

The Student t test

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1 Student t test Syntax

```
# Calculated using `t.test()`  
# x: sample data ; y: (optional) sample data  
# alternative: alternative hypothesis [two.sided, less, greater]  
#           default value = "two.sided"  
# mu: If one sample test -> true value of the mean  
#     If two sample test -> difference in means  
#     Default value = 0  
# paired: paired t-test, default value = FALSE  
  
# p-value output gotten from `$p.value`
```

2 Student t test Examples

```
# Example: One sample, two-sided test  
  
# Null: sample mean = 100  
# Alternative: sample mean != 100  
  
apples <- c(95, 104, 101, 100, 99, 102, 98, 94, 94, 93)  
t.test(apples, mu = 100)
```

```
##
## One Sample t-test
##
## data: apples
## t = -1.6514, df = 9, p-value = 0.133
## alternative hypothesis: true mean is not equal to 100
## 95 percent confidence interval:
## 95.26039 100.73961
## sample estimates:
## mean of x
## 98

# To specifically show the p-value alone
t.test(apples, mu = 100)$p.value

## [1] 0.133042

# Example: One sample, one-sided test

# Null: sample mean = 6.5
# Alternative: sample mean < 6.5

acid <- c(6.1, 6.4, 5.8, 5.8, 6.6, 5.3, 6.8, 6.4, 6.9, 5.8, 5.5, 6.3)
t.test(acid, mu = 6.5, alternative = "less")$p.value

## [1] 0.01643992

# Example: Two sample, one-sided test

# Null: vitC mean = plac mean
# Alternative: vitC mean < plac mean

vitC <- c(5.5, 6, 7, 6, 7.5, 6, 7.5, 5.5, 7, 6.5)
plac <- c(6.5, 6, 8.5, 7, 6.5, 8, 7.5, 6.5, 7.5, 6, 8.5, 7.0)

t.test(vitC, plac, alternative = "less")$p.value

## [1] 0.03428346

# Example: Paired t-test, one-sided test

# Paired t-test is used when there is a natural pairing between two populations.
```

```

# Null: patients_before mean = patients_after mean
# Alternative: patients_before mean < patients_after mean

patients_before <- c(24.2, 30.4, 32.7, 19.8, 25.1, 24.9, 22.2)
patients_after <- c(25.5, 31.2, 32.9, 20.4, 25.6, 24.7, 22.9)

t.test(patients_before, patients_after,
       alternative = "less", paired = TRUE)$p.value

## [1] 0.01025976

```

3 Confidence Interval of Sample

```

# Method 1:
# Gotten using `$conf.int`

# To calculate this:
# mu is left as 0
# no other parameters are set

heart <- c(66,73,72,80,84,60)
t.test(heart)$conf.int # 95% confidence interval by default

## [1] 63.26139 81.73861
## attr(,"conf.level")
## [1] 0.95

# Method 2:
# Calculate manually, if variance is known

loaves <- c(804, 804, 800, 797, 805, 800, 810, 803, 806, 800, 801, 802,
            800, 808, 806, 804, 810, 799, 804, 803, 805, 803, 804, 793, 808,
            810, 801, 802, 797, 802)

x_bar <- mean(loaves)
sd <- sd(loaves)
n <- length(loaves)
SEM <- sd/sqrt(n)
# For 95% confidence interval
f <- qnorm(0.975) # [100-95]/2 = 2.5% -> 100-2.5 = 97.5%

conf_int <- c(x_bar - f*SEM, x_bar + f*SEM)
conf_int

```

```
## [1] 801.6036 804.4631
```