Publication Bias

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Abstract

Meta-analysis is the statistical method for synthesizing studies on the same topic and is often used in clinical psychology to quantify the efficacy of treatments. A major threat to the validity of meta-analysis is publication bias, which implies that some studies are less likely to be published and are therefore less often included in a meta-analysis. A consequence of publication bias is the overestimation of the meta-analytic effect size that may give a false impression with respect to the efficacy of a treatment, which might result in (avoidable) suffering of patients and waste of resources. Guidelines recommend to routinely assess publication bias in meta-analyses, but this is currently not common practice. This chapter describes popular and state-of-the-art methods to assess publication bias in a meta-analysis and summarizes recommendations for applying these methods. We also illustrate how these methods can be applied to two meta-analyses that are typical for clinical psychology such that psychologists can readily apply the methods in their own meta-analyses.

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Contents

1 Introduction

A meta-analysis provides a quantitative summary of studies on the same topic, and its results are seen as the best available evidence (Aguinis, Gottfredson, and Wright 2011; Head et al. 2015). However, the quality of a meta-analysis fully depends on the quality of the included studies, and an important threat for the validity of a meta-analysis arises if the included studies are not representative for all studies conducted on this topic. Publication bias is one cause of a meta-analysis containing an unrepresentative set of studies (Rothstein, Sutton, and Borenstein 2005), which means that statistically nonsignificant studies have a lower probability of being published than significant studies. Publication bias may be caused by editors and reviewers who are more reluctant to positively evaluate statistically nonsignificant compared to significant studies or by authors who do not submit nonsignificant studies for publication (Cooper, DeNeve, and Charlton 1997; Coursol and Wagner 1986). The consequences of publication bias are severe and hamper the progress of science, because it yields overestimated effect size in the individual studies and when combining these studies in a meta-analysis (e.g., Kraemer et al. 1998; Lane and Dunlap 1978). For this reason, guidelines on how to conduct a meta-analysis such as the Meta-Analytic Reporting Standards (MARS, Appelbaum et al. 2018), Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA, Moher et al. 2009), and the Cochrane Handbook for Systematic Reviews of Interventions (Page, Higgins, and Sterne 2019) all encourage meta-analysts to routinely assess publication bias in their meta-analysis.

There is strong evidence for the presence of publication bias in the psychological literature. For example, Fanelli (2012) showed that 90% of a random sample of studies published in the psychological literature found support for their main hypothesis. This large percentage is in disagreement with the on average low statistical power of studies in psychology (Bakker, Van Dijk, and Wicherts 2012; Ellis 2010), which is too low to find support for the hypothesis this often. More direct evidence of publication bias has been observed in Franco, Malhotra, and Simonovits (2014) who determined whether the publication status of studies that were awarded a grant depended on their results. They concluded that studies with null or mixed results remained more often unpublished than studies with strong results (i.e., predominantly statistically significant results). Publication bias has also been studied in clinical psychology. For example, Driessen et al. (2015) compared the publication status of studies awarded with a grant focusing on research studying the efficacy of psychological treatments for patients with major depressive disorder. They showed that 13 out of 55 (23.6%) studies that were awarded with a grant were not published in the literature. Adding these unpublished studies to the meta-analysis of published studies resulted in a reduction in effect size estimate of 0.13 standardized mean difference.

If the efficacy of interventions is overestimated due to publication bias and publication bias remains undetected, this can have severe consequences. Taking the example of depression, efficacious treatments are essential to reduce impaired functioning and risk of suicide that are caused by depression (Holma et al. 2010). If publication bias is present, clinical guidelines may prompt psychotherapists to apply interventions in routine care that may be less efficacious than assumed. This would not only prevent individuals from receiving the best possible treatment, but also result in unnecessarily high costs for the health care system (Jaycox and

Foa 1999; Maljanen et al. 2016; Margraf 2009). Moreover, publication bias in research on etiological assumptions such as genetic predispositions, biological mechanisms, detrimental environmental exposures, cognitive distortions, or attentional biases would also be hampering knowledge accumulation about the underlying mechanisms that contribute to the onset and maintenance of mental disorders. Thus, assessing publication bias in all fields of clinical psychology is strongly recommended, but it has not been routinely done in meta-analyses. For example, Niemeyer, Musch, and Pietrowsky (2013) found that in the majority (82%) of meta-analyses on the efficacy of (psychotherapeutic) interventions for depression publication bias was not considered in the statistical analyses. In addition, 81.2% of the meta-analyses explicitly did not include unpublished studies. Publication bias is also not routinely assessed in education research where 44% (Banks, Kepes, and Banks 2012) did not assess publication bias, and industrial and organizational psychology where publication bias was not assessed in 92.7% (Aguinis et al. 2010) and 82.3% (Aytug et al. 2012) of a large number of meta-analyses.

Of note is that evidence for publication bias in psychology is, however, not always observed when published meta-analyses are reanalyzed using publication bias methods in so-called meta-meta-analyses (i.e., meta-analysis of meta-analyses). For example, publication bias was detected in approximately 15% of reanalyzed meta-analyses published on psychotherapeutic interventions for schizophrenia and depression (Niemeyer, Musch, and Pietrowsky 2012, 2013). Another study also observed only weak evidence for publication bias in reanalyzed meta-analyses published in Psychological Bulletin and the Cochrane Database of Systematic Reviews (Van Aert, Wicherts, and Van Assen 2019). A possible reason for not observing strong evidence for publication bias are the challenging conditions of the meta-analyses under study for publication bias methods. The publication bias methods that were available at that time could only be applied to a small subset of meta-analyses in these studies due to strong assumptions of the methods. For example, the applied publication bias methods assume each study in the meta-analysis to estimate the same true effect size. This implies that no heterogeneity in true effect size is allowed, which is especially uncommon in clinical psychology research where studies in psychotherapy research are, for instance, administered at different locations and by different therapists. Moreover, many disorders are heterogeneous in their symptom presentation and comorbidity is frequent (e.g., Deisenhofer et al. 2018).

Another complicating factor that is common for meta-analyses in clinical psychology research are the small number of studies included in meta-analyses. Meta-analyses containing less than five studies are not uncommon in medical research (e.g., Rhodes, Turner, and Higgins 2015; Turner et al. 2015) in general and clinical psychology research in particular (Niemeyer et al. 2020). Examining publication bias based on such a small number of studies is challenging, because the number of data points in the analysis equals the number of studies in the meta-analysis. The two complicating factors (heterogeneity and small number of studies) are also not unrelated. For example, Schumacher et al. (2018) meta-analyzed hormonal dysregulation in posttraumatic stress disorder (PTSD), but these data of 108 studies and more than 6,000 participants were very heterogeneous. An option was to create subgroups of more homogeneous studies and assessing publication bias in these subgroups, but these subgroups comprised a very small number of studies.

Simulation studies tailored to characteristics of meta-analyses on clinical psychology research

also confirmed that the conditions were unfavorable for the available publication bias methods (Niemeyer et al. 2020). However, newly developed publication bias methods are better equipped to be applied to meta-analyses that are typical for research in clinical psychology. A clear overview of the existing methods and software on how to apply these methods is currently lacking in the literature. The goal of this chapter is to provide such an overview together with summarizing recommendations for applying these methods. Many different publication bias methods have been developed, so we focus in this chapter on the most popular methods and state-of-the-art methods that have shown to outperform these most popular methods. Methods to investigate publication bias can serve two different purposes: first to estimate an effect size in the presence of publication bias, and second to assess the degree of publication bias. Publication bias methods for both purposes will be illustrated using the statistical software R (R Core Team 2020) and by applying these to two examples that are typical for meta-analyses in clinical psychology.

