

# Analysing and presenting data: practical hints

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**Course:** Ingegneria dei Tessuti Biologici

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# Outline

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- ***Basic knowledge*** of statistic and statistical inference
- «***How to use***» common software for data analysis
- ***Practical*** examples
- ***Writing a paper***: literature research and reference management



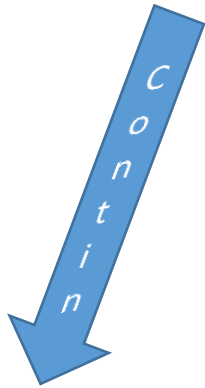
# Statistical analysis of data

## *basic knowledge*

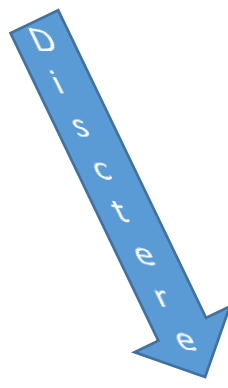
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- **Mean:** *expected value of a random variable*

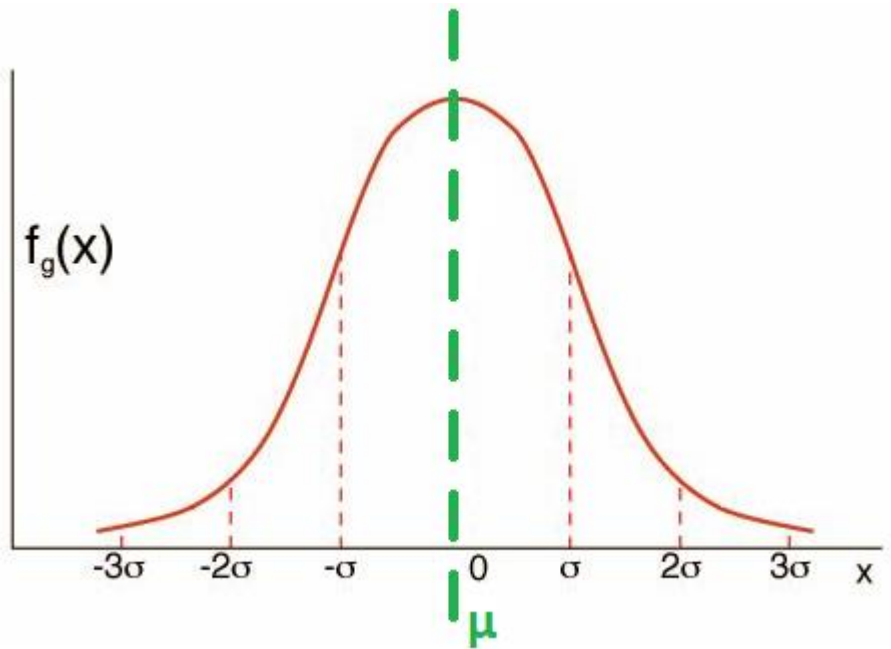
$$\mathbb{E}(X) := \int_{\Omega} X(\omega) d\mathbb{P}(\omega).$$



$$\mathbb{E}[X] = \int_{-\infty}^{\infty} x f(x) dx$$



$$\mathbb{E}[X] = \sum_{i=1}^{\infty} x_i p_i$$





# Statistical analysis of data

## *basic knowledge*

- **Variance** ( $\sigma^2$ ) and **standard deviation** ( $\sigma$ ): *measure of how far a set of numbers is spread out*

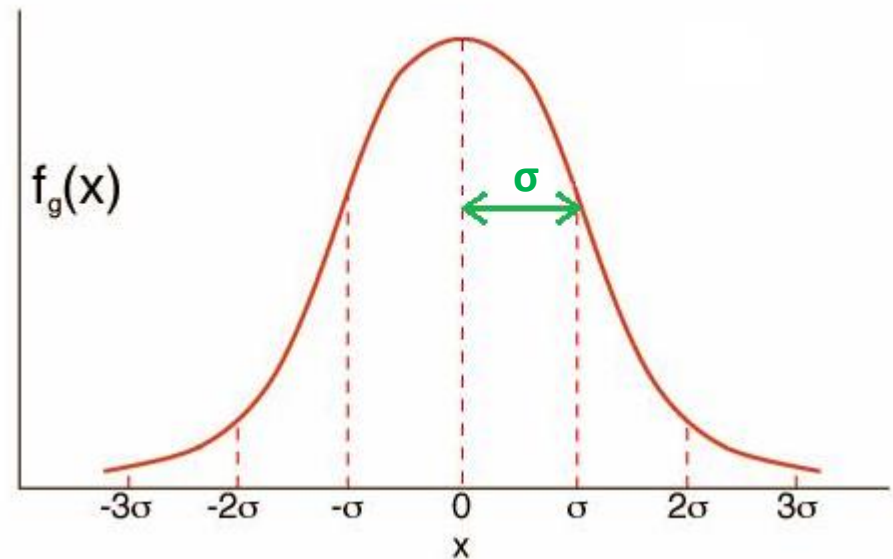
The variance of a random variable  $X$  is its **second central moment**

$$\text{Var}(X) = E[(X - \mu)^2] = E[X^2] - (E[X])^2$$

$$\begin{aligned}\text{Var}(X) &= \sigma^2 = \int (x - \mu)^2 f(x) dx \\ &= \int x^2 f(x) dx - \mu^2 \\ &= \sum_{i=1}^n p_i \cdot (x_i - \mu)^2 = \sum_{i=1}^n (p_i \cdot x_i^2) - \mu^2\end{aligned}$$

The *standard deviation* is the **square root** of the variance.

$$\sigma = \sqrt{\frac{1}{N} \sum_{i=1}^N (x_i - \mu)^2} \quad \sigma = \sqrt{\int_{\mathbf{X}} (x - \mu)^2 p(x) dx,}$$





