

بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ

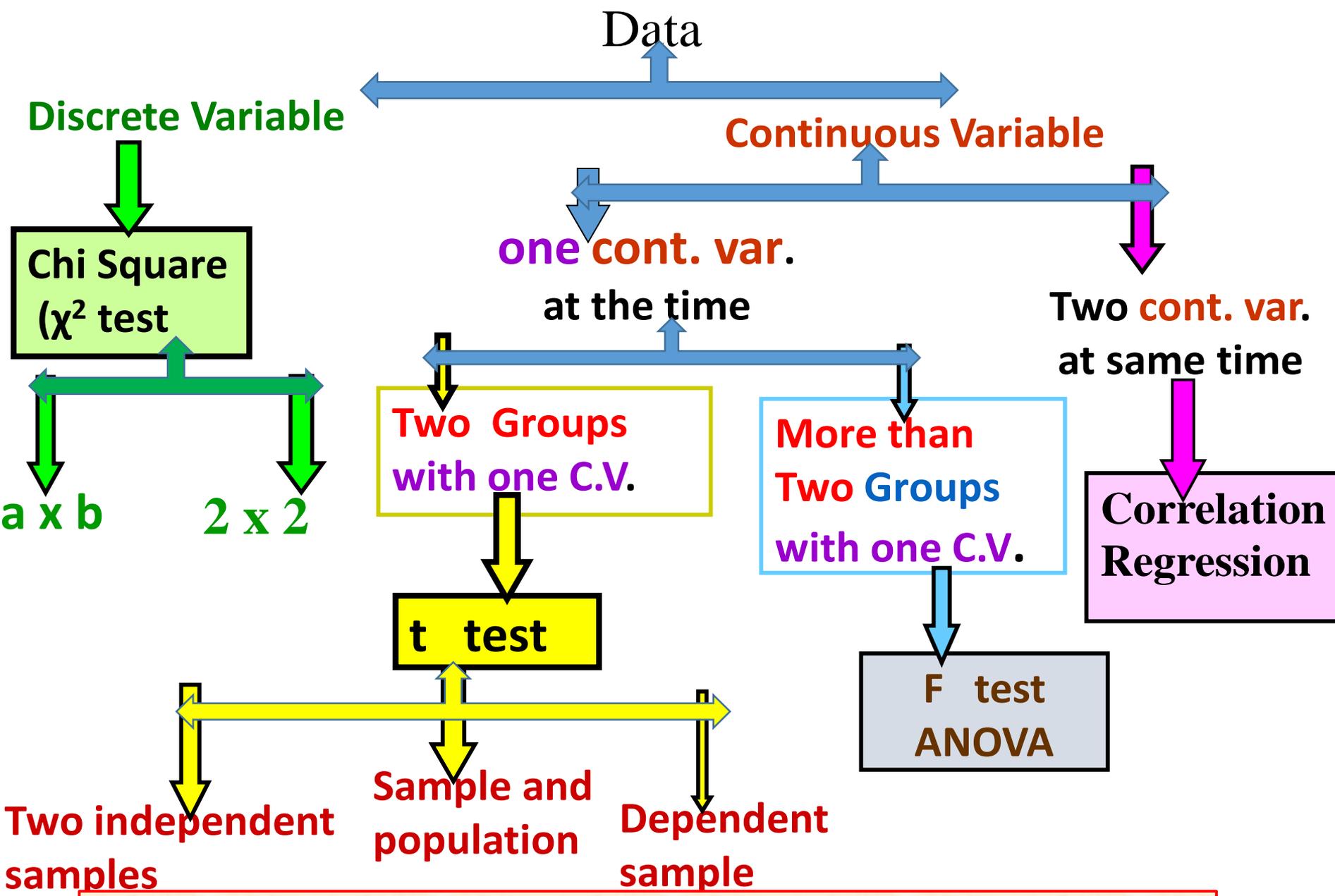


السلام عليكم ورحمة الله وبركاته

L XV

t-Tests

Part 2



An important thing is the type of the variable concerned.

It is one of the commonly test for testing Hypothesis .

It is used when we have **quantitative data** .

It is used in testing hypothesis about the **difference between Means of two populations** in comparing to the **standard error of the difference** .

to *determine in term of probability how large the observed difference is* :

$$t = \frac{m_1 - m_2}{S.E \text{ of difference}}$$

Application of t test

- (1) one-sample t-test;**
- (2) two-sample t-test; and**
- (3) two-sample paired t-test**

(1) one-sample t-test

Application of t test

I- Difference between **sample** and **population Means**

t test is used to test significance of the difference between **sample Mean** and **population mean μ** , as standard mean or standard value .

Measure the distance between , μ in relation to S.E .

