

Course 02402 Introduction to Statistics

Lecture 5: Hypothesis testing

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Overview

- 1 Motivating example - sleep medicine
- 2 One-sample t -test and p -value
- 3 Critical value and relation to the confidence interval
- 4 Hypothesis tests in general
 - The alternative hypothesis
 - The general method
 - Errors in hypothesis testing
- 5 Checking the normality assumption
 - The normal q-q plot
 - Transformation towards normality

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Motivating example - sleep medicine

Difference between sleep medicines?

In a study, the aim is to compare two kinds of sleep medicine, A and B. 10 test persons tried both kinds of medicine, and the following 10 *differences* between the two types of medicine were measured:

(For person 1, sleep medicine B was 1.2 sleep hours better than medicine A, etc.):

Sample, $n = 10$:

person	$x = \text{B effect} - \text{A effect}$
1	1.2
2	2.4
3	1.3
4	1.3
5	0.9
6	1.0
7	1.8
8	0.8
9	4.6
10	1.4

Example - sleep medicine

The hypothesis of no difference:

$$H_0 : \mu = 0$$

where μ represents mean difference in sleep length.

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Sample mean and std. deviation:

$$\bar{x} = 1.670 = \hat{\mu}$$

$$s = 1.13 = \hat{\sigma}$$

Example - sleep medicine

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where μ represents mean difference in sleep length.

Sample mean and std. deviation:

$$\bar{x} = 1.670 = \hat{\mu}$$

$$s = 1.13 = \hat{\sigma}$$

Is data in accordance with the null hypothesis H_0 ?

$$\text{Data: } \bar{x} = 1.67, H_0 : \mu = 0$$

NEW *p*-value:

$$p\text{-value} = 0.00117$$

(Computed under the scenario that H_0 is true).

NEW **Conclusion:**

As the data is far away from H_0 (unlikely under H_0), we **reject** H_0 . There is a **significant effect** of medicine B compared to A.

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Method ??: One-sample t -test and p -value

How to compute the p -value?

For a (quantitative) one sample situation, the (non-directional) p -value is given by:

$$p\text{-value} = 2 \cdot P(T > |t_{\text{obs}}|)$$

where T follows a t -distribution with $(n - 1)$ degrees of freedom. The observed value of the test statistics to be computed is

$$t_{\text{obs}} = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

where μ_0 is the value of μ under the null hypothesis:

$$H_0 : \mu = \mu_0$$

The definition and interpretation of the p -value (completely general)

The p -value expresses *evidence* against the null hypothesis – Table 3.1:

$p < 0.001$	Very strong evidence against H_0
$0.001 \leq p < 0.01$	Strong evidence against H_0
$0.01 \leq p < 0.05$	Some evidence against H_0
$0.05 \leq p < 0.1$	Weak evidence against H_0
$p \geq 0.1$	Little or no evidence against H_0

Definition 3.22 of the p -value:

The p -value is the probability of obtaining a test statistic that is at least as extreme as the test statistic that was actually observed. This probability is calculated under the assumption that the null hypothesis is true.

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Compute the test-statistic:

$$t_{\text{obs}} = \frac{1.67 - 0}{1.13/\sqrt{10}} = 4.67$$

Example - sleep medicine

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$$H_0: \mu = 0$$

where μ represents mean difference in sleep length.

Compute the p -value:

Compute the test-statistic:

$$t_{\text{obs}} = \frac{1.67 - 0}{1.13/\sqrt{10}} = 4.67$$

$$2P(T > 4.67) = 0.00117$$

```
2 * (1 - pt(4.67, df = 9))
```

Interpretation of the p -value in light of Table 3.1:

There is strong evidence against the null hypothesis.

Example - sleep medicine - in R, manually

```
# Enter data
x <- c(1.2, 2.4, 1.3, 1.3, 0.9, 1.0, 1.8, 0.8, 4.6, 1.4)
n <- length(x) # sample size

# Compute 'tobs' - the observed test statistic
tobs <- (mean(x) - 0) / (sd(x) / sqrt(n))

# Compute the p-value as a tail-probability
# in the relevant t-distribution:
2 * (1 - pt(abs(tobs), df = n-1))

## [1] 0.001166
```

Example - sleeping medicine - in R, with built-in function

```
t.test(x)

##
## One Sample t-test
##
## data:  x
## t = 4.7, df = 9, p-value = 0.001
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.8613 2.4787
## sample estimates:
## mean of x
##      1.67
```

Definition of a hypothesis test and significance (general)

Definition 3.24. Hypothesis test:

We say that we *carry out a hypothesis test* when we decide against a null hypothesis or not, using the data.

