Robust Bayesian Meta-Analysis: Addressing Publication Bias with Model-Averaging

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Abstract

Meta-analysis is an important quantitative tool for cumulative science, but its application is frustrated by publication bias. In order to test and adjust for publication bias, we extend model-averaged Bayesian meta-analysis with selection models. The resulting Robust Bayesian Meta-analysis (RoBMA) methodology does not require all-or-none decisions about the presence of publication bias, can quantify evidence in favor of the absence of publication bias, and performs well under high heterogeneity. By model-averaging over a set of 12 models, RoBMA is relatively robust to model misspecification and simulations show that it outperforms existing methods. We demonstrate that RoBMA finds evidence for the absence of publication bias in Registered Replication Reports and reliably avoids false positives. We provide an implementation in R so that researchers can easily use the new methodology in practice.

   Keywords: Evidence, Heterogeneity, Selection Models

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Meta-analysis is the method of choice for aggregating evidence across a set of primary studies. However, studies that report statistically significant results (i.e., $p < .05$) are more likely to get published (Rosenthal & Gaito, 1964; Scheel et al., 2020; Wicherts, 2017), and this preferential publishing results in an inflated effect size estimate – a phenomenon known as publication bias (Rothstein et al., 2005). A variety of methods have been developed to test and adjust for publication bias. Citation counts suggest that funnel-based methods such as trim-and-fill (Duval & Tweedie, 2000) and Egger's regression (Egger et al., 1997) are most popular.[1] Alternative methods such as p-curve (Simonsohn et al., 2014) and PET-PEESE (Carter & McCullough, 2014) have recently been proposed and are increasing in popularity (for reviews see Carter et al., 2019 and Renkewitz and Keiner, 2019). The existing methods are predominantly based on the frequentist framework for statistical inference. In other words, these methods aim to control the long-term rate of false positives such that it does not exceed some frequency α. For an individual test, the methodology usually reduces to computing a p-value (i.e., the probability of encountering a test statistic at least as extreme as the one observed, under the assumption that the null-hypothesis of no difference holds) and assessing whether or not $p < \alpha$, with α usually set to 5% (Bartoš & Maier, 2019; Neyman, 1977). However, most existing methods to test and adjust for publication bias share several limitations.

A first limitation is that frequentist methods require researchers to decide whether or not to adjust for publication bias in all-or-none fashion, based on whether the p-value is smaller than the α level. This choice fails to take model uncertainty into account and, consequently, slight differences in p-values (e.g., .049 vs. .051) can lead to consequential changes in mean estimates. This problem is exacerbated because the number of primary

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[1] At the time of writing, January 19th 2020, Google Scholar indicated that these methods had $7,710$ and $32,286$ citations, respectively.

24 studies in a meta-analysis is often so low that confident inferences about publication bias

25 are beyond reach.

26   A second limitation is that frequentist methods cannot quantify evidence in favor of

27 the absence of publication bias; a non-significant p-value may indicate evidence of absence

28 or absence of evidence (Gallistel, 2009; Rouder et al., 2009). In practice, researchers often

29 assume that they do not need to worry about publication bias whenever a test for

30 publication bias is not significant. However, publication bias might still be present, with

31 the test lacking the statistical power to detect it (Renkewitz & Keiner, 2019).

32   A third limitation is that frequentist methods assume knowledge of the sampling

33 plan with which the studies accumulate over time (ter Schure & Grünwald, 2019). When

34 executing a meta-analysis on K primary studies, the implicit assumption is that an

35 experimenter planned to conduct K studies and then stop. This sampling plan is not

36 realistic; studies accumulate over time, either indefinitely or until a point has been

37 sufficiently proven or disproven. Assume a frequentist meta-analysis has been executed

38 based on the standard assumption that K studies (no more, no less) were ever going to be

39 reported. Next, study $K + 1$ comes in. For frequentist methods, this presents a

40 conundrum, as conducting another test invokes a multiple comparisons problem, with all of

41 the α already spent on the first test.

42   A fourth limitation is that most existing methods fail under high across-study

43 heterogeneity, as shown in simulation studies (Carter et al., 2019; McShane et al., 2016;

44 Renkewitz & Keiner, 2019). A notable exception are selection models (e.g., Iyengar &

45 Greenhouse, 1988; Vevea & Hedges, 1995) which perform well even under high

46 heterogeneity, although they have other problems such as poor convergence under few

47 primary studies (Field & Gillett, 2010; Terrin et al., 2003).

48   To overcome the above limitations, we developed an extension of Bayesian

49 model-averaged meta-analysis (BMA). Below we start by introducing BMA (Gronau,

50 van Erp, et al., 2017) which is the first component of our method. Next, we introduce

selection models as a framework to test and adjust for publication bias – the second

component of our method. These two components are then brought together to yield

Robust Bayesian Meta-Analysis (RoBMA), a model-averaged meta-analytical framework in

the presence of publication bias.

We illustrate the methods by applying them to two data sets. The first data set

concerns the meta-analysis by Anderson et al. (2010) on violent video games and aggressive

behavior. Anderson et al. (2010) concluded that "exposure to violent video games is a

causal risk factor for increased aggressive behavior". However, several researchers have

questioned this conclusion, suggesting instead that the results are contaminated by

publication bias (e.g., Ferguson & Kilburn, 2010; Hilgard et al., 2017). We focus our

analysis on the 27 experimental studies that meet Anderson and colleagues' (2010) best

practice criteria.[2] The second data set concerns 28 meta-analyses from the Many Labs 2

data (Klein et al., 2018); this data set is particularly useful because we know the ground

truth: publication bias is absent. Consequently, the different tests for publication bias can

be compared based on how many false positives they produce. Finally, we present a

simulation study comparing RoBMA to other methods under different conditions for

heterogeneity, effect size, and publication bias.

Component 1: Model-Averaged Bayesian Meta-Analysis

Our method is based on BMA as introduced in Gronau, van Erp, et al. (2017). This

method applies four models simultaneously (Figure 1), differentiated according to whether

they assume an overall effect to be absent or present, and whether they assume

across-study heterogeneity to be absent (i.e., fixed effects, when the effect size is the same

across the primary studies) or present (i.e., random effects, when effect sizes differ across

the primary studies). Thus, BMA features the following four models:

1. The fixed effects null hypothesis ($\mathcal{H}_0^f$)

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[2] The data are available at https://github.com/Joe-Hilgard/Anderson-meta.

76   2. The fixed effects alternative hypothesis ($\mathcal{H}_1^f$)

77   3. The random effects null hypothesis ($\mathcal{H}_0^r$)

78   4. The random effects alternative hypothesis ($\mathcal{H}_1^r$)

79 The default setting for BMA is to assume that all four models are equally likely a priori

80 (cf. Figure 1). The relative plausibility of the four rival models is then updated according

81 to Bayes' theorem: models that predict the observed data relatively well receive a boost in

82 plausibility, whereas models that predict the data relatively poorly suffer a decline

83 (Wagenmakers et al., 2016).

Figure 1

Prior Model Probabilities of BMA
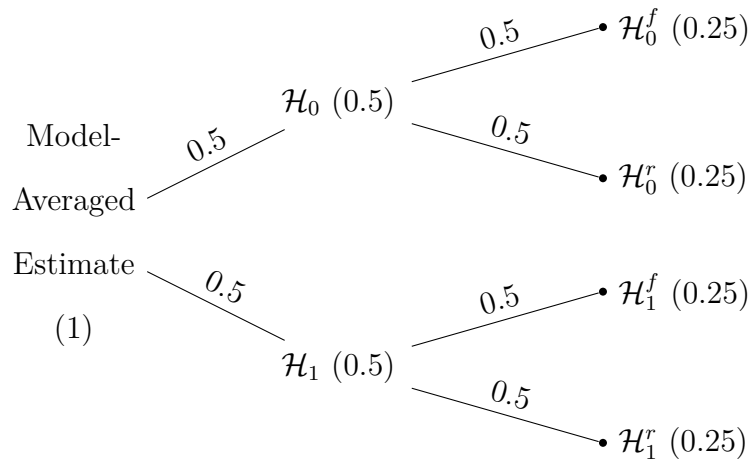
Note. Total probabilities are displayed on the nodes and conditional probabilities on the edges. $\mathcal{H}_0$ denotes the models assuming the null hypotheses to be true, $\mathcal{H}_1$ denotes the models assuming the alternative hypotheses to be true. $\mathcal{H}^f$ denotes fixed effects models, $\mathcal{H}^r$ random effects models.

