ORIGIN ≡ 0

Estimation of Sample Size and Power in t-Tests for Two Samples

Estimates for sample size (N) and power (1-β) on this page are similar to that seen in Biostatistics Worksheet 130, but here for comparing two samples.

ZAR := READPRN("c:/DATA/Biostatistics/ZarEX8.1M.txt") **< Zar Example 8.1**

$i := 0 .. 5$

$X1_i := \left(ZAR^{\langle 1 \rangle}\right)_i$ $\quad X2 := ZAR^{\langle 2 \rangle}$

$n_1 := \text{length}(X1)$ $\quad n_1 = 6$ $\quad n_2 := \text{length}(X2)$ $\quad n_2 = 7$

$X1_{bar} := \text{mean}(X1)$ $\quad X1_{bar} = 8.75$ $\quad X2_{bar} := \text{mean}(X2)$ $\quad X2_{bar} = 9.742857$

$s_1 := \sqrt{\text{Var}(X1)}$ $\quad s_1 = 0.582237$ $\quad s_2 := \sqrt{\text{Var}(X2)}$ $\quad s_2 = 0.818244$

$$s_p := \sqrt{\frac{(n_1 - 1) \cdot s_1^2 + (n_2 - 1) \cdot s_2^2}{n_1 + n_2 - 2}}$$

$s_p^2 = 0.5192857$ **< pooled variance**

ZAR =

	0	1	2
0	1	8.8	9.9
1	2	8.4	9
2	3	7.9	11.1
3	4	8.7	9.6
4	5	9.1	8.7
5	6	9.6	10.4
6	7	0	9.5

Assumptions:

- **Observed values $X_{1,1}, X_{1,2}, X_{1,3}, \dots X_{1,n}$ are a random sample from $\sim N(\mu_1, \sigma_1^2)$**
- **Observed values $X_{2,1}, X_{2,2}, X_{2,3}, \dots X_{2,n}$ are a random sample from $\sim N(\mu_2, \sigma_2^2)$**
- **Samples from the two samples are *independent***
- **Population variances $\sigma_1^2 = \sigma_2^2$**

Estimated Sample Size for a Given Resolved Distance between Populations:

Desired CI half width:

$d := 0.5$ **< This is set as desired. Note that 2d is the CI width.**

Desired Type 1 Error level:

$\alpha := 0.05$ **< Type 1 error α**

Initial Guess of Sample Size:

$N_0 := 50$ **< Initial guess of sample sample size N needed.**

$$X1 = \begin{pmatrix} 8.8 \\ 8.4 \\ 7.9 \\ 8.7 \\ 9.1 \\ 9.6 \end{pmatrix} \quad X2 = \begin{pmatrix} 9.9 \\ 9 \\ 11.1 \\ 9.6 \\ 8.7 \\ 10.4 \\ 9.5 \end{pmatrix}$$

Iterative Calculation:

$N_0 := 50$ **< Set initial guess for sample size**

$$N_1 := \frac{2 \cdot s_p^2 \cdot qt\left[1 - \frac{\alpha}{2}, 2 \cdot (N_0 - 1)\right]^2}{d^2} \qquad N_1 = 16.36004$$

$$N_2 := \frac{2 \cdot s_p^2 \cdot qt\left[1 - \frac{\alpha}{2}, 2 \cdot (N_1 - 1)\right]^2}{d^2} \qquad N_2 = 17.293$$

^ Note: input into the qt() function depends on whether the alternative hypotheses involve a one-sided or two-sided test. This example is a two-sided test. For a one-sided test, use α instead of α/2.

Prototype in R:

```
#POWER & SAMPLE SIZE CALCULATIONS
#FOR TWO SAMPLES

#ZAR EXAMPLE 8.1
ZAR=read.table("c:/DATA/Biostatistics/ZarEX8.1R.txt")
ZAR
attach(ZAR)
X1=data[group=="gpB"]
X2=data[group=="gpG"]
n1=length(X1)
n1
n2=length(X2)
n2
s1=sqrt(var(X1))
s2=sqrt(var(X2))
#POOLED VARIANCE:
sp=sqrt(((n1-1)*s1^2+(n2-1)*s2^2)/(n1+n2-2))
sp
sp^2
```

```
#ESTIMATING SAMPLE SIZE FOR CI
#SET THE FOLLOWING VALUES AS DESIRED:
d=0.5
N0=50
alpha=0.05
#ITERATE THE FOLLOWING UNTIL N IS STABILIZED:
N1=(2*sp^2*(qt(1-alpha/2,2*(N0-1)))^2)/d^2
N1
N2=(2*sp^2*(qt(1-alpha/2,2*(N1-1)))^2)/d^2
N2
N3=(2*sp^2*(qt(1-alpha/2,2*(N2-1)))^2)/d^2
N3
N4=(2*sp^2*(qt(1-alpha/2,2*(N3-1)))^2)/d^2
N4
N5=(2*sp^2*(qt(1-alpha/2,2*(N4-1)))^2)/d^2
N5
```

Estimating Sample Size for a Two Sample t-Test:

This estimation differs from the one above in being specifically tied to a distance δ defined by the alternative H_0 and H_1 hypotheses of a two-sample t-test.

