

ORIGIN ≡ 0

Paired t-Test

The Paired t-test is employed in cases, such as a longitudinal study, where two sets of measurements are exactly matched for each individual of a population. Calculations of this test are identical to the One Sample t-Test if one uses *difference between pairs of measurements* as sample data values. In this case $\mu_0 = 0$.

```
ZAR := READPRN("c:/DATA/Biostatistics/ZarEX9.1.txt")
```

< Zar Example 9.1

```
X1 := ZAR<1>
```

```
X2 := ZAR<2>
```

```
n := length(X1)    n = 10
```

```
X1_bar := mean(X1)  X1_bar = 144.7
```

```
X2_bar := mean(X2)  X2_bar = 141.4
```

ZAR =

```
s1 := sqrt(Var(X1))  s1 = 3.401
```

```
s2 := sqrt(Var(X2))  s2 = 4.0332
```

	0	1	2
0	1	142	138
1	2	140	136
2	3	144	147
3	4	144	139
4	5	142	143
5	6	146	141
6	7	149	143
7	8	150	145
8	9	142	136
9	10	148	146

Calculating difference:

```
d := X1 - X2
```

```
d_bar := mean(d)    d_bar = 3.3
```

```
s_d := sqrt(Var(d))  s_d = 3.0569
```

Assumptions:

- Observed values $X_{1,1}, X_{1,2}, X_{1,3}, \dots, X_{1,n}$ are a random sample exactly matched with Observed values $X_{2,1}, X_{2,2}, X_{2,3}, \dots, X_{2,n}$ across individuals 1,2,3, ... ,n.
- Let $d_i = X_{2,i} - X_{1,i}$ for each individual i are a random sample from $\sim N(\mu_d, \sigma_d^2)$.
- Variance σ_d^2 of the population is *unknown*.

^ Note: this test is reasonably robust for deviations from $\sim N(\mu_d, \sigma_d^2)$.

d =

	0
0	4
1	4
2	-3
3	5
4	-1
5	5
6	6
7	5
8	6
9	2

Hypotheses:

- $H_0: \mu_d = 0$ < No difference in mean between populations X_1 & X_2 .
- $H_1: \mu_d \neq 0$ < **Two Sided Case**
- $H_1: \mu_d < 0$ < **One Sided Case Lower Tail**
- $H_1: \mu_d > 0$ < **One Sided Case (Upper Tail)**

Test Statistic:

$$t := \frac{d_{bar}}{\frac{s_d}{\sqrt{n}}} \quad t = 3.4138$$

< t is the normalized mean $X_2_{bar} - X_1_{bar}$
 < s_d is the sample standard deviation of d_i

Sampling Distribution:

If Assumptions hold and H_0 is true, then $t \sim t_{(n-1)}$

Critical Values of the Test:

$\alpha := 0.05$ < **Probability of Type I error must be explicitly set**

$$C_1 := qt\left(\frac{\alpha}{2}, n - 1\right) \quad C_1 = -2.2622 \quad < \text{Two sided lower Critical Value}$$

$$C_2 := qt\left(1 - \frac{\alpha}{2}, n - 1\right) \quad C_2 = 2.2622 \quad < \text{Two sided upper Critical Value}$$

$$C := |C_2| \quad C = 2.2622 \quad < \text{Critical value used for two sided test (to simplify)}$$

$$C_3 := qt(\alpha, n - 1) \quad C_3 = -1.8331 \quad < \text{One sided lower Critical Value}$$

$$C_4 := qt(1 - \alpha, n - 1) \quad C_4 = 1.8331 \quad < \text{One sided upper Critical Value}$$

Decision Rules:

IF $|t| > C$ THEN REJECT H_0 , OTHERWISE ACCEPT H_0 < Two sided case
 IF $t < C_3$, THEN REJECT H_0 , OTHERWISE ACCEPT H_0 < One sided case lower tail
 IF $t > C_4$, THEN REJECT H_0 , OTHERWISE ACCEPT H_0 < One sided case upper tail