A null hypothesis is *rejected* if the p -value, calculated after the data has been observed, is less than some α , that is if the p -value $< \alpha$, where α is some pre-specified (so-called) *significance level*.

Otherwise, the null hypothesis is said to be '*accepted*'.

Definition 3.29. Statistical significance:

An *effect* is said to be (*statistically*) *significant* if the p -value is less than the significance level α .

Often, we use $\alpha = 0.05$.

Example - sleep medicine

With $\alpha = 0.05$:

Since the p -value is less than α , we **reject** the null hypothesis.

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Since the p -value is less than α , we **reject** the null hypothesis.

In conclusion:

We have found a **significant effect** of medicine B when compared to A (and B works better than A).

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Critical value

Definition 3.31 - the critical values of the t -test:

The $(1 - \alpha)100\%$ critical values for the (non-directional) one-sample t -test are the $(\alpha/2)100\%$ and $(1 - \alpha/2)100\%$ quantiles of the t -distribution with $n - 1$ degrees of freedom:

$$t_{\alpha/2} \text{ and } t_{1-\alpha/2}$$

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$$t_{\alpha/2} \text{ and } t_{1-\alpha/2}$$

Method 3.32: One-sample t -test by critical value:

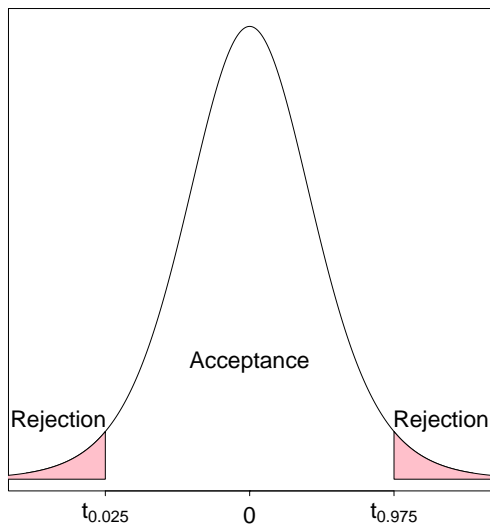
A null hypothesis is *rejected* if the observed test-statistic is more extreme than the critical values:

$$\text{If } |t_{\text{obs}}| > t_{1-\alpha/2} \text{ then } \textit{reject}$$

otherwise *accept*.

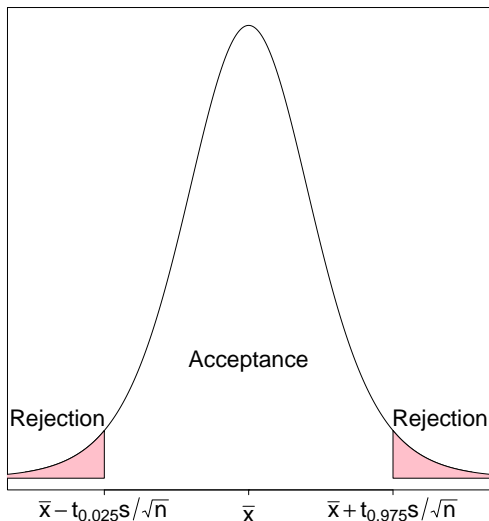
Critical value and hypothesis test

The acceptance region consists of the values of μ which are not too far away from the sample mean - here on the standardized scale:



Critical value and hypothesis test

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Critical value, confidence interval and hypothesis test

Theorem 3.33: Critical value method = Confidence interval method

We consider a $(1 - \alpha) \cdot 100\%$ confidence interval for μ :

$$\bar{x} \pm t_{1-\alpha/2} \cdot \frac{s}{\sqrt{n}}$$

The confidence interval corresponds to the acceptance region for H_0 when testing the (non-directional) hypothesis

$$H_0: \mu = \mu_0$$

Critical value, confidence interval and hypothesis test

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$$\bar{x} \pm t_{1-\alpha/2} \cdot \frac{s}{\sqrt{n}}$$

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$$H_0: \mu = \mu_0$$

(New) interpretation of the confidence interval:

The confidence interval covers those values of the parameter that we believe in given the data.