We continue this chapter by introducing the statistical software R. Subsequently, we will describe graphical methods to assess publication bias, methods to correct effect size estimates for publication bias, and methods to assess the presence of publication bias in a meta-analysis. These methods will be applied to a meta-analysis on the efficacy of cognitive-behavior therapy (CBT) for treating pathological and problem gambling (Cowlishaw et al. 2012) and a meta-analysis on the added value of collaborative care for patients with depression or anxiety problems (Archer et al. 2012). Both meta-analyses provide paradigmatic examples, because CBT is a guideline-recommended treatment for most disorders (David et al. 2018), and second, depression and anxiety are among the most prevalent disorders (Alonso et al. 2004). The chapter ends with recommendations for clinical psychologists on how to deal with publication bias in meta-analyses.

2 Software

The publication bias methods that are discussed in this chapter are illustrated using the statistical software R (Version 4.0.3; R Core Team 2020). R is free and open-source programming software with a primary focus on statistical computing and creating graphics. An important feature of R is that researchers can contribute to the software by developing so-called packages that can easily be loaded in R. Packages contain all sorts of functions to, for example, run statistical analyses and visualize data. After downloading R via https://cran.r-project.org/ and installing it, packages can be downloaded and installed by running the R code

```
install.packages("PACKAGE")
```

where `PACKAGE` needs to be replaced by the name of the package you want to download and install. The functions in a package become available by loading it using the R code

```
library("PACKAGE")
```

A popular R package for conducting meta-analyses is `metafor` (Viechtbauer 2010). This package (Version 2.5.69) will be used throughout this chapter, because it contains besides functions for conducting meta-analyses also functions for applying a large number of publica-

tion bias methods. However, we sometimes have to rely on other packages if a particular method is not included in the `metafor` package, which will be introduced when explaining these methods.

Note that we make excessive use of R for applying publication bias methods in this chapter, but familiarity with R or programming experience is not a prerequisite. All R code will be provided for applying the publication bias methods such that this code can be easily used by interested readers who want to apply these methods to their own data. An annotated version of all the codes used in this chapter is also available at https://osf.io/qjk9b/. Readers who want to learn more about R are referred to https://cran.r-project.org/doc/manuals/R-intro.pdf for an elaborate introduction or introductory books on R such as Matloff (2011) and Teetor (2011).

3 Examples

3.1 Example 1: Cowlishaw et al. (2012)

The publication bias methods will be applied to two meta-analyses that are typical for meta-analyses in clinical psychology research. The first meta-analysis synthesizes seven studies on the efficacy of CBT for treating pathological and problem gambling (analysis 1.2 in Cowlishaw et al. 2012). For each study, a standardized mean difference (i.e., Hedges' g) is computed that compares the difference in financial loss of patients who received CBT in the last three months with a control group. A positive standardized mean difference indicates that the financial loss was smaller in the group of patients who received CBT compared to those in the control group.

Cowlishaw et al. (2012) fitted a random-effects model to the included studies in the meta-analysis and, therefore, assumed that each study had its own unique true effect size (for an elaborate description of the random-effects model see Borenstein et al. 2010). This random-effects model can also be fitted to the data using the `metafor` package after creating two vectors[1] containing the standardized mean differences and corresponding sampling variances (i.e., squared standard errors). The vectors are named `yi` and `vi` and can be created using

```
yi <- c(0.587, 0.706, 0.552, 0.515, 0.566, 0.291, 0.989)
vi <- c(0.076, 0.067, 0.074, 0.217, 0.047, 0.028, 0.157)
```

the vectors are subsequently be used in the `rma()` function of the `metafor` package to fit the random-effects model,

```
res <- rma(yi = yi, vi = vi)
```

where the results are stored in the R object `res`. The average effect size in this meta-analysis was 0.519 with 95% confidence interval (CI) equal to (0.332; 0.706), and the null-hypothesis of no effect is rejected ($z = 5.432$, two-tailed p-value $< .001$). The estimated between-study

[1] A vector is R terminology for a particular data structure that contains in our case seven numeric values with the studies' standardized mean difference (`yi`) and corresponding sampling variance (`vi`).

variance in true effect size is 0 with 95% CI equal to (0; 0.125). The Q-test (Cochran 1954) for testing the null-hypothesis of no heterogeneity is not statistically significant ($Q = 3.897$, one-tailed p-value is .691). To conclude, the financial loss of the group of patients who received CBT was smaller than in the control group, and the difference between both groups was of medium size according to the rules of thumb by Cohen (1988). The between-study variance in true effect size was estimated as zero indicating that the studies' true effect size were homogeneous. However, estimation of the between-study variance was imprecise due to the small number of studies in the meta-analysis, which is apparent in the wide CI.

3.2 Example 2: Archer et al. (2012)

The second example used in this chapter is the meta-analysis by Archer et al. (2012) on the added value of collaborative care measured by patient satisfaction for patients with depression or anxiety problems. This meta-analysis consists of 24 studies and patient satisfaction was reported with a dichotomous variable in each study. The effect size measure of interest was a risk ratio (a.k.a. relative risk). The risk ratios were first transformed to log risk ratios before synthesizing these, because an assumption of common meta-analysis models is that the effect size measure follows a normal distribution. This is approximately the case for log risk ratios but not for risk ratios.

We follow Archer et al. (2012) by also fitting a random-effects model to these data. The estimated average risk ratio was 1.271 (95% CI (1.180; 1.368)), and the null-hypothesis of no effect was rejected ($z = 6.347$, two-tailed p-value $< .001$). The between-study variance was estimated as 0.021 (95% CI (0.009; 0.070)), and the null-hypothesis of no heterogeneity was rejected ($Q = 83.580$, one-tailed p-value $< .001$). These results show that patients receiving collaborative care were more satisfied than patients receiving the usual care. The true effect sizes were heterogeneous, so the effectiveness of collaborative care varied across studies.

We have presented the results of the two meta-analyses when using conventional meta-analysis methods that do not correct for publication bias in this section. We will compare these results to those obtained with publication bias methods later in this chapter. We continue by explaining the publication bias methods that are also summarized in Table 1.

Table 1: Summary of the methods described in this chapter.

	Description	Characteristics/Recommendations	R function
Graphical methods:			
Funnel plot	Figure displaying the relation between effect size and their precision (so-called small-study effects).	Small-study effects can be caused by publication bias but also by other factors. Eyeballing a funnel plot is subjective, so funnel plot asymmetry tests are recommended instead.	`funnel()` in `metafor`
Meta-plot	Figure displaying the results of cumulative meta-analysis with studies ordered by their precision.	The meta-plot can be used for assessing small-study effects and publication bias, and it is an improvement over the funnel plot.	`meta_plot()` in `puniform`
Correcting effect size for publication bias:			
Top 10% and WAAP	Meta-analysis based on the 10% most precise and adequately powered studies.	Methods only perform well if there is no heterogeneity and many studies may be discarded from the meta-analysis.	`rma()` in `metafor` after selecting studies
Trim-and-fill	Corrects for small-study effects by imputing studies in the funnel plot until symmetry is reached.	Method is discouraged to be used, because it falsely imputes studies if heterogeneity is present and is outperformed by other methods.	`trimfill()` in `metafor`
PET-PEESE	Estimate corrected for small-study effects is the intercept of regressing the effect size on either the standard error or sampling variance.	Method is discouraged to be applied in case of less than 10 studies and similar precisions of the studies.	Regression model fitted with `lm()` depending on whether true effect is zero
p-uniform and p-curve	Estimate equals the value where the p-value distribution of only the significant studies is uniform.	Methods recommended to be applied when heterogeneity is less than moderate.	`puniform()` in `puniform` for p-uniform
p-uniform*	Extension of p-uniform that does not discard nonsignificant studies and allows heterogeneous effects.	Method is discouraged to be applied if publication bias is extreme and there are only significant studies.	`puni_star()` in `puniform`

Table 1: Summary of the methods described in this chapter. *(continued)*

	Description	Characteristics/Recommendations	R function
Weight-fun.	Corrected estimates obtained by estimating and incorporating weights of studies that reflect the extent of publication bias.	Method is discouraged to be applied if publication bias is extreme and there are only significant studies. Convergence problems may arise in case of a small number of studies.	`weightfunct()` in `weightr`
Assessment of publication bias:			
Fail-safe N	Computes the number of studies that are needed to make the null-hypothesis of no meta-analytic effect nonsignificant.	Method is discouraged to be used due to, for example, the assumptions of no heterogeneity and missing studies having an effect of zero.	`fsn()` in `metafor`
Funnel plot asymmetry tests	Rank-correlation and Egger's regression test for small-study effects in a funnel plot.	Tests for small-study effects rather than publication bias. Methods are recommended to be applied with at least 10 studies in the meta-analysis.	`ranktest()` and `regtest()` in `metafor`
Test of excess significance (TES)	Tests whether more statistical significant studies are observed than expected based on their power.	Method is discouraged to be applied in case of heterogeneity and is known to be conservative.	`tes()` in `metafor`
Publication bias tests selection models	p-uniform and weight-function model test difference between models corrected and not corrected for publication bias.	p-uniform's test is conservative if true effect size is large. Properties of the test of the weight-function model are currently unknown.	`puniform()` in `puniform` and `weightfunct()` in `weightr`

Note:
WAAP = weighted average of the adequately powered studies, PET = precision-effect test, PEESE = precision-effect estimate with standard error, Weight-fun. = weight-function model.