# Statistical analysis of data

## *basic knowledge*

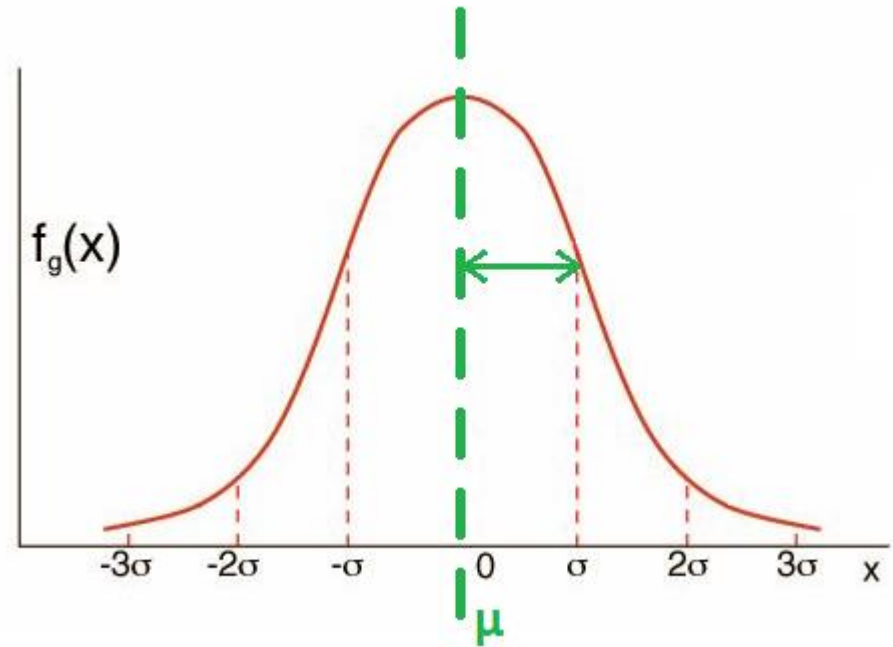
---

- **Correction for sample:** we do not use population in "real" case

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

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

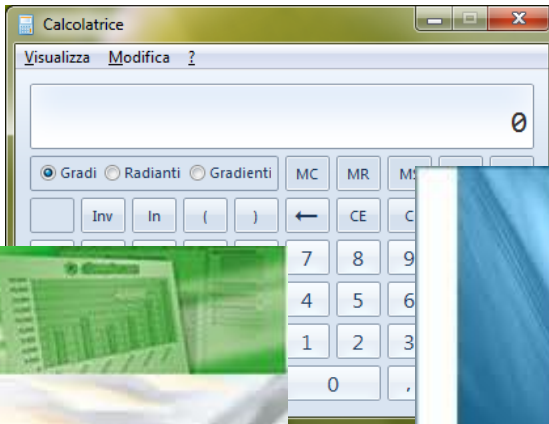
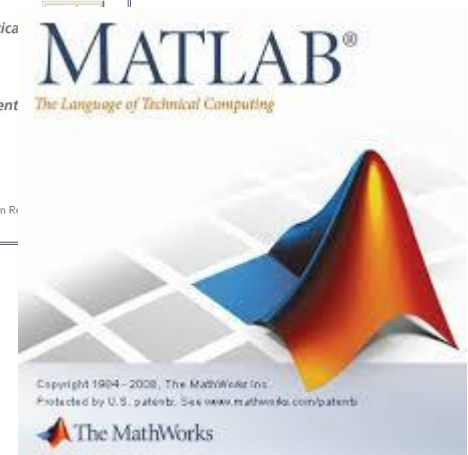
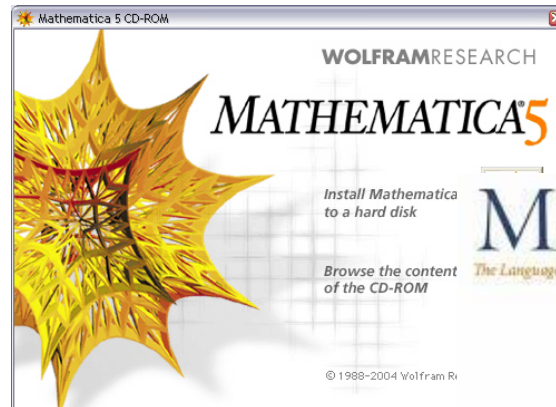
$$\mu = \frac{1}{N} \sum_{i=1}^N x_i.$$





# Data Analysis

*how people really analyse data*



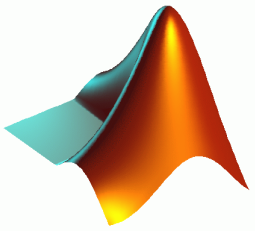


# Microsoft Excel

## *Useful shortcuts*

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- **Sum:** *sum of the selected cells*
- **Mean:** *mean of the selected cells*
- **Standard deviation (sample):**  
*=ST.DEV.C(number1,number2,...)*
- **Use of \$:** *freeze coordinates (useful when links cells and sheets)*
- **How to link cells and sheets**



# MathWorks MatLab

## *Useful Shortcuts*

---

- **Sum:**

```
S = sum(A, dim)
```

- **Mean:**

```
M = mean(A, dim)
```

- **Standard deviation (sample):**

```
s = std(X, flag, dim)
```

dim = 1  evaluation by columns (default)

dim = 2  evaluation by rows

Matlab evaluate corrected standard deviation by default





# Statistical analysis of data

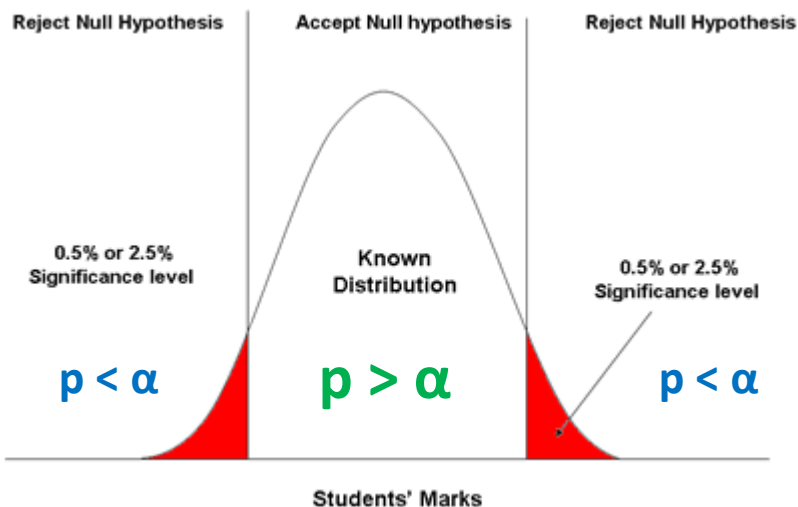
## *test of Hypothesis*

A **statistical hypothesis test** is a method of making decisions using data from a scientific study. In statistics, a result is called **statistically significant** if it has been predicted as unlikely to have occurred by chance alone, according to a pre-determined threshold probability (called *significance level,  $\alpha$* )

