

R HELP SHEET: Paired *t*-test

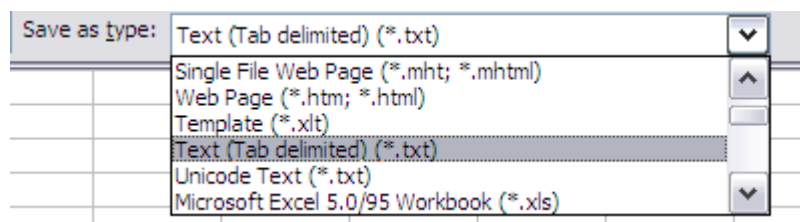
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1. Creating a tab delimited data file using Excel

Open Excel and type the data in to two columns with an appropriate heading at the top of each column (e.g., *id*, *percgr.wo*, *percgr.w*), then save the file as a **Text (Table delimited)(*.txt)** with an appropriate name (e.g., *RData_Ewes*) file using **Save as type**.

| | A | B | C |
|----|-----|-----------|----------|
| 1 | id | percgr.wo | percgr.w |
| 2 | 10 | 72 | 55.5 |
| 3 | 168 | 62.35 | 43.8 |
| 4 | 227 | 55.77 | 66.8 |
| 5 | 801 | 59.98 | 68 |
| 6 | 805 | 51.6 | 57.88 |
| 7 | 820 | 61.48 | 61.9 |
| 8 | 823 | 52.57 | 45.4 |
| 9 | 837 | 52.5 | 56.67 |
| 10 | 842 | 56.43 | 73.3 |
| 11 | 853 | 60.13 | 77.5 |
| 12 | 864 | 48.6 | 63.53 |
| 13 | 883 | 42.9 | 54.5 |
| 14 | 899 | 53.5 | 55.8 |
| 15 | 945 | 70.43 | 91.1 |
| 16 | 953 | 47.1 | 64.05 |
| 17 | 967 | 50.08 | 71.4 |



2. Conducting a paired *t*-test

The text in green after the hash (#) sign is just **notes** to help you remember what's in the output: it does not get R to actually "do" anything. The text in blue is **R code** with words in *italics* (e.g., *percgr.wo*, *percgr.w*) specific to the example data from the Biomeasurement textbook.

To get R to conduct a paired *t*-test:

Open an **R-Editor** window by selecting **File** then **New script**.

Type in (or copy and paste) the notes and code below.

Replace the stars with appropriate text as indicated in notes.

Highlight everything and press **Ctrl R**.

#Importing data from tab delimited file

#(replace stars with an appropriate object name e.g., ewes)

******<-read.table(file.choose(),header=TRUE)**

attach(**)**

names(**)**

#Conducting a paired t-test (replace stars with sample labels e.g., percgr.wo,percgr.w)

t.test(***, *****,paired=TRUE)**

3. Identifying the key elements of the output

Following the instructions above will produce the following output in the R Console window: the **key elements** are annotated in blue.

```
> #Importing data from tab delimited file (replace stars with file name)
> ewes<-read.table(file.choose(),header=TRUE)
> attach(ewes)
  id, percgr_w, percgr_wo
> names(ewes)
[1] "id"      "percgr_wo" "percgr_w"
>
> #Conducting a paired t-test (replace stars with sample labels)
> t.test(percgr_wo,percgr_w,paired=TRUE)
```

Paired t-test

data: percgr_wo and percgr_w
t = -2.2261, df = 15, p-value = 0.04176
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-13.4208576 -0.2916424
sample estimates:
mean of the differences
-6.85625

Statistic (t) **Degrees of Freedom** **P Value**

95% CI of Effect size

Effect size

In summary the key information from the test is

$t_{15} = -2.23$, $P = 0.042$

And the unstandardized effect size (estimated difference between the populations) is **difference (without-with) = -6.86, 95% CI [-13.421, -0.292]**

4. Additional notes

- Notice the full stops in the labels "*pergr.w*" and "*pergr.wo*": you must not have a space.
- The column of numbers label "id" is just for reference and not involved in the calculations.