

R HELP SHEET: Wilcoxon signed-rank test

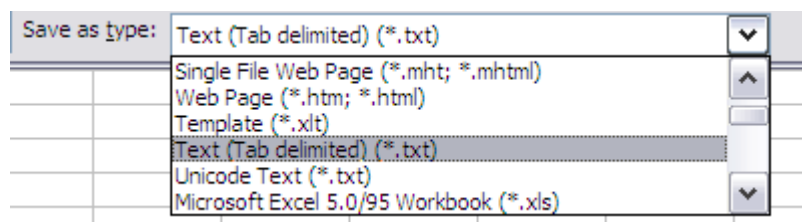
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1. Creating a tab delimited data file using Excel

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**. (Note use of full stops rather than spaces row headings.)

	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 Wilcoxon signed-rank 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 Wilcoxon signed-rank 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 Wilcoxon Matched Pairs test

#(replace stars with sample labels e.g., percgr.wo, percgr.w)

wilcox.test(***, *****,paired=TRUE,conf.int=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 orange.

```

> #Importing data from tab delimited file
> #(replace stars with an appropriate object name e.g., ewes )
> ewes<-read.table(file.choose(),header=TRUE)
> attach(ewes)
  id, percgr.w, percgr.wo
> names(ewes)
[1] "id"      "percgr.wo" "percgr.w"
>
> #Conducting a Wilcoxon Matched Pairs test
> #replace stars with sample labels e.g., pergr_wo, pergr_w)
> wilcox.test(percgr.wo,percgr.w,paired=TRUE,conf.int=TRUE)

      Wilcoxon signed rank test

data:  percgr.wo and percgr.w
V = 29, p-value = 0.04431
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -14.235 -0.185
sample estimates:
(pseudo)median
  -8.63

```

Statistic (T)
P Value

95% CI of Effect
Effect Size

NB: R reports only one T value and the order of the samples are listed determines which one. It's not clear if this is T+ or T- since, for example, without-with T=107, T+=29 but with-without T= 29, T+=107.

In summary the key information from the test is

T=29, n=16, N=16, P=0.044

And the unstandardized effect size (estimated difference between the populations) is

difference (without-with) = -8.63, 95% CI [-14.235, -0.185]

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.
- To find the sample sizes n (the number of pairs) and N (number of pairs that are not the same i.e., the difference is zero) use the following code:

```

# Code for the number of pairs (n):
length(*****)
For example: length(percgr.wo)

```

```

# Code for the number of pairs for which the difference is 0 (N)
length(*****==*****)
For example: length(percgr.wo==percgr.w)

```