

Likelihood Ratio Test

1. INTRODUCTION

- **Likelihood Ratio Test** → statistical hypothesis test that is used in the context of comparing two or more nested statistical models.
 - Determine if a more complex model, which includes more parameters, provides a significantly better fit for the data.
- **Hypothesis** → statement about a population parameter (whatever we want to test).
 - H_0 → null hypothesis.
 - H_a → alternative hypothesis.
- They are mutually exclusive → only one can be true (EXCLUSIVITY).

A hypothesis test or test procedure is a rule specifying

- for which sample values we accept H_0 as true.
- for which sample values we reject H_0 and accept H_1 .

The subset of the sample space for which we reject the null is called the critical region or rejection region. The subset of the sample space for which we accept the null is called the acceptance region.

Region reject H_0 → critical region
Region accept H_0 → acceptance region

- **ERRORS** → we do NOT choose the correct decision.
 - Type I ERROR → (reject H_0 | true H_0)
 - Type II ERROR → (accept H_0 | false H_0)

- $\alpha \equiv P(\text{Type I error}) = P(\text{Reject } H_0 | H_0 \text{ is true})$
- $\beta \equiv P(\text{Type II error}) = P(\text{Accept } H_0 | H_0 \text{ is false})$
- ideally, we would like both probabilities to be small.

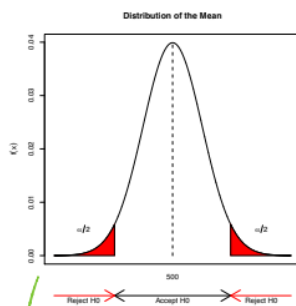
- **TEST STATISTIC** → quantity calculated on the basis of the sample, relevant for addressing the hypothesis test → **contains data info & distribution data.**
- **p-value** → probability of obtaining the observed result, assuming that the null hypothesis is true.

If the $p\text{-value} < \alpha$ then we **reject** H_0
 If the $p\text{-value} \geq \alpha$ then we **do not reject** H_0

ONE-TAILED vs TWO-TAILED:

TWO TAIL

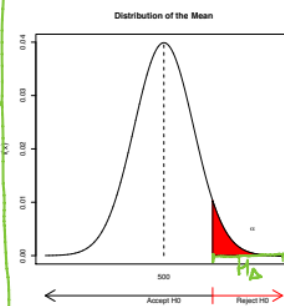
$$\begin{cases} H_0 : \mu = 500 \\ H_1 : \mu \neq 500 \end{cases}$$



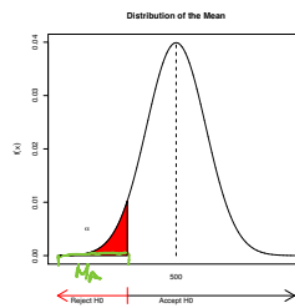
safer to use but less precision

ONE TAIL

$$\begin{cases} H_0 : \mu = 500 \\ H_1 : \mu > 500 \end{cases}$$

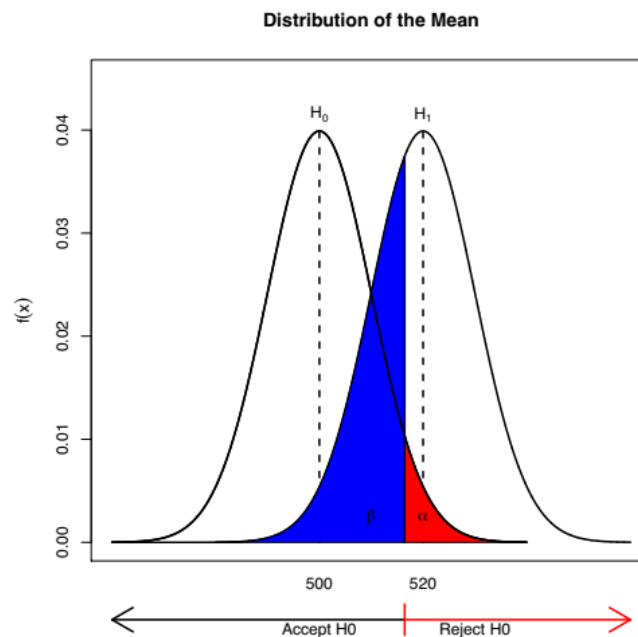


$$\begin{cases} H_0 : \mu = 500 \\ H_1 : \mu < 500 \end{cases}$$



when we have previous knowledge, more precision

ALPHA & BETA:



- **POWER** → probability of rejecting the null hypothesis.

$$\text{Power} = 1 - \beta.$$

- **Most powerful tests** → test that minimize β , for a given value α .
- If our hypothesis only contains **one** value of Θ → **SIMPLE**.
- If our hypothesis contains **more than a** Θ value → **COMPOSITE**.