**Null and alternative hypothesis** ( $H_0$  and  $H_1$ ) formulation

**Statistic Test** selection

**Significance level** ( $\alpha$ ) selection



**Reject** the null hypothesis in favor of the alternative

$$p < \alpha$$

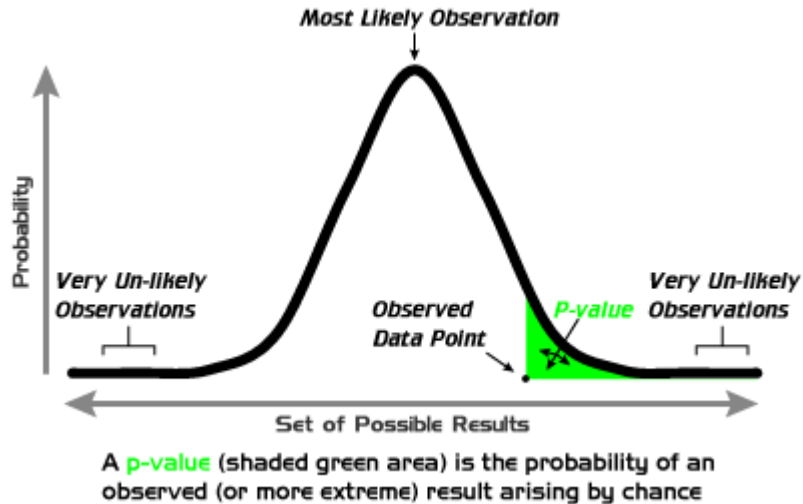
**Accept** the null hypothesis

$$p > \alpha$$

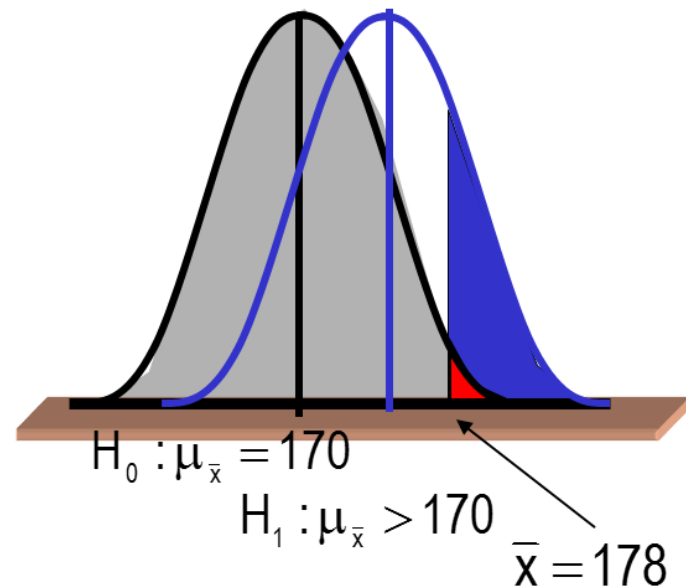
**Compute** from observation value  $t_{\text{obs}}$  and **probability** under the null hypothesis



# Interpreting the $p$ -value



In conclusion, the **smaller** the  $p$ -value the **more statistical evidence** exists to **support** the **alternative hypothesis ( $H_1$ )**





# Common Test

## *mean comparison*

---

- **Z test:** one-sample location test comparing the mean of a set of measurements to a given constant
  - **Independence** (independent and identically distributed samples, i.i.d.)
  - **Parameters variance** should be known, or estimated with high accuracy
  - The test statistic should follow a **normal distribution**.

$$z = \frac{M - \mu}{SE} \quad SE = \frac{\sigma}{\sqrt{n}}$$

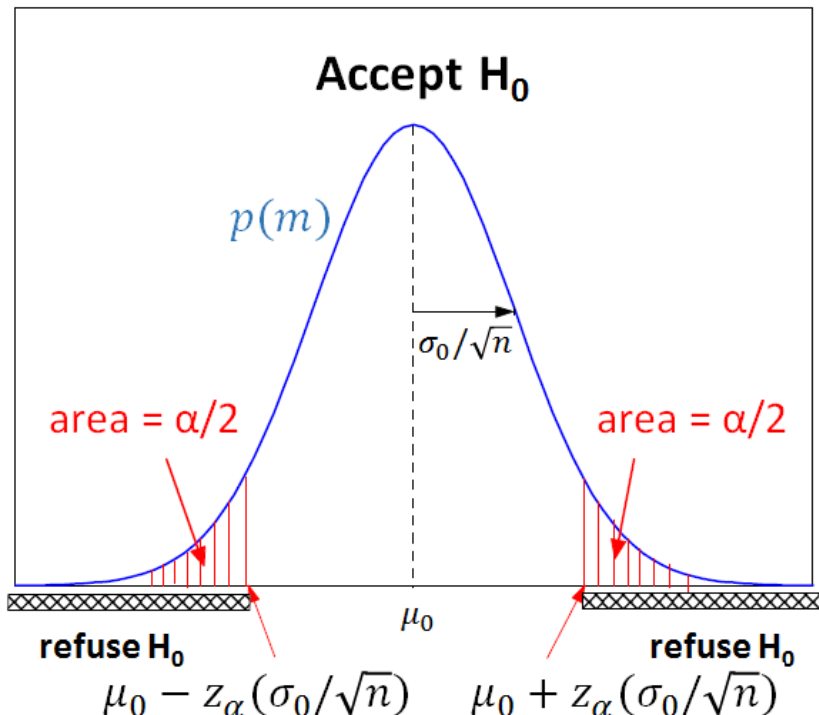
- **T test:** A **one-sample location test** of whether the mean of a population has a value specified in a null hypothesis; it is used instead of a z-test when the **sample variance is unknown** and is replaced by an estimate based on the data.
  - **Normal Population** Assumption
  - **Parameters variance** should be known, or estimated with high accuracy

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$



# Case A: unknown $\mu_0$ , known $\sigma_0$ $\bar{z}$ statistic (z-test)

- Mean survival time from the diagnosis of a given disease
  - **Population** =  $38.3 \pm 43.3$  months ( $\mu_0 \pm \sigma_0$ )
  - **100 patients treated with a new technique** = **46.9** months ( $\bar{m}$ )
- $H_0 \square \bar{m} = \mu_0$  and  $\bar{s} = \sigma_0$  and  $H_1 \square \bar{m} \neq \mu_0$



$$\bar{z} = \frac{\bar{m} - \mu_0}{\sigma_0/\sqrt{n}} = \frac{46.9 - 38.3}{43.3/\sqrt{100}} = \frac{8.6}{4.33} = 1.99$$

$H_0$  is refused with a significance level  $\alpha$  if  $\bar{z} < -z_{0.05}$  or  $\bar{z} > z_{0.05}$



Since  $z_{0.05} = 1.96$  and  $z_{0.01} = 2.58$  what can we say?

# Case b: unknown $\mu_0$ , unknown

$\sigma_0$

## $\bar{t}$ statistic (t-test)



- Rat uterine weight
  - **Population** = 24 mg ( $\mu_0$ )
  - **n=20** rats: [9, 14, 15, 15, 16, 18, 18, 19, 19, 20, 21, 22, 22, 24, 24, 26, 27, 29, 30, 32]
  - $\nu = n - 1 = 19$

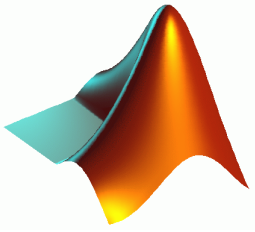
- $H_0$    $\bar{m} = \mu_0$  and  ~~$\bar{s} = \sigma_0$~~

$$\bar{t} = \frac{\bar{m} - \mu_0}{\bar{s}/\sqrt{n}} = \frac{21 - 24}{1.3219} = -2.27$$



Since  $t_{19, 0.05} = 2.093$   
and  $t_{19, 0.02} = 2.539$   
**what can we say?**

**Sample and population are significantly different with a significance level comprised between 2 % and 5 % ( $0.02 < p < 0.05$ ; calculated  $p$ -value for  $t_{19, p} = 2.27$  is  $p = 0.035$ )**



# MATLAB

## *z-test*

$H = 0$ ,  $H_0$  cannot be refused at  $\alpha$

$H = 1$ , refuse  $H_0$  at  $\alpha$

Confidence interval for the «true» value  $\mu$  at a level  $1 - \alpha$

z-statistic value

significance level

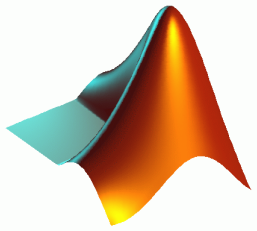
$$[H, P, CI, ZVAL] = ZTEST(X, mean, sigma, alpha, tail)$$

*p-value* (i.e. the probability of obtaining a test statistic at least as extreme as the one that was actually observed, assuming that the null hypothesis is true)

sample

population parameters

- 'both'  " $\bar{X}$  is not mean" (two-tailed test)
- 'right'  " $\bar{X}$  is greater than mean" (right-tailed test)
- 'left'  " $\bar{X}$  is less than mean" (left-tailed test)