84   With only two models under consideration, their relative predictive performance is

85 given by the Bayes factor (Etz & Wagenmakers, 2017; Kass & Raftery, 1995; Rouder &

86 Morey, 2019; Wrinch & Jeffreys, 1921). To illustrate, Equation 1 shows that the Bayes

87 factor for the random effects alternative hypothesis $\mathcal{H}_1^r$ versus the fixed effects alternative

88 hypothesis $\mathcal{H}_1^f$ equals the change from prior to posterior odds brought about by the data:

$$\underbrace{\frac{p(\text{data} \mid \mathcal{H}_1^r)}{p(\text{data} \mid \mathcal{H}_1^f)}}_{\text{Bayes factor}} = \underbrace{\frac{p(\mathcal{H}_1^r \mid \text{data})}{p(\mathcal{H}_1^f \mid \text{data})}}_{\text{Posterior odds}} \Big/ \underbrace{\frac{p(\mathcal{H}_1^r)}{p(\mathcal{H}_1^f)}}_{\text{Prior odds}} . \tag{1}$$

89 When $\mathcal{H}_1^r$ and $\mathcal{H}_1^f$ are equally plausible a priori, the prior odds equal 1 and the

90 Bayes factor reduces to the posterior odds. For instance, if $\mathcal{H}_1^r$ predicted the observed data

91 three times better than $\mathcal{H}_1^f$ (i.e., the Bayes factor equals three) then the posterior odds also

92 equal three, meaning that the posterior model probability for $\mathcal{H}_1^r$ equals $3/4 = .75$, leaving

93 .25 for $\mathcal{H}_1^f$. A common rule of thumb is to regard Bayes factors between 1 and 3 as weak or

94 anecdotal evidence, Bayes factors between 3 and 10 as moderate evidence, and Bayes

95 factors larger than 10 as strong evidence (e.g., Jeffreys, 1939, Appendix I; Lee and

96 Wagenmakers, 2013, p. 105). However, "This set of labels facilitates scientific

97 communication but should only be considered an approximate descriptive articulation of

98 different standards of evidence" (Lee and Wagenmakers, 2013, p. 105); by reducing a

99 continuous measure for the strength of evidence to a discrete category, information is

100 inevitably lost (Jeffreys, 1938).[3]

$$\underbrace{\text{BF}_{10}}_{\substack{\text{Inclusion Bayes factor} \\ \text{for effect}}} = \underbrace{\frac{p(\mathcal{H}_1^f \mid \text{data}) + p(\mathcal{H}_1^r \mid \text{data})}{p(\mathcal{H}_0^f \mid \text{data}) + p(\mathcal{H}_0^r \mid \text{data})}}_{\substack{\text{Posterior inclusion odds} \\ \text{for effect}}} \Big/ \underbrace{\frac{p(\mathcal{H}_1^f) + p(\mathcal{H}_1^r)}{p(\mathcal{H}_0^f) + p(\mathcal{H}_0^r)}}_{\substack{\text{Prior inclusion odds} \\ \text{for effect}}} . \tag{2}$$

101 The inclusion Bayes factor BF_{rf} for the test of heterogeneity is obtained similarly, by

102 contrasting $\mathcal{H}_r = \{\mathcal{H}_0^r, \mathcal{H}_1^r\}$ to $\mathcal{H}_f = \{\mathcal{H}_0^f, \mathcal{H}_1^f\}$. Note that inclusion Bayes factors are able

103 to distinguish between "absence of evidence" (i.e., when BF_{10} and BF_{rf} are close to 1) and

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[3] On p. 378, Jeffreys (1938) discusses thresholds on BF_{01} (which he termed K) as follows: "we are at

liberty to surround $K = 1$ by two other values and say that within this range the data are not sufficiently

decisive, and even this device would be purely one of convenience and sacrifice some information given by

the actual values of K."

104 "evidence of absence" (i.e., when BF_{10} and BF_{rf} are close to 0, or, equivalently, when BF_{01}

105 and BF_{fr} are much larger than 1).[4] Also note that Bayes factors quantify evidence on a

106 continuous scale, and this evidence can be seamlessly updated as more studies accumulate

107 (Berger & Wolpert, 1988; Rouder, 2014).

108   In addition to testing for effect size and across-study heterogeneity, the BMA

109 framework can also be used to estimate parameters. For instance, the overall posterior

110 distribution for the meta-analytic effect is a weighted combination of the estimates from

111 each of the four individual models, with the weights equal to the model's posterior

112 probability. This process is known as Bayesian model-averaging (Hoeting et al., 1999; for a

113 conceptual introduction see Hinne et al., in press) and it obviates the need to base

114 inference on a single model in all-or-none fashion. This is particularly advantageous when

115 there is considerable posterior uncertainty about whether a fixed effects or a random effects

116 model is most appropriate. In such scenarios, the Bayesian model-averaging result is

117 substantially influenced by both model classes.

118   Recently, BMA has been used to estimate the effect of power posing (Gronau,

119 van Erp, et al., 2017), to test compensatory control theory (Hoogeveen et al., in press),

120 study the effectiveness of descriptive social norms (Scheibehenne et al., 2017), to analyze a

121 registered replication report on facial feedback (Hinne et al., in press), to investigate how

122 researchers subjective decisions when designing studies influence the results (Landy et al.),

123 and to conduct a Bayesian multiverse analysis on the data of Many Labs 4 (Haaf et al.,

124 2020). A primer on BMA is presented in Gronau, Heck, et al. (2020). However, most past

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[4] The first and second subscript of the Bayes factor denote the model in the numerator and the denominator, respectively; so BF_{AB} means $p(\text{data} \mid \mathcal{H}_A)/p(\text{data} \mid \mathcal{H}_B)$, and BF_{BA} means $p(\text{data} \mid \mathcal{H}_B)/p(\text{data} \mid \mathcal{H}_A)$. When Bayes factors are lower than 1, it is recommended to switch numerator and denominator, because "$BF_{AB} = 0.2$, the data are 0.2 times more likely under $\mathcal{H}_A$ than under $\mathcal{H}_B$" is more difficult to interpret than the equivalent statement "$BF_{BA} = 5$, the data are 5 times more likely under $\mathcal{H}_B$ than under $\mathcal{H}_A$".

125 applications concern prospective meta-analyses, that is, meta-analyses on registered

126 reports. The main reason for this is that BMA cannot yet adjust for publication bias.

127   We illustrate BMA using the data from Anderson et al. (2010).[5] As can be seen in

128 Figure 1 we assume equal prior probabilities for the four different models. Figure 2 shows

129 the associated posterior model probabilities. The model that best predicts the data is $\mathcal{H}_1^f$,

130 the fixed effects model that assumes the presence of an effect. This model has a posterior

131 probability of 0.773. The second-best model is $\mathcal{H}_1^r$, the random effects model that assumes

132 the presence of an effect with a posterior probability of 0.277. When comparing sets of

133 models using the inclusion Bayes factor, we find weak support favoring the fixed effects

134 models over the random effects model (i.e., $\text{BF}_{fr} = 3.41$)[6] and overwhelming support for

135 the alternative of an effect of violent video games on aggressive behavior ($\text{BF}_{10} =$

136 8.75×10^9).

137   The model-averaged posterior mean effect size estimate $r = .211$, 95% CI [0.171,

138 0.247] is then obtained after weighting the effect size implied by each model according to

139 its posterior probability. In this particular case the estimate is based most strongly on $\mathcal{H}_1^f$

140 and $\mathcal{H}_1^r$, and almost not at all influenced by $\mathcal{H}_0^f$ and $\mathcal{H}_0^r$.

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[5] We fit BMA using the `metaBMA` R package (Heck et al., 2017; see also Gronau, Heck, et al., 2020).

[6] As a calculation example based on Equation 2: the prior odds are $(0.25 + 0.25)/(0.25 + 0.25) = 1$ and the posterior odds $(0.773 + 0)/(0.227 + 0) = 3.41$ corresponding to a Bayes factor of $3.41/1 = 3.41$.

Figure 2

Posterior Model Probabilities for a BMA of Anderson et al. (2010)
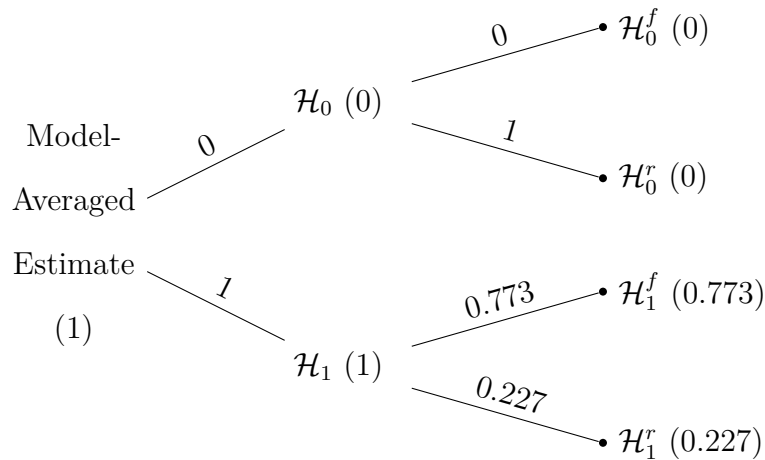
Note. Total probabilities are displayed on the nodes and conditional probabilities on the edges. $\mathcal{H}_0$ denotes the models assuming the null hypotheses to be true, $\mathcal{H}_1$ denotes the models assuming the alternative hypotheses to be true. $\mathcal{H}^f$ denotes fixed effects models, $\mathcal{H}^r$ random effects models.

However, Ferguson and Kilburn (2010) and Hilgard et al. (2017) have argued that the original effect size reported in Anderson et al. (2010) was overestimated due to publication bias. BMA cannot test or adjust for the possibility of publication bias; to do so, we now turn to selection models.