Example

Blood cholesterol level was **242 mg/100 ml** , sample of 81 individuals put on certain diet, their mean blood cholesterol was **200 \pm 45 mg/ml** **Is there a significance difference in the cholesterol level between two population?** , at level of α 0.05

Is there any **effect of diet on cholesterol level** ?

Note, that there is a quite difference between .

Is there any effect of diet on cholesterol level ?

Note, that there is a **quite difference between** .

Sampling Error .

This difference could be either

Influencing Factor (diet) .

- ❖ The group **is equal to population mean μ (242 = 200)**,
 - but the difference is **due to unusual samples that** has been drawn (**sampling error**) .
- ❖ **Or the true mean of the population of the sample is not equal to 242** . It is due to **effect** of influencing factor (diet)
- So we are **going to decide**, which **of these two** possibilities is probable or more likely . **We use t test**

Data

Data represent cholesterol level (**quantitative**) of 81 individuals under certain diet .

Assumption

We assume **that random sample** of 81 individuals was chosen randomly from **normal distribution** population with **equal variance** . Certain diet was given to this sample (81 individuals) to **see the effect of this diet on serum** cholesterol .

Mean blood cholesterol level of this random sample was found as 200 mg/100 ml .

Formulation of Hypothesis

Ho

HA

Ho

There is **no significance difference** in the **mean** cholesterol level between population mean μ (242) and **population mean of the studied (81) group** (sample) (200)

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

$$242 = 200$$

$$\mu - \bar{X} = \text{Zero}$$

$$242 - 200 = \text{Zero}$$

- ❖ **And the** observed difference between μ and \bar{X} is due to
 - **Sampling error .**
 - **Sampling variability .**
 - **Or Chance factor .**
- ❖ **There is no effect of diet on the cholesterol level .**

HA

* There is a **significance difference** in the **mean** cholesterol level between **population mean** μ and studied group \bar{X} .

$$\mu \neq \bar{X}$$

$$242 \neq 200$$

$$\mu - \bar{X} \neq \text{Zero}$$

$$242 - 200 \neq \text{Zero}$$

** This difference is **due to**

the effect of influencing factor .

the effect of diet on cholesterol .

*** This difference is **not due to chance factor**

level of significance

$$\alpha = 0.05 \quad \frac{\alpha}{2} = \frac{0.05}{2} = 0.025$$

Two tails t test .
Two sided t test .

Proper test

Because This is quantitative data .

This is difference between two means

. We use

t test

First application

$$t = \frac{\mu - \bar{X}}{S.E \text{ of difference}}$$

$$t = \frac{242 - 200}{45/\sqrt{81}} = \frac{42}{45/9} = \frac{42}{5}$$

Calculated $t = 8.4$

Tabulated t at $\alpha = 0.025$

d.F = 80

df = sample size - 1 = (N - 1)

$t_{80} = 1.993$

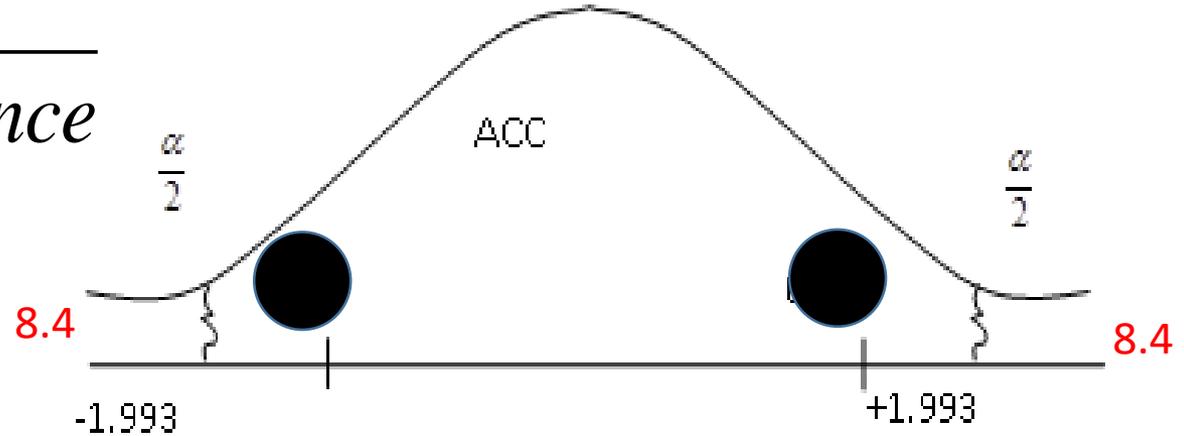
We accept that there is **a significance difference** ,
and the difference is due to **effect of the diet**
not due to sampling error .

This mean that **calculated t** fall in **Rejection region** .
This mean that the influencing factor is higher than 95%
This mean that the **chance factor is lesser than 5%** .

So, The **difference between** is **due to influencing factor** .

