

## R HELP SHEET: Spearman correlation

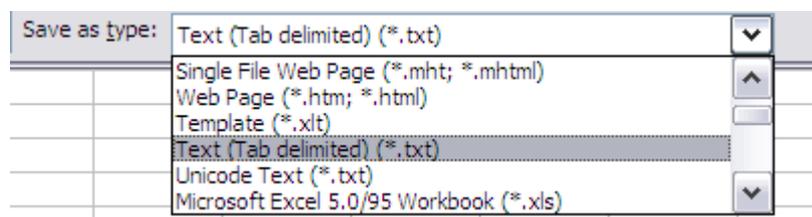
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#### 1. Creating a tab delimited data file using Excel

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., *id*, *eye*, *blood*), then save the file as a **Text (Table delimited)(\*.txt)** with an appropriate name (e.g., *RData\_EyeBlood*) file using **Save as type**.

	A	B	C
1	id	eye	blood
2		1	15.3
3		2	11.3
4		3	17.3
5		4	14.4
6		5	15.1
7		6	18.6
8		7	18.1
9		8	21.7
10		9	13.8
11		10	9.2
12		11	7.5
13		12	22.7
14		13	15.8
15		14	15.6
16		15	15.7
17		16	12.3
18		17	22.3
19		18	12.3
20		19	18.2
21		20	10.1



#### 2. Conducting an Spearman correlation

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 a Spearman correlation:

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., eye.blood)**

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

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

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

**#Conducting a Spearman correlation**

**\*(replace stars with appropriate text e.g., eye,blood)**

```
cor.test (**, ****,method="spearman")
```

### 3. Identifying the key elements of the output

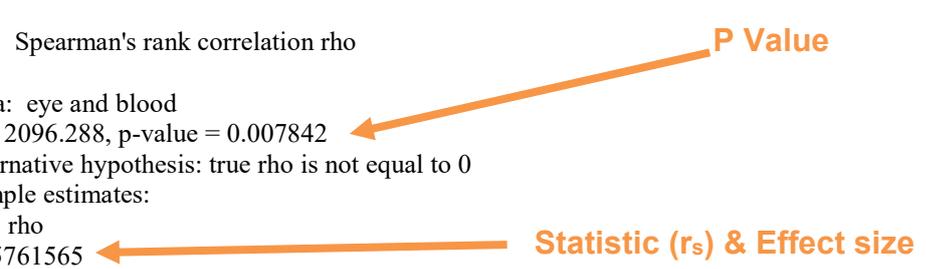
Following the instructions above will produce the following output in the **R Console** window: the **key elements** are annotated in orange.

```
> #Importing data from tab delimited file
> #(replace stars with an appropriate object name e.g.,eyes)
> eye.blood<-read.table(file.choose(),header=TRUE)
> attach(eye.blood)
> names(eye.blood)
[1] "id" "eye" "blood"
>
>> #Conducting a Spearman correlation
> #(replace stars with appropriate text e.g. eye,blood)
> cor.test(eye,blood,method="spearman")

Spearman's rank correlation rho

data: eye and blood
S = 2096.288, p-value = 0.007842
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
-0.5761565

Warning message:
In cor.test.default(eye, blood, method = "spearman") :
  Cannot compute exact p-values with ties
```



In summary the key information from the test is  
 **$r_s = -0.576$ ,  $N = 20$ ,  $P = 0.002$**

### 4. Additional notes

- Notice the full stop in “eye.blood”: 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) use the following code:

# Finding the number of pairs (N):

length(\*\*\*\*\*)

For example: length(eye)