Component 2: Selection Models

Our approach to publication bias is based on selection models that operate on p-values (e.g., Hedges, 1992; Iyengar & Greenhouse, 1988; Vevea & Hedges, 1995). These selection models use weighted distributions to account for the proportion of studies that are missing because they yielded non-significant results. The researcher specifies the p-value cut-offs that drive publication bias (usually $p = .05$). The selection model then estimates how likely studies in non-significant intervals are to be published compared to the interval with the highest publication probability (usually $p < .05$). The pooled effect

[153] size estimate accounts for the estimated publication bias by giving more weight to studies

[154] in intervals with lower publication probability (usually non-significant studies). Selection

[155] models can also test for publication bias. To do so, the unadjusted model –either a fixed or

[156] a random effects meta-analytic model– is compared to the corresponding selection model

[157] using a likelihood ratio test. This test uses a χ^2 statistic to reject the null hypothesis of no

[158] publication bias whenever the p-value is lower than the conventional 5% α level, or lower

[159] than an α level of 10%, a more lenient threshold which is sometimes advocated because it

[160] increases power (Renkewitz & Keiner, 2019).

[161] Another type of selection models, so-called "Copas" selection models, specify the

[162] probability of a study being published as a function of both effect sizes and standard errors

[163] (Copas, 1999; Copas and Li, 1997; Copas and Shi, 2001; for recent Bayesian versions see

[164] Bai et al., 2020; Mavridis et al., 2013). In this paper we focus on the selection models

[165] based on p-values; these selection models have been extensively tested in simulation studies

[166] and are most popular in practice (e.g., Carter et al., 2019).

[167] Selection models are one of the few methods that have been shown to work well

[168] even under high heterogeneity (Carter et al., 2019; McShane et al., 2016) and can be

[169] specified flexibly according to the assumed model of publication bias (e.g., assuming

[170] different probability of publication for marginally significant studies with $p \in [.05, .10]$).

[171] Finally, the assumed model of the publication process (i.e., selection based on statistical

[172] significance) is a well-founded model for how publication bias operates in practice

[173] (Masicampo & Lalande, 2012; Rosenthal & Gaito, 1964; Wicherts, 2017).

[174] To illustrate the methodology of selection models we revisit the example of

[175] Anderson et al. (2010). We use the `weightr` R package (Coburn et al., 2019) and initially

[176] specified a two-sided selection with different probabilities for significant and marginally

significant studies (i.e., with cutoffs at $p = 0.05$, 0.10).[7] Because all effects were positive we were forced to alter the model and include only p-value cut-offs in the expected direction (i.e., one-sided selection). We first tested for presence of heterogeneity (with $\alpha = 0.05$). The test is not significant, $Q(22) = 15.09$, $p = 0.89$, so we proceeded with a fixed effect model (Bartoš et al., 2020). The fixed effect model indicates significant publication bias (i.e., $X^2(2) = 13.58$, $p = 0.001$, using $\alpha = 0.10$). Estimates for the relative publication probability in the different intervals indicate that marginally significant results are only 28% as likely to be published than significant findings and non-significant results are only about 8% as likely to be published (Figure 3). Adjusting for this publication bias corrects the effect size estimate downwards although the effect remains significant, $r = .140$, 95% CI [.077, .201], $z = 4.33$, $p < .001$.

However, in addition to the general limitations of frequentist methods (i.e., ignoring model uncertainty, inability to quantify evidence for the absence of an effect, and dependence on an unknown sampling plan), selection models have more specific limitations as well. In particular, they often cannot be estimated under small sample size, especially when there are few studies in any of the p-value intervals (e.g., Terrin et al., 2003; but see Citkowicz and Vevea, 2017, for a recent attempt to solve this problem by modeling the weight function as a beta distribution). Furthermore, selection models are mainly available in the `weightr` package (Coburn et al., 2019) and the `selectMeta` package (Rufibach, 2015) in the programming language `R`, limiting their accessibility. This is arguably the reason why they have not been adopted more widely despite their desirable properties (Card, 2015, p. 275).

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[7] The `weightr` R package allows the specification of p-values cut-offs on one-sided p-values directly. To achieve two-sided selection with significant and marginally significant studies, the following one-sided p-value cutoffs need to be specified, (0.025, 0.05, 0.95, 0.975).

Figure 3

Estimated Weight Function with 95% CI for Anderson et al. (2010).
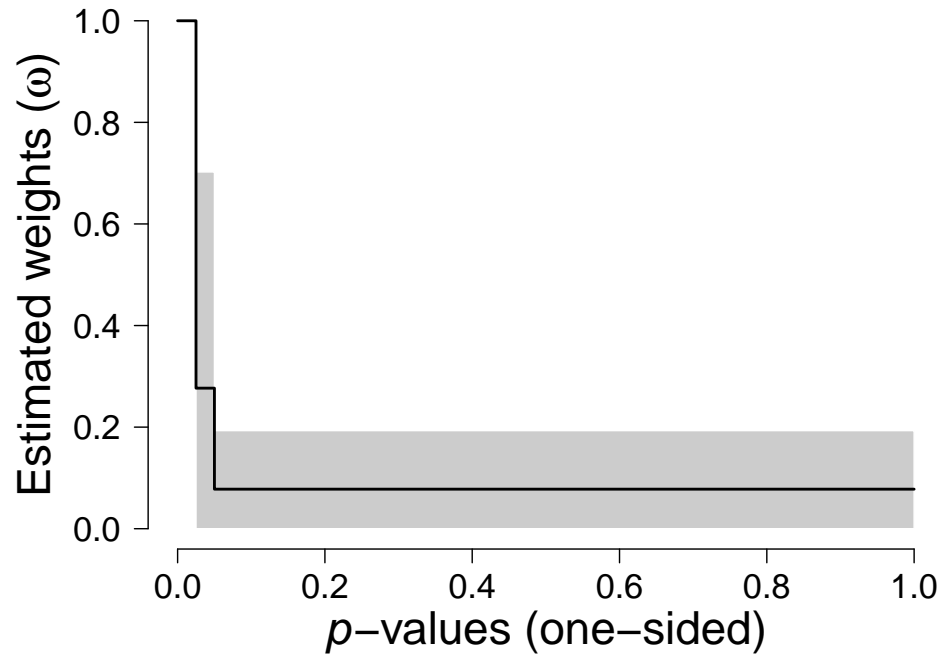
Note. Results are based on the selection model outlined in Vevea and Hedges (1995). The weight for significant studies is set to one. "Marginally" significant and non-significant studies are then weighted according to their relative probability of publication.

Combining Model-Averaged Bayesian Meta-Analysis and Selection Models: Robust Bayesian Meta-Analysis (RoBMA)

We propose Robust Bayesian Meta-Analysis (RoBMA), a Bayesian multi-model method that aims to overcome the limitations of existing procedures. RoBMA is an extension of BMA obtained by adding selection models to account for publication bias. This allows model-averaging across a larger set of models, ones that assume publication bias and ones that do not.

As shown in Figure 4, RoBMA partitions the model space according to three characteristics. As in BMA, we differentiate between models that do ($\mathcal{H}_1$) and do not ($\mathcal{H}_0$) assume the presence of an effect, and between models that assume homogeneity (fixed

₂₀₉ effects; $\mathcal{H}^f$) and heterogeneity (random effects; $\mathcal{H}^r$). RoBMA generalizes BMA by also

₂₁₀ differentiating models assuming the absence of publication bias ($\mathcal{H}^{\overline{\omega}}$) and models assuming

₂₁₁ its presence ($\mathcal{H}^{\omega}$). Comparing the predictive accuracy of the latter two model types allows

₂₁₂ us to test for the presence or absence of publication bias.

Figure 4

Different Models Included in RoBMA and Their Prior Probabilities
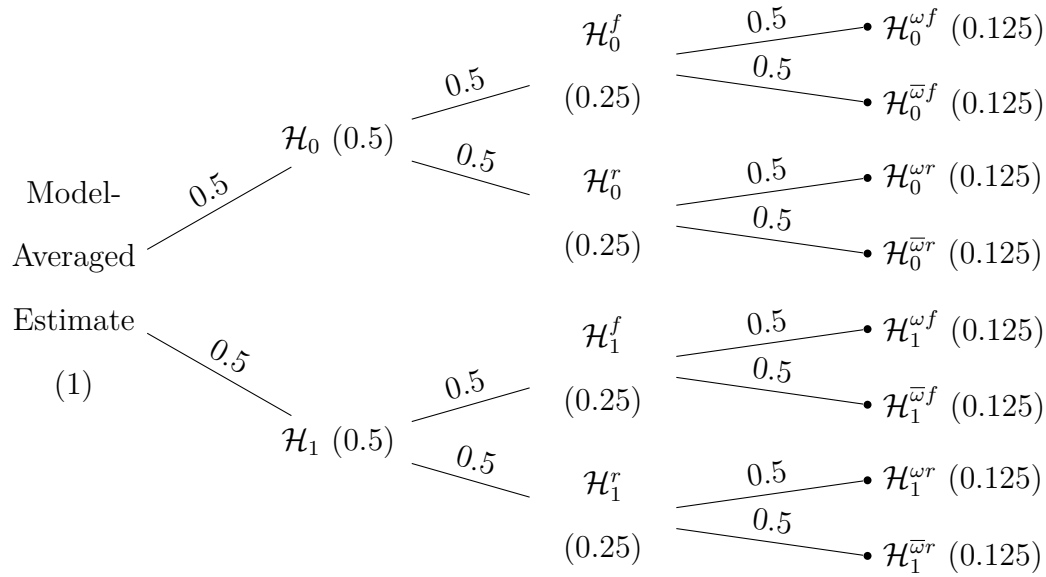
Note. RoBMA features two publication bias models (i.e., two and three-steps) that are not distinguished in the plot. Total probabilities are displayed on the nodes and conditional probabilities on the edges. $\mathcal{H}_0$ denotes the models assuming the null hypotheses to be true, $\mathcal{H}_1$ denotes the models assuming the alternative hypotheses to be true. $\mathcal{H}^f$ denotes fixed effects models, $\mathcal{H}^r$ random effects models, $\mathcal{H}^{\omega}$ publication bias models, and $\mathcal{H}^{\overline{\omega}}$ models without publication bias.