There is significance **effect of diet** on cholesterol level
This observed difference is not due to chance factor
 $P < 0.05$.

$$t = \frac{\mu - \bar{X}}{S.E \text{ of difference}}$$



Calculated t > tabulated .

So calculated t value **fall** in region of **Rejection**, so we **Reject H0** and **accept HA** .

Conclusion

There is a significance effect of diet on cholesterol level

Example

A hemoglobin level in g /dl were recorded for a sample of **20** children, who were part of a study of acute leukemia . Their **mean Hb** level was **8.5 ± 5** g/dl. Can we conclude that hemoglobin level of children with an acute leukemia differ from normal population which is **13.5** g/dl. Let alpha =0 .05

Is there any effect of acute leukemia on Hb level ?

Note, that there is a **quite difference between** .

Sampling Error .

This difference could be either

Influencing Factor (leukemia)

- The group is equal to population mean μ (**13.5 = 8.5**),
- but the difference is **due to unusual samples that** has been drawn (**sampling error**) .
- **Or** the true mean of the **population of the sample is not equal to 13.5** . It is due to effect of influencing factor (leukemia)
- ❖ So we are **going to decide**, which of these two possibilities is probable or more likely . **We use t test**

Data

Data represent **Hb level** (quantitative) of **20** children with acute leukemia.

Assumption

We assume that random sample of 20 children with acute leukemia, was chosen randomly from **normal distribution population** with equal variance . Hb measures was done to **see the effect of** leukemia **on** the Hb level.

Mean Hb level of this random sample was found as 8.5 g/dl.

Formulation of Hypothesis

Ho

HA

Ho

There is **no significance difference** in the **Hb** level between population mean μ (13.5) and **population mean of the studied** (20) group (sample) (8.5)

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

$$13.5 = 8.5$$

$$\mu - \bar{X} = \text{zero}$$

$$13.5 - 8.5 = \text{zero}$$

- ❖ **And the** observed difference between μ and \bar{X} is due to
 - **Sampling error .**
 - **Sampling variability .**
 - **Or Chance factor .**
- ❖ **There is no effect of** leukemia **on the Hb level .**

HA

* There is a **significance difference in the mean** Hb level between population mean μ and studied group \bar{X} .

$$\mu \text{ not} = \bar{X}$$

$$\mu \text{ not} = \bar{X}$$

$$13.5 \text{ not} = 8.5$$

$$13.5 - 8.5 \text{ not} = \text{zero}$$

** This difference is **due to**



the effect of influencing factor .



the effect of leukemia on Hb level .



***** This difference is not due to chance factor**

level of significance

$$\alpha = 0.05 \quad \frac{\alpha}{2} = \frac{0.05}{2} = 0.025$$

Two tails t test .
Two sided t test .

Proper test

Because This is quantitative data .

This is difference between two means

. We use

t test

First application

$$t = \frac{\mu - \bar{X}}{S.E \text{ of difference}}$$

$$t = \frac{13.5 - 8.5}{5/\sqrt{20}} = \frac{5}{5/4.47} = \frac{5}{1.12}$$

Calculated $t = 4.46$

Tabulated t at $\alpha = 0.025$

d.F = 19

df = sample size - 1 = (N - 1)

$t_{80} = 2.89$

We accept that there is **a significance difference in Hb levels** and the difference is **due to effect** of the leukemia **not due to sampling error** .

This mean that **calculated t fall in Rejection region** .

This mean that the influencing factor is higher than 95% .

This mean that the chance factor is **lesser than 5%** .

So,

The **difference in Hb levels** is due to **influencing factor** .

There is **significance effect of leukemia** on **Hb level** .

This **observed difference is not due to chance factor** .

$P < 0.05$.

