Manual for Web Application Hybrid Method

https://rvanaert.shinyapps.io/hybrid/
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This web application can be used for statistically combining an original study and a replication by means of the hybrid methods (Van Aert & Van Assen, 2016) and traditional fixed-effect meta-analysis. The hybrid methods take into account that the original study is statistically significant and therefore correct for bias in the original study. See Van Aert and Van Assen (2016) for more information about the hybrid methods and their performance compared to traditional methods.

The web application can currently handle three different effect size measures: one-sample mean, two-independent means, and raw correlation coefficients. One assumption of the hybrid methods is that the original study has to be statistically significant, so the web application cannot be used if this is not the case.

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 original study. The default alpha level is .05. Note that the web application assumes that a two-tailed test was conducted in the original study. If a one-tailed hypothesis tests was used in the original study, the alpha level has to be multiplied by two before applying the hybrid methods.
- 3) Select whether the observed effect size in the original study is in the right-tail of the distribution (i.e., positive effect) or in the left-tail of the distribution (i.e., negative effect).
- 4) Enter the data of the original study (first row) and replication (second row) in the table. One can either enter *t*-statistics and sample sizes for both studies (only for one-sample mean and two-independent means) or descriptive statistics.

For <u>one-sample mean</u> based on *t*-statistics:

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

For one-sample mean based on descriptive statistics:

- mi → group mean for each study
- *ni* → sample mean for each study
- sdi → standard deviation for each study

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

For two-independent means based on *t*-statistics:

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

For two-independent means based on descriptive statistics:

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

For one correlation:

- $ri \rightarrow$ raw correlation coefficient for each study
- $ni \rightarrow$ sample size for each study
- 5) By clicking the "Analyze" button the hybrid methods and fixed-effect meta-analysis are applied to your data.
- 6) For each method, the output contains: the effect size estimate ("estimate"), test statistic ("x", "tval", or "zval"), two-sided *p*-value ("pval"), and lower ("ci.lb") and upper bound ("ci.ub") of a 95% confidence interval. Standard errors ("se") are also reported for the replication and fixed-effect meta-analysis.

References

Van Aert, R. C. M., & Van Assen, M. A. L. M. (2016). *Examining reproducibility in psychology: A hybrid method for statistically combining a biased original study and replication*. Manuscript submitted for publication.