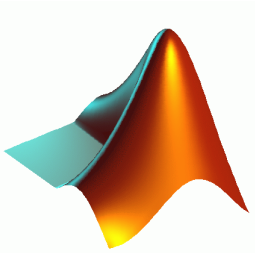


# MATLAB

## *z-test: example*

---

```
>> X=[8.3 9.2 12.5 7.6 10.2 12.9 11.7 10.8 11.7 9.6];  
>> sigma=2.1;  
>> mean=12;  
>> alpha=0.05;  
>> [H,P,CI,ZVAL]=ztest(X,mean,sigma,alpha)
```



# MATLAB

## *t*-test

---

$H = 0$ ,  $H_0$  cannot be refused at  $\alpha$   
 $H = 1$ , refuse  $H_0$  at  $\alpha$

Confidence interval for the «true»  
value  $\mu$  at a level  $1 - \alpha$

Data structure containing **t-statistics**  
value and **number of DoF**

**significance**  
level

$[H,P,CI,STATS] = TTEST(X,mean,alpha,tail)$

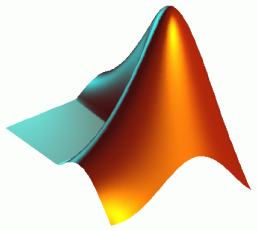
*p-value* (i.e. the probability  
of obtaining a test statistic  
at least as extreme as the  
one that was actually  
observed, assuming that  
the null hypothesis is true)

sample

population  
mean

'both'  " $\bar{X}$  is not mean" (two-tailed test)  
'right'  " $\bar{X}$  is greater than mean" (right-tailed test)  
'left'  " $\bar{X}$  is less than mean" (left-tailed test)





# MATLAB

## *t-test: example*

---

```
>> X=[22.3 25.1 27 23.4 24.7 26.5 25.7 24.1 23.9 22.8];  
>> mean=23;  
>> alpha=0.05;  
>> [H,P,CI,STAT]=ttest(X,mean,alpha)
```



# Microsoft Excel

## *Useful function*

---

- **z.test:** Returns the one-tailed probability-value of a z-test. For a given hypothesized population mean,  $x$ , **Z.TEST** returns the probability that the sample mean would be greater than the average of observations in the data set (**array**) — that is, the observed sample mean.

**=ZTEST** (*array*, *x*, *sigma* )

<b>array</b>	The array or range of data against which to test $x$ .
<b>x</b>	The value to test.
<b>sigma</b>	The population (known) standard deviation.

- **t.test:** Returns the probability that is associated with a Student's t-Test. Use **T.TEST** to determine whether two samples are likely to have come from the same two underlying populations that have the same mean

**=TTEST** (*array1*, *array2*, *tails*, *type*)

<b>Array1,</b> <b>Array2</b>	The array or range of data to test.
<b>Tails</b>	specifies the number of distribution tails: tails = 1 -> uses the one-tailed distribution tails = 2 -> uses the two-tailed distribution.
<b>Type</b>	is the kind of t-Test to perform.



# Equal or different?

## *The case of two samples*

---





# Independent two-sample *t*-test

*Equal sample sizes (n), equal variances ( $S_{X_1X_2}$ )*

---

The ***t* statistic** to test whether the **means of group 1 ( $\bar{X}_1$ )** and **group 2 ( $\bar{X}_2$ ) are different** can be calculated as follows:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{S_{X_1X_2} \cdot \sqrt{\frac{2}{n}}} \quad S_{X_1X_2} = \sqrt{\frac{1}{2}(S_{X_1}^2 + S_{X_2}^2)} \quad \text{«pooled» standard deviation}$$

$$t\text{-test DoFs} = 2n - 2$$

**$H_0$  is refused with a significance level  $\alpha$  if**

$$t < -t_{DoF,\alpha} \text{ or } t > t_{DoF,\alpha}$$



# Independent two-sample *t*-test

*Unequal sample sizes ( $n_1$  and  $n_2$ ), equal variances*  
( $S_{X_1X_2}$ )

---

The ***t* statistic** to test whether the **means of group 1 ( $\bar{X}_1$ ) and group 2 ( $\bar{X}_2$ ) are different** can be calculated as follows:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{S_{X_1X_2} \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \quad S_{X_1X_2} = \sqrt{\frac{(n_1 - 1)S_{X_1}^2 + (n_2 - 1)S_{X_2}^2}{n_1 + n_2 - 2}} \quad \text{«pooled» standard deviation}$$

$$t\text{-test DoFs} = n_1 + n_2 - 2$$

**$H_0$  is refused with a significance level  $\alpha$  if**

$$t < -t_{DoF,\alpha} \text{ or } t > t_{DoF,\alpha}$$



# Independent two-sample *t*-test

*Unequal sample sizes ( $n_1$  and  $n_2$ ), unequal variances ( $S_{X_1X_2}$ )*

---

The ***t* statistic** to test whether the **means of group 1 ( $\bar{X}_1$ ) and group 2 ( $\bar{X}_2$ ) are different** can be calculated as follows:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{s_{\bar{X}_1 - \bar{X}_2}} \quad s_{\bar{X}_1 - \bar{X}_2} = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}} \quad \text{«unpooled» standard deviation}$$

$$t\text{-test DoFs} = \frac{(s_1^2/n_1 + s_2^2/n_2)^2}{(s_1^2/n_1)^2/(n_1 - 1) + (s_2^2/n_2)^2/(n_2 - 1)} \quad \text{Welch-Satterthwaite equation}$$

**$H_0$  is refused with a significance level  $\alpha$  if**

$$t < -t_{DoF, \alpha} \text{ or } t > t_{DoF, \alpha}$$



# Independent two-sample *t*-test (*unequal sample sizes and equal variances*): an example

- Two groups of 10 *Daphnia magna* eggs, randomly extracted from the same clone, were reared in two different concentrations of hexavalent chromium
- After a month survived individuals were measured: 7 in group A and 8 in group B

	A	B
	2,7	2,2
	2,8	2,1
	2,9	2,2
	2,5	2,3
	2,6	2,1
	2,7	2,2
	2,8	2,3
		2,6

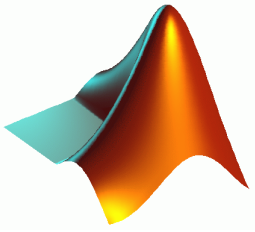
Mean      2.714      2.250

$$s_p^2 = \frac{0,10825 + 0,18000}{6 + 7} = 0,022173 \quad \text{«pooled» variance}$$

$$t_{13} = \frac{2,714 - 2,250}{\sqrt{0,022173 \cdot \left(\frac{1}{7} + \frac{1}{8}\right)}} = 6,02 \quad \text{t with 13 DoF}$$



Since  $t_{13, 0.05} = 2.160$   
what can we say?