t-test table

cum. prob	$t_{.50}$	$t_{.75}$	$t_{.80}$	$t_{.85}$	$t_{.90}$	$t_{.95}$	$t_{.975}$	$t_{.99}$	$t_{.995}$	$t_{.999}$	$t_{.9995}$
one-tail	0.50	0.25	0.20	0.15	0.10	0.05	0.025	0.01	0.005	0.001	0.0005
two-tails	1.00	0.50	0.40	0.30	0.20	0.10	0.05	0.02	0.01	0.002	0.001
df											
1	0.000	1.000	1.376	1.963	3.078	6.314	12.71	31.82	63.66	318.31	636.62
2	0.000	0.816	1.061	1.386	1.886	2.920	4.303	6.965	9.925	22.327	31.599
3	0.000	0.765	0.978	1.250	1.638	2.353	3.182	4.541	5.841	10.215	12.924
4	0.000	0.741	0.941	1.190	1.533	2.132	2.776	3.747	4.604	7.173	8.610
5	0.000	0.727	0.920	1.156	1.476	2.015	2.571	3.365	4.032	5.893	6.869
6	0.000	0.718	0.906	1.134	1.440	1.943	2.447	3.143	3.707	5.208	5.959
7	0.000	0.711	0.896	1.119	1.415	1.895	2.365	2.998	3.499	4.785	5.408
8	0.000	0.706	0.889	1.108	1.397	1.860	2.306	2.896	3.355	4.501	5.041
9	0.000	0.703	0.883	1.100	1.383	1.833	2.262	2.821	3.250	4.297	4.781
10	0.000	0.700	0.879	1.093	1.372	1.812	2.228	2.764	3.169	4.144	4.587
11	0.000	0.697	0.876	1.088	1.363	1.796	2.201	2.718	3.106	4.025	4.437
12	0.000	0.695	0.873	1.083	1.356	1.782	2.179	2.681	3.055	3.930	4.318
13	0.000	0.694	0.870	1.079	1.350	1.771	2.160	2.650	3.012	3.852	4.221
14	0.000	0.692	0.868	1.076	1.345	1.761	2.145	2.624	2.977	3.787	4.140
15	0.000	0.691	0.866	1.074	1.341	1.753	2.131	2.602	2.947	3.733	4.073
16	0.000	0.690	0.865	1.071	1.337	1.746	2.120	2.583	2.921	3.686	4.015
17	0.000	0.689	0.863	1.069	1.333	1.740	2.110	2.567	2.898	3.646	3.965
18	0.000	0.688	0.862	1.067	1.330	1.734	2.101	2.552	2.878	3.610	3.922
19	0.000	0.688	0.861	1.066	1.328	1.729	2.093	2.539	2.861	3.579	3.883
20	0.000	0.687	0.860	1.064	1.325	1.725	2.086	2.528	2.845	3.552	3.850
21	0.000	0.686	0.859	1.063	1.323	1.721	2.080	2.518	2.831	3.527	3.819
22	0.000	0.686	0.858	1.061	1.321	1.717	2.074	2.508	2.819	3.505	3.792
23	0.000	0.685	0.858	1.060	1.319	1.714	2.069	2.500	2.807	3.485	3.768
24	0.000	0.685	0.857	1.059	1.318	1.711	2.064	2.492	2.797	3.467	3.745
25	0.000	0.684	0.856	1.058	1.316	1.708	2.060	2.485	2.787	3.450	3.725
26	0.000	0.684	0.856	1.058	1.315	1.706	2.056	2.479	2.779	3.435	3.707
27	0.000	0.684	0.855	1.057	1.314	1.703	2.052	2.473	2.771	3.421	3.690
28	0.000	0.683	0.855	1.056	1.313	1.701	2.048	2.467	2.763	3.408	3.674
29	0.000	0.683	0.854	1.055	1.311	1.699	2.045	2.462	2.756	3.396	3.659
30	0.000	0.683	0.854	1.055	1.310	1.697	2.042	2.457	2.750	3.385	3.646
40	0.000	0.681	0.851	1.050	1.303	1.684	2.021	2.423	2.704	3.307	3.551
60	0.000	0.679	0.848	1.045	1.296	1.671	2.000	2.390	2.660	3.232	3.460
80	0.000	0.678	0.846	1.043	1.292	1.664	1.990	2.374	2.639	3.195	3.416
100	0.000	0.677	0.845	1.042	1.290	1.660	1.984	2.364	2.626	3.174	3.390
1000	0.000	0.675	0.842	1.037	1.282	1.646	1.962	2.330	2.581	3.098	3.300
Z	0.000	0.674	0.842	1.036	1.282	1.645	1.960	2.326	2.576	3.090	3.291
	0%	50%	60%	70%	80%	90%	95%	98%	99%	99.8%	99.9%

Example

The following are the heights in Cm of 24 two-year-old Jamaican boys with homozygous sickle cell disease (SS)

**84.4 89.9 89.0 81.9 87.0 78.5 84.1 86.3
80.6 80.0 81.3 86.8 83.4 89.9 85.4 80.6
85.0 82.5 80.7 84.3 85.4 85.0 85.5 81.9**

Height and weight standards for the UK give a reference height for two-year-old males of 86.5 cm .

Does the above sample suggest that two-year-old male SS children differ in height from the standards?

$$\bar{X} = 84.1 \text{ cm .}$$

$$\text{SD} = 3.11\text{cm}$$

$$N=24$$

$$\text{SD}/\sqrt{N} = 0.63\text{cm}$$

$$t = \frac{\mu - \bar{X}}{\text{S.E of difference}}$$

$$t = \frac{\bar{X} - 86.5}{\text{SD}/\sqrt{N}} = \frac{84.1 - 86.5}{0.63} = \frac{-2.4}{0.63} = -3.81 \text{ df } 23$$

Calculated $t = -3.81$

Tabulated t at $\alpha = 0.025$

d.F= 23

df= sample size -1= (N-1)

$t_{80} = 2.06$

Part 3

two-sample t test pooled

If the two research samples come from two different groups (e.g., a group of men and a group of women), Student's t-test is used.

