

# Topic 18: $t$ Procedures

November 19, 2009

The  $z$ -score is

$$z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}}.$$

taken under the assumption that the population standard deviation is known.

If we are forced to replace the unknown  $\sigma$  with its unbiased estimator  $s$ , then the statistic is known as  $t$ :

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

The term  $s/\sqrt{n}$  which estimate the standard deviation of the sample mean is called the **standard error**.

The remarkable discovery by William Gossett is that the distribution of the  $t$  statistic can be determined **exactly**. Moreover, the  $t$  test is a likelihood ratio test. We will save showing this result into the last section and instead focus on the applications of this widely used set of procedures.

Write

$$T = \frac{\sqrt{n}(\bar{X} - \mu)}{S}.$$

Then,

- The numerator is a standard normal random variable.
- The denominator is the square root of

$$S^2 = \frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})^2.$$

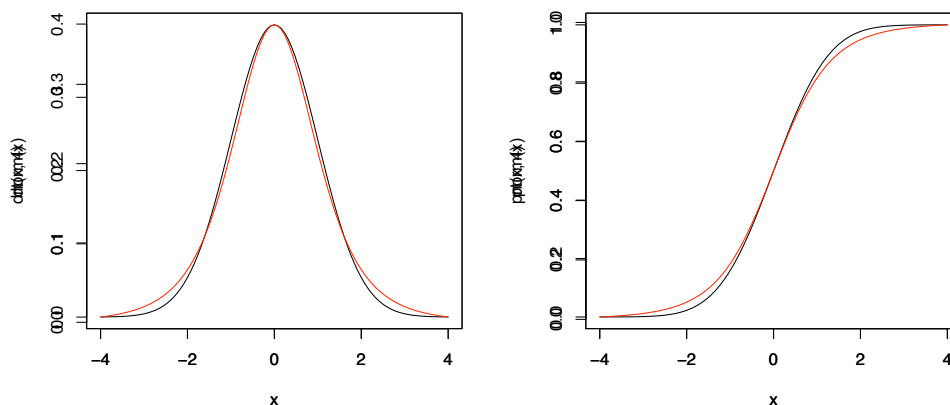
The sum is a chi-square random variable with  $n - 1$  degrees of freedom.

- The numerator and denominator are **independent**.

This is called the  $t$  distribution with  $n - 1$  degrees of freedom.

## 1 Guidelines for Using the $t$ Procedures

- Except in the case of small samples, the assumption that the data are a simple random sample from the population of interest is more important than the population distribution is normal.
- For sample sizes less than 15, use  $t$  procedures if the data are close to normal.
- For sample sizes at least 15m use  $t$  procedures except in the presence of outliers or strong skewness.
- The  $t$  procedures can be used even for clearly skewed distributions when the sample is large.



**Figure 1:** The density and distribution function for a standard normal random variable (black) and a  $t$  random variable with 4 degrees of freedom (red).

## 2 One Sample $t$ Tests

We will later explain that the likelihood ratio test for the two sided hypothesis test

$$H_0 : \mu = \mu_0 \quad \text{versus} \quad H_1 : \mu \neq \mu_0,$$

based on independent **normal** observations  $X_1, \dots, X_n$  with unknown mean  $\mu$  and **unknown** variance  $\sigma^2$  is a  $t$ -test.

So, compute the  $t$  statistic  $T(\mathbf{x})$  from the data  $\mathbf{x}$ . Then, the critical region

$$C = \{|T(\mathbf{x})| > t_{n-1, \alpha/2}\}.$$

Where  $t_{n-1, \alpha/2}$  is the upper  $\alpha/2$  tail probability of the  $t$  distribution with  $n - 1$  degrees of freedom.

