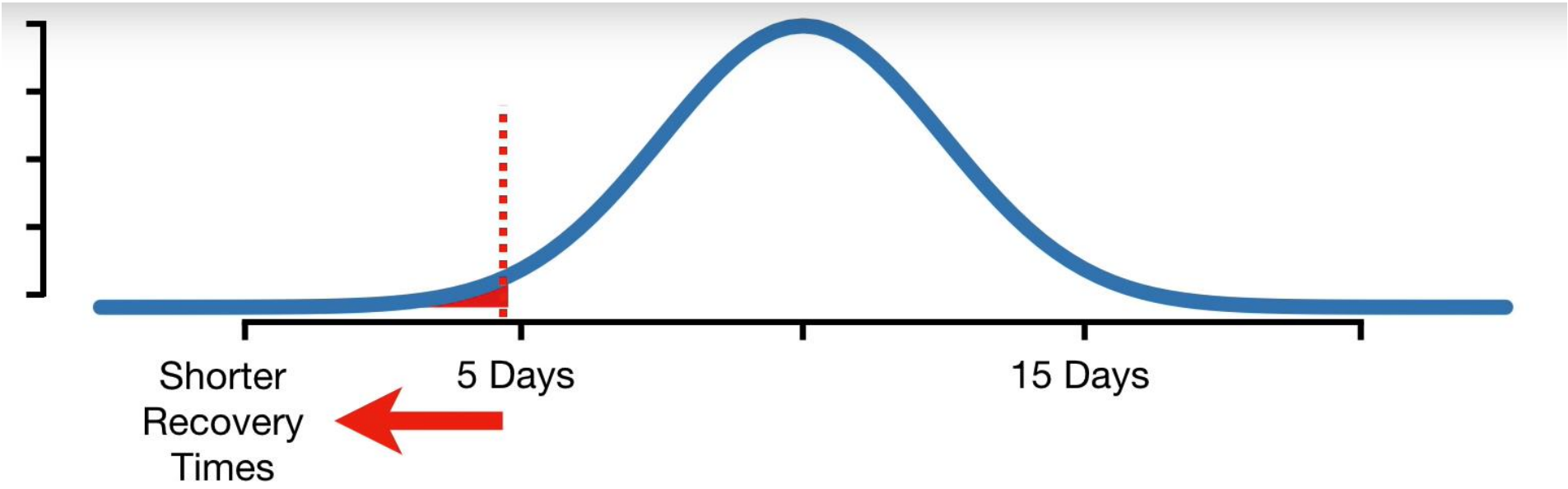
Because we want to see change in this direction, the only **more extreme** values are **< 4.5** days.


Shorter
Recovery
Times
5 Days
15 Days
All of the values > 4.5 days are
considered less extreme.



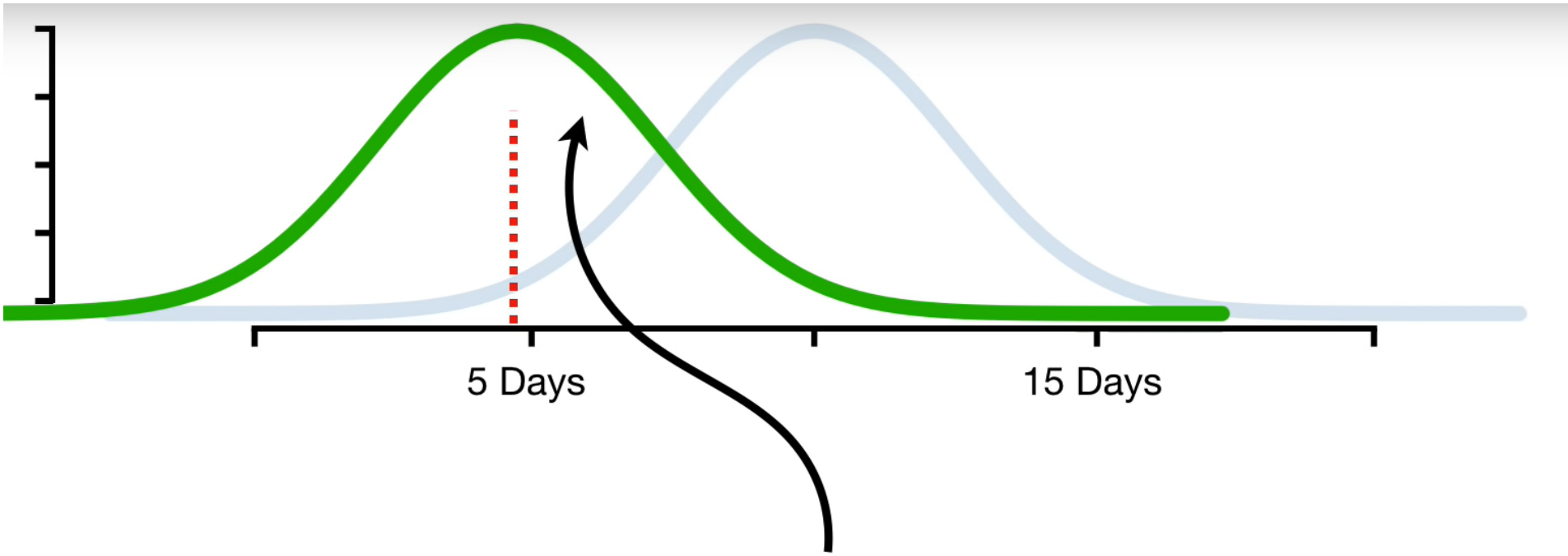
So, when we calculate a **One-Sided p-value**, we only use the area that is in the direction we want to see change, **0.016**.

One-Sided p-value for **4.5** days = 0.016



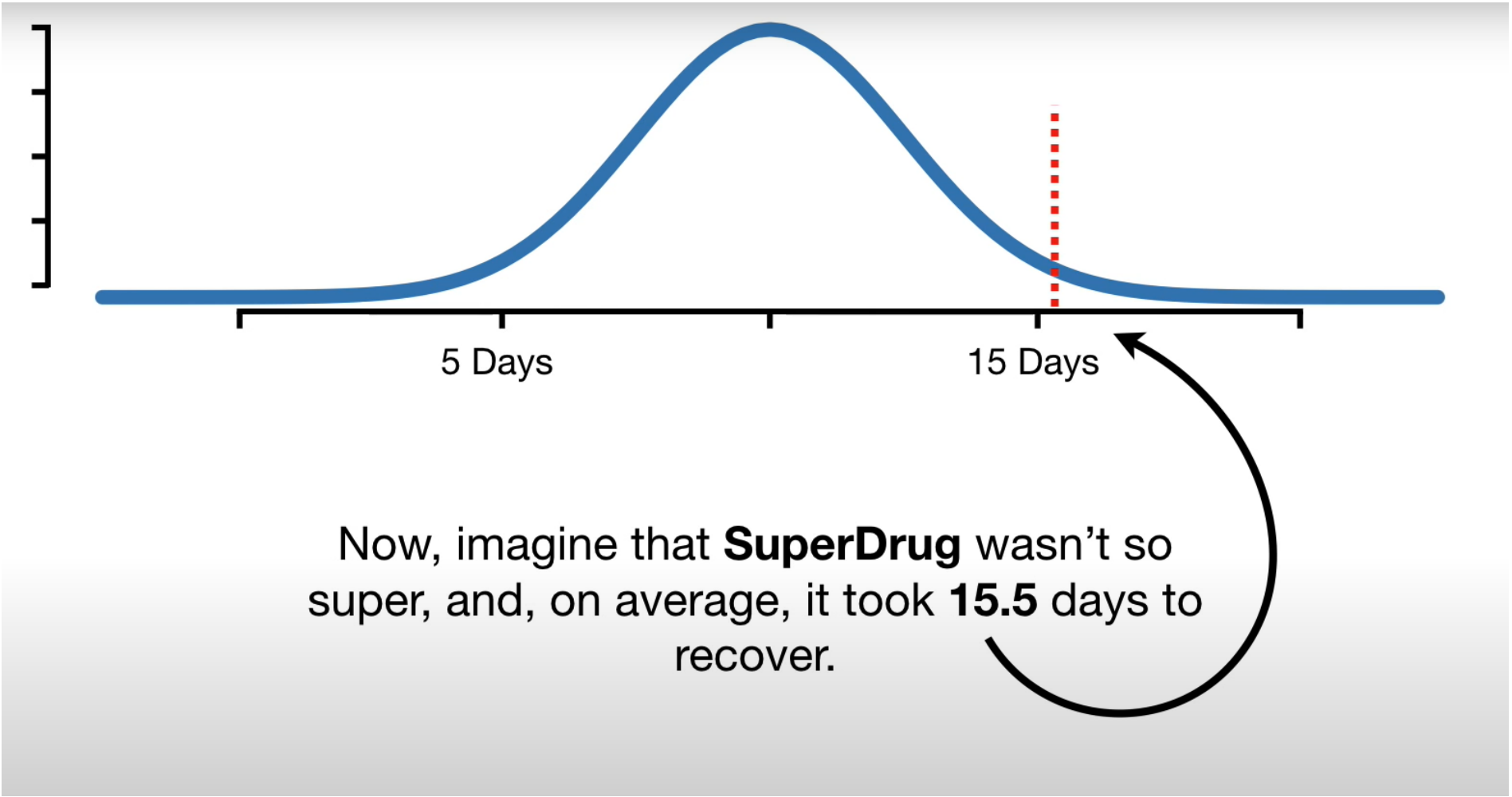
Again, since **0.016 < 0.05**, the **One-Sided p-value** would tell us that, given this distribution, **SuperDrug** did something unusual…