If the two samples come from the same group (e.g. pre treatment and post treatment values for the same study participants), the paired t-test is used.

In both types of Student's t-test, t is calculated by taking the observed difference between the means of the two groups (the numerator) and dividing this difference by the standard error of the difference between the means of the two groups (denominator).

$$t = \frac{M_1 - M_2}{SE}$$

Before t can be calculated, the standard error of the difference between the means (**SED**) must be determined. The basic formula for this is the square root of the sum of the respective population variances, each divided by its own sample size.

$$t = \frac{M_1 - M_2}{SE}$$

What is a t test? in two-sample t test

A **t test** is used to measure the difference between exactly two means.

Its focus is on the same numeric data variable rather than counts or correlations between multiple variables.

If you are taking the average of a sample of measurements t tests are the most commonly used method to evaluate that data.

For example, you might compare whether systolic blood pressure differs between a control and treated group, between men and women, or any other two groups.

This calculator uses a **two-sample t test**, which compares two datasets to see if their means are statistically different.



This calculator uses a **two-sample t test**, which compares two datasets to see if their means are statistically different.

That is different from a one sample t test, which compares the mean of your sample to some proposed theoretical value.

The most general formula for a t test is composed of two means (M1 and M2) and the overall standard error (SE) of the two samples:

Because the t-test typically is used to test a null hypothesis of no difference between two means, the assumption generally is made that there is also no difference between the variances, so a **pooled estimate of the SED (SEDP)** may be used instead

II- Difference between two sample Means (pooled t test)

**Here we have two independent samples,
two different samples,**

**and two samples from two different populations,
we use Pooled t test .**

**Two independent random samples from their respective,
different populations .**

.

Two groups (population)

Treated group

Untreated group .

by A

♂

Two groups

Two groups

by B

♀

No. of individual in each sample is not necessary be equals

we use Pooled t test .

$$Pooled\ t\ test = \frac{m_1 - m_2}{S.P \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

$$D.F = n_1 + n_2 - 2\ or\ (n_1 - 1) + (n_2 - 1)$$

$$S.P = \sqrt{\frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}}$$

S.P = pooled S.D .

n1 = No. in first group .

n2 = No. in second group

S1 = S.D in first group .

S2 = S.D in second group

Example

In order to evaluate the difference in Serum Na level between **15 normotensive** and **12 newly diagnosed hypertensive** patients not yet on Na controlled diet .

The mean Na level was **144 ± 6.2 meq/L** in **normotensive** .
 160 ± 3.9 meq/L in **hypertensive** .

Using **$\alpha 0.05$** level of significance can it be concluded that **there is a significance difference in Na level** between the two group of population ?

Data

Quantitative data of Two samples.

Sodium (Na) level in blood of two groups .

15 Normotensive with

12 Hypertensive with

Data

Quantitative data of Two samples.

Sodium (Na) level in blood of two groups .

15 Normotensive with

12 Hypertensive with

No.	\bar{X}	S.D
15	144	6.2
12	160	3.9

Assumption

We assume that both groups were independent have been chosen randomly from normal distribution population with equal variance .

To see if there is a **significance difference in the mean Sodium (Na) levels between two groups .**

Formulation of Hypothesis

Ho

There is no significance difference in the mean Na level between two groups (Normotensive and Hypertensive)

$$m_1 = m_2 , \quad m_1 - m_2 = \text{zero} .$$

The observed difference is due to Chance Factor .

Sampling Error .

Sampling Variability .

HA

There is a **significance difference** in the mean Na level between two groups (Normotensive and Hypertensive)

$$m_1 \neq m_2 , \quad m_1 - m_2 \neq \text{zero}$$

❖ This difference is **due to Influencing Factor** (Increases in Blood Pressure).

❖ The effect of Chance Factor is minimum .

Using Proper test of significance

t test .

Pooled t test .

$$t = \frac{m_1 - m_2}{S.P \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

Level of significance
two tail t test

$$\alpha = 0.05$$

$$\frac{\alpha}{2} = \frac{0.05}{2} = 0.025$$

$$\begin{aligned} D.F &= (n_1 - 1) + (n_2 - 1) = n_1 + n_2 - 2 \\ &= 15 + 12 - 2 = 25 \end{aligned}$$

$$t = \frac{m_1 - m_2}{S.P \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

$$S.P = \sqrt{\frac{(n_1 - 1) S_1^2 + (n_2 - 1) S_2^2}{n_1 + n_2 - 2}}$$

$$\begin{aligned} S.P &= \sqrt{\frac{(15 - 1) 6.2^2 + (12 - 1) 3.9^2}{15 + 12 - 2}} = \sqrt{\frac{14 \times 38.44 + 11 \times 12.96}{25}} \\ &= \sqrt{\frac{538.16 + 142.56}{25}} = \sqrt{\frac{680.72}{25}} = \sqrt{27.2285} = 5.218 \end{aligned}$$

$$S.P = 5.218$$

$$t = \frac{m_1 - m_2}{S.P \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} = \frac{160 - 144}{5.218 \sqrt{0.083 + 0.066}}$$