₂₁₃ The models assuming the absence of publication bias are identical to the models

₂₁₄ described by Gronau, van Erp, et al. (2017). For the models that assume the presence of

₂₁₅ publication bias, we specified two selection processes (not shown in Figure 4). The first

₂₁₆ selection process is a two-step model that distinguishes only between significant and

₂₁₇ non-significant studies assuming that significant studies are more likely to be published.

₂₁₈ The second selection process is a three-step model that includes marginally significant

₂₁₉ results as a separate category. We specify both processes to be independent of the direction

₂₂₀ of the effect. Therefore, marginal significance also corresponds to one-sided significance at

₂₂₁ the $\alpha = .05$ level. By including several models for publication bias the overall approach is

₂₂₂ relatively robust to model misspecification. Overall, RoBMA includes the following 12 (i.e.,

₂₂₃ 2x2x3) different models of the data generating process:

₂₂₄   1. The fixed effects null hypothesis without publication bias ($\mathcal{H}_0^{\overline{\omega}f}$)

₂₂₅   2. The fixed effects alternative hypothesis without publication bias ($\mathcal{H}_1^{\overline{\omega}f}$)

₂₂₆   3. The random effects null hypothesis without publication bias ($\mathcal{H}_0^{\overline{\omega}r}$)

₂₂₇   4. The random effects alternative hypothesis without publication bias ($\mathcal{H}_1^{\overline{\omega}r}$)

₂₂₈   5. The fixed effects weighted null hypothesis with publication bias ($\mathcal{H}_0^{\omega f}$) which

₂₂₉   subdivides into

₂₃₀   (a) a model with two-step selection ($\mathcal{H}_0^{\omega_2 f}$)

₂₃₁   (b) a model with three-step selection ($\mathcal{H}_0^{\omega_3 f}$)

₂₃₂   6. The fixed effects weighted alternative hypothesis with publication bias ($\mathcal{H}_1^{\omega f}$) which

₂₃₃   subdivides into

₂₃₄   (a) a model with two-step selection ($\mathcal{H}_1^{\omega_2 f}$)

₂₃₅   (b) a model with three-step selection ($\mathcal{H}_1^{\omega_3 f}$)

₂₃₆   7. The random effects weighted null hypothesis with publication bias ($\mathcal{H}_0^{\omega r}$) which

₂₃₇   subdivides into

₂₃₈   (a) a model with two-step selection ($\mathcal{H}_0^{\omega_2 r}$)

₂₃₉   (b) a model with three-step selection ($\mathcal{H}_0^{\omega_3 r}$)

240   8. The random effects weighted alternative hypothesis ($\mathcal{H}_1^{\omega r}$) which subdivides into

241   (a) a model with two-step selection ($\mathcal{H}_1^{\omega_2 r}$)

242   (b) a model with three-step selection ($\mathcal{H}_1^{\omega_3 r}$)

243   As can be seen in Figure 4, we distribute prior probability evenly across the

244 different pairs of model classes. In other words, a priori we assume a probability of 0.5 of

245 publication bias, a 0.5 probability for heterogeneity, and a 0.5 probability for a true effect

246 (Figure 4). In the case of the publication bias models, the prior probability is further

247 divided, assigning 0.5 probability to the two-step models and 0.5 probability to the

248 three-step models. Regarding the probability of the individual models, this results in a

249 probability of 0.125 (0.5/4) for each of the models assuming no publication bias and 0.0625

250 (0.5/8) for each of the models assuming publication bias.

251   Regarding the parameter prior distributions, we used a normal distribution with

252 mean zero and a standard deviation of 1 for the effect size. This prior distribution assigns

253 high probability to a wide range of effect sizes, without being as heavy-tailed as the

254 popular Cauchy distribution. For heterogeneity, we used inverse gamma with $\alpha = 1$ and

255 $\beta = 0.15$. This estimate is based on empirical heterogeneities for the field of Psychology

256 (van Erp et al., 2017). The prior distribution on the weights parameter is the cumulative

257 sum of the Dirichlet distribution with α set to (1,1) for the two-interval model and (1,1,1)

258 for the three-interval model. Thus, the weight for the significant studies is always equal to

259 one and the weights increase monotonically with decreasing p-values. We fit the models

260 with the `RoBMA` (Bartoš & Maier, 2020) R package. The package estimates the individual

261 models via MCMC sampling using `JAGS` (Plummer, 2003), specifically the `runjags` R

262 package (Denwood, 2016). While `JAGS` incorporates most common distributions we also

263 added custom weighted distributions that were required to implement the selection models.

264 To obtain the marginal likelihoods, the package uses bridge sampling (Gronau, Sarafoglou,

265 et al., 2017) implemented in the `bridgesampling` R package (Gronau, Singmann, et al.,

266 2020). More detailed specifications of RoBMA can be found in Appendix A.

267   Although this is the default setup and the setup that will be used in the examples

268 and in the simulation study of this paper, we wish to stress that RoBMA can be

269 customized in several ways. For example, some methodologists have argued that only

270 random effects meta-analysis should be used (e.g., Borenstein, 2019). This advice can be

271 followed by simply removing the fixed effects models from RoBMA. Apart from adding and

272 removing models one can also alter the assignment of prior model probabilities. For

273 instance, the belief that the null hypothesis is relatively unlikely may be incorporated by

274 lowering the prior model probabilities for the associated models. Finally, in practice

275 researchers should also feel free to use different parameter prior distributions when

276 conducting meta-analyses, depending on their prior knowledge and the specific hypotheses

277 under consideration. For example, when the possibility of very large effect sizes cannot be

278 ruled out a Cauchy prior might be preferable over the normal prior distribution. An R

279 vignette that explains how to modify RoBMA is available at

280 https://cran.microsoft.com/web/packages/RoBMA/vignettes/CustomEnsembles.html.

281   To illustrate, we apply RoBMA to the example of Anderson et al. (2010). As can be

282 seen in Figure 4, all model pairs are equally likely a priori. Figure 5 shows the associated

283 posterior probabilities. After updating by the data the two most likely models are the

284 weighted fixed effects alternative ($H_1^{\omega f}$) and the weighted random effects ($H_1^{\omega r}$) alternative.

285 Those two models take up almost all posterior probability (86% and 13.6%). When

286 comparing sets of models using the inclusion Bayes factor the data overwhelmingly support

287 the presence of effect size ($\text{BF}_{10} = 1.05 \times 10^7$) and publication bias ($\text{BF}_{\omega\overline{\omega}} = 381.69$), while

288 support for the fixed effects models is moderate ($\text{BF}_{fr} = 6.29$). The final inference is,

289 therefore, based most strongly on the effect-present fixed and random effects models that

290 include publication bias; consequently, the model-averaged posterior mean corrects the

291 meta-analytical effect size estimate downwards in comparison to BMA, $r = .151$, 95% CI

292 [.094, .207].

Figure 5

Posterior Model Probabilities for the Different Types of Models in RoBMA After Updating on the Data of Anderson et al. (2010)
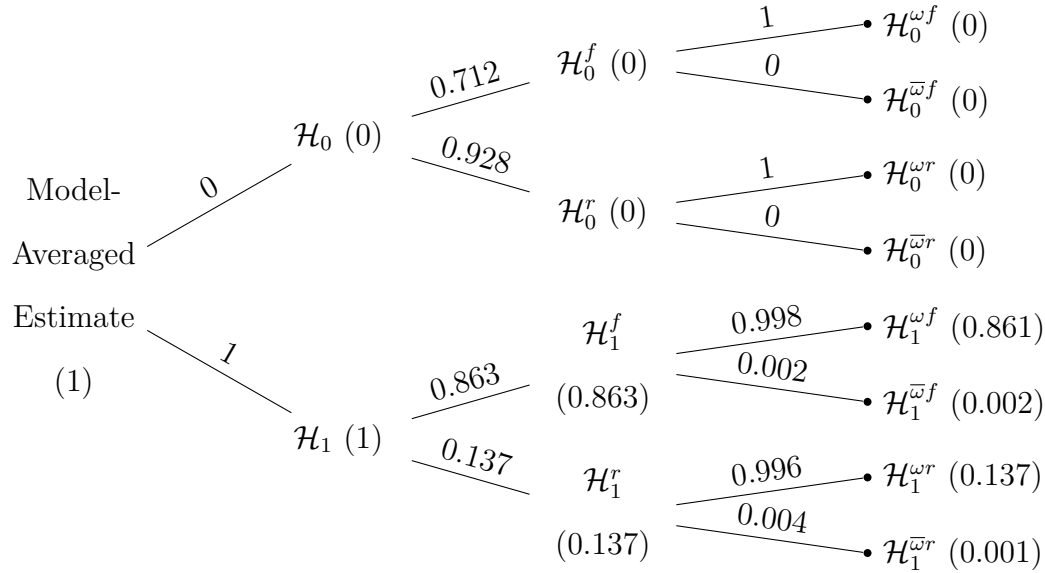
Note. RoBMA features two publication bias models (i.e., two and three-steps) that are not distinguished in the plot. Total probabilities are displayed on the nodes and conditional probabilities on the edges. $\mathcal{H}_0$ denotes the models assuming the null hypotheses to be true, $\mathcal{H}_1$ denotes the models assuming the alternative hypotheses to be true. $\mathcal{H}^f$ denotes fixed effects models, $\mathcal{H}^r$ random effects models, $\mathcal{H}^\omega$ publication bias models and $\mathcal{H}^{\overline{\omega}}$ models without publication bias.