One-Sided p-value for **4.5** days = 0.016

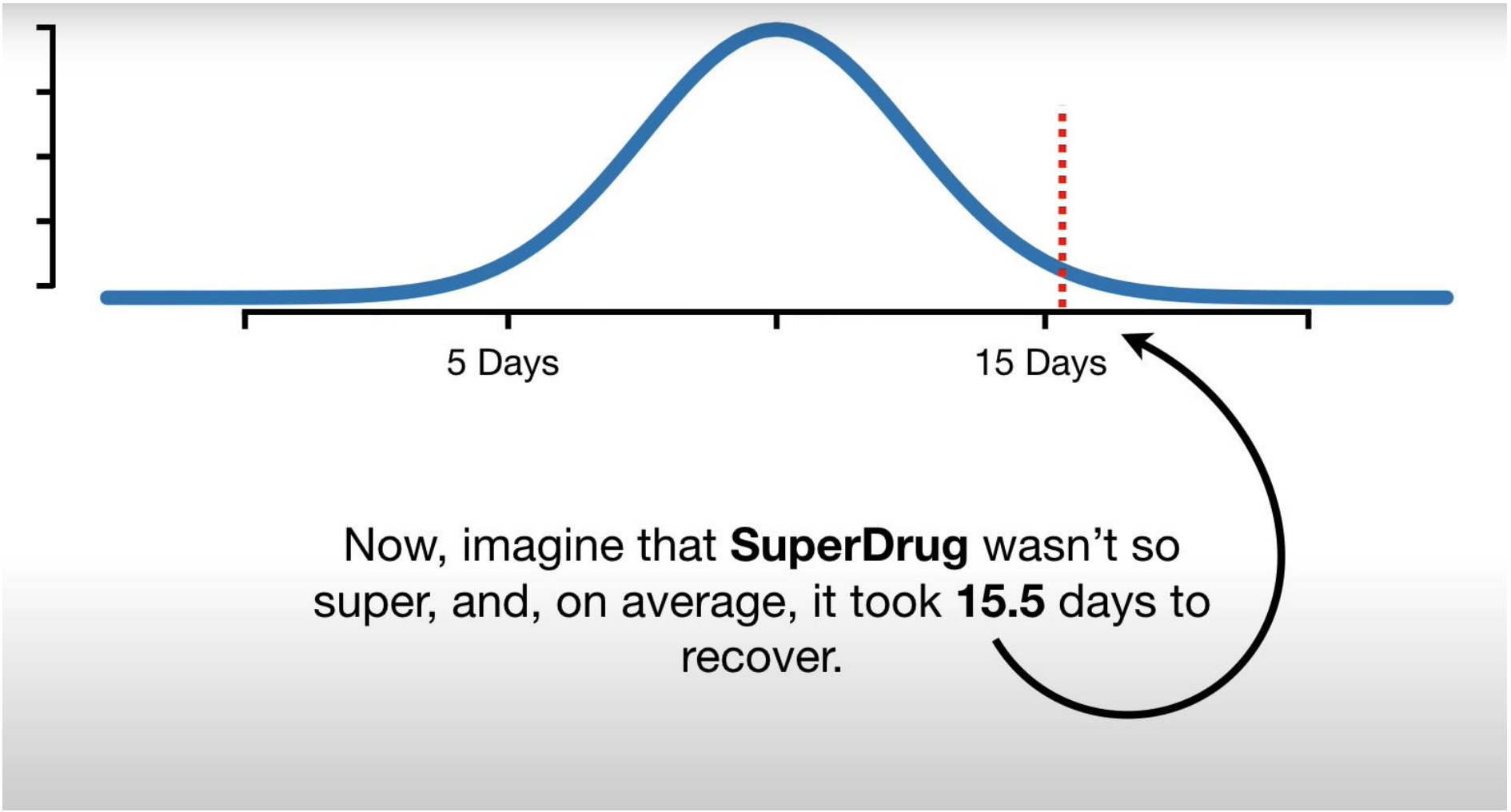


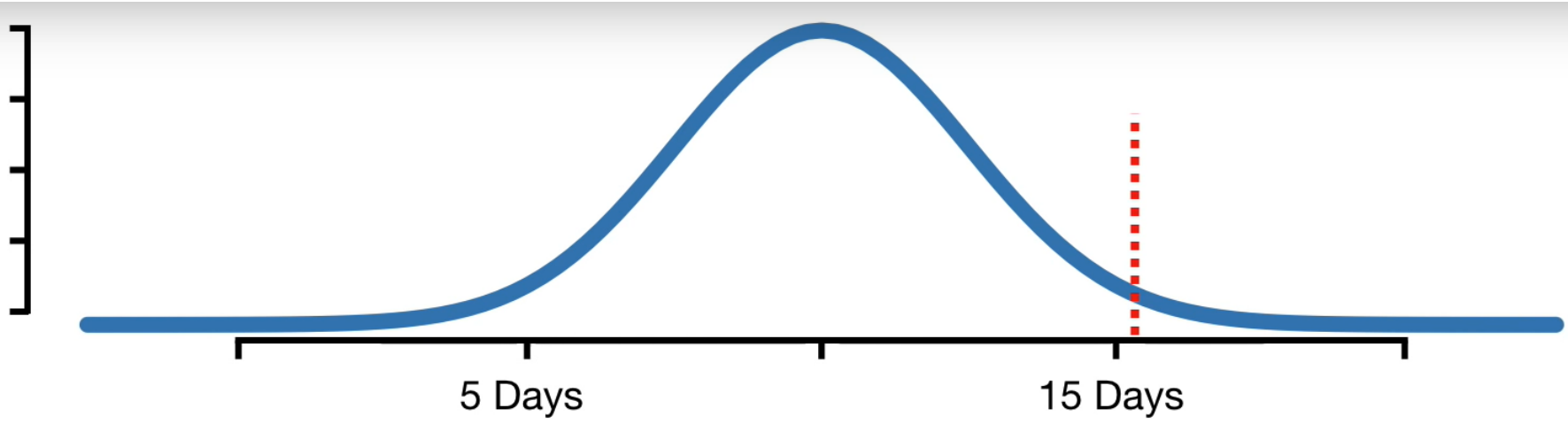
…and that some other distribution
makes more sense.

One-Sided p-value for **4.5** days = 0.016

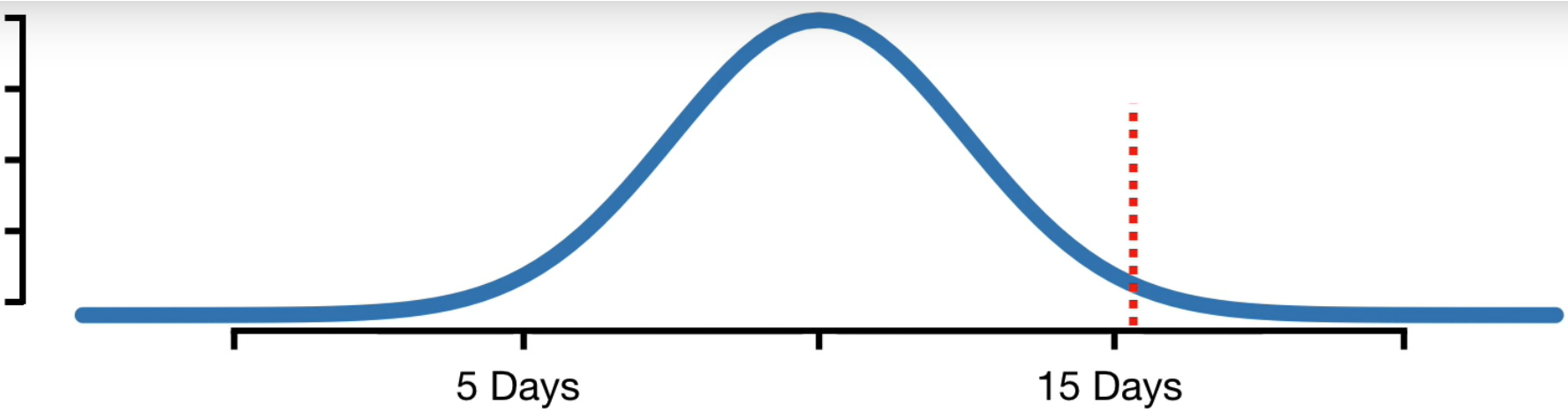


Now, imagine that **SuperDrug** wasn't so super, and, on average, it took **15.5** days to recover.