**Example 1.** To check the reliability of radon detector, a university placed 12 detectors in a chamber having 105 picocuries of radon. The two sided hypothesis test

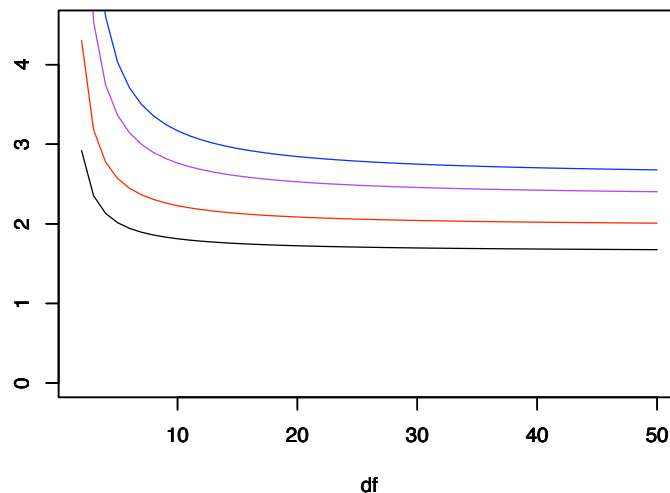
$$H_0 : \mu = 105 \quad \text{versus} \quad H_1 : \mu \neq 105,$$

The detector readings were:

91.9 97.8 111.4 122.3 105.4 95.0 103.8 99.6 96.6 119.3 104.8 101.7

Our basic issue is the loss of vitamin C contain R, we find

```
> radon<-c(91.9, 97.8, 111.4, 122.3, 105.4, 95.0, 103.8, 99.6, 96.6, 119.3, 104.8, 101.7)
> hist(radon)
> mean(radon)
[1] 104.1333
> sd(radon)
[1] 9.39742
> length(radon)
[1] 12
> qt(0.975, 11)
[1] 2.200985
```



**Figure 2:** Critical values for the two sided  $t$  test with  $\alpha = 0.10, 0.05, 0.02$ , and  $0.01$

Thus, the  $t$ -statistic is

$$t = \frac{105 - 104.1333}{9.39742/\sqrt{12}} = -0.3195.$$

Thus, for a 5% significance test,  $|t| < 2.200985$ , the critical value and we fail to reject  $H_0$ .

```
> t.test(radon, alternative=c("two.sided"), mu=105)
```

One Sample t-test

```
data: radon
t = -0.3195, df = 11, p-value = 0.7554
alternative hypothesis: true mean is not equal to 105
95 percent confidence interval:
 98.1625 110.1042
sample estimates:
mean of x
104.1333
```

The output also gives the 95% confidence interval

$$\bar{x} \pm \frac{s}{\sqrt{n}} t_{0.025, 11}.$$

The power against an alternative of 110 is

```
> power.t.test(n=12, delta=5, sd=sd(radon), type=c("one.sample"))
```

One-sample t test power calculation

```
      n = 12
  delta = 5
     sd = 9.39742
```

```
sig.level = 0.05
power = 0.3907862
alternative = two.sided
```

*If we want 80% power against an alternative of 110, then we need to make 30 measurements.*

```
> power.t.test(power=0.80, delta=5, sd=sd(radon), type=c("one.sample"))
```

One-sample t test power calculation

```
n = 29.70383
delta = 5
sd = 9.39742
sig.level = 0.05
power = 0.8
alternative = two.sided
```

### 3 Matched Pairs Procedure

A **matched pair procedure** is called for when a pair of quantitative measurements from a simple random sample

$$X_1, X_2, \dots, X_n, \quad \text{and} \quad Y_1, Y_2, \dots, Y_n$$

are made on the same subjects.

The null hypothesis says that the two populations are the same

$$H_0 : \mu_X = \mu_Y$$

The alternative can be either one-sided or two sided. Underlying this assumption is that the populations are the same under the null hypothesis. In particular, the standard deviations, although unknown, are equal.  $\sigma_X = \sigma_Y = \sigma$ .