293 ## RoBMA Benefits

294   The first benefit of RoBMA is that Bayes factors can quantify evidence for the

295 absence of publication bias. This is especially important since frequentist tests for

296 publication bias usually have low power to detect publication bias if it is present

297 (Renkewitz & Keiner, 2019). Therefore, a non-significant test for publication bias does not

298 usually imply the absence of publication bias. RoBMA allows researchers to differentiate

299 between absence of evidence and evidence of absence.

300   The second benefit of RoBMA is that the Bayesian framework mitigates the

301 estimation problems that arise when some of the p-value intervals contain only few studies.

302 If one of the p-value intervals misses sufficient observations, the weights are still

303 constrained by prior distributions. Therefore, the model can also be estimated on few

304 primary studies. However, in this context it is important to choose priors carefully and

305 evaluate the robustness to prior specification by examining how the conclusions change

306 when using different parameter priors on the weights.

307   The third benefit of RoBMA is that the Bayesian model-averaging removes the need

308 for a variety of all-or-none p-value-based decisions required by frequentist methods. In

309 other words, RoBMA allows researchers to retain all models, weighting their inferential

310 impact by their posterior probability. The option to include multiple models of the

311 publication process also makes selection models more robust to model misspecification.

312 Model-averaging should be especially beneficial when there is substantial uncertainty about

313 the best model. In addition, model-averaging avoids the danger of making incorrect

314 analysis choices since the data will directly guide the inference to be based most strongly

315 on the best model.

316   Unsurprisingly, we are not the first to realize these benefits. Non model-averaging

317 Bayesian selection models have been proposed over 20 years ago (Givens et al., 1995;

318 Larose & Dey, 1998; Silliman, 1997; Smith et al., 2001) and more recently Guan and

319 Vandekerckhove (2016) showed model-averaging over fixed effects models. However,

320 heterogeneous effect sizes are the norm, rather than the exception in psychology (e.g.,

321 McShane et al., 2016). Therefore, we extend model-averaging to include random effects

322 models. In addition, we add Bayes factor tests for the presence or absence of publication

323 bias. Finally, we implement the Bayesian model-averaged meta-analysis in an `R` package

324 `RoBMA` (Bartoš & Maier, 2020) and we also recently developed a version for the the

open-source statistical software program JASP (Bartoš et al., 2020; JASP Team, 2020) .

This allows researchers without programming experience to conduct state-of-the-art

publication bias-adjusted meta-analysis.

In the remainder of this paper, we test RoBMA and compare it with existing

meta-analytic techniques. First, we used the 28 studies from Many Labs 2 –here we know

that publication bias is absent– to assess the possible tendency to produce false positives

when testing for publication bias. Second we performed a simulation study to compare

RoBMA with other methods under different conditions for publication bias, effect size,

heterogeneity, and number of primary studies.

Testing False Positives on Many Labs 2

It is hard to assess the performance of different methods on published meta-analyses

since the true parameters are usually unknown. However, it is possible to assess the false

positive rate of tests for publication bias using Registered Reports (Chambers, 2013, 2019).

Registered Reports are subject to a two-stage peer review process. In the first, pre-data

stage, peer review concerns only the introduction and method sections; when the

experimental design and data analysis plan are sufficiently convincing, the manuscript

receives "in principle acceptance", which means that the journal commits to publishing the

results independent of the outcome (Chambers et al., 2015). Therefore, in the case of

Registered Reports we know that all primary studies are published regardless of the result;

in other words, if a method detects publication bias, this is a false positive finding. In

addition, Registered Reports allow an empirical test of RoBMA's ability to quantify

evidence in favor of the absence of publication bias. Therefore, we compared RoBMA to

different methods for publication bias using the registered replication report Many Labs 2

(Klein et al., 2018). This large-scale project attempted to replicate 28 classic and

contemporary effects from psychology. Each effect was subject to a replication attempt

from about half of the 125 participating labs (comprising $15,305$ participants from 36

countries in total). The median Cohen's d across the 28 replicated effects was 0.15. One

effect had τ larger .2, while the others all had values near $\tau = .10$.[8]

In addition to RoBMA, we included Vevea and Hedges (1995) selection models with

two-steps or three-steps and two-sided selection. Similar to the Anderson example, we first

applied the test for heterogeneity before proceeding to the test for publication bias.[9] In

addition to RoBMA and the selection models, we also test for publication bias using Trim

and Fill (Duval & Tweedie, 2000), Replicability Index (Schimmack, 2020), Egger

Regression (Egger et al., 1997 ; which corresponds to testing for publication bias using the

PET part of PET-PEESE; Stanley and Doucouliagos, 2014), and the Test for Excess

Significance (Ioannidis & Trikalinos, 2007). For an explanation of these methods see

Renkewitz and Keiner (2019) and Schimmack (2020). For Egger Regression we used code

from Carter et al. (2019); for Replicability Index and Test for Excess Significance we used

code provided by dr. Schimmack; for Trim and Fill we used the `trimfill` function from

the `metafor` (Viechtbauer, 2010) R package with the RO estimator; for selection models

we used the `weightr` R package (Coburn et al., 2019); and for the RoBMA models we used

the `RoBMA` R package (Bartoš & Maier, 2020). For frequentist methods we used $\alpha = .10$ as

significance level (Renkewitz & Keiner, 2019) whereas for RoBMA we used the inclusion

$\text{BF}_{w\overline{w}} > 3$ as a discrete "evidence threshold" (e.g., Jeffreys, 1939). In practice, we

recommend researchers interpret Bayes factors as a continuous measure of evidence rather

---

[8] We used the reported t-statistics and sample sizes for studies analyzed using (Welch) t-tests (16 effects).
For the remaining 12 effects, we computed t-statistic from the reported correlation coefficients.

[9] Because the frequentist implementation of selection models requires at least 3 p-values in each interval,
we join intervals with fewer than 3 p-values. If there was only one interval left, we used either a random or
fixed meta-analytical model based on the test of residual heterogeneity (with $\alpha = .05$). Otherwise, we
fitted a selection model, first tested for residual heterogeneity (with $\alpha = .05$), selected either fixed or
random effect model and then used a likelihood ratio test (with $\alpha = .10$) to determine whether or not to
use an adjusted model. If an adjusted model was selected but all of the estimated weights were higher than
1, we set the publication bias p-value to 1 and proceeded with the unadjusted model.

370 than by reference to discrete thresholds. We use thresholds here only to interpret

371 RoBMA's performance in terms of false positive rate and power, thereby enabling a

372 comparison to frequentist methods.

373   As can be seen in Figure 6, RoBMA, the two selection models (i.e., 'SM2' and

374 'SM3'), and Trim and Fill had either no or few false positives (0% for SM2 and SM3; 3.6%

375 or 1/28 for RoBMA; 7.1% or 2/28 for Trim and Fill; i.e., results with $p < .10$ or

376 $\mathrm{BF}_{w\overline{w}} > 3$). However, in contrast to the two frequentist selection models, RoBMA also

377 provided evidence in favor of the absence of publication bias in 43% of cases (i.e., for 12/28

378 studies). The other methods (i.e., Replicability Index, Egger regression, and the Test for

379 Excess Significance) fare worse and incorrectly find evidence for publication bias in 29% of

380 cases or more (i.e., 8/28 for Replicability Index, 9/28 for Egger regression, 11/28 for the

381 Test for Excess Significance).

Figure 6

False Positives of Different Methods Using the 28 Effects Studied in Many Labs 2 (Klein et al., 2018)
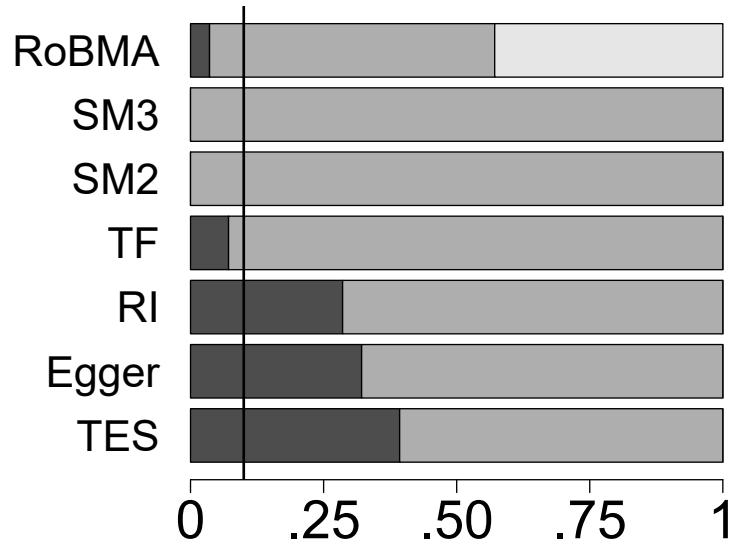
Note. SM3 = three-step selection model, SM2 = two-step selection model, RI = Replicability Index, TES = Test for Excess Significance. Black areas indicate evidence for publication bias (BF > 3, $p < .10$), grey areas indicate ambiguous evidence regarding publication bias (1/3 < BF < 3, $p > .10$), and white areas indicate evidence for the absence of publication bias (BF < 1/3, only applicable to RoBMA).

