MetaNSUE tutorial, version Dec 2018

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The aim of this tutorial is to show how to conduct a meta-analysis using MetaNSUE software, using either the Graphical User Interface (for non-R meta-analysts) or the R package. To this end, you will perform some of the analyses conducted in:

Albajes-Eizagirre A, Solanes A and Radua J. Meta-analysis of non-statistically significant unreported effects. *Stat Methods Med Res, in Press* https://doi.org/10.1177/0962280218811349.

Note that we distribute this tutorial in the hope that it will be useful, but without any warranty on the accuracy of the text or the data.
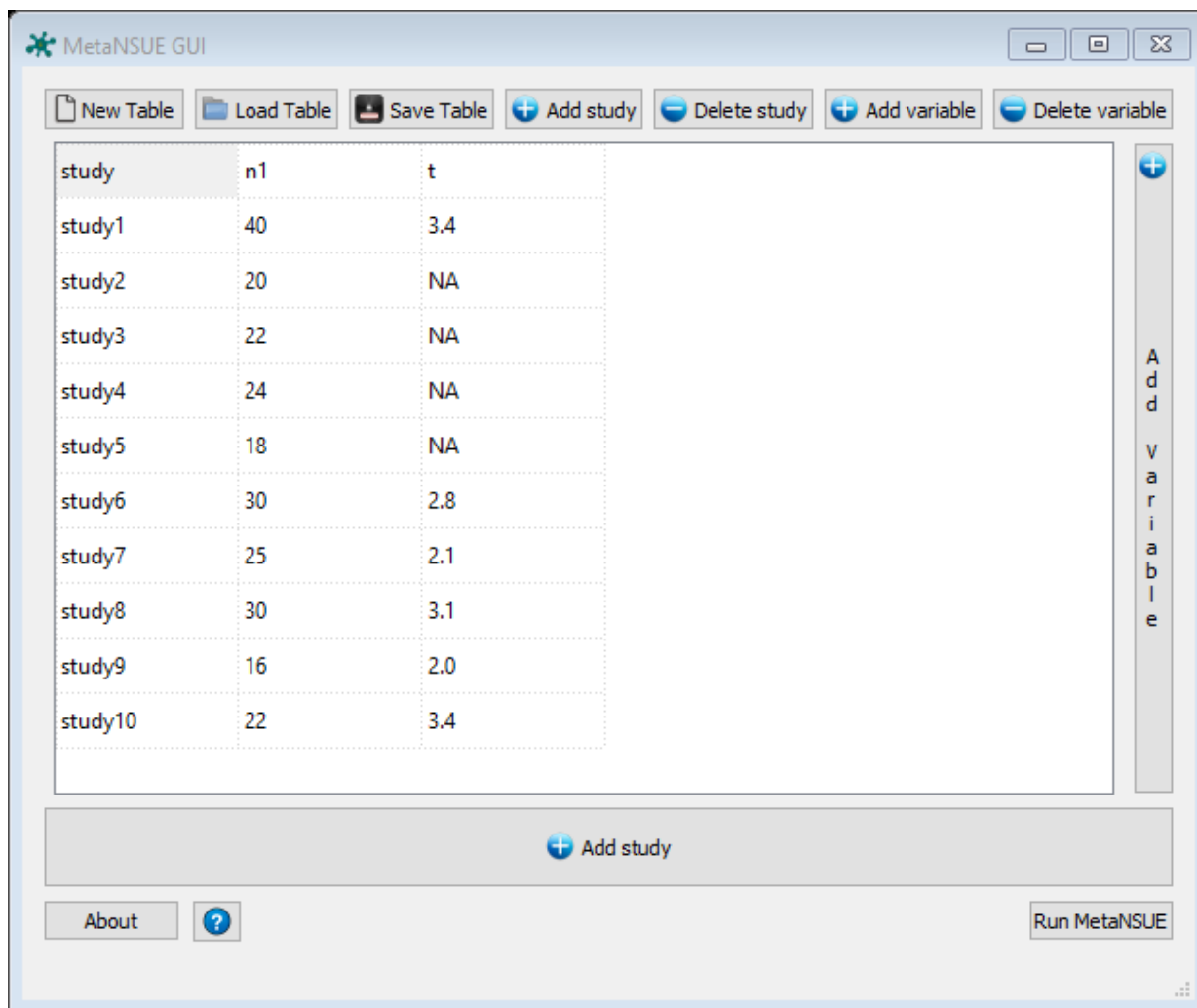
Preparation of the data

For this tutorial, we will use the example in the above paper. As we described there, we may imagine that we want to conduct a meta-analysis of studies of the change in blood pressure after the administration of a drug. Out of the 10 included studies, we would have the necessary data for six of such studies (i.e., their t-value). For the other four studies, we would only know that they were not statistically significant ($p > 0.05$). These four latter studies would be Non-statistically Significant Unreported Effects (NSUEs).

To prepare the data, you may create the text file with Microsoft Excel or any other software, or manually enter the values in MetaNSUE GUI as follows:

- Click the button "Add study" ten times to create the ten rows, optionally writing a name for each study.

- Enter the following values in the cells of column "n1" (sample sizes of the studies): 40, 20, 22, 24, 18, 30, 25, 30, 16, and 22.

- Click the button "Add variable" to create a column called "t" (t-values of the studies).

- Enter the following values in the cells of column "t": 3.4, NA, NA, NA, NA, 2.8, 2.1, 3.1, 2.0, and 3.4. Note that we coded the four NSUEs as "NA".

- Click the button "Save Table" to save the table (specify any name you want).

The MetaNSUE GUI should look similar to the following figure:

study	n1	t
study1	40	3.4
study2	20	NA
study3	22	NA
study4	24	NA
study5	18	NA
study6	30	2.8
study7	25	2.1
study8	30	3.1
study9	16	2.0
study10	22	3.4

How to do it using the R console

Create a vector with the sample sizes, a vector with the t-values, and use the function "smc_from_t" to create the NSUE object. Note that for standardized mean differences you should use the function "smd_from_t", and for correlations the function "zcor_from_r".

```
library(metansue)
n1 <- c(40, 20, 22, 24, 18, 30, 25, 30, 16, 22)
t <- c(3.4, NA, NA, NA, NA, 2.8, 2.1, 3.1, 2.0, 3.4)
x <- smc_from_t(t, n1)
```

Main / mean meta-analysis

Very easy:

- Click the button "Run MetaNSUE".

- In the first dialog, ensure that the outcome is a "standard mean change", that the outcome variable is "t", and that the type of meta-analysis is a "main analysis".

- Click the button "Next".

- In the second dialog, select the optional analyses that you want to conduct.

- Click the button "Next".

- In the last dialog, specify the name of the results (type any name you want), and check the binary path for the program "Rscript".

- Click the button "Launch MetaNSUE".

After a while, the program will open a website with the results.

How to do it using the R console

To conduct the main meta-analysis, simply use the function "meta". You may conduct the optional analyses using the functions "leave1out", "metabias", "forest" and "funnel".
 	
`meta(x)`
 	
`leave1out(x)`
 	
`m = meta(x)`
`metabias(m)`
`forest(m)`
`funnel(m)`

Meta-regression and other linear models.

After clicking the button "Run MetaNSUE", select that the type of meta-analysis that you want to conduct is a "meta-regression", and in the next dialog specify the regressors and the hypothesis. For a standard meta-regression, simply select the regressor of interest.

How to do it using the R console
Specify the regressors as a formula and the hypothesis as a matrix in the function "meta". For a standard meta-regression, the formula should simply be "~" plus the name of the regressor of interest, and the hypothesis "c(0, 1)".