Manual for Web Application Snapshot Method

https://rvanaert.shinyapps.io/snapshot/

Author: Robbie C.M. van Aert, R.C.M.vanAert@tilburguniversity.edu

This web application computes the posterior probability for four effect sizes (zero, small, medium, and large) when combining an original study and replication. The snapshot method takes into account that the original study is probably biased due to its statistical significance. We also included in the web application a method that does not take into account bias in the original study (uncorrected method) and traditional fixed-effect meta-analysis. The web application also enables researchers to compute the required sample size of the replication for a particular desired posterior probability (*a*) with a desired probability of observing a posterior probability larger than *a* (*b*). This procedure is akin to power analysis in null hypothesis significance testing. See van Aert and van Assen (2016) for more information about the snapshot method.

The web application can currently handle two different effect size measures: two-independent means and raw correlation coefficients. One assumption of the snapshot method 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 and computing the posterior probabilities:

1) Select the effect size measure (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 snapshot method.

3) 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 two-independent means) or descriptive statistics.

   For two-independent means based on *t*-statistics:
   - *tobs* → *t*-statistic for each study
   - *n1i* → sample size in group 1 for primary study
   - *n2i* → sample size in group 2 for primary study

   For two-independent means based on descriptive statistics:
   - *m1i* → mean in group 1 for each study
   - *m2i* → mean in group 2 for each study
   - *n1i* → sample size in group 1 for each study
   - *n2i* → sample size in group 2 for each study
   - *sd1i* → standard deviation in group 1 for each study
   - *sd2i* → standard deviation in group 2 for each study

   For one correlation:
   - *ri* → raw correlation coefficient for each study
   - *ni* → sample size for each study

4) Enter the prior probabilities for no, small, medium, and large true effect in the next table. Rules of thumb as proposed by Cohen (1988) were used for determining no, small, medium, and large true effect. For two-independent means, $\delta=0$ (no), $\delta=0.2$ (small), $\delta=0.5$ (medium), and $\delta=0.8$ (large). For one correlation coefficient, $\rho=0$ (no), $\rho=0.1$ (small), $\rho=0.3$ (medium), $\rho=0.5$ (large). The default prior probabilities are 0.25 for each true effect size (uniform prior probabilities).

5) By clicking the "Analyze" button the snapshot method is applied to your data.

6) The output contains a table with posterior probabilities based on uniform prior probabilities for the snapshot and uncorrected method and the results of traditional fixed-effect meta-analysis. A second table with posterior probabilities is presented if prior probabilities are specified by the user.

Step-by-step guide for using the web application and computing the required sample size in the replication:

1) Select the effect size measure (two-independent means or one raw correlation).

2) 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 two-independent means) or descriptive statistics.

    For <u>two-independent means</u> based on *t*-statistics:
        - *tobs* → *t*-statistic for each study
        - *n1i* → sample size in group 1 for primary study
        - *n2i* → sample size in group 2 for primary study

    For <u>two-independent means</u> based on descriptive statistics:
        - *m1i* → mean in group 1 for each study
        - *m2i* → mean in group 2 for each study
        - *n1i* → sample size in group 1 for each study
        - *n2i* → sample size in group 2 for each study
        - *sd1i* → standard deviation in group 1 for each study
        - *sd2i* → standard deviation in group 2 for each study

    For <u>one correlation</u>:
        - *ri* → raw correlation coefficient for each study
        - *ni* → sample size for each study

3) Enter values for *a* and *b*. The web application computes the required sample size where $P(\pi_x \geq a)=b$ with *a* being the desired posterior probability and *b* the desired probability of observing a posterior probability larger than *a*.

4) By clicking the "Analyze" button the required sample size in the replication is computed by means of the snapshot method.

5) The output contains a table with required total sample size in the replication when information of the original study is included (second column) and excluded (final column).

References

Cohen, J. (1988). *Statistical power analysis for the behavioral sciences* (2nd ed.). Hillsdale, NJ: Lawrence Erlbaum Associates.

van Aert, R. C. M., & van Assen, M. A. L. M. (2016). *Bayesian evaluation of effect size after replicating an original study*. Manuscript submitted for publication.