

Manual for web application p -uniform*

<https://rvanaert.shinyapps.io/p-uniformstar>

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Meta-analysis based on p -uniform* can be conducted by means of this web application.¹ P -uniform* is a method for estimating effect size and between-study variance, testing the null hypothesis of no effect and no between-study variance, and testing for publication bias while taking into account publication bias. The p -uniform* method is based on the statistical theory that the distribution of p -values is uniform conditional on the population effect size. See van Aert and van Assen (2018) for more information.

The web application can currently handle three different effect size measures: one-sample mean, two-independent means, and raw correlation coefficients.

Step-by-step guide for using the web application:

- 1) Select the effect size measure in the meta-analysis (one-sample mean, two-independent means, or one raw correlation).
- 2) Select the alpha level which is used in the primary studies. The default alpha level is .05. Note that p -uniform* assumes that two-tailed tests were conducted in the primary studies. If one-tailed hypothesis tests were used in the primary studies, the alpha level has to be multiplied by two before applying p -uniform*.
- 3) Select whether the effect sizes in the primary studies are in the right-tail of the distribution (i.e., positive effects) or in the left-tail of the distribution (i.e., negative effects).
- 4) Three different methods are currently implemented for the p -uniform* method. The ML method refers to maximum likelihood estimation of the effect size and the between-study variance. Profile likelihood confidence intervals around the estimates are computed by means of inverting the likelihood-ratio test. Likelihood-ratio tests are used for the publication bias test and testing the null hypotheses of no effect and no between-study variance. The ML method is the recommended method for applying p -uniform*.

The two other methods (P and LNP) are moment based estimators. The method P is based on the distribution of the sum of independent uniformly distributed random variables (Irwin-Hall distribution) and the LNP method refers to Fisher's method (1950, Chapter 4). For these methods, a p -value for testing the null hypothesis of no between-study variance can also be obtained by means of a parametric bootstrap. This is necessary since the data is otherwise first used for estimating the effect size in the procedure for testing the null hypothesis of no

¹ This web application is based on the R package `puniform` which can be downloaded from GitHub by running the following lines of code inside R: `devtools::install_github("RobbievanAert/puniform"); library(puniform)`

between-study variance and then also used for computing a p-value. The test of no effect is not available for the methods P and LNP and the publication bias test for these methods is not yet implemented.

- 5) Two options are available for entering the data in the web application. Data can be entered via a CSV file or manually in a table in the web browser.

Manually in table:

If “Manually in table” is selected, you can choose between supplying p -uniform* with t -statistics and sample sizes for each primary study (only for one-sample mean and two-independent means) or with descriptive statistics. Note that extra rows can be added to the table by clicking the “plus” sign above the table. The following information has to be entered:

For one-sample mean based on t -statistics:

- $tobs \rightarrow t$ -statistic for each primary study
- $ni \rightarrow$ sample size for each primary study

For one-sample mean based on descriptive statistics:

- $mi \rightarrow$ group mean for each primary study
- $ni \rightarrow$ sample mean for each primary study
- $sdi \rightarrow$ standard deviation for each primary study

For two-independent means based on t -statistics:

- $tobs \rightarrow t$ -statistic for each primary study
- $n1i \rightarrow$ sample size in group 1 for each primary study
- $n2i \rightarrow$ sample size in group 2 for each primary study

For two-independent means based on descriptive statistics:

- $m1i \rightarrow$ mean in group 1 for each primary study
- $m2i \rightarrow$ mean in group 2 for each primary study
- $n1i \rightarrow$ sample size in group 1 for each primary study
- $n2i \rightarrow$ sample size in group 2 for each primary study
- $sd1i \rightarrow$ standard deviation in group 1 for each primary study
- $sd2i \rightarrow$ standard deviation in group 2 for each primary study

For one correlation:

- $ri \rightarrow$ raw correlation coefficient for each primary study
- $ni \rightarrow$ sample size for each primary study

Via CSV file:

If “via CSV file” is selected, a comma separated file has to be uploaded with a comma as separator and a period indicating the decimal point. The first row should *exactly* match the

names of the variables as described above for supplying the data manually in the table. To give an example, the CSV file for two-independent means has to be structured as follows

For t -statistics:

	A	B	C
1	tobs	n1i	n2i
2	4	200	200
3	4	200	200

For descriptive statistics:

	A	B	C	D	E	F
1	m1i	m2i	n1i	n2i	sd1i	sd2i
2	0.2	0	200	200	1	1
3	0.2	0	200	200	1	1

- 6) By clicking the “Analyze” button p -uniform is applied to your data.

References

van Aert, R. C. M., & van Assen, M. A. L. M. (2018). Manuscript in preparation.