2. NEYMAN-PEARSON LEMMA

- Let X_1, \dots, X_n be a random sample of a random variable with $f(x; \theta)$.
- We wish to test $H_0: \theta = \theta_0$ versus $H_1: \theta = \theta_1$.
- Let $L(\theta | \mathbf{x})$ be the likelihood function
- The most powerful test of size α has critical region

test that minimizes β for some constant $C_\alpha > 0$.

$$CR = \left\{ \mathbf{x} \in \mathcal{X}^n : \frac{L(\theta_1 | \mathbf{x})}{L(\theta_0 | \mathbf{x})} \geq C_\alpha \right\}$$

Alternative

Null

- Note this lemma involves the ratio of two likelihoods.

critical region

- GENERALIZED LIKELIHOOD RATIO TEST:

- Let X_1, \dots, X_n be a random sample of X with density $f(x | \theta)$ for some $\theta \in \Omega$. We wish to test

$$\begin{cases} H_0: \theta \in \Omega_0 \\ H_1: \theta \in \Omega_1 \end{cases}$$

where $\Theta = \Omega_0 \cup \Omega_1$ and $\Omega_0 \cap \Omega_1 = \emptyset$.

We define the likelihood ratio statistic as

$$\lambda = \lambda(\mathbf{x}) = \frac{\max_{\theta \in \Omega_0} L(\theta | \mathbf{x})}{\max_{\theta \in \Omega} L(\theta | \mathbf{x})}$$

or $\lambda = \lambda(\mathbf{x}) = \frac{L(H_0)}{L(H_1)}$

The likelihood ratio test, also called the generalized likelihood ratio test in order to distinguish it from the test obtained by the lemma of Neyman-Pearson, has a critical region of the form

$$C = \{ \mathbf{x} : \lambda(\mathbf{x}) \leq A \}$$

for some constant A to be determined such that the size of the test is α .

Note that $0 \leq \lambda \leq 1$. The closer λ is to 1, the more likely it is that $\theta \in \Omega_0$, whereas if λ is far from 1 the more likely is the alternative hypothesis $\theta \in \Omega_1$.

Null

$\lambda \Rightarrow$ close 1 = H_0

$\lambda \Rightarrow$ close 0 = H_1

Null

Alternative

- ASYMPTOTIC DISTRIBUTION OF THE LIKELIHOOD RATIO STATISTIC:

Theorem:

Let X_1, \dots, X_n be a random sample, where X_i has density $f(x | \theta)$ for some $\theta \in \Omega$. We wish to test

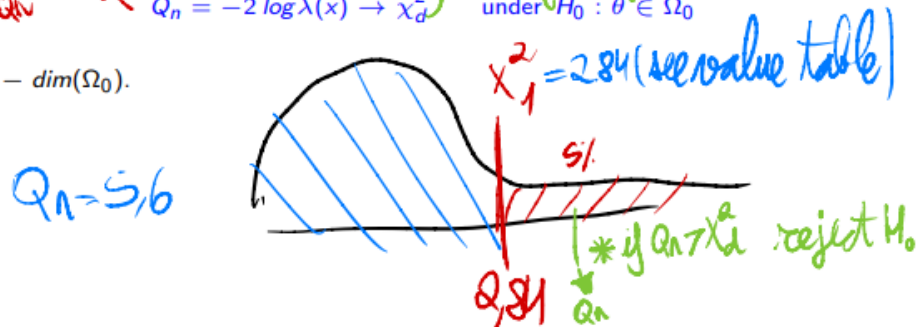
$$\begin{cases} H_0 : \theta \in \Omega_0 \\ H_1 : \theta \in \Omega_1 \end{cases}$$

where $\Omega = \Omega_0 \cup \Omega_1$ i $\Omega_0 \cap \Omega_1 = \emptyset$.

Assuming that the derivatives of the likelihood function exist and are continuous, and that the support of the distribution does not depend on the parameter. Given these conditions, the statistic

formula find Qn $Q_n = -2 \log \lambda(x) \rightarrow \chi_d^2$ *degree freedom* *under $H_0 : \theta \in \Omega_0$*

with $d = \dim(\Omega) - \dim(\Omega_0)$.



