

Topic 20

t Procedures

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Matched Pairs Procedures

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 alternative can be either one-sided or two-sided. Underlying this assumption is that the populations are the same under the null hypothesis.

Thus, when H_0 holds and if in addition, if the data are **normal**, then $\bar{X} - \bar{Y}$ is also normal and so

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

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

Vitamin C Reduction

- Researchers are concerned about the impact of **vitamin C** content reduction due to 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 milligrams of vitamin C per **100g** of wheat soy blend.

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		



Vitamin C Reduction

Because we are concerned that the vitamin C is *reduced*, we use the hypothesis

$$H_0 : \mu_F \leq \mu_H \quad \text{versus} \quad H_1 : \mu_F > \mu_H$$

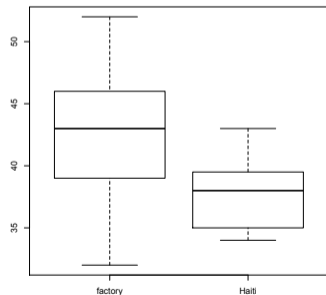
where μ_F and μ_H are the mean amount of vitamin C for the wheat soy blend for, respectively, at the factory and in Haiti.

```
> t.test(factory, haiti, alternative
= c("greater"), mu = 0, paired = TRUE)
```

Paired t-test

```
data: factory and haiti t = 4.9589,
df = 26, p-value = 1.872e-05
alternative hypothesis: true
difference in means is greater than 0
```

Note the very low *p*-value.



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 **independent** but are **not paired**. If the first sample has common mean μ_X and variance σ_X^2 and the second sample has common mean μ_Y and variance σ_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

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

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.

Two Sample Procedures

- Unlike the match pairs procedures, this test statistic does *not* have a t distribution under the null hypothesis.
- We make what is commonly known in statistics as a *conservative* approximation.
 - We replace the actual distribution of the t statistic in with one which has slightly bigger tails.
- Thus, the computed p -value which are just integrals of the density function will be slightly larger.
- In this way, a conservative procedures is one that does not decrease the **type I error** probability.

This goal can be accomplished with Student's t distribution with the **effective degrees of freedom** ν calculated using the **Welch-Satterthwaite** equation:

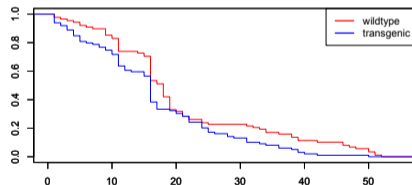
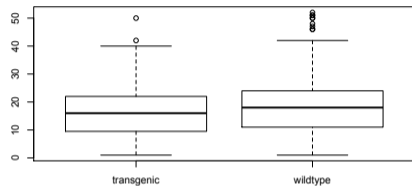
$$\nu = \frac{(s_X^2/n_X + s_Y^2/n_Y)^2}{(s_X^2/n_X)^2/(n_X - 1) + (s_Y^2/n_Y)^2/(n_Y - 1)}$$

Mosquito Life Span

Anopheles mosquitoes are the carrier of parasitic protozoans of the genus *Plasmodium*. The blood obtained from a bite from a female mosquito is used as a source of protein for the production of eggs. In this way inflected mosquitoes transmit malaria to humans.

We test to see if overstimulation of the insulin signaling cascade in the midgut of transgenic mosquitoes reduces the μ_t , the mean life span of these transgenic mosquitoes from that of the wildtype μ_{wt} .

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



Boxplot and survival function of lifespan in days for transgenic and wildtype mosquitoes.

Mosquito Life Span

R easily handles the analysis.

```
> 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
```

NB. the number of degrees of freedom $\nu = 169.665$.

Mosquito Life Span

Exercise. For the data set on the lifespan of transgenic and wildtype mosquitoes,

- modify the commands in `t.test` to find a 98% confidence interval for the difference $\mu_t - \mu_{wt}$.
- Notice that the 98% confidence interval does not contain 0. What can be said about a two-sided test at the 2% significance level?
- Based on this information, what can be said about the p -value for a one-sided test?