4 Graphical methods to assess publication bias

4.1 Funnel plot

A regularly reported figure for assessing publication bias in a meta-analysis is the funnel plot (Light and Pillemer 1984). A funnel plot of the meta-analysis by Cowlishaw et al. (2012) is presented in the left panel of Figure 1.[2] The x-axis of a funnel plot shows the observed effect sizes of the studies included in the meta-analysis, and a measure of the studies' precision is depicted on the y-axis. The standard error is displayed on the y-axis of the funnel plot in Figure 1, but other measures of a study's precision can also be displayed (e.g., sampling variance, sample size, or the inverse of the standard error). A funnel plot can be created using the `funnel()` function incorporated in the `metafor` package by using the code

```
funnel(res)
```

where `res` is the object that was created earlier when conducting the random-effects meta-analysis.

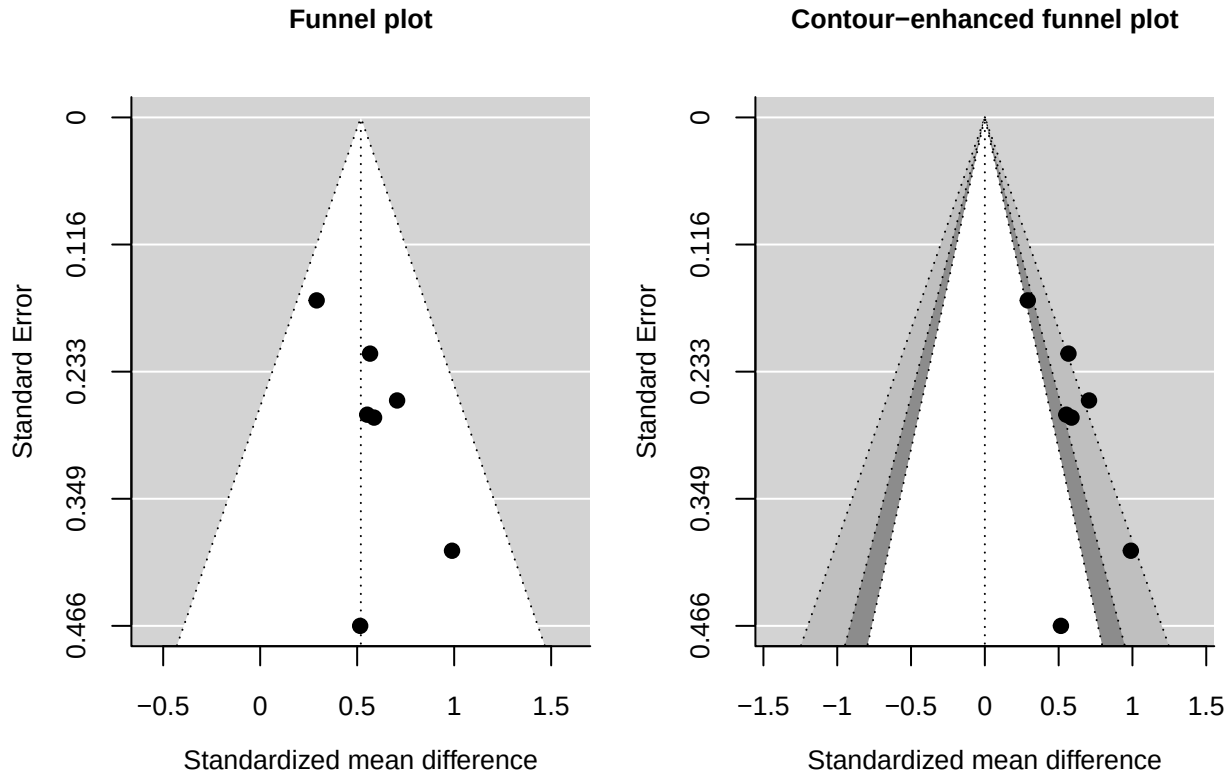

Figure 1: Funnel plot (left panel) and contour-enhanced funnel plot (right panel) for the meta-analysis by Cowlishaw et al. (2012).

[2]The funnel plot based on the data of the meta-analysis by Archer et al. (2012) is available in the annotated R codes (https://osf.io/qjk9b/).

Publication bias can be assessed using a funnel plot by examining whether the studies resemble the shape of an inverted funnel. Some studies in the left bottom corner are missing in the funnel plot in the left panel of Figure 1 to closely resemble an inverted funnel. This implies that studies with a negative observed effect size might be suppressed from being published in the literature, and therefore could not be included in the meta-analysis. It is important to emphasize that funnel plots not resembling an inverted funnel can also be caused by other factors than publication bias. An asymmetric funnel plot is indicative for larger observed effect sizes going along with larger imprecision (i.e., larger standard errors) of studies. These so-called small-study effects (Egger et al. 1997) may be caused by publication bias but also by other factors such as heterogeneity in true effect size. Heterogeneity is common for meta-analyses in clinical psychology, so prudence is in order when concluding that publication bias is present solely based on visually inspecting a funnel plot.

Another reason why meta-analysts should be cautious when drawing conclusions by inspecting funnel plots is that funnel plots can be misleading. Based on a large number of funnel plots, researchers correctly identified publication bias in only 52.5% of the funnel plots (Terrin, Schmid, and Lau 2005). Moreover, changing the study's precision on the y-axis may also have a major impact on the on the shape of the funnel plot. The contour-enhanced funnel plot (Peters et al. 2008) was proposed to counteract the drawbacks of the funnel plot. The contour-enhanced funnel plot of the meta-analysis by Cowlishaw et al. (2012) is presented in Figure 1 and modifies the funnel plot in two important ways. First, the contour-enhanced funnel plot is always centered at an effect size of zero whereas the funnel plot is centered at the meta-analytic effect size estimate. Second, contour lines are added to the plot reflecting the p-values of studies. That is, studies in the white area of the contour-enhanced funnel plot have two-tailed p-values between 0.1 and 1 whereas studies in the dark gray, gray, and outside the funnel have two-tailed p-values in the intervals 0.05 and 0.1, 0.01 and 0.05, and 0 and 0.01, respectively. These contour lines help evaluating whether publication bias is the cause of funnel plot asymmetry, because they show whether statistically nonsignificant studies are missing in the meta-analysis. A contour-enhanced funnel plot can also be created using the `funnel()` function,

```
funnel(res, refline = 0, level = c(90, 95, 99),
       shade = c("white", "gray55", "gray75"))
```

where `refline = 0` is the center of the funnel, `level = c(90, 95, 99)` defines the contour lines, and `shade = c("white", "gray55", "gray75")` specifies the colors of the areas created by adding the contour lines.