Thus, when  $H_0$  holds

$$E[\bar{X} - \bar{Y}] = \mu_X - \mu_Y \quad \text{and} \quad \text{Var}(\bar{X} - \bar{Y}) = \text{Var}(\bar{X}) + \text{Var}(\bar{Y}) = \frac{\sigma^2}{n} + \frac{\sigma^2}{n} = \frac{2\sigma^2}{n}.$$

In addition, if the data are normal, then  $\bar{X} - \bar{Y}$  is also and so

$$T = \frac{\bar{X} - \bar{Y}}{S_{X-Y}/\sqrt{n}}$$

has a  $t$  distribution with  $n - 1$  degrees of freedom.

The  $\gamma$ -level confidence interval for the difference in the population means is

$$\bar{x} - \bar{y} \pm \frac{s_{X-Y}}{n} t_{(1-\gamma)/2, n-1}.$$

**Example 2.** *Researchers are concerned about the impact of vitamin C content reduction due to and storage and shipment. To test this, researchers randomly chose a collection of bags of wheat soy blend bound for Haiti, marked them, and measured vitamin C from a sample of the contents. Five months later, the bags were opened and a second sample was measured for vitamin C content. The units are mg/100g.*

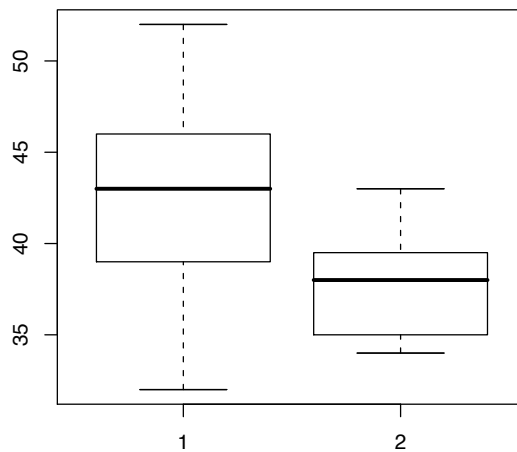
| Factory | Haiti | Factory | Haiti | Factory | Haiti | Factory | Haiti |
|---------|-------|---------|-------|---------|-------|---------|-------|
| 44      | 40    | 45      | 38    | 39      | 43    | 50      | 37    |
| 50      | 37    | 32      | 40    | 52      | 38    | 40      | 34    |
| 48      | 39    | 47      | 35    | 45      | 38    | 39      | 38    |
| 44      | 35    | 40      | 38    | 37      | 38    | 39      | 34    |
| 42      | 35    | 38      | 34    | 38      | 41    | 37      | 40    |
| 47      | 41    | 41      | 35    | 44      | 40    | 44      | 36    |
| 49      | 37    | 40      | 34    | 43      | 35    |         |       |

*Here is the R output with the 95% confidence interval.*

```
> factory<-c(44, 50, 48, 44, 42, 47, 49, 45, 32, 47, 40, 38, 41, 40, 39, 52, 45, 37, 38, 44, 43, 50, 40, 39, 39, 37,
> haiti<-c(40, 37, 39, 35, 35, 41, 37, 38, 40, 35, 38, 34, 35, 34, 43, 38, 38, 38, 41, 40, 35, 37, 34, 38, 34, 40, 3
> boxplot(factory, haiti)
> t.test(factory, haiti, alternative = c("two.sided"), mu = 0, paired = TRUE)
```

Paired t-test

```
data: factory and haiti
t = 4.9589, df = 26, p-value = 3.745e-05
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 3.122616 7.544050
sample estimates:
mean of the differences
          5.333333
```



**Figure 3:** Vitamin C content in milligrams per 100 grams, measured at the factory and measured 5 month later in Haiti.

*The input*

```
> t.test(factory - haiti, alternative = c("two.sided"), mu = 0)
```

*gives essentially the same output.*

*In addition, the output*

```
> t.test(haiti, alternative = c("less"), mu = 40)
```

One Sample t-test

```

data: haiti
t = -5.3232, df = 26, p-value = 7.175e-06
alternative hypothesis: true mean is less than 40
95 percent confidence interval:
  -Inf 38.23811
sample estimates:
mean of x
  37.40741

```

shows that we would reject the one sided test

$$H_0 : \mu \geq 40 \quad \text{versus} \quad H_1 : \mu < 40,$$

based on a goal of having 40mg/100g vitamin C in the wheat consumed by the Haitians.