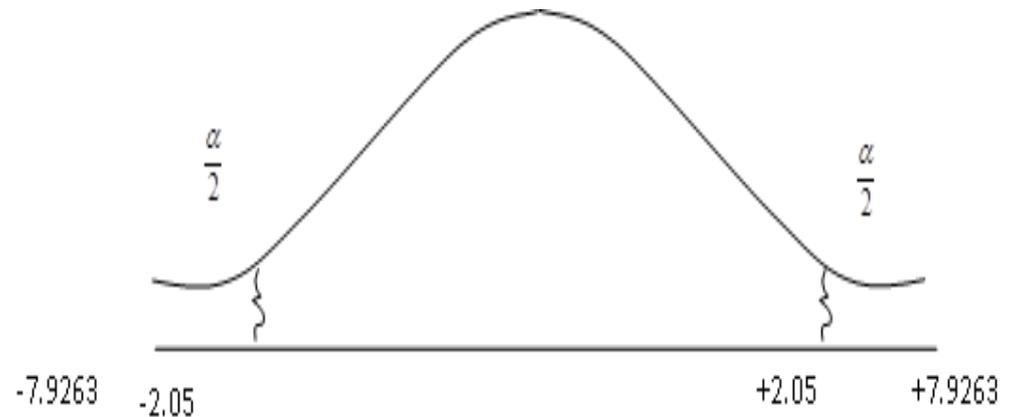
$$t = \frac{160 - 144}{5.218 \sqrt{0.1496}} = \frac{160 - 144}{5.218 \times 0.3868} = \frac{16}{2.0186}$$

$$t = 7.9263$$

Tabulated $t_{25}^{0.025} = 2.05$

d.F = 25

Calculated $t = 7.9263$



Calculated t > tabulated

Calculated t fall in area of **Rejection**,
so we reject H_0 .

This mean that we reject that **there is no significance difference in Na level between Normotensive and Hypertensive** :

❖ **there is a significance difference .**

This difference is due to **influencing factor** .

This difference is **due to increase in B.P.**

❖ **There** is a significance effect of Na on B.P.

Calculated t fall in area of **Rejection** .

❖ **Calculated t fall behind the critical region, so there is an**

❖ **increase of the influencing factor**, and there is

❖ **a decrease in chance factor**,

Therefore

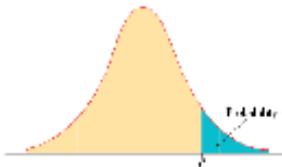
$P < 0.05$.