Simulation Study

Methods

To test the performance of RoBMA under different conditions we designed a simulation study in which we manipulated the following four parameters:

1. The population mean: $\mu = (0, 0.2, 0.5)$

2. The heterogeneity: $\tau = (0, 0.2)$

3. The number of primary studies in each meta-analysis: K = (10, 30, 100)

4. Three different conditions for publication bias with ω denoting the probability of publication for (1) non-significant findings (2) marginally significant findings, and (3) significant findings:

   (a) No publication bias: $\omega_1 = 1$, $\omega_2 = 1$, $\omega_3 = 1$

   (b) Moderate publication bias: $\omega_1 = 0.2$, $\omega_2 = 0.5$, $\omega_3 = 1$

   (c) Severe publication bias: $\omega_1 = 0$, $\omega_2 = 0$, $\omega_3 = 1$

Significance was assessed based on two-sided p-values. The sample size of the primary studies in the meta-analysis was sampled from a negative binomial distribution based on empirical sample sizes that we extracted from Stanley et al. (2018, Figure in Appendix B). We also conducted one simulation to assess method performance under extreme p-hacking of a null effect ($\mu = 0$, $\tau = 0$). The results of this simulation can be found in Appendix C. Each of the presented conditions was repeated 500 times.

In all simulations, we compared the performance of RoBMA to that of several different methods. To test for publication bias we used the same methods as in the Many Labs 2 example presented above. For effect size estimation and testing, we kept RoBMA, two and three-step selection models, and Trim and Fill, since the other methods are only suited to test for publication bias. Instead we added p-curve (Simonsohn et al., 2014), PET-PEESE (Stanley & Doucouliagos, 2014) and vanilla BMA (Gronau, van Erp, et al., 2017) to test for and estimate the meta-analytical effect size. A review and explanation of the different frequentist methods can be found in (Carter et al., 2019; Renkewitz & Keiner, 2019; Schimmack, 2020). The implementation of the additional methods for effect size estimation and testing, PET-PEESE, p-curve and Trim and Fill (estimation)[10] was based on code from Carter et al. (2019). For the frequentist methods, we used $\alpha = .05$ as significance level for the effect size test and $\alpha = .10$ for the test of publication bias. For the

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[10] Carter et al. (2019) used Trim and Fill with the default *L0* estimator that does not allow to test for publication bias.

₄₁₃ Bayesian methods, we used BF > 10 as "evidence threshold" for effect size testing and BF

₄₁₄ > 3 for the test of publication bias. For estimation with RoBMA and BMA we used the

₄₁₅ model-averaged posterior mean as the point estimate. As before we do not recommend

₄₁₆ interpreting Bayes factors in terms of these thresholds; we used them here solely to

₄₁₇ facilitate the comparison to frequentist methods.

Results

₄₁₉   Our results indicate that RoBMA outperforms other meta-analytic methods in most

₄₂₀ conditions. Averaging across all conditions RoBMA usually had the lowest root mean

₄₂₁ squared error (RMSE) and bias (cf. Figure 7). RoBMA performs best in 65% of conditions

₄₂₂ when ranked according to RMSE (Figure 8a) and in 36% of conditions when ranked

₄₂₃ according to bias (Figure 8b). Results were computed conditional on method convergence.

₄₂₄ *P*-curve converged in 95.5% of effect size estimations and tests, Trim and Fill in 99.8% of

₄₂₅ effect size estimations. All other methods converged in 100% of cases.

Figure 7

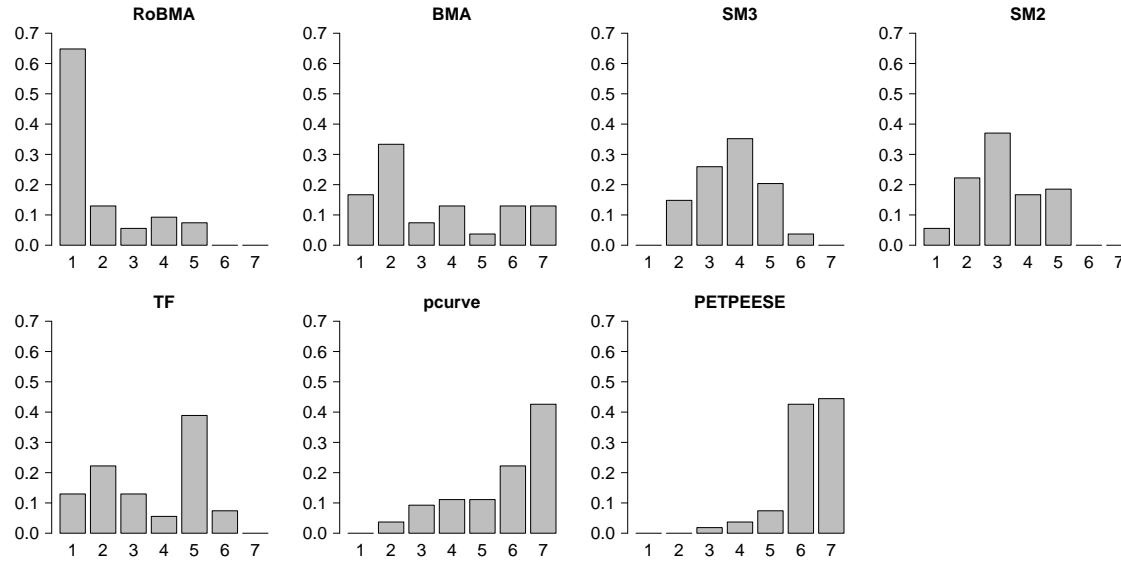*Boxplots of RMSE and Bias Across Simulation Conditions*
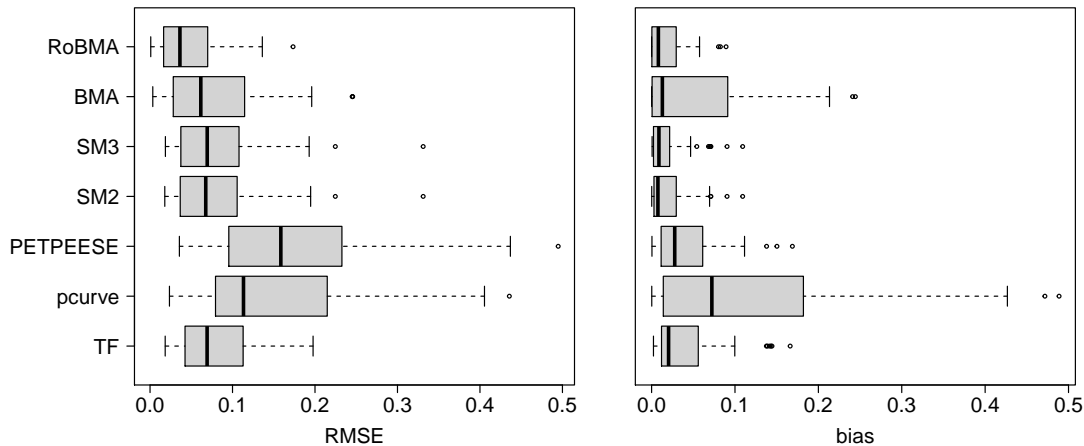
Note. SM3 = three-step selection model, SM2 = two-step selection model, TF = Trim and Fill. We omit 10 conditions with RMSE > .5 for *p*-curve, 1 condtion with RMSE > .5 for PET-PEESE, and 4 conditions with bias > .5 for *p*-curve.
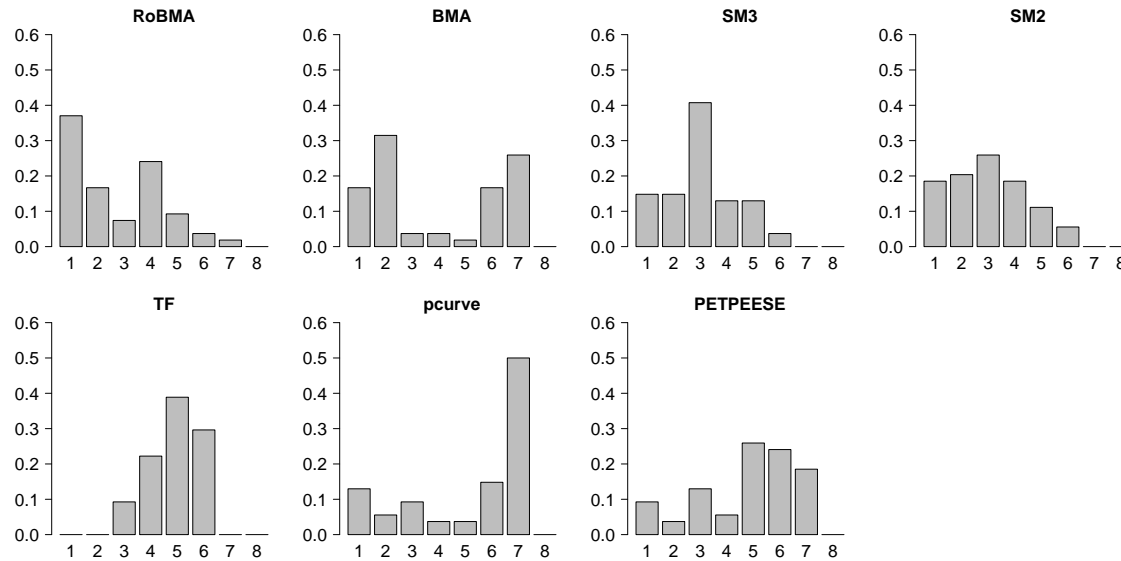
Figure 8