4.2 Meta-plot

Another graphical method that was recently proposed to assess publication bias in a meta-analysis is the meta-plot (Van Assen et al. 2020). The meta-plot of the meta-analysis by Cowlishaw et al. (2012) is shown in Figure 2. It shows the precision of a study (i.e., reciprocal of its standard error) on the x-axis and the effect size on the y-axis. The circles in the meta-plot are the average effect size estimates of a cumulative random-effects meta-analysis. In a cumulative meta-analysis (Lau et al. 1992), multiple meta-analyses are conducted where

the first meta-analysis is based on a single study and in each subsequent meta-analysis a study is added. The order of the studies being added to the cumulative meta-analysis in the meta-plot is based on studies' precision. That is, the rightmost dot is the meta-analysis based on only the study that is most precise and the leftmost dot is the meta-analysis based on all studies. Each dot is accompanied by its 95% CI. The meta-plot in Figure 2 shows a decreasing trend in the cumulative meta-analysis from left to right. This is indicative for small-study effects, because the average effect size estimate of the meta-analysis based on all studies is larger than meta-analyses based on more precise studies. An advantage of the meta-plot over the funnel plot is that small-study effects are more visible as the effect size in the plot refers to the results of meta-analyses rather than individual studies.

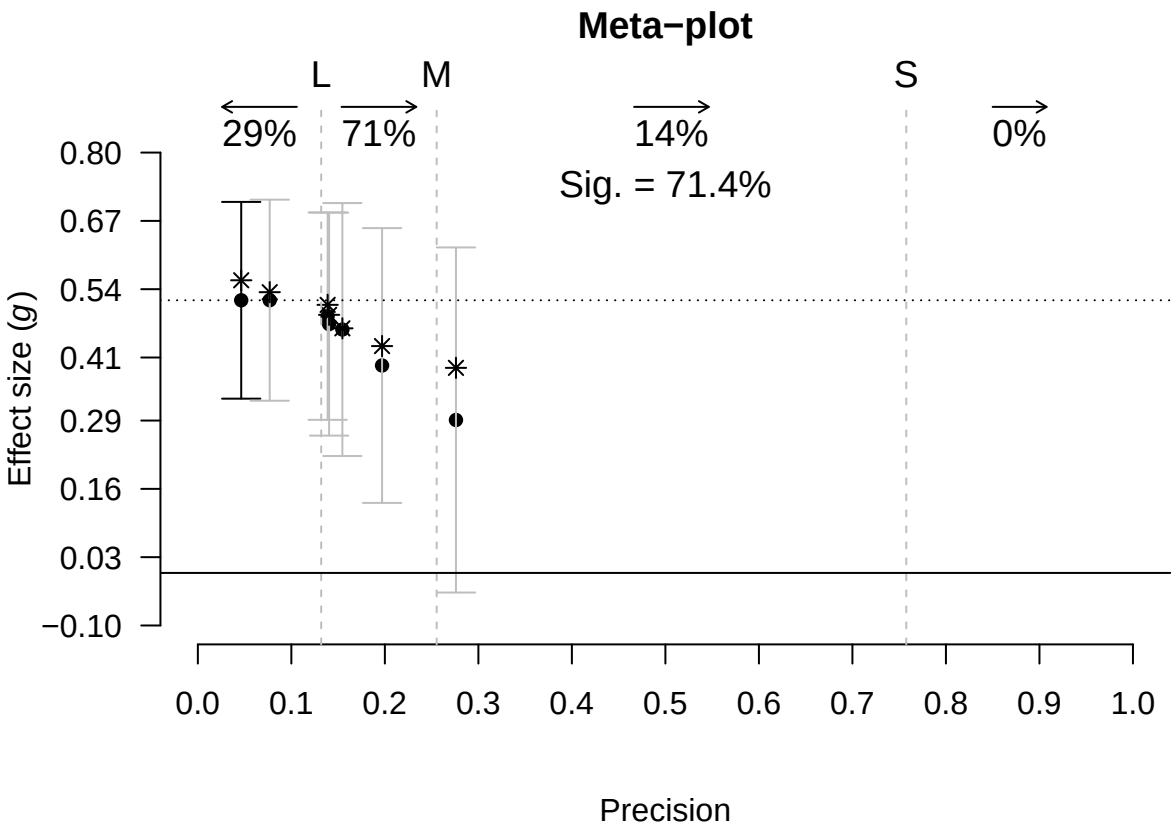

Figure 2: Meta-plot of the meta-analysis by Cowlishaw et al. (2012).

The meta-plot also contains other relevant information for meta-analysts. First, it states the percentage of statistically significant results in the meta-analysis (71.4% in the meta-analysis of Cowlishaw et al. (2012)). Second, it shows information about the statistical power of the studies in the meta-analysis at the top of the plot. The leftmost percentage indicates the percentage of studies whose statistical power was insufficient (less than 80%) to detect a large population effect. The remaining three percentages at the top of the plot describe the percentages of studies with sufficient statistical power to detect a large (L), medium (M), and small (S) effect, respectively. Finally, the asterisks in the meta-plot refer to the expected estimates in the cumulative meta-analysis if the population effect size is zero in

combination with extreme publication bias (i.e., only statistically significant studies get published). Asterisks that are larger than the dots imply that the results of the meta-analysis can also be explained by extreme publication bias in combination with no effect. This is the case for the meta-plot in Figure 2, so authors are recommended to be cautious when interpreting the results of this meta-analysis.

Functions for creating the meta-plot are available in the R package `puniform` (Version 0.2.4; Van Aert 2020). After installing and loading this package as described above, the meta-plot can be created using the code

```
meta_plot(m1i = m1i, m2i = m2i, n1i = n1i, n2i = n2i, sd1i = sd1i,
          sd2i = sd2i, pub_bias = TRUE)
```

where `m1i`, `n1i`, and `sd1i` are the study's mean, sample size, and standard deviation of patients receiving usual care and `m2i`, `n2i`, and `sd2i` are the study's mean, sample size, and standard deviation of patients receiving collaborative care.[3] Setting the argument `pub_bias` to `TRUE` makes sure that the asterisks are plotted.

The above introduced funnel plot and meta-plot enable to visually inspect whether small-study effects or publication bias are present in a meta-analysis. For an applied researcher, it is usually more of interest what the impact is of these biases on the results of a meta-analysis. In the next section, we will introduce methods that can be used for this purpose.

5 Methods to estimate effect size in the presence of publication bias

5.1 WAAP and Top 10%

Two intuitive approaches to estimate the effect size in the presence of publication bias are the weighted average of the adequately powered (WAAP) studies (Ioannidis, Stanley, and Doucouliagos 2017) and the Top 10% approach (Stanley, Jarrell, and Doucouliagos 2010). Both approaches rest on the idea that the effect sizes of the most precise studies (i.e., studies with the largest sample size) in a meta-analysis are less overestimated due to publication bias. Less precise studies are more vulnerable to publication bias, because overestimation of effect size needs to be larger in these studies in order to be statistically significant. The WAAP uses this idea by meta-analyzing only the studies whose statistical power to reject the null-hypothesis of no effect is larger than 80%.[4] The Top 10% does not take statistical power into account, but meta-analyzes only the 10% most precise studies. Others have argued to not focus on the 10% most precise studies, but interpret the study with the largest precision as the best effect size estimate if publication bias is present (Ioannidis 2013). Although, the intuition of these approaches is appealing, they should only be used if there is no heterogeneity

[3]The study's mean, sample size, and standard deviation of both groups are available on page 73 of Cowlishaw et al. (2012).

[4]Statistical power of the studies is computed using the estimate of the fixed-effect model as proxy for the true effect size and a two-tailed hypothesis with significance level 0.05 (Stanley, Doucouliagos, and Ioannidis 2017).

in the meta-analysis. Drawing conclusions based on only a subset of studies is ill-advised in case of heterogeneity, because the true effect size of studies are different and a subset of studies is not a good representation of all studies in the meta-analysis.

