

Statistical Inference and Hypothesis Testing

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Quantitative Research Methods

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- 1 Statistical inference
- 2 Hypothesis testing
- 3 Type I and type II errors
- 4 Replication crisis

1 Statistical inference

2 Hypothesis testing

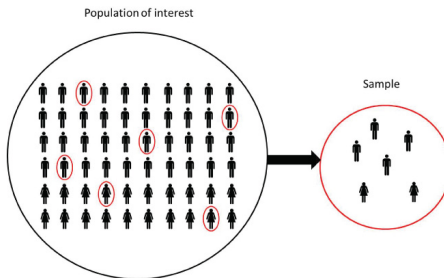
3 Type I and type II errors

4 Replication crisis

Statistics is a branch of mathematics dealing with the collection, analysis, interpretation, presentation, and organization of data.

Descriptive statistics is solely concerned with properties of the observed data.

The aim of **inferential statistics** is to deduce properties about the probability distribution of a **population** analyzing data from a **sample**.



Source: <https://ies.ed.gov/blogs/nces/2016/04/05/default>

1 Statistical inference

2 Hypothesis testing

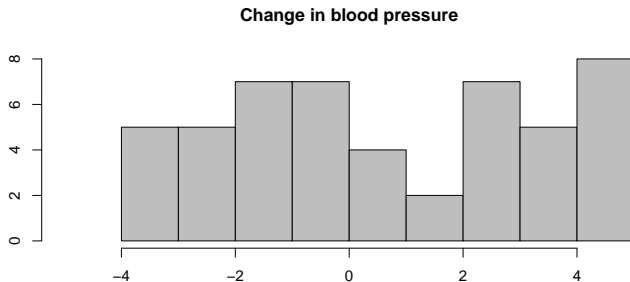
3 Type I and type II errors

4 Replication crisis

Statistical hypothesis testing is an attempt to **detect an effect** on a **population** from data taken from a **sample**.

Detecting an effect (mean)

Change in blood pressure after taking experimental drug A in $n = 50$ participants:



Has the drug any effect? \Rightarrow Is the **population mean** of change of blood pressure **different from zero**?

The first step to hypothesis testing is to define null and alternative hypothesis:

- **Null hypothesis:** there is no effect in the population.
- **Alternative hypothesis:** there is effect in the population.

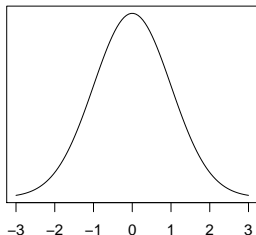
In this case, absence of effect means that the population mean μ of differences is equal to zero:

- $H_0 : \mu = 0$
- $H_1 : \mu \neq 0$

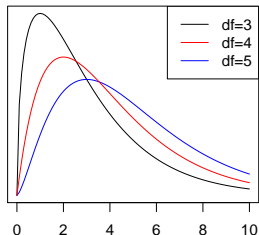
Then we need to know what is the **probability distribution of sample variable** if H_0 is true.

Normal $N(\mu, \sigma)$ and the **chi-square** χ^2 .

Normal distribution



Chi-squared distribution



Any normal distribution can be transformed into the **standard normal distribution** $N(0, 1)$ by:

$$\bar{z} = \frac{x - \mu}{\sigma}$$

The **central limit theorem** for the sample mean establishes that the sample mean \bar{x} computed with n elements of a random variable x of mean μ and variance σ follows a normal distribution with mean μ and variance σ/\sqrt{n} .

The variable:

$$z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}}$$

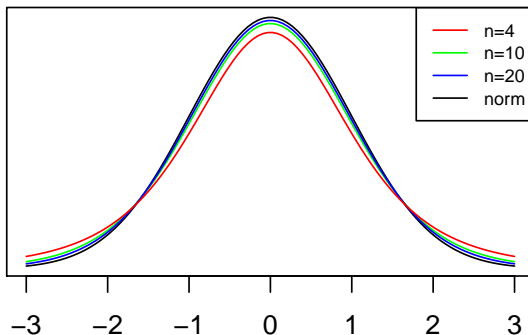
follows a $N(0, 1)$ distribution.

Usually we don't know the population standard deviation σ , but the sample standard deviation s . The variable:

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

Follows a Student's t -distribution of $n - 1$ degrees of freedom.

Student's t -distribution



For large enough values of n , Student's t is similar to a normal distribution.

We have to test the null hypothesis:

- $H_0 : \mu = 0$
- $H_1 : \mu \neq 0$

Now we know that, **if H_0 is true**, the variable:

$$t = \frac{\bar{x}}{s/\sqrt{n}}$$

follows a Student's t -distribution of $n - 1 = 49$ degrees of freedom.