# MATLAB

## *Independent two-sample t-test*

$H = 0$ ,  $H_0$  cannot be refused at  $\alpha$   
 $H = 1$ , refuse  $H_0$  at  $\alpha$

Confidence interval for the «true»  
difference of population means

Data structure containing t-statistics  
value and number of DoF

significance  
level

$$[H,P,CI,STATS] = TTEST2(X,Y,alpha,tail,vartype)$$

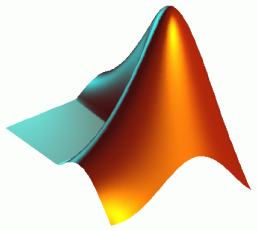
samples

*p-value* (i.e. the probability  
of observing the given  
result, or one more  
extreme, by chance if the  
null hypothesis is true)

'equal' or  
'unequal'

- 'both'  "means are not equal" (two-tailed test)
- 'right'  " $\bar{X}$  is greater than  $\bar{Y}$ " (right-tailed test)
- 'left'  " $\bar{X}$  is less than  $\bar{Y}$ " (left-tailed test)





# MATLAB

## *Ind. 2-sample t-test: an example*

---

```
>> X=[2.7 2.8 2.9 2.5 2.6 2.7 2.8]';
```

```
>> Y=[2.2 2.1 2.2 2.3 2.1 2.2 2.3 2.6]';
```

```
>> [H,P,CI,STATS] = ttest2(X,Y,0.05,'both','equal')
```



# Dependent two-sample *t*-test

*one sample tested twice or two “paired” samples*

---

$$t = \frac{\overline{X}_D - \mu_0}{s_D / \sqrt{n}}$$

- Calculate the differences between all  $n$  pairs ( $X_D$ ), then substitute their average ( $\overline{X}_D$ ) and standard deviation ( $s_D$ ) in the equation above to test if the average of the differences is significantly different from  $\mu_0$  ( $\mu_0 = 0$  under  $H_0$ , **DoFs =  $n - 1$** )
- The “pairs” can be either one person's pre-test and post-test scores (repeated measures) or persons matched into meaningful groups (e.g. same age)

<i>Example of repeated measures</i>			
Number	Name	Test 1	Test 2
1	Mike	35%	67%
2	Melanie	50%	46%
3	Melissa	90%	86%
4	Mitchell	78%	91%

<i>Example of matched pairs</i>			
Pair	Name	Age	Test
1	John	35	250
1	Jane	36	340
2	Jimmy	22	460
2	Jessy	21	200



# Dependent two-sample *t*-test: an example

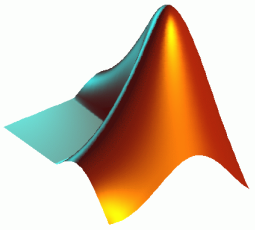
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Student	Pre-module score	Post-module score	Difference
1	18	22	+4
2	21	25	+4
3	16	17	+1
4	22	24	+2
5	19	16	-3
6	24	29	+5
7	17	20	+3
8	21	23	+2
9	23	19	-4
10	18	20	+2
11	14	15	+1
12	16	15	-1
13	16	18	+2
14	19	26	+7
15	18	18	0
16	20	24	+4
17	12	18	+6
18	22	25	+3
19	15	19	+4
20	17	16	-1

$$t = \frac{2.05}{0.634} = 3.231 \quad \text{on 19 df}$$



Since  $t_{19, 0.05} = 2.093$   
what can we say?



# MATLAB

## *Dependent two-sample t-test*

$H = 0$ ,  $H_0$  cannot be refused at  $\alpha$   
 $H = 1$ , refuse  $H_0$  at  $\alpha$

Confidence interval for the «true»  
difference of population means

Data structure containing **t-statistics**  
value and number of DoF

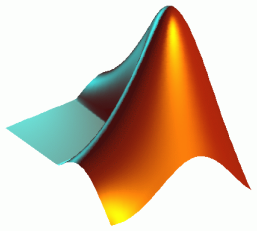
significance  
level

$$[H,P,CI,STATS] = \text{TTEST}(X,Y,\alpha,\text{tail})$$

samples

*p-value* (i.e. the probability  
of observing the given  
result, or one more  
extreme, by chance if the  
null hypothesis is true)

- 'both'  "means are not equal" (two-tailed test)
- 'right'  " $\bar{X}$  is greater than  $\bar{Y}$ " (right-tailed test)
- 'left'  " $\bar{X}$  is less than  $\bar{Y}$ " (left-tailed test)



# MATLAB

## *Dep. 2-sample t-test: an example*

---

```
>> X=[22 25 17 24 16 29 20 23 19 20 15 15 18 26 18 24 18 25 19 16]';  
>> Y=[18 21 16 22 19 24 17 21 23 18 14 16 16 19 18 20 12 22 15 17]';  
>> [H,P,CI,STATS] = ttest(X,Y,0.05,'both')
```



# Equal or different? *more than two samples*

---





# ANalysis Of VAriance (ANOVA)

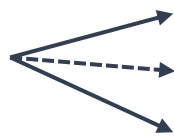
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- More than 2 groups: **NO pairwise comparisons (*t-test*)**

↑ groups □ ↑ overall probability that at least one of them is significant  
(e.g.  $\alpha=0.05$  and  $n=20$  □ in average 1 group will be significantly different for the case, even if  $H_0$  is true)

$$H_0: \mu_1 = \mu_2 = \mu_3 = \dots = \mu_k$$

$H_1$ : not all means are equal



**all means are different**

...

**one mean is different** from the others, which are all equals

- **ANOVA**

- uses **Fisher's distribution (F-distribution)**
- the **sources of variations** on observed values of **two or more groups** can be **decomposed** and **accurately measured**
- the **source of variation** is called **EXPERIMENTAL FACTOR** (or **TREATMENT**) and can be multi-levelled
- each **unit or observation** of the experimental factor is called **REPLICATION**



# 1- and 2-way ANOVA

---

- **ANOVA (1way)**: The ANOVA tests the null hypothesis that samples in *two or more groups* are drawn from populations with the *same* mean values. To do this, two assumption are made about the population variance.
  - Response variable are **normally distributed** (or approximately normally distributed), and **independent** and **identically** distributed
  - **Variances** of populations are **equal**.
- **ANOVA (2way)**: is an extension of the one-way ANOVA test that examines the *influence of different categorical* independent variables on one dependent variable. The two-way ANOVA can determine the main **effect of contributions** of each independent variable and identifies if there is a **significant interaction effect** between the independent variables.
  - The populations from which the samples are obtained must be **normally distributed**, with a **correct** sampling. Observations for within and between groups must be **independent**.
  - The variances among populations must be equal (**homoscedastic**).





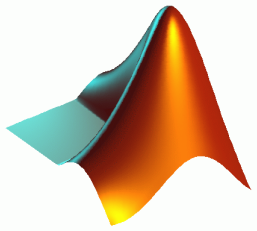
# one-way ANOVA: an example

## The problem

---

- Content of iron in air in 3 different zones (A, B, C) of a city ( $\mu\text{g}/\text{N mc}$  at  $0^\circ\text{C}$  and  $1013\text{ mbar}$ )

EXPERIMENTAL FACTOR						
		A	B	C		
		2,71	1,75	2,22		
		2,06	2,19	2,38		
		2,84	2,09	2,56		
		2,97	2,75	2,60		
		2,55		2,72		
		2,78				
$\sum X_j$		15,91	8,78	12,48	$\sum X$	37,17
$n_i$		6	4	5	<b>n</b>	15
$\bar{X}_{.j}$		2,652	2,195	2,496	$\bar{X}_{..}$	2,478



# MATLAB

## *one-way ANOVA*

$p$ -value for  $H_0$   
(means of the  
groups are equal)

ANOVA table  
values

Structure of statistics useful for performing a  
multiple comparison of means with the  
MULTCOMPARE function