5.2 Trim-and-fill

The trim-and-fill method (Duval and Tweedie 2000a, 2000b) is the most often used method to correct effect size for publication bias. The trim-and-fill method is an iterative procedure that *trims* the most extreme effect sizes from the right hand side of the funnel plot and *fills* these in the funnel plot until it is symmetric. The meta-analytic estimate corrected for bias is the estimate based on the observed studies as well as the imputed studies. The left panel of Figure 3 visually shows the procedure for the meta-analysis of Cowlishaw et al. (2012) where the solid and open circles are the observed and filled studies, respectively.

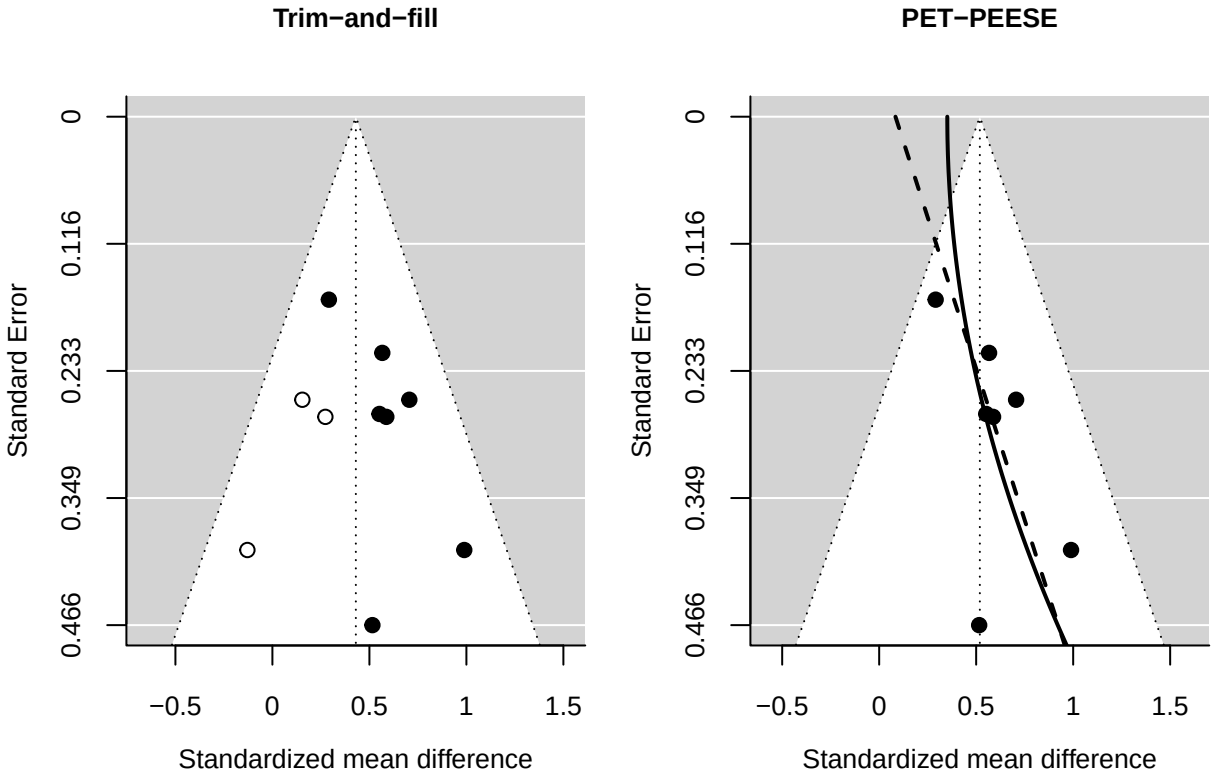

Figure 3: Illustration of the trim-and-fill method (left panel) and the PET-PEESE method (right panel) when applied to the meta-analysis by Cowlishaw et al. (2012). The dashed line in the right panel refers to the PET analysis and the solid line to the PEESE analysis.

Multiple researchers have criticized the trim-and-fill method and discourage meta-analysts to use the method. A prevalent issue with the trim-and-fill method is that it is based on the funnel plot and therefore actually corrects for small-study effects rather than publication bias. Simulation studies have confirmed that the trim-and-fill method yields misleading results if

heterogeneity is present in a meta-analysis (Terrin et al. 2003; Peters et al. 2007). Moreover, the trim-and-fill method is outperformed by other methods (e.g., Van Assen, Van Aert, and Wicherts 2015; Moreno et al. 2009; Simonsohn, Nelson, and Simmons 2014) that will be discussed next making it a method that should better be avoided. Nevertheless, if researchers want to report the results of the trim-and-fill method in their meta-analysis, they can apply the method using this line of code

```
trimfill(res)
```

5.3 PET-PEESE

Another method that uses the relationship between studies' effect size and precision is the PET-PEESE method (Stanley and Doucouliagos 2014; Moreno et al. 2009). PET-PEESE is a combination of two distinct methods: the *precision-effect test* (PET) and the *precision-effect estimate with standard error* (PEESE). The rationale of this method can best be explained by the funnel plot based on the meta-analysis by Cowlishaw et al. (2012) in the right panel of Figure 3. PET and PEESE both fit a regression line through the points in the funnel plot. The lines of PET (dashed line) and PEESE (solid line) in Figure 3 are based on a linear regression with the study's standard error and sampling variance as predictor, respectively. The effect size estimates of PET and PEESE are the values where the slope of the regression line is 0 (i.e., the estimate of the intercept). This occurs in the right panel of Figure 3 at the top of the funnel plot where the lines end, because this is the point where the standard error equals zero. The rationale of both methods is that these estimates resemble a study with an infinite sample size, and they are therefore expected to be closer to the true effect size than conventional meta-analysis.

The PET-PEESE method is a combination of PET and PEESE, because simulation studies have shown that PEESE is the least biased when the true effect is different from zero (Stanley and Doucouliagos 2014). Hence, it was proposed to first test whether the null-hypothesis of no effect is rejected in PET using a one-tailed test and significance level of 10%, and then interpret the estimate of PET if this test is not statistically significant and the estimate of PEESE if it is significant (Stanley 2017). Limitations of the method are that it actually corrects the effect size for small-study effects rather then publication bias. Hence, the method becomes biased if there is large heterogeneity in a meta-analysis (Alinaghi and Reed 2018). Moreover, applying the method is also discouraged if there are less than 10 studies in the meta-analysis or the precision of the studies are similar, because this makes it difficult to fit the regression lines and results in an imprecise estimate (Stanley, Doucouliagos, and Ioannidis 2017; Stanley 2017; Niemeyer et al. 2020).

PET can be applied using the following line of code

```
lm(yi ~ I(sqrt(vi)), weights = 1/vi)
```

where `yi ~ I(sqrt(vi))` specifies that the effect size is regressed on the standard error and `weights = 1/vi` make sure that studies in the analysis are weighted by the reciprocal of their sampling variance. If the null-hypothesis of no effect is statistically significant in PET, PEESE can be applied using the code

```
lm(yi ~ vi, weights = 1/vi)
```

5.4 Selection model approaches

Selection model approaches are nowadays seen as the state-of-the-art methods to correct for publication bias in a meta-analysis (McShane, Böckenholt, and Hansen 2016). These selection model approaches assign weights to studies to take into account that some studies are less likely to be published than others. For example, statistical nonsignificant studies will most likely receive a larger weight than significant studies to compensate for nonsignificant studies being less likely to be published. These weights are then taken into account when meta-analyzing studies using a conventional meta-analysis model such as the random-effects model that does not correct for publication bias.

Selection model approaches were known to suffer from convergence problems if less than 100 studies are included in a meta-analysis (e.g., Borenstein et al. 2009; Terrin et al. 2003). However, these convergence problems were less of an issue in recent studies (McShane, Böckenholt, and Hansen 2016; Carter et al. 2019; Van Aert and Van Assen 2020), which was probably caused by the development of new selection model approaches in combination with improved software implementation. Many different selection model approaches exist (for an overview see Marks-Anglin and Chen (2020), Jin, Zhou, and He (2014), and the supplements of Van Aert and Van Assen (2020)) that mainly differ on how the weights of the studies are computed. We will focus in this book chapter on three selection model approaches that do not require the meta-analyst to make sophisticated choices and are therefore easy to implement, have shown to outperform the existing methods that were introduced above, or are regularly used in practice.