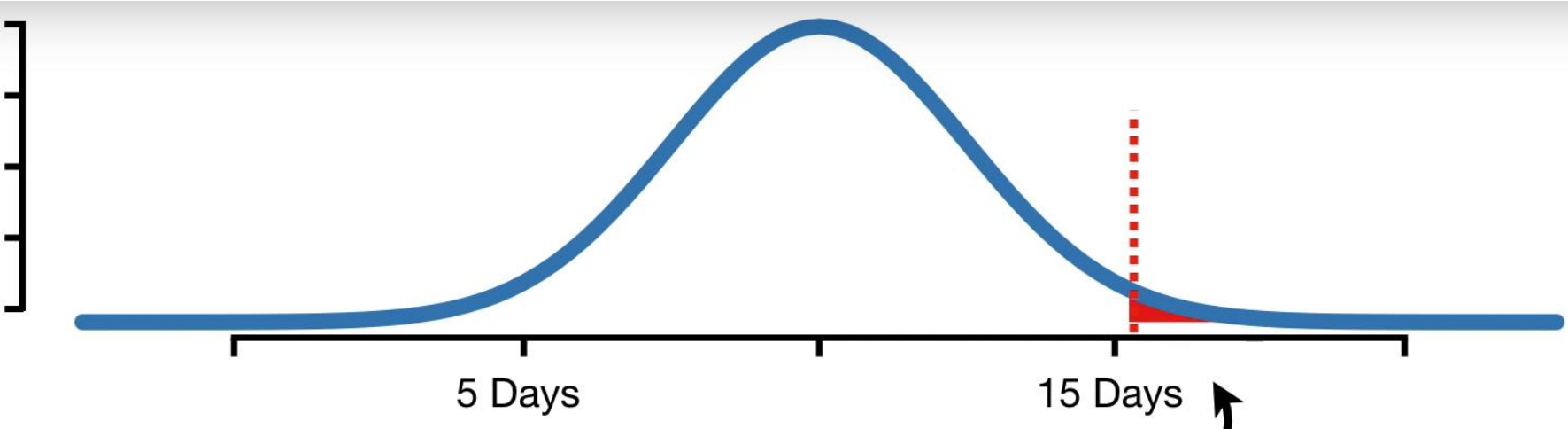

5 Days
15 Days
Now, imagine that **SuperDrug** wasn't so super, and, on average, it took **15.5** days to recover.



Just like before, the **Two-Sided p-value** would be…

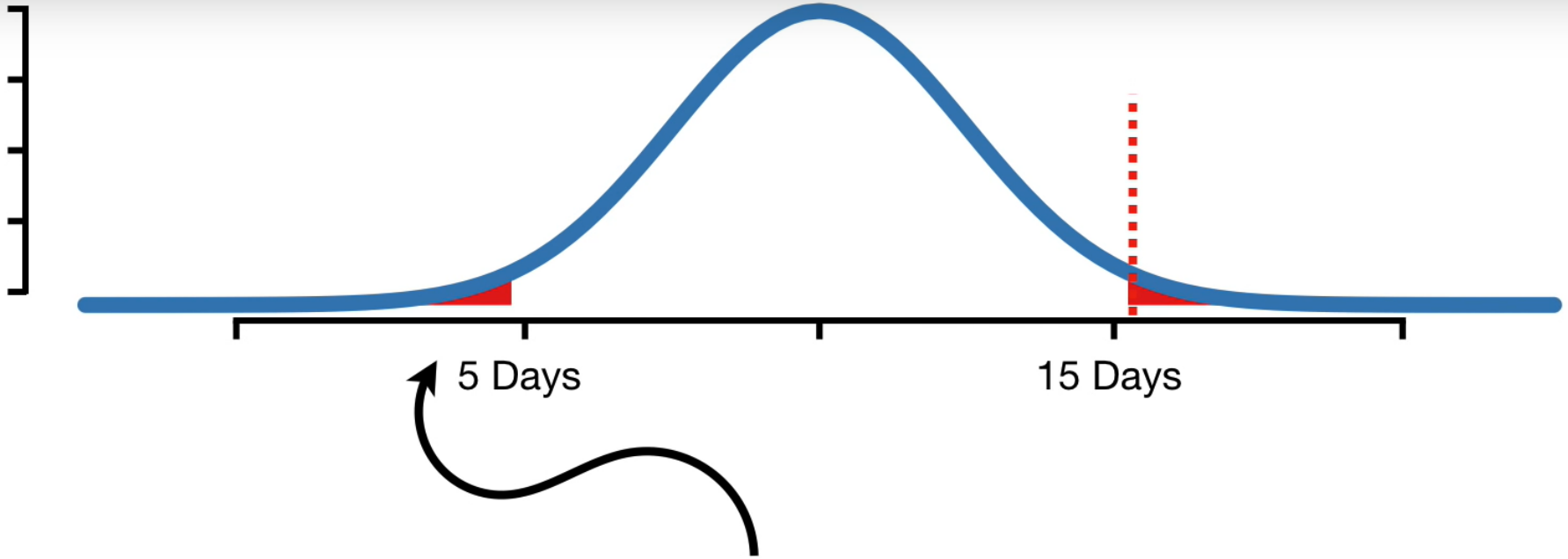


Just like before, the **Two-Sided p-value** would be…



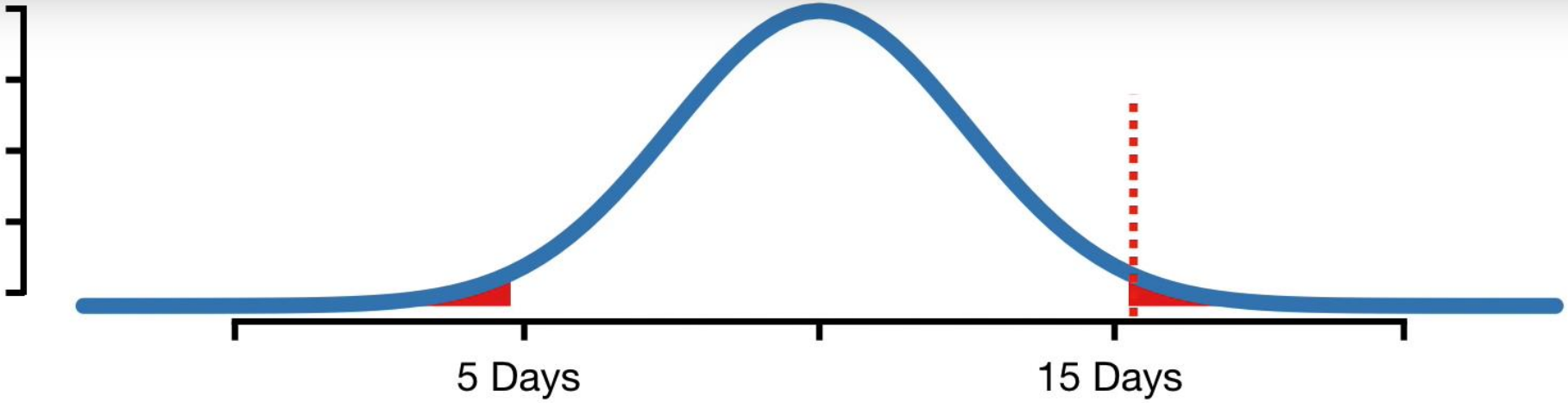
…the sum of *this* area under the curve, **0.016**…

Two-Sided p-value for **15.5** days = 0.016



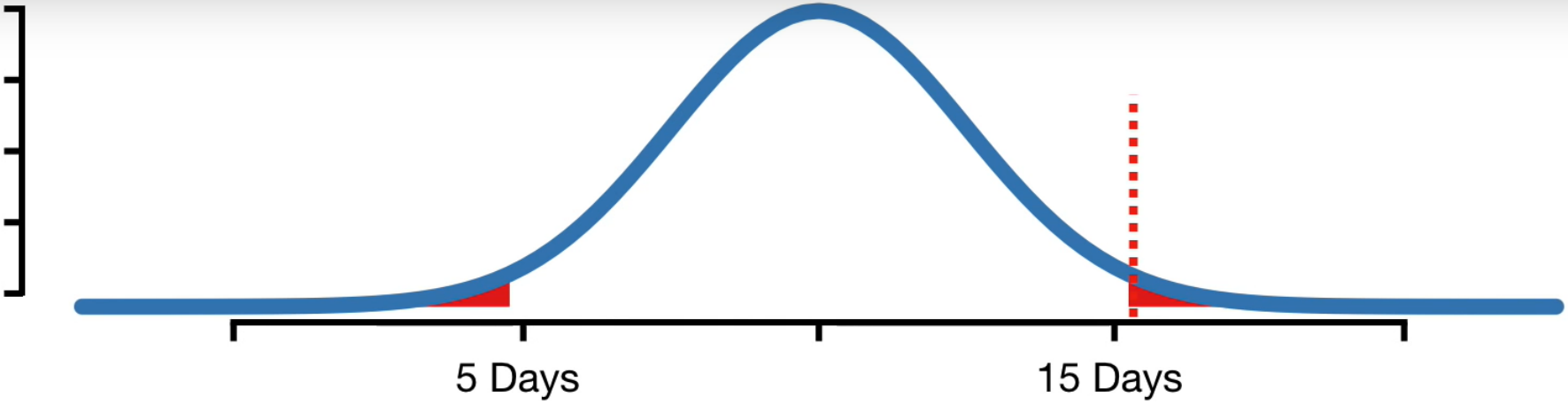
…plus *this* area under the curve, **0.016**…

Two-Sided p-value for **15.5** days = 0.016 + 0.016

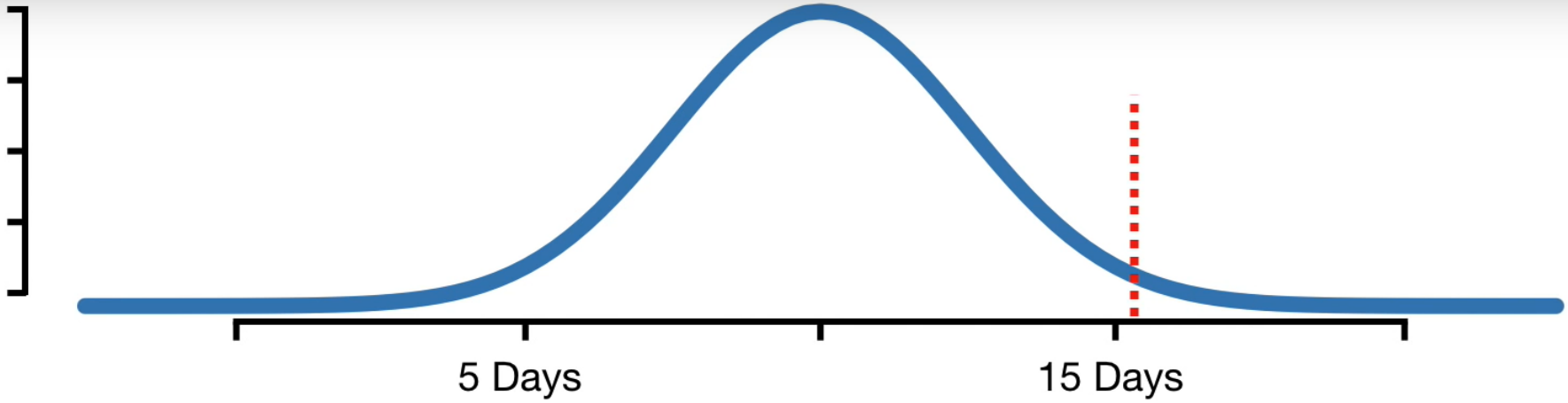


…and the total is **0.03**.