(Those values that we accept by the corresponding hypothesis test.)

Proof:

Remark 3.34

A μ_0 inside the confidence interval satisfies that

$$|\bar{x} - \mu_0| < t_{1-\alpha/2} \cdot \frac{s}{\sqrt{n}}$$

which is equivalent to

$$\frac{|\bar{x} - \mu_0|}{\frac{s}{\sqrt{n}}} < t_{1-\alpha/2}$$

and again to

$$|t_{\text{obs}}| < t_{1-\alpha/2}$$

which then exactly states that μ_0 is accepted, since the t_{obs} is within the critical values.

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The alternative hypothesis

So far - implied: (= non-directional)

The alternative to $H_0 : \mu = \mu_0$ is $H_1 : \mu \neq \mu_0$.

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BUT there are other possible settings, e.g. one-sided (= directional), "less":

The alternative to $H_0 : \mu = \mu_0$ is $H_1 : \mu < \mu_0$.

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BUT there are other possible settings, e.g. one-sided (= directional), "less":

The alternative to $H_0 : \mu = \mu_0$ is $H_1 : \mu < \mu_0$.

We stick to the "non-directional" in this course!

Steps of a hypothesis test - an overview

Generally, a hypothesis test consists of the following steps:

- 1 Formulate the hypothesis and choose the level of significance α (choose the "risk-level").
- 2 Calculate, using the data, the value of the test statistic.
- 3 Calculate the p -value using the test statistic and the relevant distribution. Compare the p -value to the significance level α and make a conclusion.

OR:

Alternatively, make a conclusion based on the relevant critical value(s).

The one-sample t-test again

Method 3.36 The level α one-sample t-test:

- 1 Compute t_{obs} as before.
- 2 Compute evidence against the *null hypothesis* $H_0 : \mu = \mu_0$ vs. the *alternative hypothesis* $H_1 : \mu \neq \mu_0$ by the

$$p\text{-value} = 2 \cdot P(T > |t_{\text{obs}}|),$$

where the t -distribution with $n - 1$ degrees of freedom is used.

- 3 If $p\text{-value} < \alpha$, we reject H_0 . Otherwise, we accept H_0 .

OR:

The rejection/acceptance conclusion could alternatively, but equivalently, be made based on the critical value(s) $\pm t_{1-\alpha/2}$:

If $|t_{\text{obs}}| > t_{1-\alpha/2}$ we reject H_0 , otherwise we accept H_0 .

Errors in hypothesis testing

Two kind of errors can occur (but only one at a time!):

Type I: Rejection of H_0 when H_0 is true.

Type II: Non-rejection (acceptance) of H_0 when H_1 is true.

The risks of the two types of errors are:

$$P(\text{Type I error}) = \alpha$$

$$P(\text{Type II error}) = \beta$$

Court of law analogy

A man is standing in a court of law:

A man is standing in a court of law, accused of criminal activity.

The null- and the alternative hypotheses are:

H_0 : The man is not guilty.

H_1 : The man is guilty.

Court of law analogy

A man is standing in a court of law:

A man is standing in a court of law, accused of criminal activity.

The null- and the alternative hypotheses are:

H_0 : The man is not guilty.

H_1 : The man is guilty.

Not being able to prove that the man is guilty is not the same as *proving* that he is innocent.

Or, put differently:

Accepting a null hypothesis is NOT a statistical proof of the null hypothesis being true!

