

## R HELP SHEET: Kruskal-Wallis test

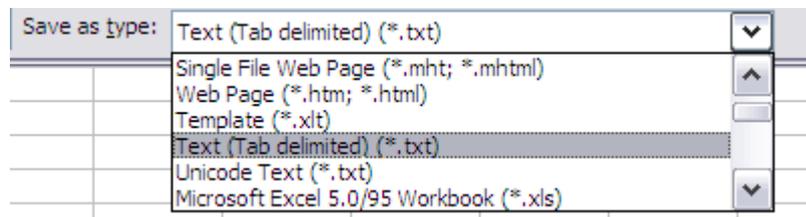
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#### 1. Creating a tab delimited data file using Excel

Open Excel and type data from your dependent variable into one column and data from your independent variable into another column with appropriate headings at the top of each column (e.g., *site*, *nitrogen*) then save the file as a **Text (Table delimited)(\*.txt)** with an appropriate name (e.g., *RData\_Reedbeds*) file using **Save as type**.

|    | A    | B        |
|----|------|----------|
| 1  | site | nitrogen |
| 2  | 1    | 2.92     |
| 3  | 1    | 2.88     |
| 4  | 1    | 3.25     |
| 5  | 1    | 2.64     |
| 6  | 1    | 3.28     |
| 7  | 2    | 3.06     |
| 8  | 2    | 2.6      |
| 9  | 2    | 2.55     |
| 10 | 2    | 2.42     |
| 11 | 2    | 2.35     |
| 12 | 3    | 3.41     |
| 13 | 3    | 3.23     |
| 14 | 3    | 3.93     |
| 15 | 3    | 3.74     |
| 16 | 3    | 3.18     |



(Note this example has site coded as numbers 1, 2 and 3 but it could also be written in words e.g., Site1, Site2, Site3).

#### 2. Conducting an Kruskal-Wallis Anova

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 stars representing words that are specific to the example: you need to replace this with text specific to your data as shown in the output in section 3.

To get R to conduct an Anova:

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 e.g., reeds )

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

```
attach(*****)
```

```
names(*****)
```

#Conducting a Kruskal-Wallis Anova

\*(replace stars with appropriate text e.g. ,nitrogen,site)

```
kruskal.test(*****~*****)
```

### 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.,reeds)
> reeds<-read.table(file.choose(),header=TRUE)
> attach(reeds)
> names(reeds)
[1] "site" "nitrogen"

> #Conducting a Kruskal-Wallis Anova
> #(replace stars with appropriate text e.g., nitrogen,site)
> kruskal.test(nitrogen~site)

Kruskal-Wallis rank sum test

data: nitrogen by site
Kruskal-Wallis chi-squared = 9.26, df = 2, p-value = 0.009755
```



In summary the key information from the test is  
 **$X^2=9.26$ ,  $n_1=5$ ,  $n_2=5$ ,  $n_3=5$ ,  $P=0.010$**

### 4. Additional note

To find the sample sizes  $n_1$ ,  $n_2$  and  $n_3$  use the following code:

```
#To find sample sizes
```

```
tapply(*****,*****,length)
```

For example: `tapply(site,site,length)`