`[P, ANOVATAB, STATS] = anova1(X, GROUP, DISPLAYOPT)`

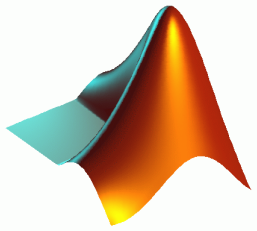
Matrix with 1 group per column  
(requires equal-sized samples)

Vector of data

Character array: one row per column  
of X, containing the group names

Vector: one group name for each  
element of X

'on' (the default) to **display figures containing a standard one-way anova table and a boxplot**, or 'off' to omit these displays

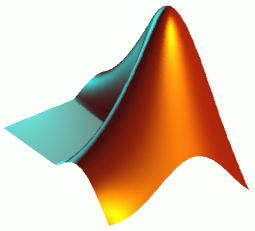


# MATLAB

## *one-way ANOVA: example*

---

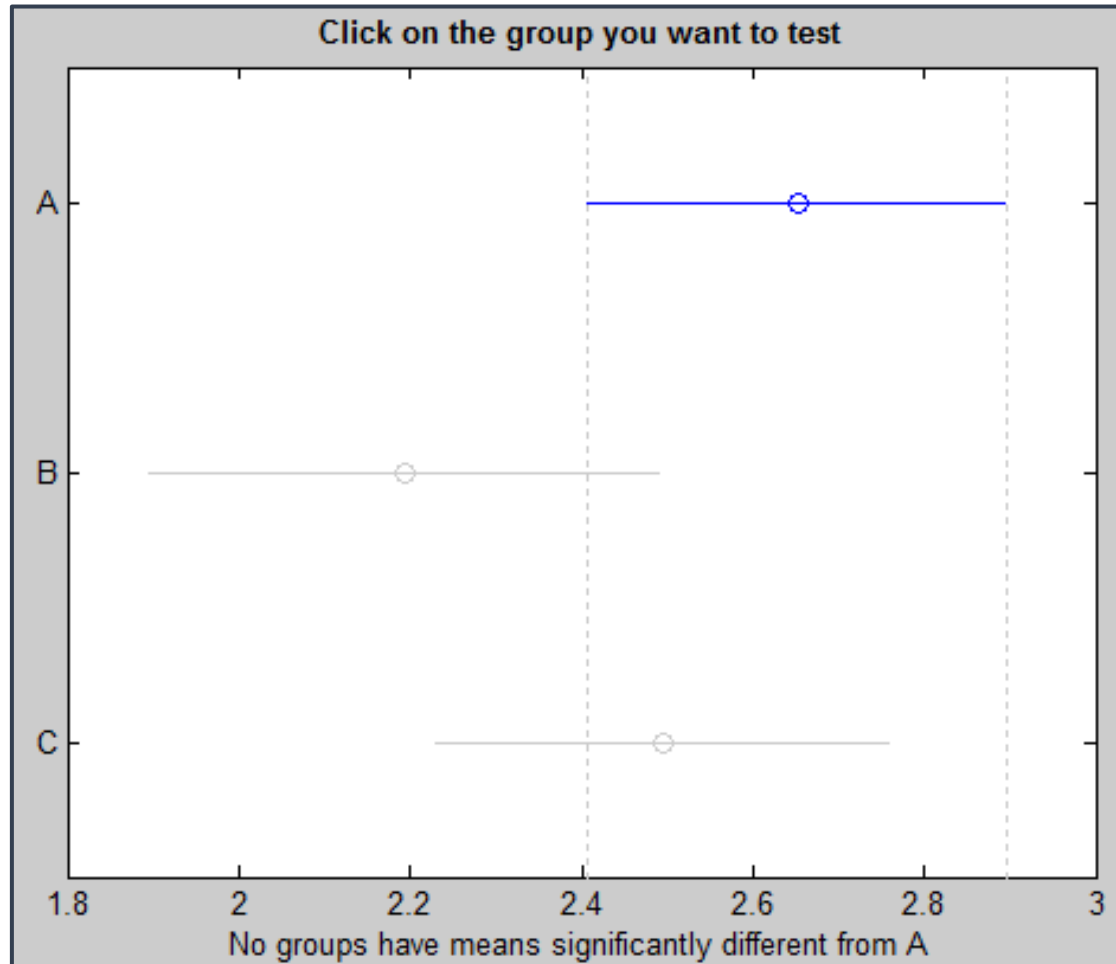
```
>> X=[2.71,2.06,2.84,2.97,2.55,2.78,1.75,2.19,2.09,2.75,2.22,2.38,2.56,2.6,2.72]';  
>> GROUP=['A','A','A','A','A','A','B','B','B','B','C','C','C','C','C'];  
>> [P,ANOVATAB,STATS] = anova1(X,GROUP)
```



# MATLAB

## *one-way ANOVA: example*

COMPARISON = multcompare(STATS)





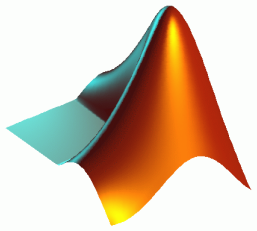
# two-way ANOVA: an example

## The problem

---

- **Content of Pb** in air in **5 different urban zones** revealed every **6 hours** during the day

BLOCKS (time)	TREATMENTS (urban zone)					$X_{ij}$	
	1	2	3	4	5	sums	means
6 am	28	25	30	22	26	131	26,2
12 am	34	32	37	31	30	164	32,8
6 pm	22	21	24	20	19	106	21,2
12 pm	36	31	40	33	29	169	33,8
sums	120	109	131	106	104	570	
means	30,00	27,25	32,75	26,50	26,00		28,50



# MATLAB

## *two-way ANOVA*

$p$ -value for  $H_0$   
(means of the  
groups are equal)

ANOVA table  
values

Structure of statistics useful for performing a  
multiple comparison of means with the  
MULTCOMPARE function

`[P, ANOVATAB, STATS] = anova2(X, REPS, DISPLAYOPT)`

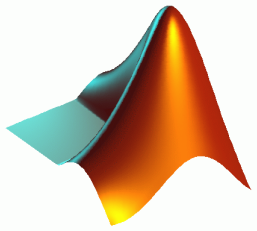
**Matrix of data** (balanced ANOVA  
□ equal number of repetitions)

**Columns:** 1<sup>st</sup> factor  
**Rows:** 2<sup>nd</sup> factor

**REPS** indicates the **number of  
observations per "cell"**

A **"cell"** contains REPS number of  
**rows**

'on' (the default) to **display a standard two-way anova table**, or 'off' to skip the display