Errors in hypothesis testing

Theorem 3.39: Significance level = The risk of a Type I error

The significance level α in hypothesis testing is the overall Type I risk:

$$P(\text{Type I error}) = P(\text{Rejection of } H_0 \text{ when } H_0 \text{ is true}) = \alpha$$

Errors in hypothesis testing

Theorem 3.39: Significance level = The risk of a Type I error

The significance level α in hypothesis testing is the overall Type I risk:

$$P(\text{Type I error}) = P(\text{Rejection of } H_0 \text{ when } H_0 \text{ is true}) = \alpha$$

Two possible truths vs. two possible conclusions:

	Reject H_0	Fail to reject H_0
H_0 is true	Type I error (α)	Correct acceptance of H_0
H_0 is false	Correct rejection of H_0 (Power)	Type II error (β)

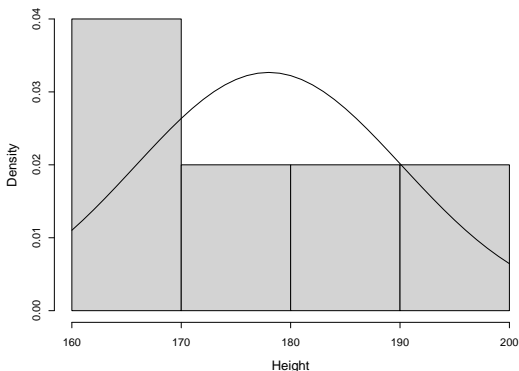
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Example - student heights

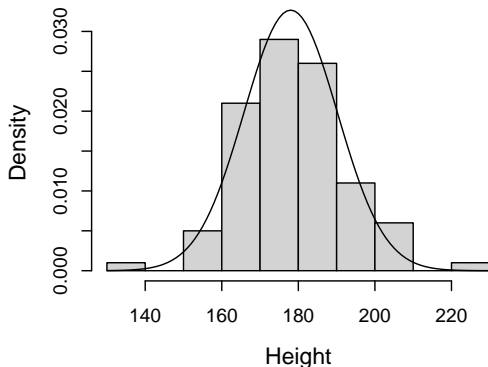
```
# Student heights data
x <- c(168, 161, 167, 179, 184, 166, 198, 187, 191, 179)

# Density histogram of student height data together with normal pdf
hist(x, xlab = "Height", main = "", freq = FALSE)
lines(seq(160, 200, 1), dnorm(seq(160, 200, 1), mean(x), sd(x)))
```



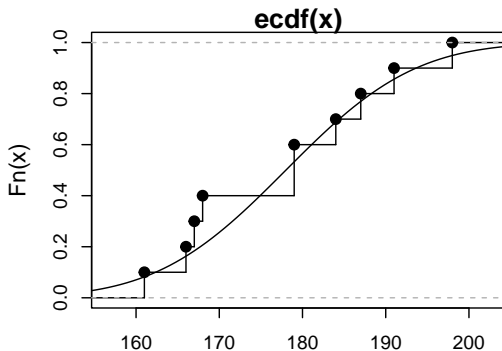
Example - 100 observations from a normal distribution

```
# Density histogram of simulated data from normal distribution  
# (n = 100) together with normal pdf  
xr <- rnorm(100, mean(x), sd(x))  
hist(xr, xlab = "Height", main = "", freq = FALSE, ylim = c(0, 0.032))  
lines(seq(130, 230, 1), dnorm(seq(130, 230, 1), mean(x), sd(x)))
```



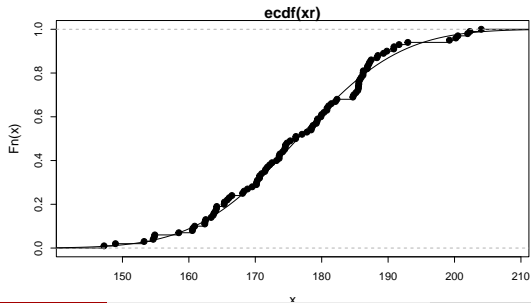
Example - student heights - ecdf

```
# Empirical cdf for student height data together  
# with normal cdf  
plot(ecdf(x), verticals = TRUE)  
xp <- seq(0.9*min(x), 1.1*max(x), length.out = 100)  
lines(xp, pnorm(xp, mean(x), sd(x)))
```



Example - 100 observations from a normal distribution - ecdf

```
# Empirical cdf of simulated data from normal distribution  
# (n = 100) together with normal cdf  
xr <- rnorm(100, mean(x), sd(x))  
plot(ecdf(xr), verticals = TRUE)  
xp <- seq(0.9*min(xr), 1.1*max(xr), length.out = 100)  
lines(xp, pnorm(xp, mean(xr), sd(xr)))
```