## 4 Two Sample Procedures

Now we consider the situation in which the two samples

$$X_1, X_2, \dots, X_{n_X}, \quad \text{and} \quad Y_1, Y_2, \dots, Y_{n_Y}$$

are not paired.

If the first sample has common mean  $\mu_X$  and variance  $\sigma_X^2$  and the second sample has common mean  $\mu_Y$  and variance  $\sigma_Y^2$ , then

$$E[\bar{X} - \bar{Y}] = \mu_X - \mu_Y \quad \text{and} \quad \text{Var}(\bar{X} - \bar{Y}) = \frac{\sigma_X^2}{n_X} + \frac{\sigma_Y^2}{n_Y}.$$

For the two sided hypothesis test

$$H_0 : \mu_X = \mu_Y \quad \text{versus} \quad H_1 : \mu_X \neq \mu_Y,$$

The corresponding  $t$ -statistic is

$$t = \frac{\bar{x} - \bar{y}}{\sqrt{\frac{s_X^2}{n_X} + \frac{s_Y^2}{n_Y}}}$$

with  $s_X^2$  and  $s_Y^2$  the unbiased sample variances. The distribution is not a  $t$  distribution. However, its tails can be approximated using an ordinary Student's  $t$  distribution with the degrees of freedom  $\nu$  calculated using the **Welch-Satterthwaite** equation:

$$\nu = \frac{(s_X^2/n_X + s_Y^2/n_Y)^2}{(s_X^2/n_X)^2/(n_X - 1) + (s_Y^2/n_Y)^2/(n_Y - 1)}.$$

This also gives a  $\gamma$ -level confidence interval for the difference in the means  $\mu_x$  and  $\mu_y$ .

$$\bar{x} - \bar{y} \pm t_{(1-\gamma)/2, \nu} \sqrt{\frac{s_X^2}{n_X} + \frac{s_Y^2}{n_Y}}.$$

**Example 3.** To investigate the effect on blood pressure of added calcium in the diet, a researchers conducts a double blind randomized experiment. In the treatment group, each individual receives a calcium supplement. In the control group, the individual takes a placebo. The response variable is the decrease in systolic blood pressure, measured in millimeters of mercury, after 12 weeks. The test subjects are all male.

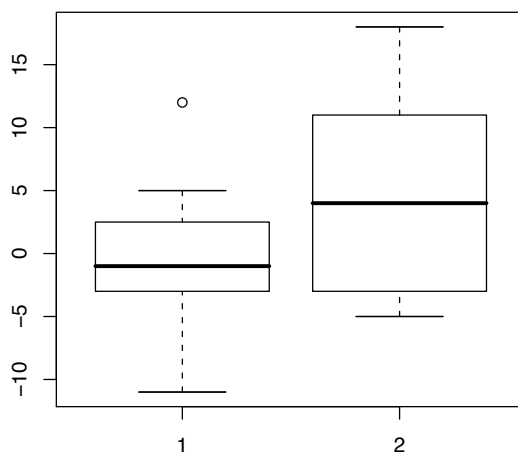
```

> calcium<-c(7,-4,18,17,-3,-5,1,10,11,-2)
> mean(calcium)
[1] 5
> sd(calcium)
[1] 8.743251
> placebo<-c(-1,12,-1,-3,3,-5,5,2,-11,-1,-3)
> mean(placebo)
[1] -0.2727273
> sd(placebo)
[1] 5.900693
> boxplot(placebo,calcium)

```

The null hypothesis is that the treatment did not reduce  $\mu_t$  the mean blood pressure of the treatment any more than it did the mean  $\mu_c$  for the control group. The alternative is that it did reduce blood pressure more. Formally the hypothesis test is

$$H_0 : \mu_c \leq \mu_t \quad \text{versus} \quad H_1 : \mu_c > \mu_t.$$



The *t*-statistic is

$$t = \frac{5.000 + 0.273}{\sqrt{\frac{8.743^2}{10} + \frac{5.901^2}{11}}} = 1.604.$$

```

> t.test(calcium,placebo,alternative = c("greater"))