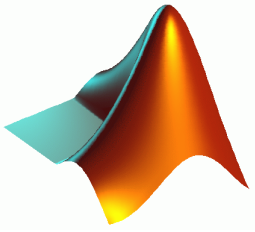


# MATLAB

## *two-way ANOVA: example*

---

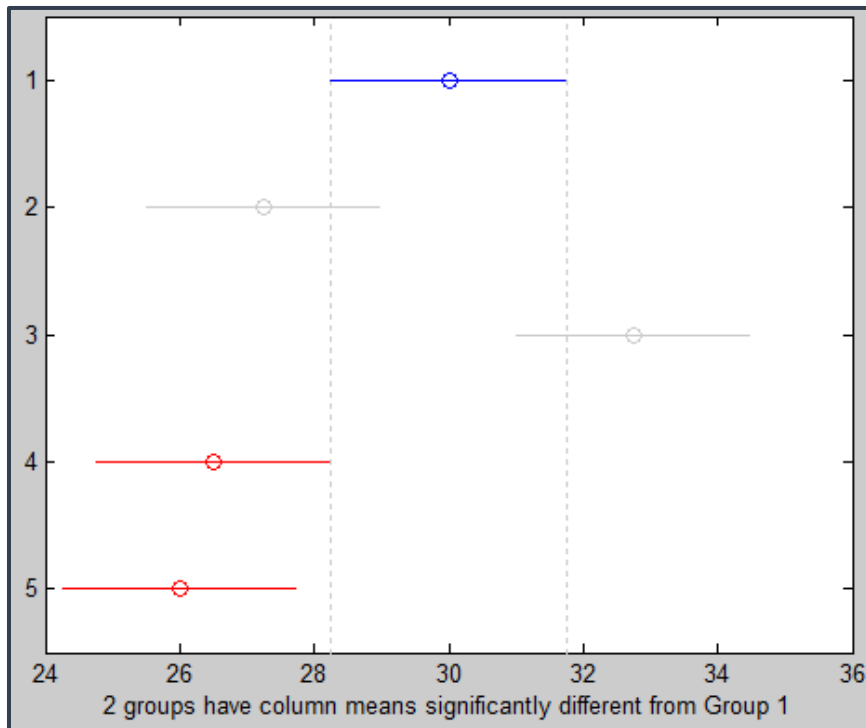
```
>> X=[28 25 30 22 26;  
34 32 37 31 30;  
22 21 24 20 19;  
36 31 40 33 29];  
>> [P,ANOVATAB,STATS] = anova2(X)
```



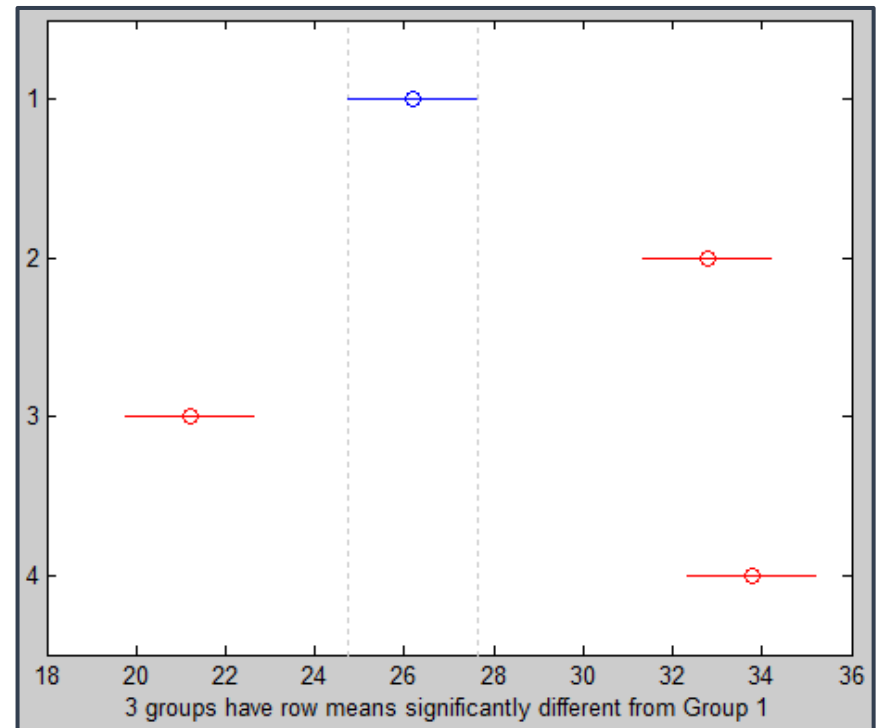
# MATLAB

## *two-way ANOVA: example*

COMPARISON = multcompare(STATS, 'estimate', 'column' (default) or 'row')

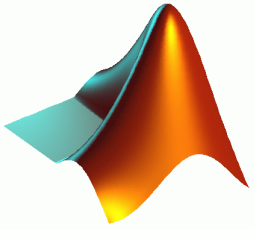


**Columns (i.e. urban zones)**



**Rows (i.e. times)**





# MATLAB

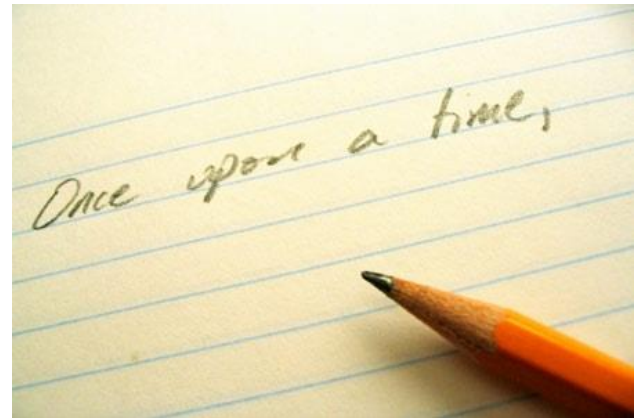
## *anovan: N-way analysis of variance*

---



# How to write a paper

Literature research and reference management





# The Sections of a Paper

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- Most journal-style scientific papers are subdivided into sections which usually appear in the following prescribed order:

Experimental process	Section of Paper
What did I do in a nutshell?	<a href="#"><u>Abstract</u></a>
What is the problem?	<a href="#"><u>Introduction</u></a>
How did I solve the problem?	<a href="#"><u>Materials and Methods</u></a>
What did I find out?	<a href="#"><u>Results</u></a>
What does it mean?	<a href="#"><u>Discussion</u></a>
Who helped me out?	<a href="#"><u>Acknowledgments</u></a> (optional)
Whose work did I refer to?	<a href="#"><u>Literature Cited</u></a>
Extra Information	<a href="#"><u>Appendices</u></a> (optional)



# Literature research

PubMed, Web of Science, or Google Scholar?

---

## Major differences you must know

1. **Pubmed and Web of Science are human-curated databases. Google Scholar is not.** This is the key to most of the differences you will find in your search results.
2. **Web of Science and Google Scholar track citations, but PubMed does not.**
3. **Google Scholar searches full text of articles but PubMed and Web of Science search only the citation, abstract, and tagging information.**



# Pubmed

<http://www.ncbi.nlm.nih.gov/pubmed>

## PubMed Advanced Search Builder

Tutorial

Use the builder below to create your search

[Edit](#)

[Clear](#)

### Builder

All Fields



[Show index list](#)

AND

All Fields



[Show index list](#)

or [Add to history](#)

### History

There is no recent history

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[NCBI Help Manual](#)

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[Data & Software](#)

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# Web of Science

<http://apps.webofknowledge.com/>

Web of Science™ InCites® Journal Citation Reports® Essential Science Indicators™ EndNote® Sign In Help English

WEB OF SCIENCE™ THOMSON REUTERS™

Search All Databases My Tools Search History Marked List

Welcome to the new Web of Science! View a brief tutorial.

**Basic Search**

Example: oil spill\* mediterranean Topic Search

+ Add Another Field

**TIMESPAN**

All years

From 1950 to 2014

▶ MORE SETTINGS








# Google Scholar

<http://scholar.google.it/>

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Web Immagini Altro...