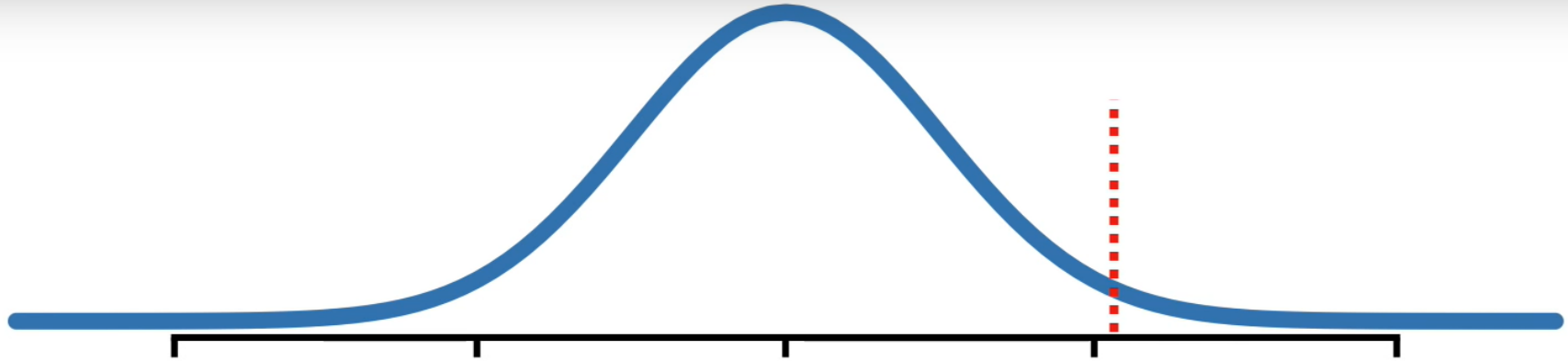
Two-Sided p-value for **15.5** days = 0.016 + 0.016 = 0.03



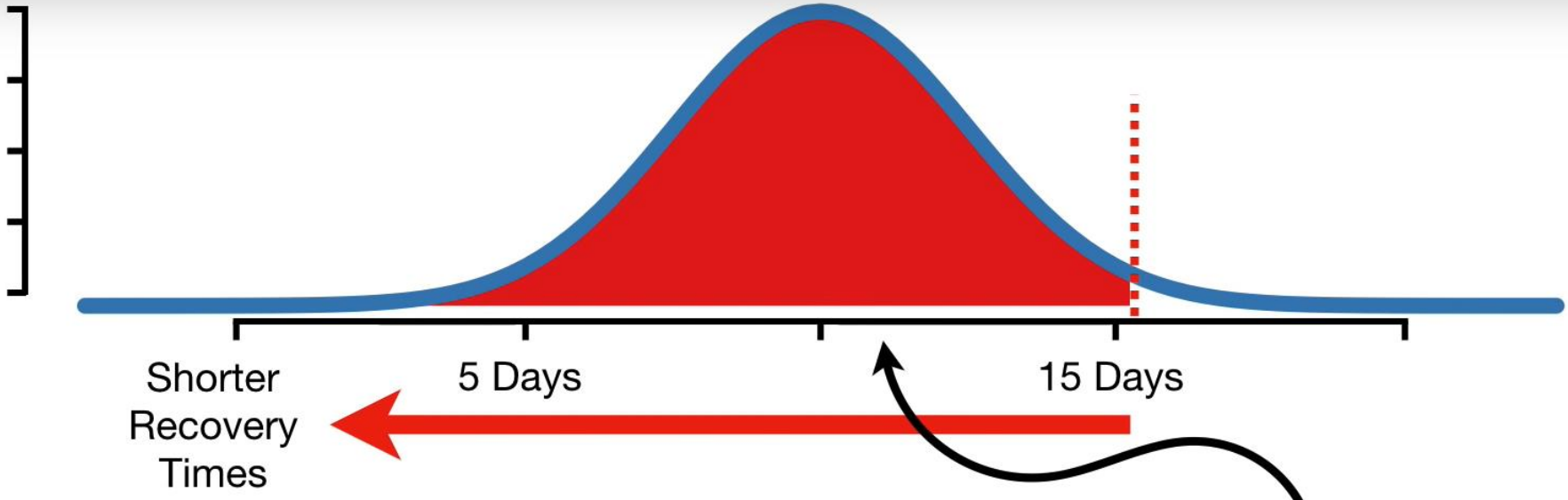
In other words, regardless of whether **SuperDrug** is super and makes things better, or if is not so super and makes things worse, a **Two-Sided p-value** will detect something unusual happened.



For a **One-Sided p-value**, the first thing we do is decide which direction we want to see change in.

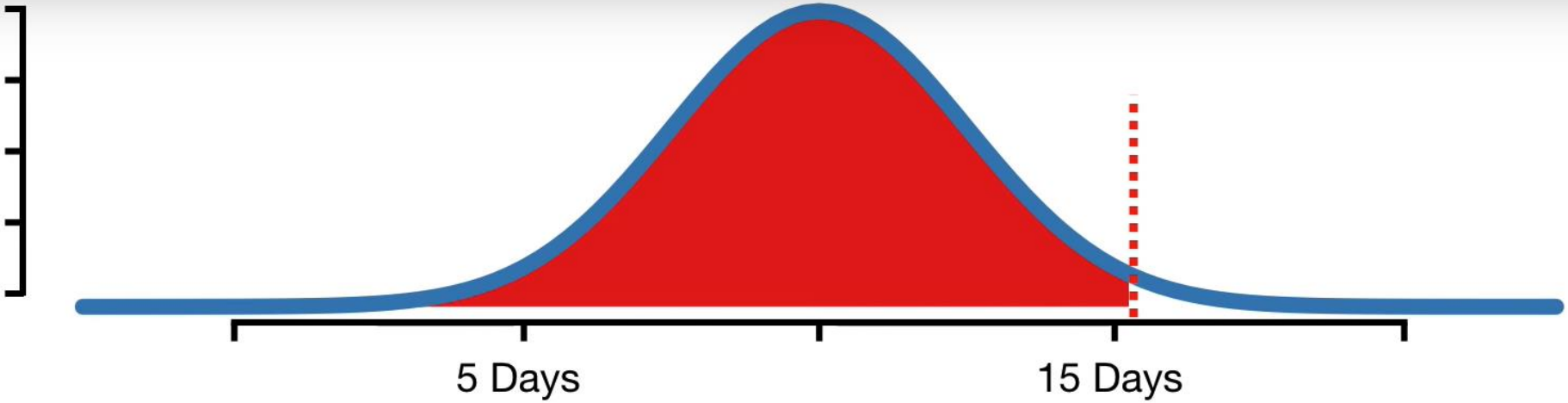


…and just like before, that means we want to see if recovery times are shorter.



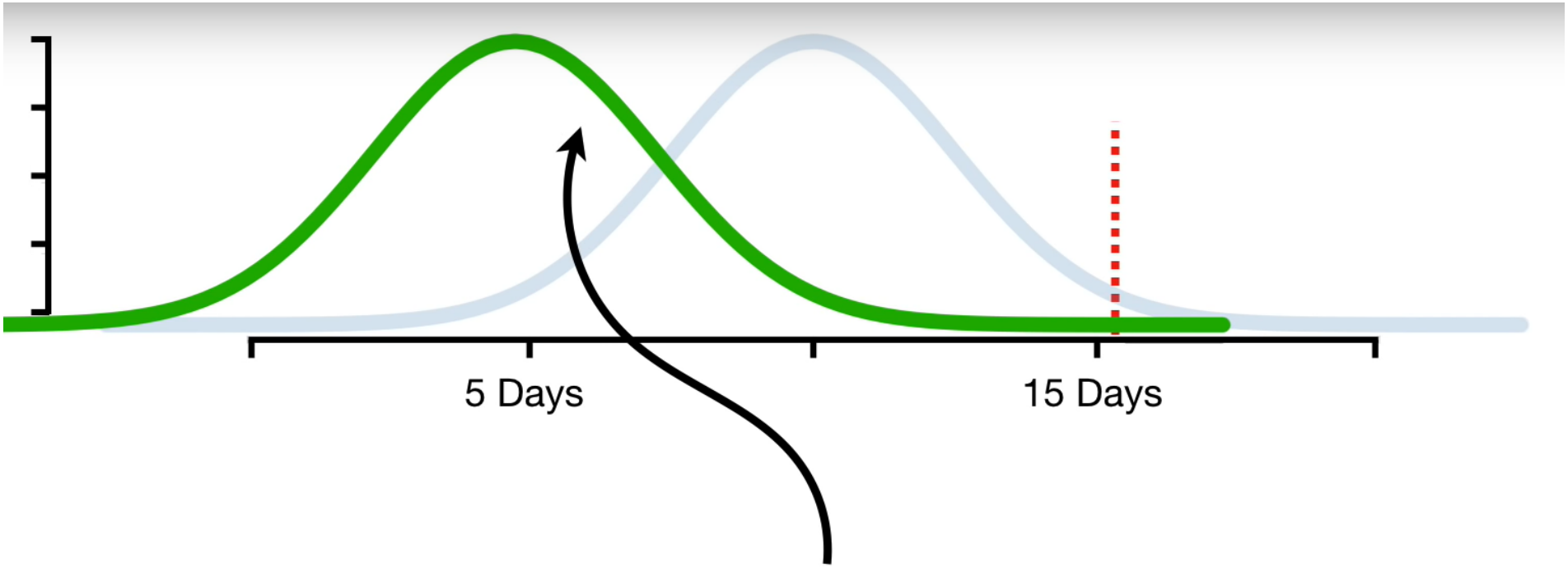
So the **One-Sided p-value** is this huge area, **0.98**, because it is ***more extreme*** in the direction we want to see change.

One-Sided p-value for **15.5** days = 0.98



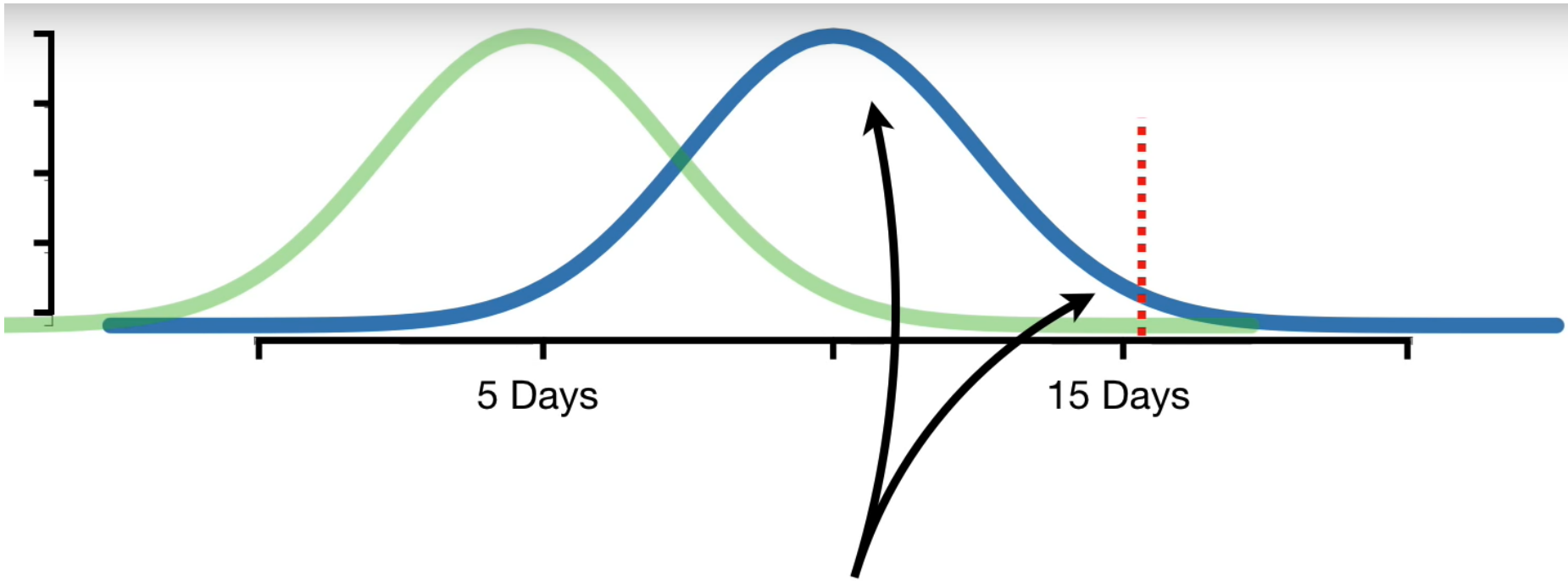
And since **0.98 > 0.05**, the **One-Sided p-value** would not detect that **SuperDrug** was doing anything unusual.