```

Welch Two Sample t-test

```

data: calcium and placebo
t = 1.6037, df = 15.591, p-value = 0.06442
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
-0.476678      Inf

```

```
sample estimates:
mean of x  mean of y
5.0000000 -0.2727273
```

Thus, the evidence against the null hypothesis is modest with a  $p$ -value of about 6%.  
To see a 90% confidence interval

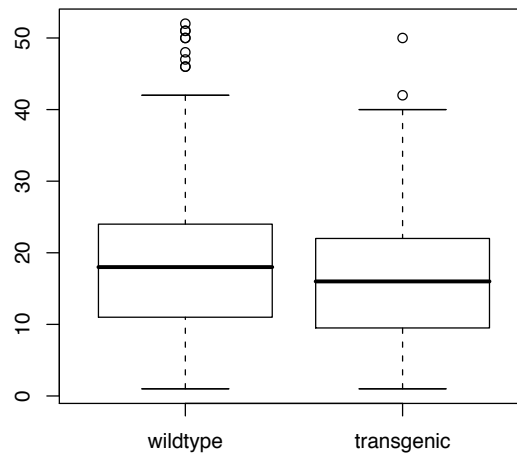
```
> t.test(calcium,placebo,conf.level = 0.9)
```

Welch Two Sample t-test

```
data:  calcium and placebo
t = 1.6037, df = 15.591, p-value = 0.1288
alternative hypothesis: true difference in means is not equal to 0
90 percent confidence interval:
 -0.476678 11.022133
sample estimates:
mean of x  mean of y
5.0000000 -0.2727273
```

**Example 4.** The life span in days of 88 wildtype and 99 transgenic mosquitoes is given in the following data set.

```
> mosquitoes<-read.delim("http://math.arizona.edu/~jwatkins/mosquitoes.txt")
> boxplot(mosquitoes)
```



The goal is to see if overstimulation of the insulin signaling cascade in the mosquito midgut reduces the  $\mu_t$ , the mean life span of these transgenic mosquitoes from that of the wild type  $\mu_{wt}$ .

$$H_0 : \mu_{wt} \leq \mu_t \quad \text{versus} \quad H_1 : \mu_{wt} > \mu_t.$$



```
> wildtype<-mosquitoes[1:88,1]
> transgenic<-mosquitoes[,2]
> t.test(transgenic,wildtype,alternative = c("less"))
```

Welch Two Sample t-test

```
data: transgenic and wildtype
t = -2.4106, df = 169.665, p-value = 0.008497
alternative hypothesis: true difference in means is less than 0
95 percent confidence interval:
 -Inf -1.330591
sample estimates:
mean of x mean of y
 16.54545  20.78409
```

```
> t.test(transgenic,wildtype,conf.level=0.98)
```

Welch Two Sample t-test

```
data: transgenic and wildtype
t = -2.4106, df = 169.665, p-value = 0.01699
alternative hypothesis: true difference in means is not equal to 0
98 percent confidence interval:
 -8.3680812 -0.1091915
sample estimates:
mean of x mean of y
 16.54545  20.78409
```

## 5 A Note on the Delta Method

For a one sample test hypothesizing a value for  $g(\mu)$ , we use the  $t$  statistic

$$t = \frac{g(\bar{x}) - g(\mu_0)}{|g'(\bar{x})|s/\sqrt{n}}$$

and base the test on the  $t$  distribution with  $n - 1$  degrees of freedom.