t-test table

cum. prob	$t_{.50}$	$t_{.75}$	$t_{.80}$	$t_{.85}$	$t_{.90}$	$t_{.95}$	$t_{.975}$	$t_{.99}$	$t_{.995}$	$t_{.999}$	$t_{.9995}$
one-tail	0.50	0.25	0.20	0.15	0.10	0.05	0.025	0.01	0.005	0.001	0.0005
two-tails	1.00	0.50	0.40	0.30	0.20	0.10	0.05	0.02	0.01	0.002	0.001
df											
1	0.000	1.000	1.376	1.963	3.078	6.314	12.71	31.82	63.66	318.31	636.62
2	0.000	0.816	1.061	1.386	1.886	2.920	4.303	6.965	9.925	22.327	31.599
3	0.000	0.765	0.978	1.250	1.638	2.353	3.182	4.541	5.841	10.215	12.924
4	0.000	0.741	0.941	1.190	1.533	2.132	2.776	3.747	4.604	7.173	8.610
5	0.000	0.727	0.920	1.156	1.476	2.015	2.571	3.365	4.032	5.893	6.869
6	0.000	0.718	0.906	1.134	1.440	1.943	2.447	3.143	3.707	5.208	5.959
7	0.000	0.711	0.896	1.119	1.415	1.895	2.365	2.998	3.499	4.785	5.408
8	0.000	0.706	0.889	1.108	1.397	1.860	2.306	2.896	3.355	4.501	5.041
9	0.000	0.703	0.883	1.100	1.383	1.833	2.262	2.821	3.250	4.297	4.781
10	0.000	0.700	0.879	1.093	1.372	1.812	2.228	2.764	3.169	4.144	4.587
11	0.000	0.697	0.876	1.088	1.363	1.796	2.201	2.718	3.106	4.025	4.437
12	0.000	0.695	0.873	1.083	1.356	1.782	2.179	2.681	3.055	3.930	4.318
13	0.000	0.694	0.870	1.079	1.350	1.771	2.160	2.650	3.012	3.852	4.221
14	0.000	0.692	0.868	1.076	1.345	1.761	2.145	2.624	2.977	3.787	4.140
15	0.000	0.691	0.866	1.074	1.341	1.753	2.131	2.602	2.947	3.733	4.073
16	0.000	0.690	0.865	1.071	1.337	1.746	2.120	2.583	2.921	3.686	4.015
17	0.000	0.689	0.863	1.069	1.333	1.740	2.110	2.567	2.898	3.646	3.965
18	0.000	0.688	0.862	1.067	1.330	1.734	2.101	2.552	2.878	3.610	3.922
19	0.000	0.688	0.861	1.066	1.328	1.729	2.093	2.539	2.861	3.579	3.883
20	0.000	0.687	0.860	1.064	1.325	1.725	2.086	2.528	2.845	3.552	3.850
21	0.000	0.686	0.859	1.063	1.323	1.721	2.080	2.518	2.831	3.527	3.819
22	0.000	0.686	0.858	1.061	1.321	1.717	2.074	2.508	2.819	3.505	3.792
23	0.000	0.685	0.858	1.060	1.319	1.714	2.069	2.500	2.807	3.485	3.768
24	0.000	0.685	0.857	1.059	1.318	1.711	2.064	2.492	2.797	3.467	3.745
25	0.000	0.684	0.856	1.058	1.316	1.708	2.060	2.485	2.787	3.450	3.725
26	0.000	0.684	0.856	1.058	1.315	1.706	2.056	2.479	2.779	3.435	3.707
27	0.000	0.684	0.855	1.057	1.314	1.703	2.052	2.473	2.771	3.421	3.690
28	0.000	0.683	0.855	1.056	1.313	1.701	2.048	2.467	2.763	3.408	3.674
29	0.000	0.683	0.854	1.055	1.311	1.699	2.045	2.462	2.756	3.396	3.659
30	0.000	0.683	0.854	1.055	1.310	1.697	2.042	2.457	2.750	3.385	3.646
40	0.000	0.681	0.851	1.050	1.303	1.684	2.021	2.423	2.704	3.307	3.551
60	0.000	0.679	0.848	1.045	1.296	1.671	2.000	2.390	2.660	3.232	3.460
80	0.000	0.678	0.846	1.043	1.292	1.664	1.990	2.374	2.639	3.195	3.416
100	0.000	0.677	0.845	1.042	1.290	1.660	1.984	2.364	2.626	3.174	3.390
1000	0.000	0.675	0.842	1.037	1.282	1.646	1.962	2.330	2.581	3.098	3.300
Z	0.000	0.674	0.842	1.036	1.282	1.645	1.960	2.326	2.576	3.090	3.291
	0%	50%	60%	70%	80%	90%	95%	98%	99%	99.8%	99.9%

t-distribution table

Areas in the upper tail are given along the top of the table. Critical t^* values are given in the table.



df	0*	0.05	0.025	0.02	0.01	0.005
1	0.000	0.000	0.000	0.000	0.000	0.000
2	0.000	0.000	0.000	0.000	0.000	0.000
3	0.000	0.000	0.000	0.000	0.000	0.000
4	0.000	0.000	0.000	0.000	0.000	0.000
5	0.000	0.000	0.000	0.000	0.000	0.000
6	0.000	0.000	0.000	0.000	0.000	0.000
7	0.000	0.000	0.000	0.000	0.000	0.000
8	0.000	0.000	0.000	0.000	0.000	0.000
9	0.000	0.000	0.000	0.000	0.000	0.000
10	0.000	0.000	0.000	0.000	0.000	0.000
11	0.000	0.000	0.000	0.000	0.000	0.000
12	0.000	0.000	0.000	0.000	0.000	0.000
13	0.000	0.000	0.000	0.000	0.000	0.000
14	0.000	0.000	0.000	0.000	0.000	0.000
15	0.000	0.000	0.000	0.000	0.000	0.000
16	0.000	0.000	0.000	0.000	0.000	0.000
17	0.000	0.000	0.000	0.000	0.000	0.000
18	0.000	0.000	0.000	0.000	0.000	0.000
19	0.000	0.000	0.000	0.000	0.000	0.000
20	0.000	0.000	0.000	0.000	0.000	0.000
21	0.000	0.000	0.000	0.000	0.000	0.000
22	0.000	0.000	0.000	0.000	0.000	0.000
23	0.000	0.000	0.000	0.000	0.000	0.000
24	0.000	0.000	0.000	0.000	0.000	0.000
25	0.000	0.000	0.000	0.000	0.000	0.000
26	0.000	0.000	0.000	0.000	0.000	0.000
27	0.000	0.000	0.000	0.000	0.000	0.000
28	0.000	0.000	0.000	0.000	0.000	0.000
29	0.000	0.000	0.000	0.000	0.000	0.000
30	0.000	0.000	0.000	0.000	0.000	0.000
31	0.000	0.000	0.000	0.000	0.000	0.000
32	0.000	0.000	0.000	0.000	0.000	0.000
33	0.000	0.000	0.000	0.000	0.000	0.000
34	0.000	0.000	0.000	0.000	0.000	0.000
35	0.000	0.000	0.000	0.000	0.000	0.000
36	0.000	0.000	0.000	0.000	0.000	0.000
37	0.000	0.000	0.000	0.000	0.000	0.000
38	0.000	0.000	0.000	0.000	0.000	0.000
39	0.000	0.000	0.000	0.000	0.000	0.000
40	0.000	0.000	0.000	0.000	0.000	0.000
41	0.000	0.000	0.000	0.000	0.000	0.000
42	0.000	0.000	0.000	0.000	0.000	0.000
43	0.000	0.000	0.000	0.000	0.000	0.000
44	0.000	0.000	0.000	0.000	0.000	0.000
45	0.000	0.000	0.000	0.000	0.000	0.000
46	0.000	0.000	0.000	0.000	0.000	0.000
47	0.000	0.000	0.000	0.000	0.000	0.000
48	0.000	0.000	0.000	0.000	0.000	0.000
49	0.000	0.000	0.000	0.000	0.000	0.000
50	0.000	0.000	0.000	0.000	0.000	0.000