One-Sided p-value for **15.5** days = 0.98



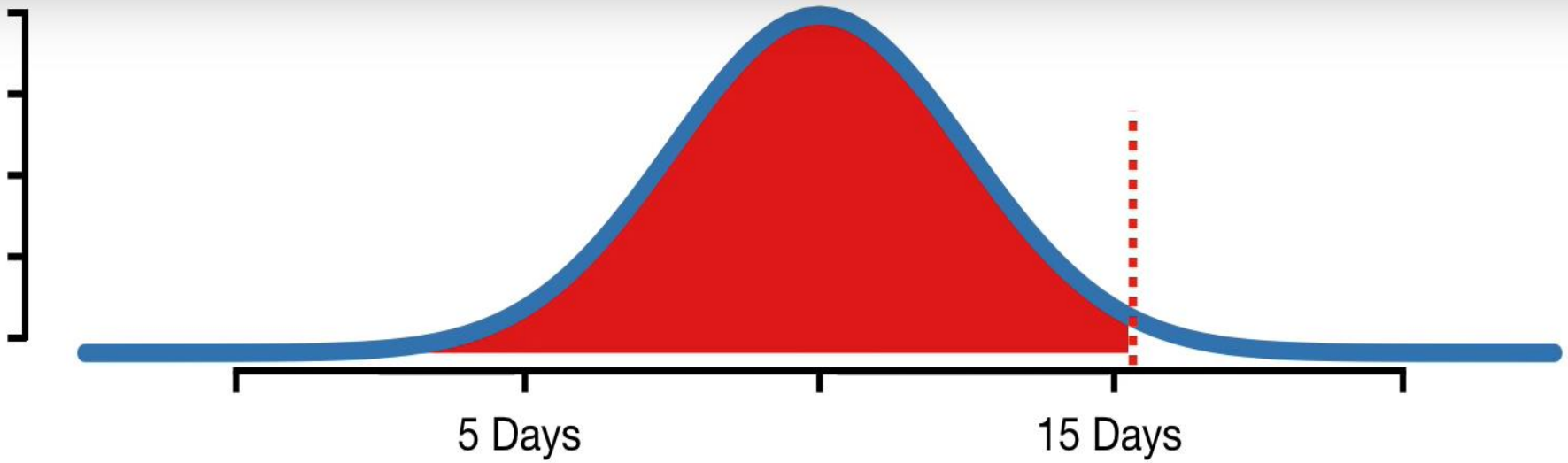
In other words, the **One-Sided p-value** is only looking to see if a distribution to the left of the original mean makes more sense…

One-Sided p-value for **15.5** days = 0.98



…and since the observation is on the right side of the mean, we fail to reject the hypothesis that the original distribution makes sense.

One-Sided p-value for **15.5** days = 0.98



Since failing to detect that **SuperDrug** is making things worse would be bad, **One-Sided p-values** are tricky and should be avoided….*or you should really know what you are doing.*

Example for a single mean

- **Problem 1:**

  We believe that the average “normal” weight of ravens in Yukon is 1kg. In a sample of 10 ravens, the average bird weight is 0.8 kg, and the sample standard deviation was 0.15 kg. At 0.05 significance level, can we reject the null hypothesis that the mean raven weight does not differ from the “normal” weight?

script 2_hypothesistests.R

Example for a single mean

- **Solution**

$$H0: \mu = 1$$
$$H1: \mu \neq 1$$

we can use a t-test. (why not a z-test?)

Mean: 0.8

sample standard deviation: *s* = 0.15

Standard Error of the Mean:

Example for a single mean

Test -statistic: t-distribution

Under H0: this will follow a t-distribution with df = n-1

The idea is:

The sample means are normally distributed with

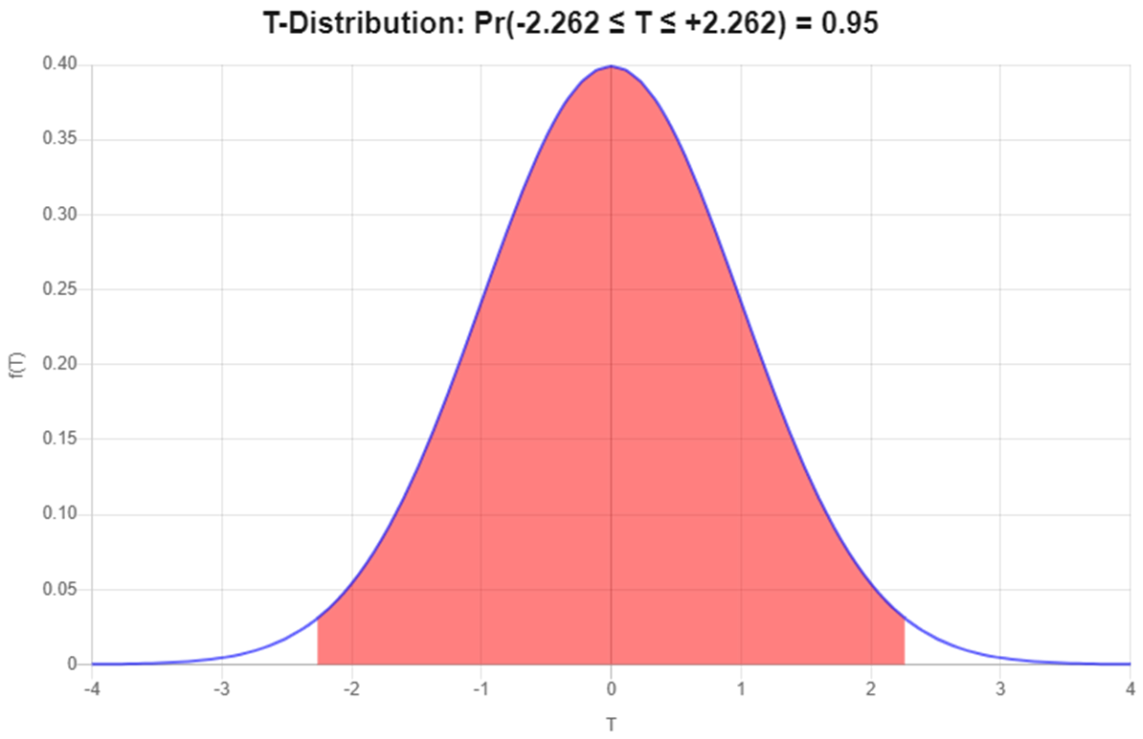
- *mean = population mean (Under H0: population mean = 1)*
- *sd = standard error of the mean*

The standardized sample means (= the number of standard deviations that the sample means are away from the population mean) will follow a z-distribution or, if the population variance is unknown, a t-distribution

For what values of t will we reject H0?

Find the critical t-value for α=0.05 from t-table and compare:

$$t_{n-1,1-\frac{\alpha}{2}} = t_{9,\,0.975} = 2.262$$



Example for a single mean

Conclude:

|t-statistic| > critical value

➔it is not a usual value

The test statistic -4.2 is not between the critical values -2.262, and 2.262. Hence, at 0.05 significance level, we **reject the null hypothesis** that the mean bird weight does not differ from the assumed “normal” weight of 1 kg.

We reject H0 with 5% chance that it was true (type I error)

R code

```
> samplemean <- 0.8# sample mean
> mu0 <- 1              # hypothesized population mean
> s <- 0.15                # sample standard deviation
> n <- 10                 # sample size
> sem <- s/sqrt(n)
> sem    #standard error of the mean
[1] 0.04743416
> t <- (samplemean-mu0)/sem
> t                       # test statistic
[1] -4.21637
> alpha <- 0.05
> t.half.alpha <- qt(1-alpha/2, df=n-1)
> c(-t.half.alpha, t.half.alpha) #critical values
[1] -2.262157  2.262157
```

P-value

Alternatively:

Find the **probability** of getting this test statistic -4.2 :

In the table:

look across the row with df = 9: you see that the absolute value of the test statistic is higher than 3.25, corresponding to alpha 0.01 in a two-tailed test. Hence, P-value < 0.01.

We reject the null hypothesis that $\mu = 1$.