Accedi

 La mia biblioteca  Le mie citazioni  Avvisi  Metriche  Impostazioni



Cerca nel Web  Pagine in Italiano

**Sali sulle spalle dei giganti**



# Reference management

## Mendeley desktop: a free citation manager

The screenshot shows the Mendeley Desktop application window. The main area displays a list of references under the heading "Amine quantification in gel". The selected reference is:

★	●	📄	Authors	Title	Year	Published In	Added
☆	●	📄	Bang, Tami; Ford, Millicent; ...	A Quantitative Study of Poly-L-Lysine Poly ( ethylene glycol ) Hydrogels Quantification of Amines			15/06/12
☆	●	📄	Gebeyehu, Setegn	Physiological response to drought stress of common bean (Phaseolus vulgaris L.) genotypes differing in drought resist...	2006		15/12/13
☆	●	📄	Lee, Sang-Won; Lim, Jong-...	Colorimetric determination of amino acids using genipin from Gardenia jasminoides	2003	Analytica Chimica Acta	15/10/12
☆	●	📄	Leslie-Barbick, Julia E; Moo...	Covalently-immobilized vascular endothelial growth factor promotes endothelial cell tubulogenesis in poly(ethylene gly...	2009	Journal of biomaterials scien...	15/06/12
☆	●	📄	Lévesque, Stéphane G; Sho...	Synthesis of cell-adhesive dextran hydrogels and macroporous scaffolds.	2006	Biomaterials	15/06/12
☆	●	📄	Liu, Y; Griffith, M; Watsky, ...	Properties of porcine and recombinant human collagen matrices for optically clear tissue engineering applications.	2006	Biomacromolecules	15/06/12
☆	●	📄	Lutolf, M P; Lauer-Fields, J ...	Synthetic matrix metalloproteinase-sensitive hydrogels for the conduction of tissue regeneration: engineering cell-inv...	2003	Proceedings of the National Academ...	15/10/12
☆	●	📄	McCaldin, D. J.	The Chemistry of Ninhydrin.	1960	Chemical Reviews	15/12/13
☆	●	📄	Yeo, Giselle C; Baldock, Clai...	Tropoelastin bridge region positions the cell-interactive C terminus and contributes to elastic fiber assembly.	2012	Proceedings of the National Academ...	05/12/12
☆	●	📄	Yeo, Giselle C; Baldock, Clai...	Tropoelastin bridge region positions the cell-interactive C terminus and contributes to elastic fiber assembly.	2012	Proceedings of the National Academ...	05/12/12

The right-hand pane shows the details for the selected article:

Type: Journal Article

**Colorimetric determination of amino acids using genipin from Gardenia jasminoides**

Authors: S. Lee, J. Lim, S. Bhoo et al.

Journal: *Analytica Chimica Acta*

Year: 2003

Volume: 480

Issue: 2

Pages: 267-274

**Abstract:**

**Tags:**

**Author Keywords:** amino acids; genipin; geniposide; molar absorptivity; ninhydrin; uv-vis spectrophotometry

**URL:** <http://linkinghub.elsevier.com/retrieve/pii/S00...>

Downloadable at <http://www.mendeley.com>





# Mendeley's features

## Reference Manager

Generate citations and bibliographies in Microsoft Word, LibreOffice, and LaTeX.



## Read and Annotate

Open PDFs and capture your thoughts through sticky notes and highlights.

**Content-based recommendations:** The user is recommended items similar to the ones preferred in the past;

**Collaborative recommendations:** The user is recommended items that people with similar interests and preferences liked in the past;

## Add and Organize

Import and organize PDFs from your computer, EndNote™, Papers or Zotero.



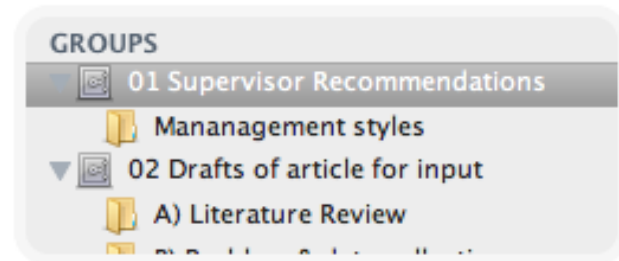


# Mendeley's features

---

## Collaborate

Connect with colleagues and securely share your papers, notes and annotations.



## Backup, Sync and Mobile

Access your papers on the web, iPhone or iPad.



## Network and Discover

Discover papers, people and public groups.





# Add papers from anywhere

---



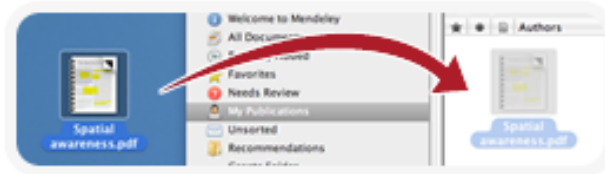
## Import from websites

The **web importer** allows you to import papers, web pages and other documents into your library from search engines and academic databases.



## Import from existing software

Mendeley can import BibTeX, RIS and EndNote™ XML files so you can easily transfer your library from EndNote™, Papers and Zotero.



## Drag and drop

Drag any PDF directly into Mendeley from your desktop or folders which you can then instantly annotate, cite, and highlight.



## Automatically watch folders

Choose a folder on your computer to “watch”. When you next add papers to that folder, they are also automatically added to your Mendeley library.

Source: <http://www.mendeley.com/features/add-and-organize/>



# Reference manager

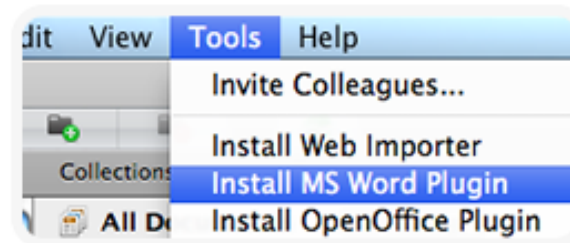
## Free and fully compatible with...

- ✓ Windows Word 2003, 2007, 2010
- ✓ Mac Word 2008, 2011
- ✓ LibreOffice
- ✓ BibTeX



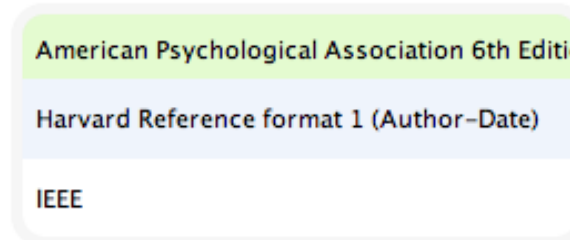
## Quick and simple installation

Once you download the Mendeley reference manager, you can install the Word Plugin in 3 clicks. Hey presto – you are ready to create your bibliography.



## Citation styles for thousands of journals

Quickly search and select your citation style from a rapidly growing **community managed database**, or create new styles with the new CSL Editor.



Source: <http://www.mendeley.com/features/reference-manager/>



# Reference manager

## Create bibliographies instantly

Cite seamlessly without leaving Word. Format your citations and bibliography according to your chosen style.



## Flexible formatting

Hanging indents, the use of "Ibid.", author disambiguation. Mendeley looks after the details of creating a bibliography so you can focus on writing.

- [1] W. W. Lee, L. T. Nguyen, applicability to chip scale
- [2] S.-W. R. Lee and X. Zhan

## Collaborate on bibliographies

Share bibliographies with your colleagues through a private group. Any member can add or edit any cited references.



Source: <http://www.mendeley.com/features/reference-manager/>