df	0.1	0.05	0.025	0.02	0.01	0.005
51	1.298	1.675	2.008	2.108	2.407	2.675
52	1.299	1.675	2.007	2.107	2.407	2.675
53	1.298	1.674	2.006	2.106	2.406	2.674
54	1.297	1.674	2.005	2.105	2.405	2.673
55	1.297	1.673	2.004	2.104	2.405	2.673
56	1.297	1.673	2.003	2.103	2.404	2.672
57	1.297	1.672	2.002	2.102	2.404	2.672
58	1.296	1.672	2.002	2.101	2.403	2.671
59	1.296	1.671	2.001	2.100	2.403	2.671
60	1.295	1.671	2.000	2.099	2.402	2.670
61	1.295	1.670	2.000	2.099	2.402	2.670
62	1.295	1.670	1.999	2.098	2.401	2.669
63	1.294	1.669	1.998	2.097	2.401	2.669
64	1.294	1.669	1.998	2.096	2.400	2.668
65	1.294	1.669	1.997	2.096	2.400	2.668
66	1.294	1.668	1.997	2.095	2.399	2.667
67	1.294	1.668	1.996	2.095	2.399	2.667
68	1.294	1.668	1.995	2.094	2.398	2.666
69	1.294	1.667	1.995	2.093	2.398	2.666
70	1.293	1.667	1.994	2.093	2.397	2.665
71	1.293	1.667	1.994	2.092	2.397	2.665
72	1.293	1.666	1.993	2.092	2.396	2.664
73	1.293	1.666	1.993	2.091	2.396	2.664
74	1.293	1.666	1.993	2.091	2.395	2.663
75	1.293	1.665	1.992	2.090	2.395	2.663
76	1.293	1.665	1.992	2.090	2.394	2.662
77	1.293	1.665	1.991	2.089	2.394	2.661
78	1.292	1.665	1.991	2.089	2.393	2.661
79	1.292	1.664	1.990	2.088	2.393	2.660
80	1.292	1.664	1.990	2.088	2.392	2.660
81	1.292	1.664	1.990	2.087	2.392	2.659
82	1.292	1.664	1.989	2.087	2.392	2.659
83	1.292	1.663	1.989	2.087	2.391	2.658
84	1.292	1.663	1.989	2.086	2.391	2.658
85	1.292	1.663	1.988	2.086	2.391	2.657
86	1.291	1.663	1.988	2.085	2.390	2.657
87	1.291	1.663	1.988	2.085	2.390	2.656
88	1.291	1.662	1.987	2.085	2.389	2.655
89	1.291	1.662	1.987	2.084	2.389	2.655
90	1.291	1.662	1.987	2.084	2.388	2.654
91	1.291	1.662	1.986	2.084	2.388	2.654
92	1.291	1.662	1.986	2.083	2.387	2.653
93	1.291	1.661	1.986	2.083	2.387	2.653
94	1.291	1.661	1.986	2.083	2.386	2.652
95	1.291	1.661	1.985	2.082	2.386	2.652
96	1.291	1.661	1.985	2.082	2.385	2.651
97	1.291	1.661	1.985	2.082	2.385	2.651
98	1.291	1.661	1.984	2.081	2.384	2.650
99	1.291	1.660	1.984	2.081	2.384	2.650
100	1.291	1.660	1.984	2.081	2.383	2.649

Thank You