P-value

Alternatively:

Find the **probability** of getting this test statistic -4.2

OR something else, equally extreme

OR something else more extreme :

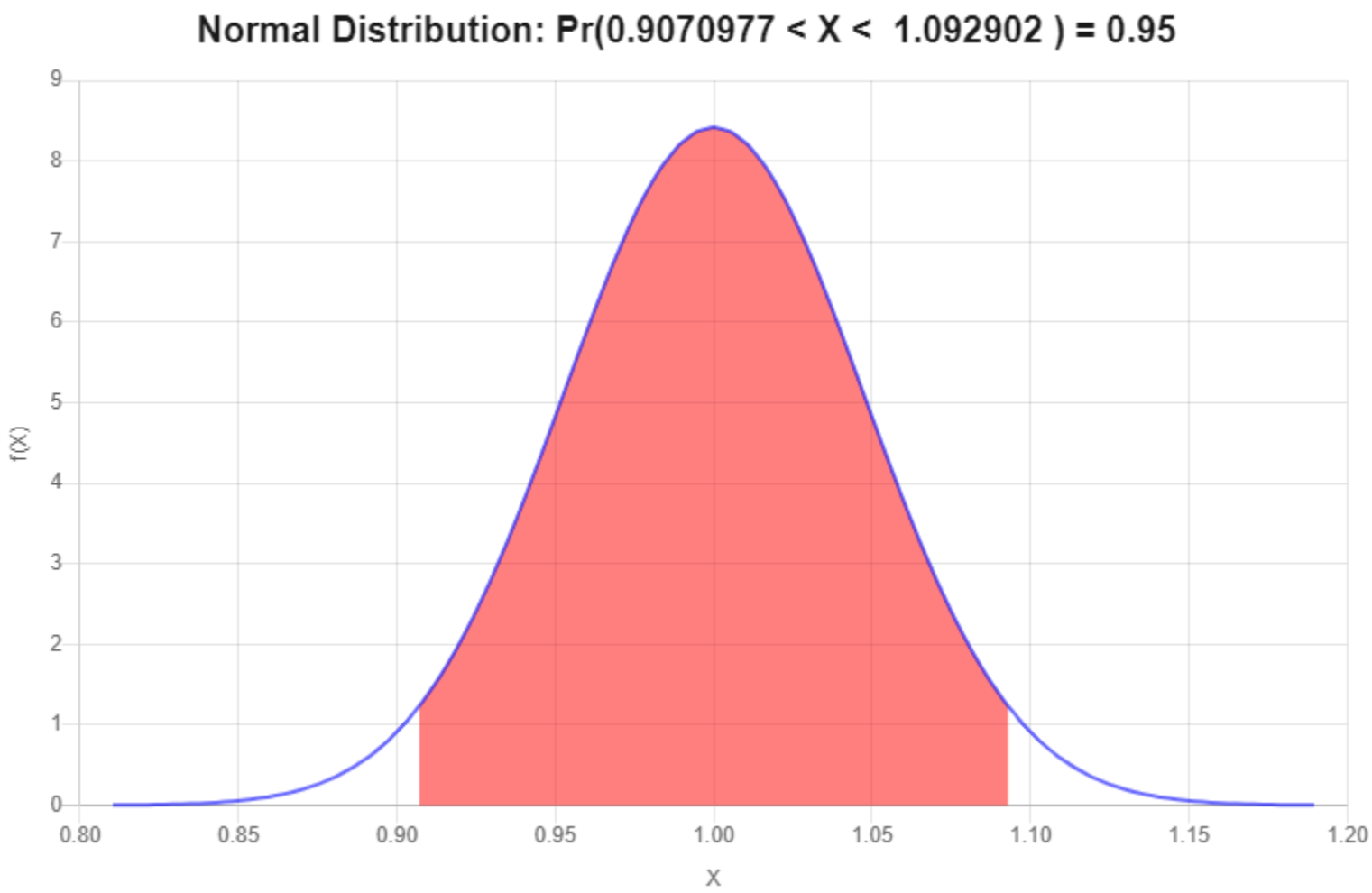
In R:

We apply the pt() function to compute the two-tailed **p-value** of the test statistic. We need to double the *lower* tail p-value to know what is the chance of getting such extreme value. Since the p-value turns out to be smaller than the 0.05 significance level, we reject the null hypothesis that $\mu = 1$.

```
> pval <- 2 * pt(-4.2, df = 9)  # lower tail
> pval                          # two-tailed p-value
[1] 0.002306693
```

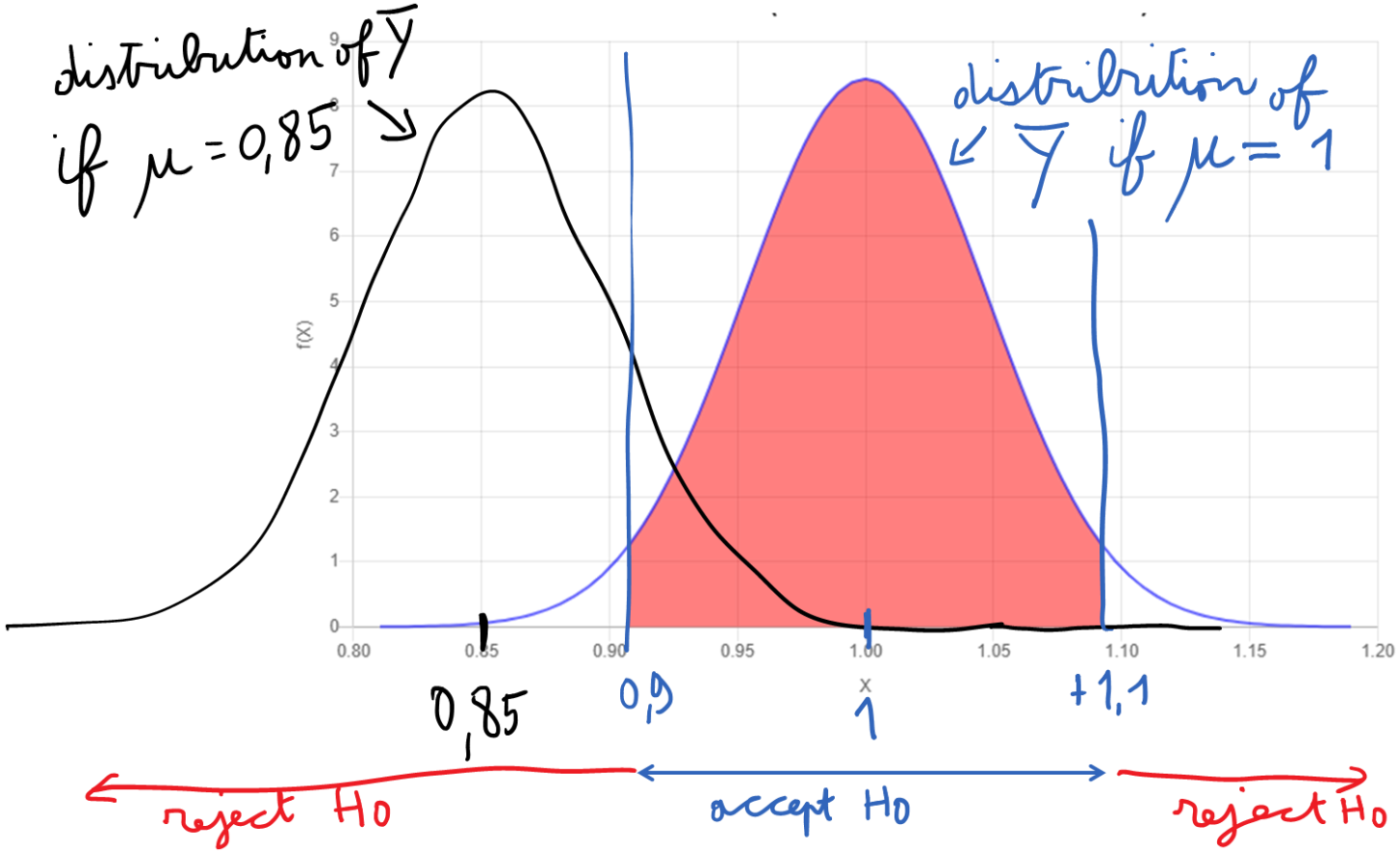
For what values of $\overline{Y}$ will we reject H0?

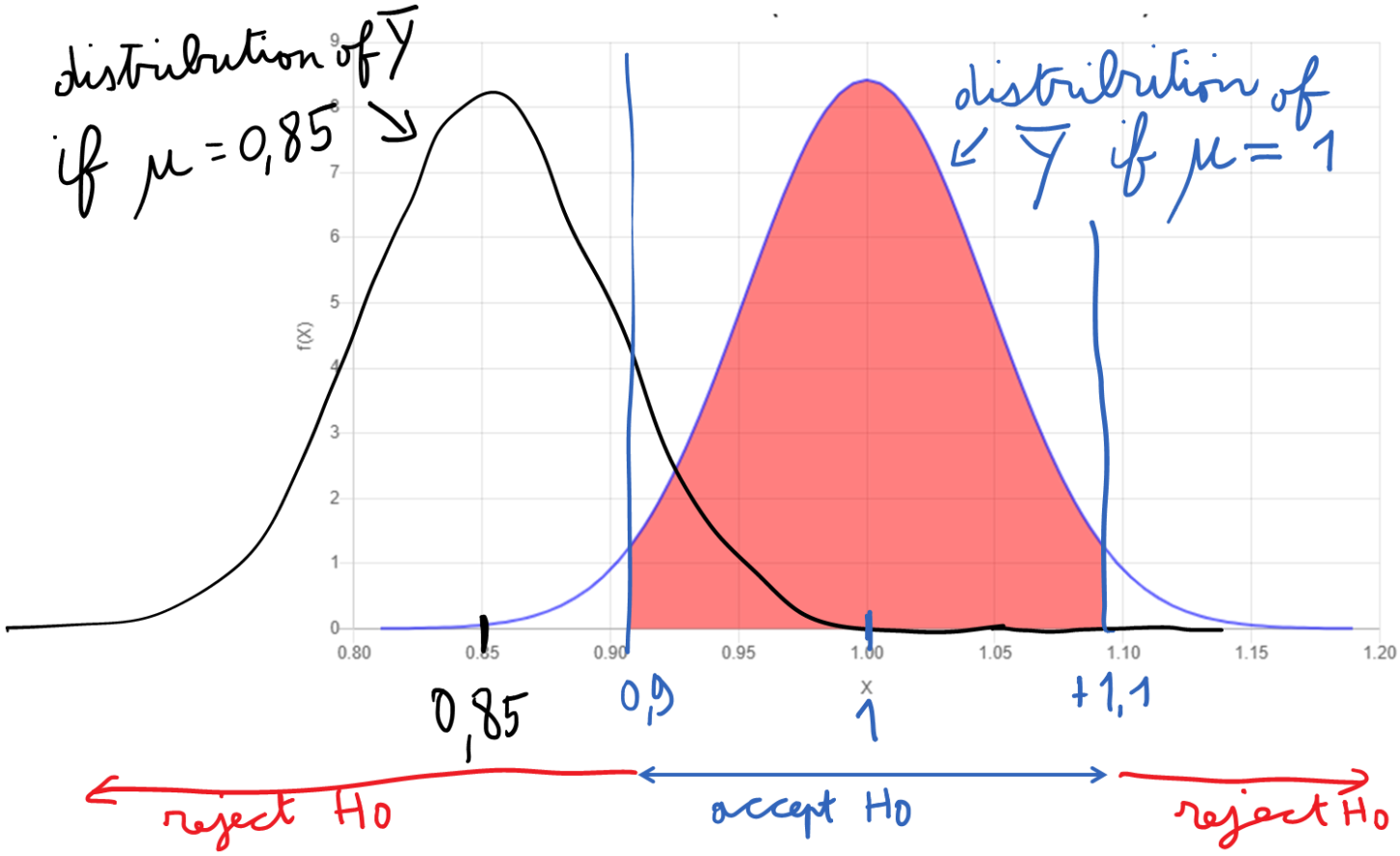
$$t_{n-1,1-\frac{\alpha}{2}} = t_{9,\,0.975} = 2.262$$