For a test that compare a function of the mean of a two samples  $g(\mu_X)$  and  $g(\mu_Y)$  we can use the test statistic

$$t = \frac{g(\bar{x}) - g(\bar{y})}{\sqrt{\frac{(g'(\bar{x})s_X)^2}{n_X} + \frac{(g'(\bar{y})s_Y)^2}{n_Y}}}$$

The degrees of freedom  $\nu$  can be computed from the Welch-Satterthwaite equation specialized to this circumstance.

$$\nu = \frac{(g(\bar{x})s_X)^2/n_X + (g(\bar{y})s_Y)^2/n_Y}{((g'(\bar{x})s_X)^2/n_X)^2/(n_X - 1) + ((g'(\bar{y})s_Y)^2/n_Y)^2/(n_Y - 1)}$$

## 6 The $t$ Test as a Likelihood Ratio Test

Again, we begin with independent normal observations  $X_1, \dots, X_n$  with unknown mean  $\mu$  and unknown variance  $\sigma^2$ . The likelihood function

$$L(\mu, \sigma^2 | \mathbf{x}) = \frac{1}{(2\pi\sigma^2)^{n/2}} \exp -\frac{1}{2\sigma^2} \sum_{i=1}^n (x_i - \mu)^2$$

$$\ln L(\mu, \sigma^2 | \mathbf{x}) = -\frac{n}{2}(\ln 2\pi + \ln \sigma^2) - \frac{1}{2\sigma^2} \sum_{i=1}^n (x_i - \mu)^2$$

$$\frac{\partial}{\partial \mu} \ln L(\mu, \sigma^2 | \mathbf{x}) = -\frac{1}{\sigma^2} \sum_{i=1}^n (x_i - \mu)$$

Thus,  $\hat{\mu} = \bar{x}$ .

$$\frac{\partial}{\partial \sigma^2} \ln L(\mu, \sigma^2 | \mathbf{x}) = -\frac{n}{2\sigma^2} + \frac{1}{2(\sigma^2)^2} \sum_{i=1}^n (x_i - \mu)^2.$$

Thus,

$$\hat{\sigma}^2 = \frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})^2.$$

For the hypothesis

$$H_0 : \mu = \mu_0 \quad \text{versus} \quad H_1 : \mu \neq \mu_0,$$

the **likelihood ratio test**

$$\Lambda(x) = \frac{L(\mu_0, \hat{\sigma}_0^2 | \mathbf{x})}{L(\hat{\mu}, \hat{\sigma}^2 | \mathbf{x})}$$

where the value

$$\hat{\sigma}_0^2 = \frac{1}{n} \sum_{i=1}^n (x_i - \mu_0)^2$$

gives the maximum likelihood on the set  $\mu = \mu_0$ .

$$L(\mu_0, \hat{\sigma}_0^2 | \mathbf{x}) = \frac{1}{(2\pi \hat{\sigma}_0^2)^{n/2}} \exp -\frac{1}{2\hat{\sigma}_0^2} \sum_{i=1}^n (x_i - \mu_0)^2 = \frac{1}{(2\pi \hat{\sigma}_0^2)^{n/2}} \exp -\frac{2}{n},$$

$$L(\hat{\mu}, \hat{\sigma}^2 | \mathbf{x}) = \frac{1}{(2\pi \hat{\sigma}^2)^{n/2}} \exp -\frac{1}{2\hat{\sigma}^2} \sum_{i=1}^n (x_i - \bar{x})^2 = \frac{1}{(2\pi \hat{\sigma}^2)^{n/2}}, \exp -\frac{2}{n},$$

and

$$\Lambda(x) = \left( \frac{\hat{\sigma}^2}{\hat{\sigma}_0^2} \right)^{n/2} = \left( \frac{\sum_{i=1}^n (x_i - \mu_0)^2}{\sum_{i=1}^n (x_i - \bar{x})^2} \right)^{-n/2}$$

The critical region  $\lambda(\mathbf{x}) \leq \lambda_0$  is equivalent to

$$c \leq \frac{\sum_{i=1}^n (x_i - \mu_0)^2}{\sum_{i=1}^n (x_i - \bar{x})^2} = 1 + \frac{n(\bar{x} - \mu_0)^2}{\sum_{i=1}^n (x_i - \bar{x})^2}$$

or

$$T(x)^2 \geq (c - 1)(n - 1)$$

where

$$T(x) = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

and we write  $s$  for the square root of the *unbiased* estimator of the variance

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