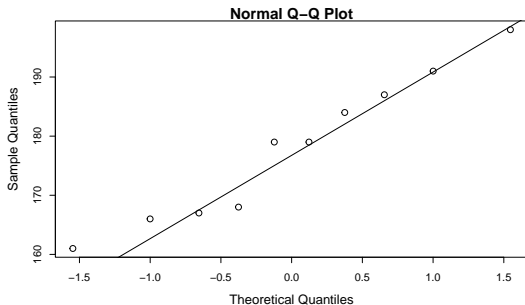


Example - student heights - normal q-q plot

```
# Normal q-q plot of student heights
```

```
qqnorm(x)
```

```
qqline(x)
```



Normal q-q plot

Method 3.42- The formal definition

The ordered observations $x_{(1)}, \dots, x_{(n)}$ are plotted versus a set of expected normal quantiles z_{p_1}, \dots, z_{p_n} . Different definitions of p_1, \dots, p_n exist:

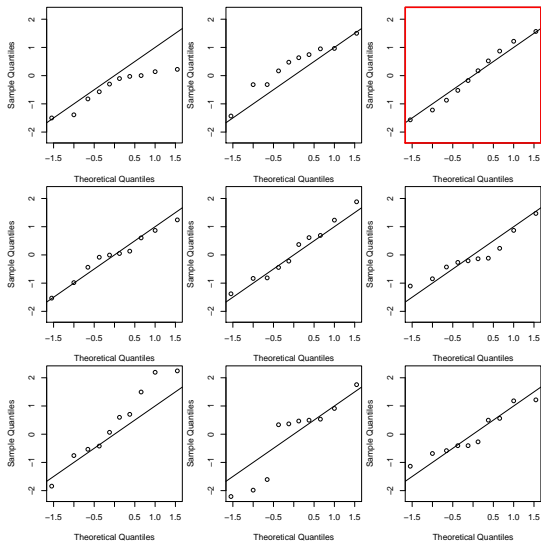
- In R, when $n > 10$:

$$p_i = \frac{i - 0.5}{n}, \quad i = 1, \dots, n$$

- In R, when $n \leq 10$:

$$p_i = \frac{i - 3/8}{n + 1/4}, \quad i = 1, \dots, n$$

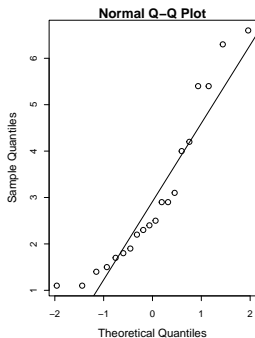
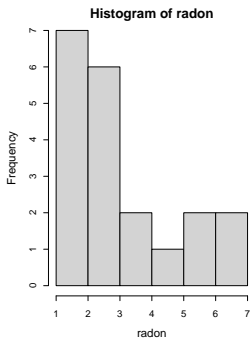
Example - student heights - compare with other simulated normal distributed data



Example - Radon data

```
## Reading in the data
radon <- c(2.4, 4.2, 1.8, 2.5, 5.4, 2.2, 4.0, 1.1, 1.5, 5.4, 6.3,
          1.9, 1.7, 1.1, 6.6, 3.1, 2.3, 1.4, 2.9, 2.9)

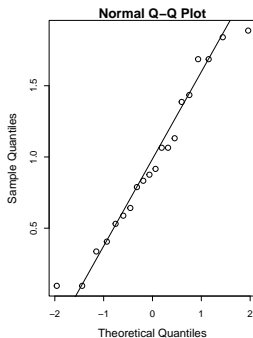
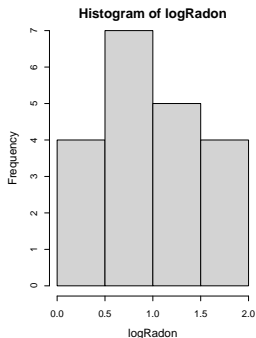
## Histogram and q-q plot of data
par(mfrow = c(1,2))
hist(radon)
qqnorm(radon)
qqline(radon)
```



Example - Radon data - log-transformed data are closer to a normal distribution

```
# Transform data using the natural logarithm
logRadon<-log(radon)

## Histogram and q-q plot of transformed data
par(mfrow = c(1,2))
hist(logRadon)
qqnorm(logRadon)
qqline(logRadon)
```



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