5.4.1 P-uniform and p-curve

P-uniform (Van Assen, Van Aert, and Wicherts 2015) and *p*-curve (Simonsohn, Nelson, and Simmons 2014) are two methods based on the same methodology that slightly differ in how they are implemented (for a description of the differences see Van Aert, Wicherts, and Van Assen 2016). Both methods correct for publication bias in a meta-analysis by only focusing on the statistically significant studies and discarding the nonsignificant studies. The methods use the distribution of statistically significant *p*-values for effect size estimation. The estimate of both methods equals zero if this *p*-value distribution is uniformly distributed under the null-hypothesis. A *p*-value distribution with small *p*-values being overrepresented is indicative for an effect larger than zero whereas a distribution with an overrepresentation of *p*-values close to the significance level is evidence for an effect smaller than zero. The effect size estimate of *p*-uniform and *p*-curve is obtained by means of an iterative procedure to find the effect size where the *p*-values are uniformly distributed. The methods assume that each statistically significant study is equally likely to be published (i.e., the same weight for each study).

P-uniform and *p*-curve have shown to yield accurate estimates in the presence of publication bias and homogeneous true effect size and outperformed the trim-and-fill method (Van Assen,

Van Aert, and Wicherts 2015; Simonsohn, Nelson, and Simmons 2014). However, the methods overestimate effect size if a meta-analysis is heterogeneous (Van Aert, Wicherts, and Van Assen 2016; McShane, Böckenholt, and Hansen 2016; Carter et al. 2019). For that reason, Van Aert, Wicherts, and Van Assen (2016) recommended to only interpret the effect size estimate of both methods as the estimate of the population effect if the true effect sizes are homogeneous or if heterogeneity is less than moderate.[5] Another limitation of the methods is that effect size estimates may become unrealistically low in case of *p*-uniform or peculiar in case of *p*-curve if a preponderance of studies has *p*-values just under the significance level (Van Aert, Wicherts, and Van Assen 2016). This may be caused by researchers having used questionable research practices (a.k.a. *p*-hacking or researcher degrees of freedom, Simmons, Nelson, and Simonsohn 2011; Wicherts et al. 2016) in the studies to get *p*-values below the threshold of statistical significance.

We only show how *p*-uniform can be applied, because there is no R package that contains functions for applying *p*-curve and, in contrast to *p*-curve, a publication bias test and 95% CIs have been developed for *p*-uniform. *P*-uniform can be applied by using the `puniform()` function in the `puniform` package,

```
puniform(yi = yi, vi = vi, side = "right")
```

where `side = "right"` specifies that the method should be applied to the studies that are statistically significant based on a right-tailed test. Specifying `side = "left"` allows applying *p*-uniform to studies that are based on a left-tailed test.

5.4.2 P-uniform*

The *p*-uniform* method (Van Aert and Van Assen 2020) is an extension of *p*-uniform that solves the problem of overestimation of effect size if there is heterogeneity in a meta-analysis. Furthermore, it also enables, in contrast to *p*-uniform and also *p*-curve, estimation of heterogeneity and testing the null-hypothesis of no heterogeneity. *P*-uniform* is based on the same rationale as *p*-uniform and *p*-curve, but also includes statistically nonsignificant studies. That is, the method implicitly assigns different weights to statistically significant and nonsignificant studies by taking into account the likelihood of a study getting published given its statistical (non)significance (for technical details see Van Aert and Van Assen 2020). An important assumption of *p*-uniform* is that all statistically significant studies are assumed to be equally likely published and the same holds for all statistically nonsignificant studies. This implies that studies with statistically nonsignificant *p*-values of, for instance, 0.1 and 0.9 are assumed to be published with the same probability, but that this probability might differ for a study with a statistically significant *p*-value of 0.04.[6]

[5] Moderate heterogeneity is defined in terms of the I^2-statistic that is commonly used in meta-analysis to quantify the heterogeneity. The I^2-statistic (Higgins and Thompson 2002) indicates the proportion of total variance that can be attributed to heterogeneity in true effect size. Moderate heterogeneity is $I^2 = 0.5$ according to the rules-of-thumb proposed in Higgins et al. (2003).

[6] Research is currently ongoing to study whether this assumption can be relaxed by not only weighing statistically significant and nonsignificant studies differently in *p*-uniform* but also allow more complex weighting schemes. For example, marginally significant studies (i.e., studies with *p*-values just above the significance threshold) may have a different probability of being published than other nonsignificant studies.

A recent simulation study (Van Aert and Van Assen 2020) has shown that p-uniform* is indeed an improvement over p-uniform if heterogeneity is present and both statistically significant and nonsignificant studies are included in a meta-analysis. Researchers should, however, be cautious when interpreting the results of p-uniform* when publication bias is expected to be extreme in combination with only statistically significant studies in a meta-analysis. P-uniform*'s performance was not good in this condition and was outperformed by p-uniform if there was no heterogeneity. P-uniform* might also yield a very negative effect size estimate if many studies with p-values just below the significance threshold are included, but this was less of a problem than with p-uniform due to the inclusion of also statistically nonsignificant studies in p-uniform*.

P-uniform* can be applied by using the `puni_star()` function included in the `puniform` package,

```
puni_star(yi = yi, vi = vi, side = "right")
```

5.4.3 Weight-function model

The weight-function model (Hedges 1992; Vevea, Clements, and Hedges 1993) also enables estimation of the average effect size as well as between-study variance in a meta-analysis. The method creates intervals based on p-values, and then estimates the weights for the studies with p-values belonging to these intervals. Studies in the same interval get the same weight in the weight-function model. The intervals have to be specified by the meta-analyst and a reasonable choice is to create two intervals such that statistically significant and nonsignificant studies are treated differently. This model with two intervals is sometimes also referred to as the three-parameter selection model, because three parameters are estimated: the average effect size, between-study variance in true effect size (i.e, heterogeneity), and the relative weight specifying how much less likely a statistically nonsignificant study is published compared to a significant study.

The weight-function model outperformed the trim-and-fill method, p-uniform, and p-curve in simulation studies (McShane, Böckenholt, and Hansen 2016; Carter et al. 2019). A recent study (Van Aert and Van Assen 2020) comparing the weight-function model to p-uniform* revealed that the performance of both methods was comparable. Performance of the weight-function model was, just as of p-uniform*, not good in case of extreme publication bias in combination with only statistically significant studies in a meta-analysis, so the method is not recommended to be applied in meta-analyses with these characteristics. The weight-function model requires, in contrast to p-uniform, p-curve, and p-uniform*, estimation of the weights of the studies. This may cause convergence problems if a small number of studies is included in some of the intervals. Furthermore, Hedges and Vevea (1996) showed that estimation of the weights is often inaccurate, but that this hardly affected estimation of the average effect size and heterogeneity.

The weight-function model can be applied by using the `weightfunct()` function in the `weightr` package (Version 2.0.2, Coburn and Vevea 2016),

Weighing these studies differently may improve estimation and drawing inferences.

```
weightfunct(effect = yi, v = vi)
```

where the study's effect sizes and corresponding sampling variances can be supplied using the arguments `effect` and `v`, respectively.

6 Assessment of publication bias

We focused in the previous section on methods to correct for bias in the meta-analysis. Meta-analysts might, however, also want to quantify whether publication bias is likely present in their meta-analysis or test whether the hypothesis of no publication bias is rejected. We discuss methods for these purposes in this section.

6.1 Fail-safe *N*

The most popular method to study the impact of publication bias in a meta-analysis is the fail-safe N method (Rosenthal 1979). This method quantifies how many studies with an effect size of zero need to be added to a meta-analysis such that the meta-analytic effect size changes from being statistically significant to nonsignificant. Publication bias is unlikely if the fail-safe N is large, because many studies with an effect size of zero are then needed to no longer reject the null-hypothesis of no effect in the meta-analysis.