Normal Distribution: Pr(0.9070977 < X < 1.092902) = 0.95
f(X)
X
0
1
2
3
4
5
6
7
8
9
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
1.20

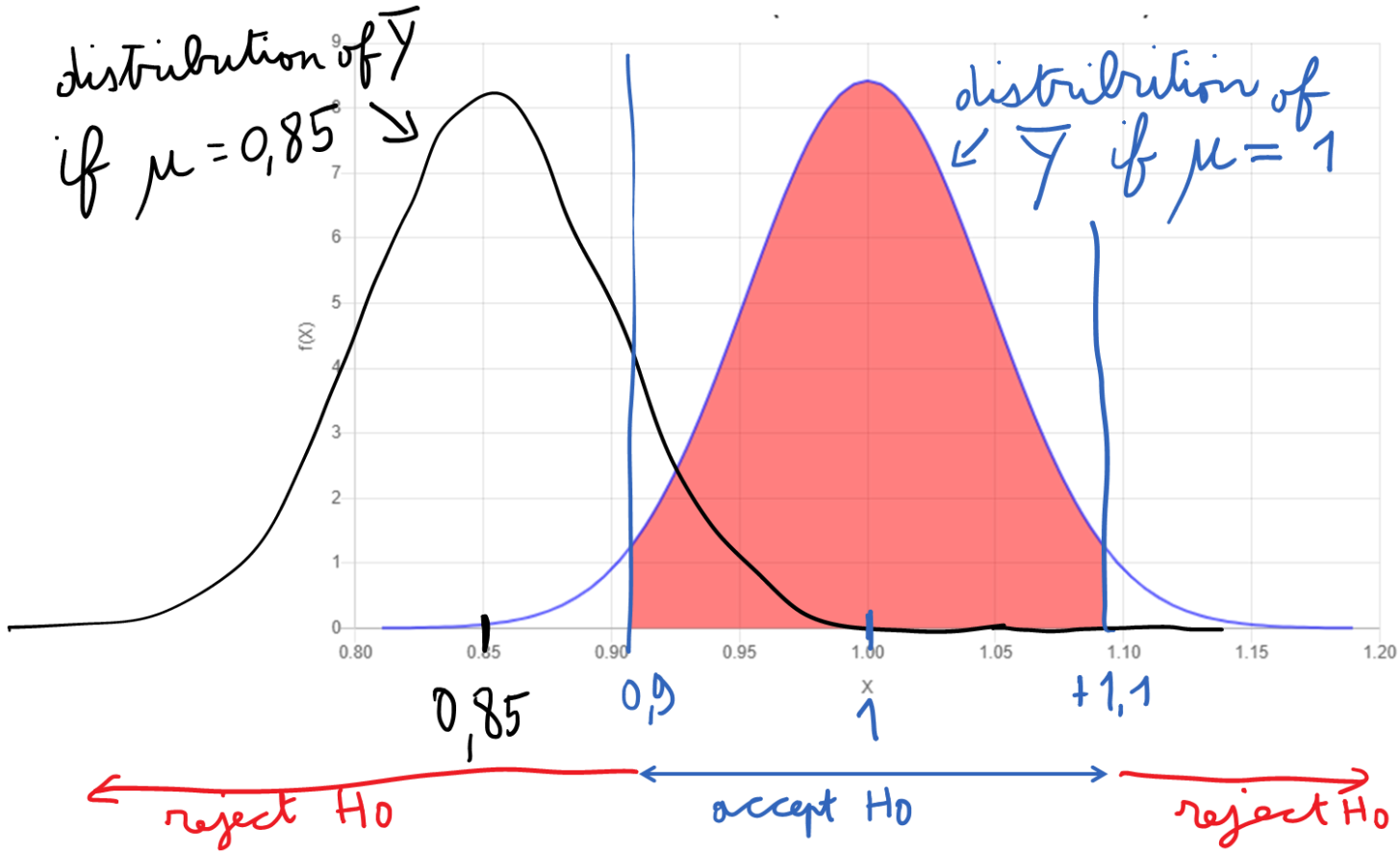
Calculating the probability of committing a type II error = β

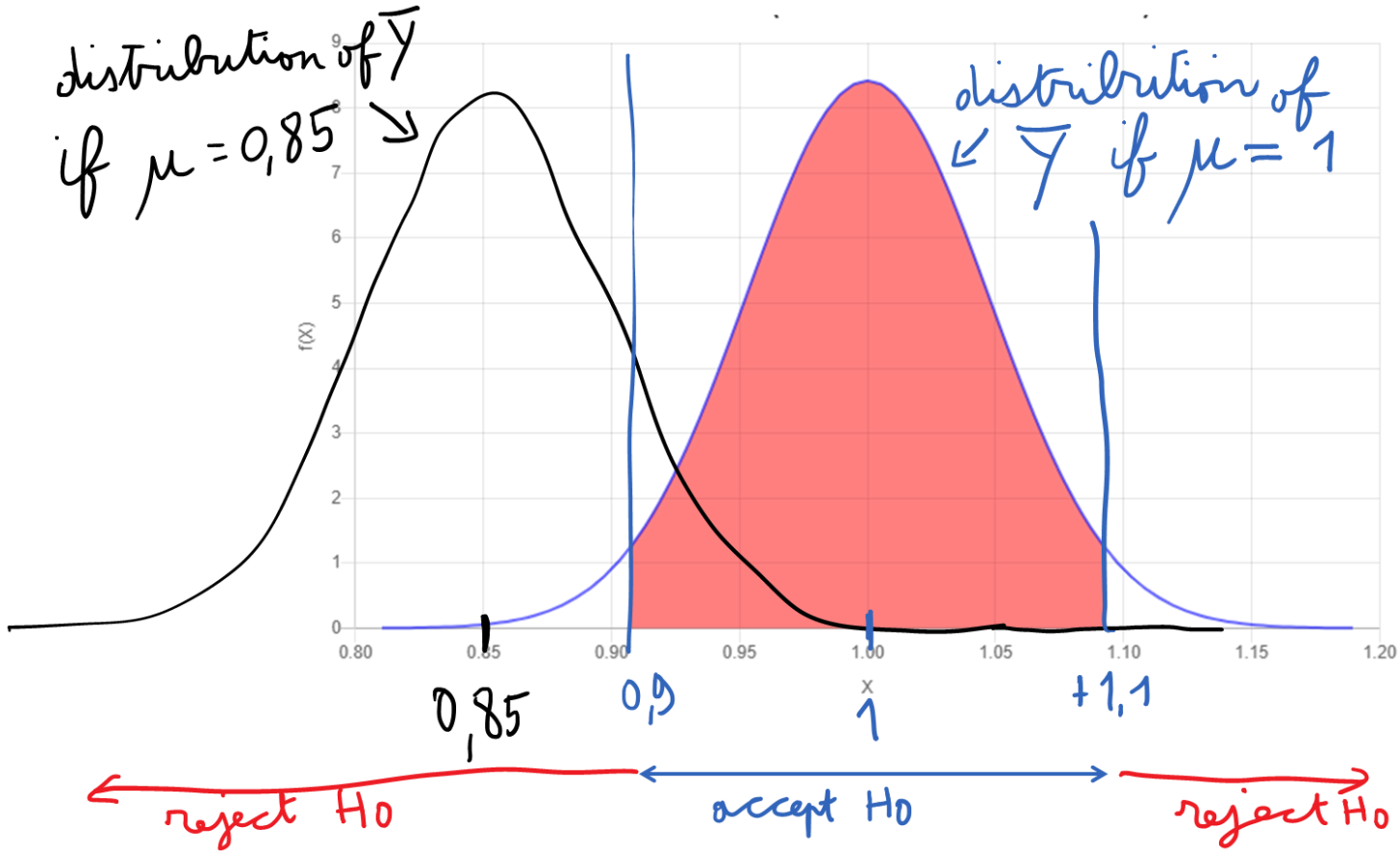
- If the sample of 10 ravens with sample mean 0.8 kg came from *another population*, of which the *true mean weight is 0.85*, what is then the probability that we commit a type II error?


distribution of $\bar{Y}$ if $\mu = 0{,}85$
distribution of $\bar{Y}$ if $\mu = 1$
f(X)
X
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
1.20
0,85
0,9
1
1,1
reject H0
accept H0
reject H0


distribution of $\bar{Y}$ if $\mu = 0{,}85$
distribution of $\bar{Y}$ if $\mu = 1$
f(X)
X
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
1.20
0
1
2
3
4
5
6
7
9
0,85
0,9
1
1,1
reject H_0
accept H_0
reject H_0