Ranked RMSE and Bias of the Population Mean Estimates of Different Methods Across Conditions

(a) *RMSE*

(b) *Bias*

Note. SM3 = three-step selection model, SM2 = two-step selection model, TF = Trim and Fill. A rank of one means that a method performed best in a simulation condition while rank seven indicates that a method performed worst. The y-axis indicates in which share of simulations a given method achieved a rank.

⁴²⁶   While presenting all individual conditions is beyond the scope of this paper (they

⁴²⁷ can be found at https://osf.io/buk8g/), we show the results from three conditions that we

⁴²⁸ find of particular interest to psychologists in Figure 9 since they seem to cover a range of

⁴²⁹ values typical for meta-analysis in psychology (e.g., Stanley et al., 2018). These are K =

⁴³⁰ 30, $\mu = 0$, $\tau = 0$, $\omega = (0.2, 0.5, 1)$; K = 30, $\mu = 0.2$, $\tau = 0.2$, $\omega = (1, 1, 1)$; and K = 30, μ

⁴³¹ = 0.2, $\tau = 0.2$, $\omega = (0.2, 0.5, 1)$.

Figure 9

Results for Selected Scenarios with 30 Primary Studies
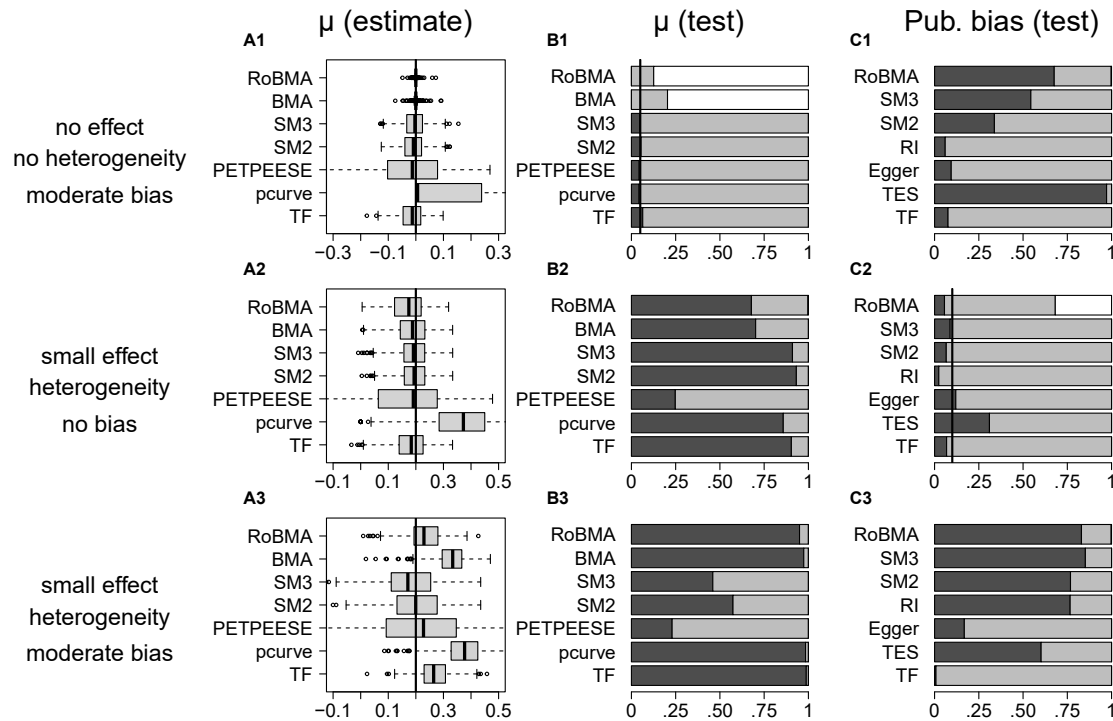
Note. For testing black lines indicate evidence for the alternative, white indicates evidence

for the null (only applicable for Bayesian methods), and grey undecided. BMA = Bayesian

meta-analysis, SM3 = Selection model with three-steps, SM2 = selection model with two-

steps, TF = Trim and Fill, RI = Replicability Index, TES = Test for Excess Significance.

⁴³²   As can be seen in panel A, RoBMA estimates the pooled mean usually precise,

⁴³³ although sometimes with slight underestimation due to model-averaging involving the null

hypotheses (A2) or a slight overestimation due to the involvement of models assuming no bias (A3). For the effect size test (panel B) RoBMA has high power to detect a null effect (B1) and few false positives. Panels B2 and B3 show that power to detect a true effect is also satisfactory. The test for publication bias in panel C shows that only the Test for Excess Significance seems to have higher power (C1 and C3), however, that is mitigated by a false positive rate of 30% under no publication bias (C2). RoBMA, on the other hand, shows few false positives as well as high power to detect publication bias. RoBMA's test for the absence of publication bias has lower power (C1), however, the other simulation conditions (https://osf.io/buk8g/) show that the power increases with more primary studies. In addition, the conditions available at https://osf.io/buk8g/ show that RoBMA sometimes overestimates or underestimates when there are only 10 primary studies in the meta-analysis, although performance is still good compared to other methods. In addition, Appendix C shows that RoBMA leads to substantial overestimation under strong p-hacking. Although this limitation is shared with most other methods, it should be noted that Vevea and Hedges (1995) selection models perform better than RoBMA under strong p-hacking.

To summarize, RoBMA outperformed the other methods in most conditions examined here. In some conditions, RoBMA has lower power than other methods; however, these methods suffer from an inflated false positive rate in other conditions. In addition, RoBMA has a tendency to underestimate effect size whenever the alternative is true (due to the inclusion of the null models) and overestimate effect size under publication bias (due to the inclusion of the models assuming no publication bias). However, as can be seen in the online materials, these biases are slight and disappear under larger sample sizes, when almost all weight is given to the correct models. Finally, RoBMA fares noticeably worse than Vevea and Hedges (1995) selection model under strong p-hacking.

Concluding Comments

In this paper, we introduced a robust Bayesian meta-analysis that model-averages over selection models as well as fixed and random effects models. By applying a set of twelve models simultaneously our method respects the underlying uncertainty when deciding between different meta-analytical models and is comparatively robust to model misspecification. RoBMA also performs well in different simulation conditions and correctly finds support for the absence of publication bias in the Many Labs 2 example. Besides this ability to quantify the evidence for absence of publication bias, the Bayesian approach also allows updating evidence sequentially as studies accumulate, addressing recent concerns about accumulation bias (ter Schure & Grünwald, 2019).

As are all models, our model is based on assumptions. First, the test statistics follow a (weighted) normal distribution around the true effect size with additive heterogeneity. Second, we make assumptions about the publication process, specifically, that selection is based on p-values and that studies with smaller p-values are more likely to be published. Other methods, such as Egger regression (Egger et al., 1997) are based on different assumptions of the publication process. Therefore, these methods were disadvantaged in our simulation in which we operationalized publication bias based on significance. However, our model is supported by empirical findings regarding the publication process and p-value distributions (e.g., Masicampo & Lalande, 2012) and outperforms other methods on the real data example of Many Labs 2.

We are currently investigating the possibility of adding more models to the RoBMA ensemble such as different weight functions (Citkowicz & Vevea, 2017; Iyengar & Greenhouse, 1988; Patil & Taillie, 1989), "Copas" selection models (Copas, 1999; Copas & Li, 1997; Copas & Shi, 2001), or PET-PEESE models (Stanley & Doucouliagos, 2014). While these additions are beyond the scope of the current paper, the RoBMA methodology is sufficiently flexible to include any plausible model for publication bias and unify different competing approaches under a single model-averaging umbrella.