The fail-safe N method has been heavily criticized (e.g., Becker 2005; Iyengar and Greenhouse 1988; Orwin 1983; Scargle 2000; Schonemann and Scargle 2008) for multiple reasons. First, the method does not take the sample size of studies into account by treating all studies as if they are equally precise. Second, there is no clear criterion defining what a large fail-safe N is. Third, only studies with an effect size of zero are assumed to be missing. For this reason, Orwin (1983) extended the fail-safe N method by allowing meta-analysts to specify an average effect size of the missing studies that may differ from zero, and allowing computing the number of studies needed to get a meta-analytic estimate smaller than an user-specified effect size. A drawback of the originally proposed fail-safe N method as well as Orwin's extension is that heterogeneity in the meta-analysis is not taken into account, because all missing studies are assumed to have a common effect size. Due to these limitations, the fail-safe N method and Orwin's extension are discouraged to be used (Becker 2005; Vevea and Woods 2005; Jin, Zhou, and He 2014), and meta-analysts are referred to other methods that will be discussed next.

Nevertheless, the fail-safe N can be computed using

```
fsn(yi = yi, vi = vi)
```

6.2 Funnel plot asymmetry tests

The funnel plot introduced earlier can be used to examine visually whether small-study effects are present in a meta-analysis. However, eyeballing a funnel plot to assess small-study effects is known to be difficult (Terrin, Schmid, and Lau 2005). Hence, hypothesis tests were

developed to test whether a funnel plot is asymmetric and thus small-study effects are present in a meta-analysis. The rank-correlation test (Begg and Mazumdar 1994) tests whether the Kendall's rank correlation between the studies' effect sizes and sampling variances differs from zero after first stabilizing the sampling variances by standardizing the effect sizes (for technical details see Begg and Mazumdar 1994). A positive correlation implies that large effect sizes go along with large sampling variances and is indicative for small-study effects.

Another funnel plot asymmetry test is Egger's regression test (Egger et al. 1997) that actually formed the basis of the PET-PEESE method to correct effect size estimates. In Egger's regression test, the slope of the regression line fitted by applying PET is tested for statistical significance, and evidence for small-study effects is observed if this slope is significantly larger than zero. Egger's regression test has been modified in various ways where especially other predictors than the studies' standard error are used as predictor (for an overview see Jin, Zhou, and He 2014).

Simulation studies have shown that statistical power of Egger's regression test is generally larger than of the rank-correlation test (Sterne, Gavaghan, and Egger 2000). However, statistical power of both methods is low when a small number of studies are included in the meta-analysis (Macaskill, Walter, and Irwig 2001; Deeks, Macaskill, and Irwig 2005). Hence, both methods are recommended to be only applied if a meta-analysis contains more than ten studies (Sterne et al. 2011), and a significance level of 0.1 is recommended to be used for hypothesis testing (Egger et al. 1997). Another limitation of funnel plot asymmetry tests is that these, just as the funnel plot itself and other methods based on the funnel plot, test whether small-study effects are present and not explicitly test for publication bias.

The rank-correlation test can be applied using the following code

```
ranktest(res)
```

Egger's regression test is incorporated in the PET analysis when testing whether the slope coefficient is statistically significant and can also be obtained using the code

```
regtest(res)
```

6.3 Test of excess significance

The test of excess significance (TES, Ioannidis and Trikalinos 2007) tests whether more studies in a meta-analysis are statistically significant than expected. The expected number of statistically significant studies is obtained by taking the sum of each study's statistical power given that the meta-analytic effect size estimate is the true effect size. A hypothesis test (e.g., an exact, binomial, or Pearson's χ^2-test) can subsequently be used to test whether the observed number of statistically significant studies is larger than expected.

A problem with the TES is that the expected number of statistically significant studies is based on the meta-analytic effect size estimate that is likely to be overestimated if publication bias is present. Consequently, the statistical power of the studies and, in turn, also the expected number of statistically significant studies will be overestimated. This has also been observed in simulation studies where the TES was conservative (Francis 2013; Van

Assen, Van Aert, and Wicherts 2015; Vandekerckhove, Guan, and Styrcula 2013). Hence, it is recommended to apply the TES using 0.1 as significance level (Ioannidis and Trikalinos 2007). It is important to emphasize that publication bias is not the only cause of an excess of significant studies. Another reason is considerable heterogeneity, and the TES is therefore advised to be not applied when this is present in a meta-analysis (Ioannidis and Trikalinos 2007).

The TES can be applied using the code

```
tes(res)
```

6.4 Publication bias tests based on selection model approaches

The selection model approaches p-uniform and the weight-function model also implemented publication bias tests. In these methods, the estimated model that corrects for publication bias is compared with the conventional meta-analysis model that does not correct for bias. A statistically significant difference between these two models indicates that a selection model approach better fits the data, and that publication bias might be present.

Simulation studies have shown that p-uniform's publication bias test is conservative if the true effect size is large, and that statistical power of p-uniform's test was generally higher than of TES except for meta-analyses with a large true effect and more than 30 studies in the meta-analysis (Van Assen, Van Aert, and Wicherts 2015; Renkewitz and Keiner 2019). The properties of the publication bias test of the weight-function model are unknown and are therefore topic for future research. These publication bias tests are reported in the output of p-uniform and the weight-function model that can be obtained by applying these methods as described in the section on correcting effect size estimation corrected for bias.

7 Applying methods to examples

We apply the described methods to the earlier introduced meta-analyses of Cowlishaw et al. (2012) and Archer et al. (2012). Annotated R code of all analyses is available at https://osf.io/qjk9b/ to facilitate the application of these methods.

7.1 Example 1: Cowlishaw et al. (2012)

Table 2 shows the earlier described results of applying the random-effects meta-analysis to the data of Cowlishaw et al. (2012), and the results of the methods that correct for bias. This meta-analysis only contains seven studies and is therefore typical for meta-analyses in clinical psychology. All methods that estimate the between-study variance in true effects estimate it as zero and testing the null-hypothesis of homogeneity is for none of the methods statistically significant. Hence, the results of the methods that require homogeneous true effect size in the meta-analysis (WAAP, Top 10%, trim-and-fill, and p-uniform) can also be safely interpreted. Note that some results regarding estimation and testing the between-study variance are missing in Table 2 and denoted by "-", because these results could not be computed or are not reported by the methods.

Table 2: Results of applying random-effects meta-analysis and methods to correct for bias to the meta-analysis by Cowlishaw et al. (2012).

		Overall mean			Between-study variance		
	k	Estimate (SE)	(95% CI)	Test of no effect	Estimate (SE)	(95% CI)	Test of homogeneity
RE	7	0.519 (0.096)	(0.332;0.706)	z=5.432, p< .001	0 (0.035)	(0;0.125)	Q=3.897, p=.691
WAAP	1	0.291 (0.168)	(-0.037;0.619)	z=1.737, p =.082	$-^b$	$-^b$	Q=0, p=1
Top 10%	1	0.291 (0.168)	(-0.037;0.619)	z=1.737, p =.082	$-^b$	$-^b$	Q=0, p=1
Trim-and-fill	10	0.430 (0.083)	(0.267;0.593)	z=5.162, p< .001	0 (0.030)	(0;0.202)	Q=8.204, p=.514
PET-PEESE[a]	7	0.084 (0.195)	(-0.418;0.586)	t=0.430, p =.685	$-^c$	$-^c$	$-^c$
p-uniform	5	0.218 (-)	(-0.787;0.656)	L_0=-0.672, p =.251	$-^c$	$-^c$	$-^c$
p-uniform*	7	0.394 (-)	(0.059;0.721)	L_0=5.414, p =.020	0 (-)	(0;0.064)	L_{het}=0, p=1
Weight-fun.	7	0.328 (0.156)	(0.022;0.634)	z=2.100, p =.036	0 ($-^b$)	$-^b$	$-^c$

Note:
For the random-effects model and Trim-and-fill, between-study variance is estimated with the restricted maximum likelihood estimator (Raudenbush, 2009) and corresponding confidence intervals are created using the Q-profile method (Viechtbauer, 2007). RE = random-effects model, WAAP = weighted average of the adequately powered studies, PET = precision-effect test, PEESE = precision-effect estimate with standard error, Weight-fun. = weight-function model; k = number of studies in the analysis, SE = standard error, CI = confidence interval; [a] = results of PET analysis; -[b] = could not be computed by the method; -[c] = estimation or testing of the between-study variance is not included by the method.