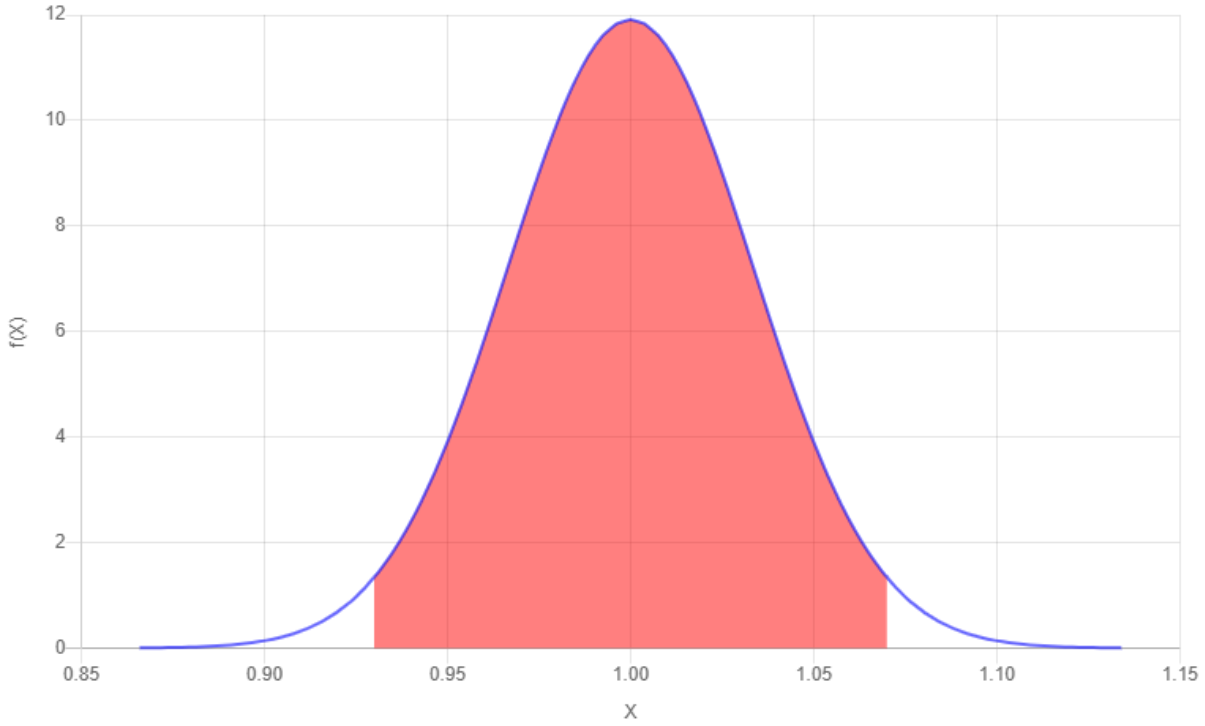
```
> pt(q=1.05, df=9, lower.tail=FALSE)
[1] 0.160547
> pt(q=5.27, df=9, lower.tail=FALSE)
[1] 0.0002569349
```

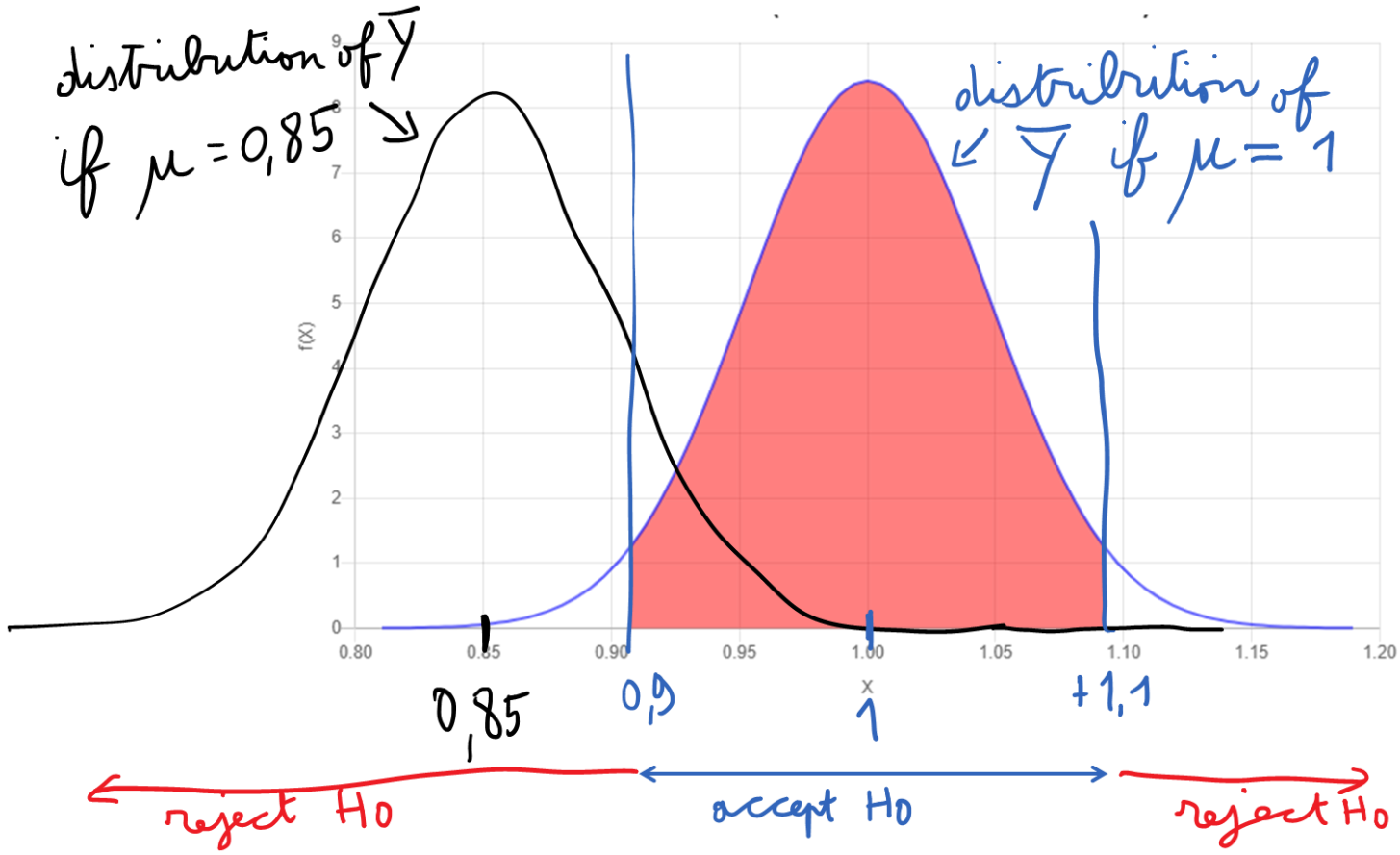

distribution of $\bar{Y}$ if $\mu = 0{,}85$
distribution of $\bar{Y}$ if $\mu = 1$
f(X)
X
0,85
0,9
1
1,1
reject H_0
accept H_0
reject H_0


distribution of $\bar{Y}$ if $\mu = 0{,}85$
distribution of $\bar{Y}$ if $\mu = 1$
f(X)
X
0,85
0,9
1
1,1
reject H_0
accept H_0
reject H_0

- If the sample size $n = 20$ ravens, and $\mu = 0.85$, what is the power of the test?

```
> pt(q=2.7, df=19, lower.tail=TRUE)
[1] 0.9929054
> pt(q=7.3, df=19, lower.tail=FALSE)
[1] 3.175725e-07
```


12
10
8
6
4
2
0
f(X)
0.85
0.90
0.95
1.00
1.05
1.10
1.15
X


distribution of $\bar{Y}$ if $\mu = 0{,}85$
distribution of $\bar{Y}$ if $\mu = 1$
f(X)
X
0,85
0,9
1
1,1
reject H_0
accept H_0
reject H_0

Example for a single mean (2)

- If you have the sample data:

```
>t.test(sampledata, mu, alternative="two.sided")
```

- **Problem 2**

  We assume that students are on average 20 years old. Using the sample of the student population in the data set survey of the package “MASS”, at 0.05 significance level, can we reject the null hypothesis that the mean student age is 20 years?

script 2_hypothesistests.R

Example for a single mean (2)

Solution:

```
> t.test(age, mu=20, alternative="two.sided")

        One Sample t-test

data:  age
t = 0.8905, df = 236, p-value = 0.3741
alternative hypothesis: true mean is not equal to 20
95 percent confidence interval:
 19.54600 21.20303
sample estimates:
mean of x
 20.37451
```

Example for a single mean (2)

Solution:

t.test()says: t-statistic = 0.89 p-value = 0.37

Look in the t-distribution table:

When the degrees of freedom are 29 or more, the row ∞ is used. Note that the values in this row are the same as the values for the z-distribution, since, as the sample size increases, the t-distribution approaches the z-distribution. When the sample size is 30 or more, the two distributions are considered identical

the test statistic lies between 0.674 and 1.282, corresponding to alpha 0.50 and 0.20 in a **two-tailed test**.

Hence, 0.2 < P-value < 0.5.

R was right.

The chance of getting this t-statistic is not extreme and therefore we do not reject the null hypothesis

Example for comparing two means

- **Problem 3:**

  We believe that the average weight of male ravens differs from female ravens.

$$\mathrm{H0}: \mu_1 = \mu_2 \text{ or } \mu_1 - \mu_2 = 0$$

$$\mathrm{H1}: \mu_1 \neq \mu_2 \text{ or } \mu_1 - \mu_2 \neq 0$$

  A sample of 20 birds is taken and each bird is weighed and released. 12 birds were males with an average weight of 1.2 kg and a standard deviation of 0.02 kg. 8 birds were females with an average weight of 0.8 and a standard deviation of 0.01 kg.

script 2_hypothesistests.R

Example for comparing two means

Test -statistic: t-distribution

$$t = \frac{(\bar{y}_1 - \bar{y}_2) - 0}{s_{\bar{y}_1 - \bar{y}_2}} = \frac{\bar{y}_1 - \bar{y}_2}{\sqrt{\frac{(n_1 - 1)s_1^{\,2} + (n_2 - 1)s_2^{\,2}}{n_1 + n_2 - 2}}}$$

Under H0: this will follow a t-distribution with df =($n_1 + n_2 - 2$)

The idea is:

The sample means are normally distributed and thus also the difference between sample means is normally distributed, with

- *mean = population mean (Under H0: population mean = 0)*
- *sd = standard error of the difference between the means*

The standardized difference between sample means will follow a z-distribution or, if the population variance is unknown, a t-distribution

Example for comparing two means

Find the critical t-values and compare to the t-statistic, or use the p-value

Example for comparing two means

- **In R:** can **split the dataframe by a factor** column and do t-test on the colunm pairs t.test(numericvariable ~factor)
- **Problem 4:**

  Using the sample of the student population in the data set survey of the package "MASS", at 0.05 significance level, can we reject the null hypothesis that the mean height of male and female students is equal?

script 2_hypothesistests.R

Exercise 2

- In the Survey dataset of the MASS package, is there a significant difference between males and females for the following variables: pulse, height et age.

➔do all the tests together (NOT variable by variable)

➔create a table representing the mean values per category (male and female), the t-statistic and the p-value for all variables

script TADE_exercise_2.R