Hypotheses:

$H_0: \mu_1 = \mu_2$ < μ_0 is a specified value for μ

$H_1: \mu \neq \mu_0$ < Two sided test

Desired Precision δ:

$\delta := 0.5$ < Set as desired for precision in estimating μ_1-μ_2. We want to reject H_0 if $|\mu_1-\mu_2| > \delta$

Desired Type 1 & 2 Error levels:

$\alpha := 0.05$ < Type 1 error α

$\beta := 0.10$ < Type 2 error β

Initial Guess of Sample Size:

$N_0 := 100$ < Initial guess of sample sample size N needed.

Iterative Calculation:

$$N_1 := \frac{2 \cdot s_p^2}{\delta^2} \cdot \left[qt\left[\frac{\alpha}{2}, 2 \cdot (N_0 - 1)\right] + qt(\beta, N_0 - 1)\right]^2 \qquad N_1 = 44.20912$$

$$N_2 := \frac{2 \cdot s_p^2}{\delta^2} \cdot \left[qt\left[\frac{\alpha}{2}, 2 \cdot (N_1 - 1)\right] + qt(\beta, N_1 - 1)\right]^2 \qquad N_2 = 44.94591$$

< This process is continued until the value of N_i stabilizes. Then use the next largest interger value as an estimate of minimum sample size needed.

^ Note: input into the qt() function depends on whether the alternative hypotheses involve a one-sided or two-sided test. This example is a two-sided test. For a one-sided test, use α instead of $\alpha/2$.

Prototype in R:

```
#ESTIMATING SAMPLE SIZE FOR TWO SAMPLE T-TEST
#SET THE FOLLOWING VALUES AS DESIRED:
delta=0.5
alpha=0.05
beta=0.10
N0=100
#ITERATE THE FOLLOWING UNTIL N IS STABILIZED:
N1=(2*sp^2/delta^2)*(qt(alpha/2,2*(N0-1))+qt(beta,N0-1))^2
N1
N2=(2*sp^2/delta^2)*(qt(alpha/2,2*(N1-1))+qt(beta,N1-1))^2
N2
N3=(2*sp^2/delta^2)*(qt(alpha/2,2*(N2-1))+qt(beta,N2-1))^2
N3
N4=(2*sp^2/delta^2)*(qt(alpha/2,2*(N3-1))+qt(beta,N3-1))^2
N4
N5=(2*sp^2/delta^2)*(qt(alpha/2,2*(N4-1))+qt(beta,N4-1))^2
N5
```

Estimating Detectable Difference of a given Sample Size for a Two Sample t-Test:

For a given sample with size n, one can estimate $\delta = \mu_1 - \mu_2$ directly.

Desired Sample Size:

$N := 20$ **< set for desired sample size N**

Desired Type 1 & 2 Error levels:

$\alpha := 0.05$ **< Type 1 error α**

$\beta := 0.10$ **< Type 2 error β**

Calculation:

$$\delta := \sqrt{\frac{2 \cdot s_p^{\,2}}{N}} \cdot \left[qt\left[\frac{\alpha}{2}, 2 \cdot (N-1)\right] + qt\left[\beta, 2 \cdot (N-1)\right]\right]$$

$\delta = -0.7585216$ **< Note: sign of δ doesn't matter**

^ Note: input into the qt() function depends on whether the alternative hypotheses involve a one-sided or two-sided test. This example is a two-sided test. For a one-sided test, use α instead of $\alpha/2$.

Prototype in R:

```
#ESTIMATING DETECTABLE DIFFERENCE GIVEN N
#FOR ONE SAMPLE t-TEST
#SET THE FOLLOWING VALUES AS DESIRED:
N=20
alpha=0.05
beta=0.10

delta=sqrt(2*sp^2/N)*(qt(alpha/2,2*(N-1))+qt(beta,2*(N-1)))
delta
```

Estimating POWER of a Two Sample t-test:

POWER (1-β) of a test is the probability of properly rejecting H_0 when it is false. It is the converse of Type 2 error β. We would like POWER to be as high as possible.

Desired Sample Size:

$N := 15$ **< set for desired sample size N**

Desired Precision δ:

$\delta := 1.0$ **< Set as desired for precision in estimating μ_1-μ_2. We want to reject H_0 if $|\mu_1-\mu_2| > \delta$**

Desired Type 1 Error level:

$\alpha := 0.05$ **< Set Type 1 error α**

Calculation:

$$B := \frac{\delta}{\sqrt{\frac{2 \cdot s_p^{\,2}}{N}}} - \left| qt\left[\frac{\alpha}{2}, 2 \cdot (N-1)\right]\right| \qquad B = 1.751977$$

^ Note: absolute value used here to allow use of standard qt() function whereas Zar uses a *partial* table that only has positive values.

$POWER := pt[B, 2 \cdot (N-1)]$ $POWER = 0.9546375$ **< Exact calculation using pt() function**

$POWER_N := pnorm(B, 0, 1)$ $POWER_N = 0.960111$ **< Approximate calculation using pnorm() function assuming s=σ.**

^ POWER = (1-β)
Note use of the probability functions.

Prototype in R:

```
#ESTIMATING POWER OF TWO SAMPLE t-TEST
#SET THE FOLLOWING VALUES AS DESIRED:
N=15
delta=1.0
alpha=0.05

B=(delta/sqrt(2*sp^2/N))-abs(qt(alpha/2,2*(N-1)))
B
POWER=pt(B,2*(N-1))
POWER
POWERN=pnorm(B,0,1)
POWERN
```