Probability Value:

$t = 3.4138$

$$P := 2 \cdot pt(t, n - 1) \quad P = 1.9923 \quad < \text{if } t \leq 0$$

$$P := 2 \cdot (1 - pt(t, n - 1)) \quad P = 0.007703 \quad < \text{if } t > 0 \quad < \text{Two sided case}$$

$$P := pt(t, n - 1) \quad P = 0.996148 \quad < \text{One sided case lower tail}$$

$$P := 1 - pt(t, n - 1) \quad P = 0.003852 \quad < \text{One sided case upper tail}$$

Confidence Intervals for the mean:

$\bar{d} = 3.3$

$$CI := \left(\bar{d} - C \cdot \frac{sd}{\sqrt{n}}, \bar{d} + C \cdot \frac{sd}{\sqrt{n}} \right) \quad CI = (1.113248 \quad 5.486752) \quad < \text{Two sided case}$$

$$CIL := \bar{d} - C_3 \cdot \frac{sd}{\sqrt{n}} \quad \text{minus infinity to} \quad CIL = 5.072009 \quad < \text{One sided case lower tail}$$

$$CIU := \bar{d} - C_4 \cdot \frac{sd}{\sqrt{n}} \quad CIU = 1.527991 \quad \text{to infinity} \quad < \text{One sided case upper tail}$$

Prototype in R:

```
#ZAR EXAMPLE 9.1
ZAR=read.table("c:/DATA/Biostatistics/ZarEX9.1.txt")
ZAR
attach(ZAR)
X1=hindlen
X2=forlen
d=X1-X2
n=length(d)
n
dbar=mean(d)
dbar
sd=sqrt(var(d))
sd
```

#PERFORMING PAIRED t-TEST:**?t.test****#TWO SIDED CASE:****t.test(X1,X2,alternative="two.sided",paired=T,conf.level=0.95)****t.test(d,alternative="two.sided",conf.level=0.95)****#NOTE ABOVE APPROACHES ARE EQUIVALENT**

Paired t-test

data: X1 and X2

t = 3.4138, df = 9, p-value = 0.007703

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

1.113248 5.486752

sample estimates:

mean of the differences

3.3

> t.test(d,alternative="two.sided",conf.level=0.95)

One Sample t-test

data: d

t = 3.4138, df = 9, p-value = 0.007703

alternative hypothesis: true mean is not equal to 0

95 percent confidence interval:

1.113248 5.486752

sample estimates:

mean of x

3.3

> #NOTE ABOVE APPROACHES ARE EQUIVALENT

#ONE SIDED CASE UPPER TAIL:**t.test(X1,X2,alternative="greater",paired=T,conf.level=0.95)****t.test(d,alternative="greater",conf.level=0.95)**

Paired t-test

data: X1 and X2

t = 3.4138, df = 9, p-value = 0.003852

alternative hypothesis: true difference in means is greater than 0

95 percent confidence interval:

1.527991 Inf

sample estimates:

mean of the differences

3.3

> t.test(d,alternative="greater",conf.level=0.95)

One Sample t-test

data: d

t = 3.4138, df = 9, p-value = 0.003852

alternative hypothesis: true mean is greater than 0

95 percent confidence interval:

1.527991 Inf

sample estimates:

mean of x

3.3

#ONE SIDED CASE LOWER TAIL:**t.test(X1,X2,alternative="less",paired=T,conf.level=0.95)****t.test(d,alternative="less",conf.level=0.95)**

Paired t-test

data: X1 and X2

t = 3.4138, df = 9, p-value = 0.9961

alternative hypothesis: true difference in means is less than 0

95 percent confidence interval:

-Inf 5.072009

sample estimates:

mean of the differences

3.3

> t.test(d,alternative="less",conf.level=0.95)

One Sample t-test

data: d

t = 3.4138, df = 9, p-value = 0.9961

alternative hypothesis: true mean is less than 0

95 percent confidence interval:

-Inf 5.072009

sample estimates:

mean of x

3.3