Table 3: Results of applying tests for small-study effects and publication bias to the meta-analyses of Cowlishaw et al. (2012) and Archer et al. (2012).

	Cowlishaw et al. (2012)	Archer et al. (2012)
Fail-safe N	N=75	N=1216
Rank-cor. test	τ=0.238, p=.562	τ=0.391, p=.007
Egger's test	z=1.426, p=.154	z=3.17, p=.002
TES[a]	Exact p=.192	χ^2=1.545, p=.107
p-uniform	L_{pb}=1.284, p=.100	L_{pb}=-0.552, p=.709
Weight-fun.	χ^2=3.292, p=.070	χ^2=4.687, p=.030

Note:
[a] the default implementation of the Test of Excess Significance (TES) in the `tes()` function was used. Using this implementation an exact test was conducted for the meta-analysis by Cowlishaw et al. (2012) and a Pearson's χ^2-test for the meta-analysis by Archer et al. (2012).

The average effect size estimate of all methods was closer to zero than of the random-effects model. The smallest correction was by trim-and-fill that imputed three missing studies and the largest correction was by PET-PEESE that yielded an estimate close to zero. The results of WAAP and Top 10% have to be interpreted with caution, because estimates of these methods were only based on the most precise study in the meta-analysis. For this reason, the between-study variance in true effect size could also not be estimated for these methods. Only trim-and-fill, p-uniform*, and the weight-function model rejected the null-hypothesis of no effect and corroborated the hypothesis test of the random-effects model. Table 3 shows in the first column the results of the tests for small-study effects and publication bias. No method rejected the null-hypothesis of no bias in this meta-analysis. However, this may be caused by the small number of studies resulting in low statistical power of these tests. To conclude, correcting for bias yielded estimates closer to zero of all methods, and the null-hypothesis of no effect was not rejected by some methods. Although the tests for bias were not statistically significant, we argue that the evidence for CBT resulting in less financial loss of patients is weak at best.

7.2 Example 2: Archer et al. (2012)

Table 4 shows the results of effect size estimation and drawing inferences for the meta-analysis by Archer et al. (2012). This meta-analysis is typical for clinical psychology, because there is a large amount of heterogeneity in the meta-analysis. All methods estimated the between-study variance as positive and rejected the null-hypothesis of homogeneity. Hence, interpreting the results of the methods that do not perform well if large heterogeneity is present should best be avoided (WAAP, Top 10%, trim-and-fill, PET-PEESE, and p-uniform) and are only reported for completeness. The methods that allow large heterogeneity (p-uniform* and the weight-function model) estimated a lower average effect size than the random-effects model

that was statistically significant. Estimates of the between-study variance were similar of the random-effects model and p-uniform* and the weight-function model. The rank-correlation test, Egger's test, and the publication bias test of the weight-function model were statistically significant (second column of Table 3). This suggests that small-study effects or publication bias were present and might be the cause of the large effect size of the random-effects model compared to the other methods. To conclude, there is evidence for bias in the meta-analysis by Archer et al. (2012), because tests for small-study effects and publication bias were statistically significant and the corrected average effect size for bias were smaller than the one of the random-effects meta-analysis. However, the effect was larger than zero after correcting for bias, so collaborative care appeared to be beneficial for patients with depression or anxiety problems.

8 Summary

It is of utmost importance to address publication bias in every meta-analysis, which has also been advised by MARS (Appelbaum et al. 2018), PRISMA (Moher et al. 2009), and the Cochrane Collaboration (Page, Higgins, and Sterne 2019). We believe that publication bias should also be routinely assessed when developing and revising evidence-based clinical guidelines, such as the NICE guidelines in the UK or the AWMF guidelines in Germany, and when identify empirically supported treatments (ESTs) by the American Psychological Association's (APA) Division 12 (Tolin et al. 2015). In this chapter, we have described methods that can be applied for this purpose and summarized recommendations on when to apply each method (see Table 1).

Clinical psychologists who conduct a meta-analysis often encounter difficulties when addressing publication bias, because meta-analyses in clinical psychology are usually heterogeneous and contain a small number of studies, which are unfavorable conditions for the vast majority of publication bias methods (Niemeyer et al. 2020). However, recent research has shown that selection model approaches perform reasonably well when the number of studies in the meta-analysis is at least ten (Van Aert, Wicherts, and Van Assen 2019). Despite the promising results of selection model approaches, it is important that meta-analysts apply multiple publication bias methods in a so-called triangulation approach (Kepes et al. 2012; Coburn and Vevea 2015), because there is no publication bias method that outperformed all other methods in all conditions (Carter et al. 2019; Renkewitz and Keiner 2019). Such a triangulation approach should be preceded by a performance check to assess which methods perform well for the characteristics of the meta-analysis under study (Carter et al. 2019; Niemeyer et al. 2020). A performance check can be conducted by scrutinizing the literature on publication bias methods or assessing the performance of publication bias methods in a simulation study that resembles the characteristics of the meta-analysis as closely as possible.

We hope that this chapter helps clinical psychologists to apply state-of-the-art publication bias methods in their meta-analyses. Application of these publication bias methods has high potential for yielding relevant scientific insights, and will benefit policy-making and treatment of patients that is commonly based on the conclusions of meta-analyses.

Table 4: Results of applying random-effects meta-analysis and methods to correct for bias to the meta-analysis by Archer et al. (2012).

		Overall mean			Between-study variance		
	k	Estimate (SE)	(95% CI)	Test of no effect	Estimate (SE)	(95% CI)	Test of homogeneity
RE	24	0.240 (0.038)	(0.166;0.314)	z=6.347, p< .001	0.021 (0.010)	(0.009;0.070)	Q=83.580, p< .001
WAAP	6	0.155 (0.068)	(0.022;0.289)	z=2.285, p =.022	0.024 (0.018)	(0.008;0.164)	Q=47.556, p< .001
Top 10%	2	0.287 (0.135)	(0.023;0.550)	z=2.131, p =.033	0.034 (0.051)	(0.005;36.862)	Q=16.416, p< .001
Trim-and-fill	27	0.210 (0.041)	(0.130;0.290)	z=5.136, p< .001	0.029 (0.012)	(0.016;0.105)	Q=100.725, p< .001
PET-PEESE[a]	24	0.160 (0.042)	(0.073;0.247)	t=3.835, p =.001	−[c]	−[c]	−[c]
p-uniform	16	0.240 (-)	(0.154;0.374)	L_0=-4.309, p< .001	−[c]	−[c]	−[c]
p-uniform*	24	0.175 (-)	(0.067;0.280)	L_0=9.913, p =.002	0.015 (-)	(0.005;0.040)	L_{het}=29.502, p< .001
Weight-fun.	24	0.148 (0.057)	(0.036;0.261)	z=2.593, p =.010	0.017 (0.009)	(0;0.035)	−[b]

Note:
Estimates and confidence intervals are log-transformed risk ratios. For the random-effects model, WAAP, Top 10%, and Trim-and-fill, between-study variance is estimated with the restricted maximum likelihood estimator (Raudenbush, 2009) and corresponding confidence intervals are created using the Q-profile method (Viechtbauer, 2007). RE = random-effects model, WAAP = weighted average of the adequately powered studies, PET = precision-effect test, PEESE = precision-effect estimate with standard error, Weight-fun. = weight-function model; k = number of studies in the analysis, SE = standard error, CI = confidence interval; [a] = results of PEESE analysis; -[b] = could not be computed by the method; -[c] = estimation or testing of the between-study variance is not included by the method.

9 References

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