For the sample of drug A, we know that:

$$\bar{x} = 0.5872$$

$$s = 2.762$$

If H_0 is true, then $\mu = 0$ so the standardized value is:

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}} = \frac{0.5872 - 0}{2.762/\sqrt{50}} = 1.503$$

Is this a surprising value on a t_{49} distribution?

To rate the extent to an observed value of the probability distribution is surprising, we use p-values.

A **p-value** is the probability of getting the observed or a more extreme value, assuming that the null hypothesis is true.

The p-value for $t_{49} = 1.503$ is $p = 0.1392$.

We can observe a value of 1.503 or higher coming from a t_{49} distribution with a probability of 13.92%. **Is this p-value high or low?**

Thresholds of p-values

We can consider that we have found a significant effect when $p < 0.05$.
This is an arbitrary value, arising from common practice.

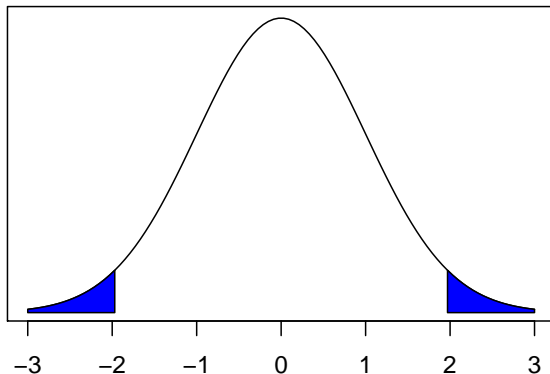
<u>p-VALUE</u>	<u>INTERPRETATION</u>
0.001	HIGHLY SIGNIFICANT
0.01	
0.02	
0.03	
0.04	SIGNIFICANT
0.049	
0.050	OH CRAP. REDO CALCULATIONS.
0.051	ON THE EDGE OF SIGNIFICANCE
0.06	
0.07	HIGHLY SUGGESTIVE, SIGNIFICANT AT THE $P < 0.10$ LEVEL
0.08	
0.09	
0.099	HEY, LOOK AT THIS INTERESTING SUBGROUP ANALYSIS
≥ 0.1	

Source: <https://xkcd.com/1478/>.

Thresholds of p-values

In a two-tailed test, we assume that values can be positive or negative, so the probability is split on both sides. This are the tails of a two-tailed test for $p = 0.05$ (values ± 1.96):

Two-tails with $\alpha=0.05$



In the example of drug A we have that the p-value obtained is larger than 0.05, so we **cannot reject the null hypothesis**.

We can do it faster with **R** using the `t.test` function (values are stored in vector `a`):

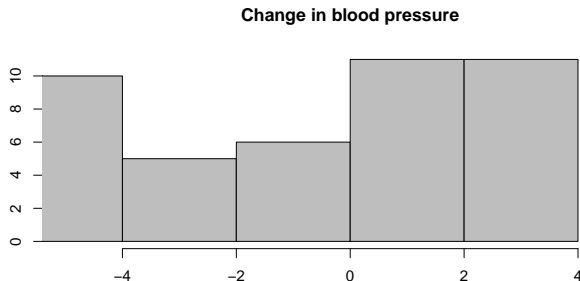
```
> t.test(a)
```

One Sample t-test

```
data:  a
t = 1.5032, df = 49, p-value = 0.1392
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.1978011  1.3721480
sample estimates:
mean of x
0.5871735
```

Testing the null hypothesis

We have made another test with a drug B, obtaining the following values:



For this sample, we obtain that $p < 0.01$, therefore we can reject the null hypothesis:

```
> t.test(b)
```

One Sample t-test

```
data:  b
t = -2.8835, df = 49, p-value = 0.005827
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -2.449835 -0.437545
sample estimates:
mean of x
 -1.44369
```

Two possible contexts for mean comparison:

- **Paired data:** comparison of two observations taken from the same sample (e.g., scores before and after taking a course).
- **Non-paired data:** comparison of means of two independent samples.

See details of implementation in **R** in:

<https://www.statmethods.net/stats/ttest.html>.

The test $H_0 : \rho = 0$ for the population Pearson correlation let us know if a relationship exists between two variables.

If H_0 is true and r is the sample correlation taken from n observations, the value:

$$\frac{r}{\sqrt{1 - r^2}} \sqrt{n - 2}$$

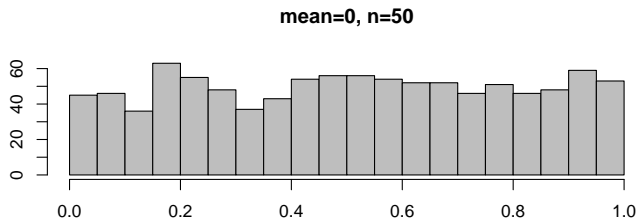
follows a t_{n-2} distribution.