A summary of classical statistical tests

Test	Hypothesis	Statistic	Distribution
One-sample Z	$H_0 : \mu = \mu_0$ $H_1 : \mu \neq \mu_0$	$Z = \frac{\bar{x} - \mu_0}{\sigma / \sqrt{n}}$	$N(0, 1)$
One-sample Z (proportion)	$H_0 : p = p_0$ $H_1 : p \neq p_0$	$Z = \frac{\hat{p} - p_0}{\sqrt{\hat{p}(1-\hat{p})/n}}$	$N(0, 1)$
One-sample T	$H_0 : \mu = \mu_0$ $H_1 : \mu \neq \mu_0$	$T = \frac{\bar{x} - \mu_0}{s / \sqrt{n}}$	t_{n-1}
Two-sample T (paired)	$H_0 : \mu_D = 0$ $H_1 : \mu_D \neq 0$	$T = \frac{\bar{D} - \mu_D}{s_D / \sqrt{n}}$	t_{n-1}
Two-sample T (independent)	$H_0 : \mu_x = \mu_y$ $H_1 : \mu_x \neq \mu_y$	$T = \frac{\bar{X}_m - \bar{Y}_n - (\mu_1 - \mu_2)}{s_p \sqrt{\frac{1}{m} + \frac{1}{n}}}$	t_{m+n-2}
Two-sample T (independent)	$H_0 : \mu_x = \mu_y$ $H_1 : \mu_x \neq \mu_y$	$T = \frac{\bar{X}_m - \bar{Y}_n - (\mu_1 - \mu_2)}{\sqrt{\frac{s_m^2}{m} + \frac{s_n^2}{n}}}$	$t_{\hat{p}}$
Two-sample F	$H_0 : \sigma_x^2 = \sigma_y^2$ $H_1 : \sigma_x^2 \neq \sigma_y^2$	$F = \frac{s_x^2}{s_y^2}$	$F(n_x - 1, n_y - 1)$

3. EXAMPLES

In Spain, in 1983, 475743 children were born, 246124 boys and 229619 girls.
Is it true that $P(\text{"newborn child is a boy"}) = P(\text{"newborn child is girl"}) = 0.5$?

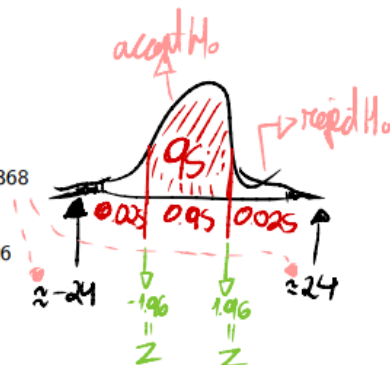
$$\begin{cases} H_0 : p_{\text{boy}} = p_{\text{girl}} = p = 0.5 \\ H_1 : p \neq 0.5 \end{cases}$$

$$\hat{p} = 0.5173466$$

$$Z = \frac{0.5173466 - 0.50}{\sqrt{0.5173466(1 - 0.5173466)/475743}} = 23.94368$$

$$\text{p-value} = 2 \cdot P(Z \geq 23.94368) = 1.075362e - 126$$

$$CI_{0.95} = (0.5159266, 0.5187665)$$



if we only see CI we can reject because 0.5 is NOT included
we also know that 0.5 is not included in CI 0.95 because
0.5 is included in 0.95, if not in 0.95 not in 0.95

```
> prop.test(boy,tot)
```

1-sample proportions test with continuity correction

data: boy out of tot, null probability 0.5 = H_0

X-squared = 572.5402, df = 1, p-value < 2.2e-16

alternative hypothesis: true p is not equal to 0.5 = H_A

95 percent confidence interval:

0.5159254 0.5187674

sample estimates:

0.5173466 \rightarrow p-value

```
> prop.test(boy,tot,correct=FALSE)
```

1-sample proportions test without continuity correction

data: boy out of tot, null probability 0.5

X-squared = 572.6096, df = 1, p-value < 2.2e-16

alternative hypothesis: true p is not equal to 0.5

95 percent confidence interval:

0.5159265 0.5187663

sample estimates:

p
0.5173466

Example: student weight and height

```
out1.lm <- lm(Pes~Alçada+Edat+Sexe+germans+Esports+Alç.pare+Alç.mare+Pes.pare+Pes.mare+germ.mare+germ.)
> summary(out1.lm)
```

Call:

```
lm(formula = Pes ~ Alçada + Edat + Sexe + germans + Esports +
    Alç.pare + Alç.mare + Pes.pare + Pes.mare + germ.mare + germ.pare,
    data = X)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-62.962540	29.861521	-2.108	0.0385 *
Alçada	0.840958	0.157498	5.339	1.04e-06 ***
Edat	0.768634	0.718386	1.070	0.2882
Sexe	-3.334807	3.094713	-1.078	0.2848
germans	0.964057	0.812694	1.186	0.2394
Esports	2.063933	1.771648	1.165	0.2479
Alç.pare	-0.315586	0.156447	-2.017	0.0474 *
Alç.mare	0.003795	0.148619	0.026	0.9797
Pes.pare	0.077042	0.090486	0.851	0.3974
Pes.mare	0.200909	0.103468	1.942	0.0561 .
germ.mare	-0.145142	0.332750	-0.436	0.6640
germ.pare	0.358032	0.463533	0.772	0.4424

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.314 on 72 degrees of freedom

(7 observations deleted due to missingness)

Multiple R-squared: 0.5838, Adjusted R-squared: 0.5202

F-statistic: 9.181 on 11 and 72 DF, p-value: 5.117e-10