Much of our inference has been for **population proportions** and the **population means**. Our methods are sometimes reserved for those cases in which the **central limit theorem** applies and thus the estimates, the sample proportions and the sample means, have approximately a **normal distribution**.

General Guidelines

- Hypotheses are stated in terms of a *population parameter*.
- The **null hypothesis** H_0 is a statement that no effect is present.
- The **alternative hypothesis** H_1 is a statement that a parameter differs from its null value in a **specific direction** (one-sided alternative) or in **either direction** (two-sided alternative).
- A **test statistic** is designed to assess the strength of evidence against H_0 .
- If a decision must be made, specify the **significance level** α .
- Assuming H_0 is true, the **p -value** is the probability that the test statistic would take a value **as extreme or more extreme** than the value observed.
- If the **p -value** is **smaller** than the significance level α , then H_0 is **rejected** and the data are said to be **statistically significant at level** α .

Tests for Population Proportion

The design is based on **Bernoulli trials**. For this we have

- A fixed **number** of trials n .
- The **outcome** of each trial is **independent** of the other trials.
- Each trial has one of two outcomes **success** and **failure**.
- The **probability of success** p is the same for each trial.
- This **test statistic** is the z -score and thus is based the applicability of the central limit theorem on using the **standard normal distribution**.
 - This procedure is considered valid is the sample is small ($< 10\%$) compared to the total population and both np_0 and $n(1 - p_0)$ is at least **10**.
- For **small sample sizes**, use the **number of successes** and **binomial distribution** directly for the **test statistic**.

Test for Population Proportion

The statistics \hat{p} for a one-sample procedure and \hat{p}_1, \hat{p}_2 for a two-sample procedure are the appropriate proportions of success.

	null hypothesis		
sample proportions	one-sided	two-sided	test statistic
single proportion	$H_0 : p \geq p_0$ $H_0 : p \leq p_0$	$H_0 : p = p_0$	$z = \frac{\hat{p} - p_0}{\sqrt{p_0(1-p_0)/n}}$
two proportions	$H_0 : p_1 \geq p_2$ $H_0 : p_1 \leq p_2$	$H_0 : p_1 = p_2$	$z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})(\frac{1}{n_1} + \frac{1}{n_2})}}$

The pooled sample proportion $\hat{p} = (x_1 + x_2)/(n_1 + n_2)$ where x_i is the number of successes in the n_i Bernoulli trials from group i .

Tests for Population Means

- Use the z -statistic when the standard deviations are known.
- Use the t -statistic when the standard deviations are computed from the data.

	null hypothesis	
t or z -procedure	one-sided	two-sided
single sample	$H_0 : \mu \leq \mu_0$ $H_0 : \mu \geq \mu_0$	$H_0 : \mu = \mu_0$
two samples	$H_0 : \mu_1 \leq \mu_2$ $H_0 : \mu_1 \geq \mu_2$	$H_0 : \mu_1 = \mu_2$

Tests for Population Means

The test statistic,

$$t = \frac{\text{estimate} - \text{parameter}}{\text{standard error}}.$$

<i>t</i> -procedure	parameter	estimate	standard error	degrees of freedom
one sample	μ	\bar{x}	$\frac{s}{\sqrt{n}}$	$n - 1$
two sample	$\mu_1 - \mu_2$	$\bar{x}_1 - \bar{x}_2$	$\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$	ν in W-S equation
pooled two sample	$\mu_1 - \mu_2$	$\bar{x}_1 - \bar{x}_2$	$s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$	$n_1 + n_2 - 2$

For one-sample and two-sample *z* procedures, replace the values *s* with σ and s_1 and s_2 with σ_1 and σ_2 , respectively. Use the normal distribution for these tests.