We can perform correlational analysis using functions of `psych` and `corrplot` packages.

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Distribution of p-values when H_0 is true

Let's obtain 1,000 mean samples of $n = 50$ from a variable with $\mu = 0$, and let's compute the p-value of $H_0 : \mu = 0$ for each:



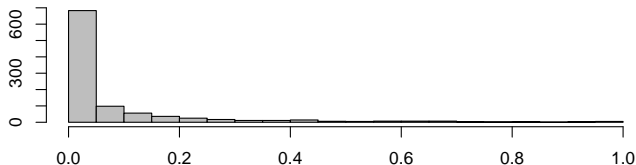
We observe that:

- p-values are uniformly distributed, if the number of samples is large enough.
- There is a probability $p = 0.05$ of rejecting H_0 when it is true. This is a **Type I error**.

Distribution of p-values when H_0 is false

Let's obtain 1,000 mean samples of $n = 50$ from a variable with $\mu = -1$, and let's compute the p-value of $H_0 : \mu = 0$ for each:

mean -1 , $n=50$

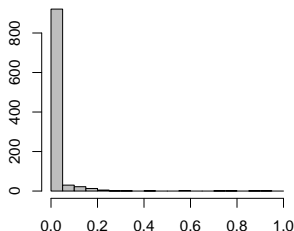


Now most of the p-values are smaller than 0.05, but the 34.2 % are larger. In this cases we are accepting H_0 when it is false. This is a **Type II error**.

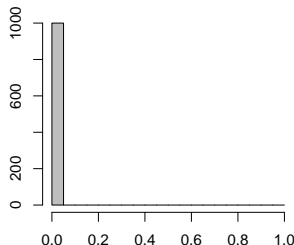
Distribution of p-values when H_0 is false

We can **reduce the Type II error rate increasing the sample size** (rate is 7.9% for $n = 100$ and 0% for $n = 1000$):

mean -1, $n=100$



mean -1, $n=1000$



Type I and type II errors

	H_0 true	H_0 false
Accept H_0 : non-significant finding.	Correct inference ($1 - \alpha$): true negative.	Type II error β : false negative.
Reject H_0 : significant finding.	Type I error α : false positive.	Correct inference ($1 - \beta$): true positive.

- α is the Type I error rate. Can be controlled setting a p-value.
- β is the Type II error rate, and $1 - \beta$ the statistical power of the test.

Type I and type II errors

Let's consider that:

- There is a 50% probability that an effect really exists.
- We have fixed a Type I error rate of $\alpha = 0.05$ and $1 - \beta = 0.8$.

	H_0 true 50%	H_0 false 50%
Accept H_0 : non-significant finding.	Correct inference: true negative. $0.5 * 0.95 =$ 0.475	Type II error: false negative. $0.5 * 0.2 =$ 0.1
Reject H_0 : significant finding.	Type I error: false positive. $0.5 * 0.05 =$ 0.025	Correct inference: true positive. $0.5 * 0.8 =$ 0.4

... the most likely result is true negative.

Learn more at: <http://rpsychologist.com/d3/NHST/>

Performing an analysis with multiple tests may lead to **error inflation**. If we set a Type I error rate of α , the probability of having at least one Type I error when performing k tests is:

$$1 - (1 - \alpha)^k$$

Some values of errors:

k	error
1	0.05
2	0.0975
5	0.226
10	0.401

Type I error inflation can be corrected being more exigent with α when multiple test are performed.

Bonferroni correction: set Type I error rate to α/k . It is considered too conservative, and can yield to higher Type II errors. Other methods can be found in:

https://en.wikipedia.org/wiki/Family-wise_error_rate.

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Hypothesis testing is a powerful tool to make scientific discoveries through statistical inference.

A careless use of hypothesis testing may lead to misleading results, as unnoticed Type I or Type II error rates:

- **p-hacking**: making multiple (unreported) statistical tests until a “good” p-value appears (e.g., optional stopping).
- **HARKing**: hypothesizing after the results are known.
- **Publication bias**: journal editors discourage publication of non-significant results and replication studies.

https://en.wikipedia.org/wiki/Replication_crisis

Replication crisis



Source: <https://xkcd.com/882/>.

Remedies for replication crisis:

- Larger samples, lower Type I error rates.
- Encourage replication studies.
- Tackling publication bias with pre-registration of studies.
- Sharing raw data in online repositories.