As a general methodological point, we acknowledge that some researchers believe that testing null hypotheses is not meaningful or interesting; instead, these researchers wish to focus on estimation (e.g., Cumming, 2014; Cumming, 2013; Gelman et al., 2014; Kruschke, 2015). This philosophy can be accommodated within the framework of RoBMA. To do so, researchers can simply remove the null models (i.e., the model assuming no effect, the fixed-effects model, and the model assuming no publication bias) and then proceed with estimating RoBMA as usual (e.g., see the vignettes for the R package on https://cran.r-project.org/web/packages/RoBMA/). Also, the R package allows researchers to retrieve the conditional parameter estimates. In other words, after fitting RoBMA –including the null models for testing– researchers may decide to engage in estimation using only those models that assume the effect of interest to be present.

To conclude, this work offers applied researchers a new, conceptually straightforward method to conduct meta-analysis. Instead of basing conclusions on a single model, our method is based on keeping all models in play, with the data determining model importance according to predictive success. The simulations and the example suggest that RoBMA is a promising new method in the toolbox of various approaches to test and adjust for publication bias in meta-analysis.

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Appendix A

Specifications of RoBMA

In the previous version of our manuscript and the `RoBMA` package (Bartoš & Maier, 2020, versions < 1.2), we followed a description of the Bayesian version of selection models outlined in Equations 2 and 3 of Larose and Dey (1998). However, after the selection process has filtered out the observed effects that are relatively small, the true random effects will no longer be normally distributed. Especially under high heterogeneity, the Larose and Dey assumption may distort the model fit and unduly lower the marginal likelihood. Therefore, motivated by the frequentist specification of selection models (Vevea & Hedges, 1995) we adapted our model such that it does not estimate the true effects directly but rather marginalizes them out of the likelihood. A similar approach to a Bayesian random effects meta-analysis was recently described as a "marginalized random-effects meta-analysis" (van Aert & Mulder, 2020).

A Bayesian selection model with a three-step weight function, assuming a standard normal prior distributions for the meta-analytic effect size μ, inverse-gamma distribution for between-study heterogeneity τ, and a cumulative sum of Dirichlet distribution for the weights ω, with y_k and σ_k denoting the observed effect sizes and standard errors for the k in 1:K studies, can be denoted as,

$$\mu \sim \text{Normal}(0, 1)$$
$$\tau \sim \text{Inverse-gamma}(1, 0.15)$$
$$\omega \sim \text{Cumulative-Dirichlet}(1, 1, 1) \tag{3}$$
$$y_k \sim \text{Weighted-normal}(\mu, \tau^2 + \sigma_k^2, \omega).$$

745 *Weighted-normal* stands for a likelihood function of a weighted normal distribution, with

746 mean μ, variance $\tau^2 + \sigma_k^2$, weights ω, and a cumulative probability function of a standard

747 normal distribution Φ,

$$\text{Weighted-normal}(y_k|\mu, \tau^2 + \sigma_k^2, \omega) = \frac{\text{Normal}(y_k|\mu, \tau^2 + \sigma_k^2) \times w(\omega, p_k)}{\int \text{Normal}(x|\mu, \tau^2 + \sigma_k^2) \times w(\omega, (1 - \Phi(x/\sigma_k)) * 2)dx},$$

(4)

748 where the weights ω are assigned based on the two-sided p-values, p_k, through the weight

749 function w,

$$w(\omega, p_k) = \begin{cases} \omega_1, & \text{if } p_k > 0.10 \\ \omega_2, & \text{if } 0.05 < p_k \le .10 \\ 1, & \text{if } p_k \le .05 \end{cases}$$

(5)

750   The remaining models can be obtained either by restricting $\mu = 0$ for models

751 assuming no effect size, restricting $\tau = 0$ for fixed effect models, by changing the weight

752 functions w (and the prior on ω) to use only two steps for the two-steps weight function, or

753 by using normal distribution for the observed effect sizes for the models assuming no
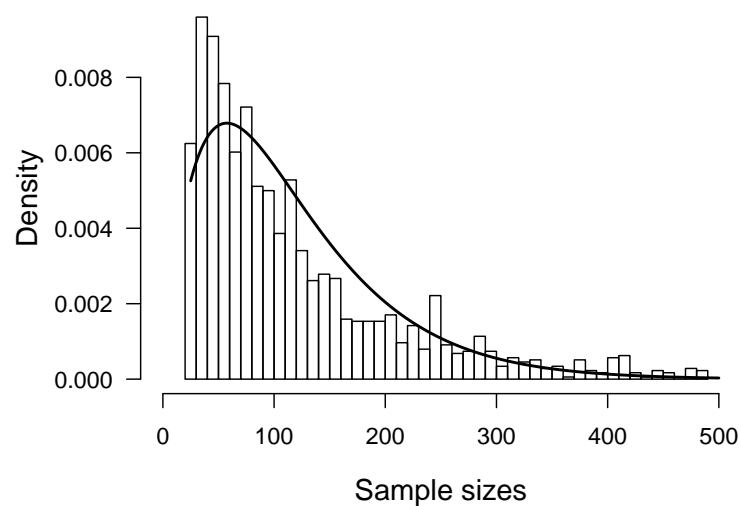
754 publication bias.

Appendix B

Sample Sizes

755   Sample sizes where extracted from empirical meta-analyses in Stanley et al. (2018). The

756   data can be found at https://osf.io/2vfyj/files/.

Figure B1

*Distribution of Sample Sizes Used for the Simulation*

Note. The histogram is overlaid with Negative binomial distribution with shape $r = 2$ and scale $\theta = 58$, truncated at 25 and 500 which was used for generating sample sizes for the simulation.

Appendix C

P-**hacking Simulation**

We operationalized strong *p*-hacking by starting with two groups of 10 participants, testing the difference after adding one additional participant to a condition, and stopping either upon reaching significance or collecting 100 participants overall. Then, the K = (10, 30) studies are presented as being in the expected direction and published under either moderate or severe publication bias. Trim and Fill did not converge in 0.35% of cases, other methods always converged. The simulations for intense *p*-hacking show that RoBMA overestimates the effect size by about 0.2. This is less than many other methods but more than frequentist selection models (Figure C1) . Since *p*-hacking is common in psychological literature (e.g., Simmons et al., 2011) this shows that effect sizes might still be overestimated even after adjusting for publication bias.

Figure C1

Effect Size Estimation Under Strong p-*Hacking*
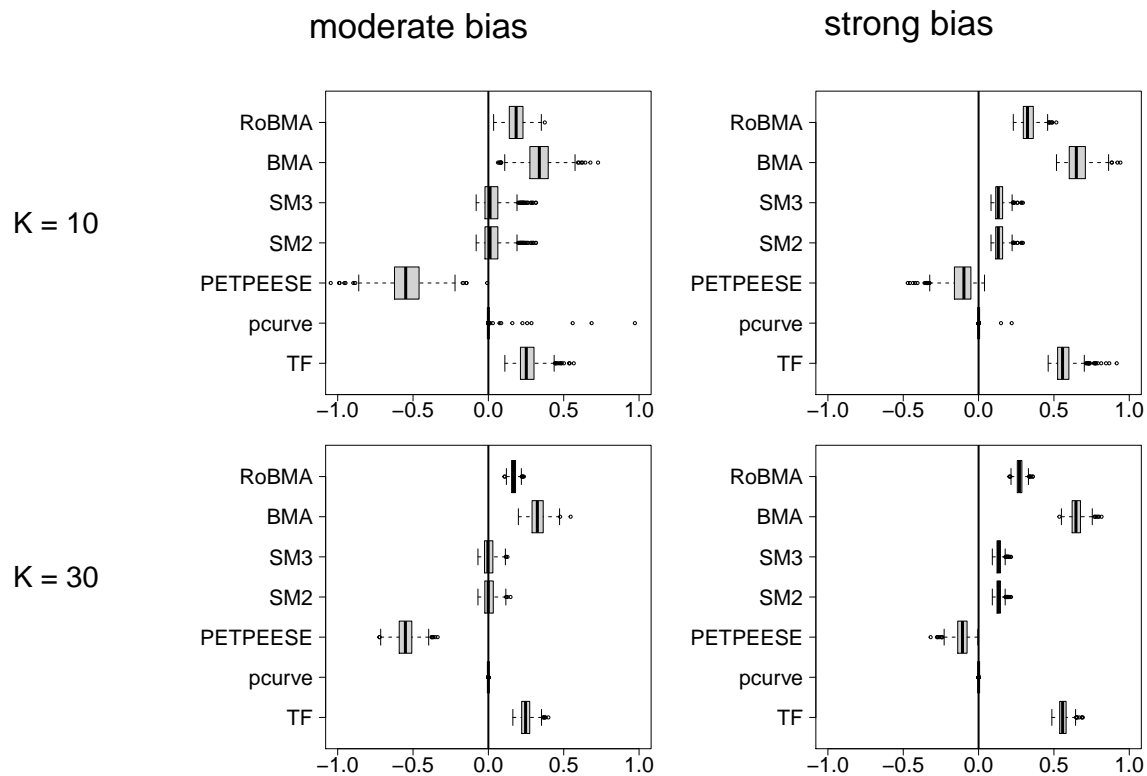
Note. BMA = Bayesian meta-analysis, SM2 = two-parameter selection model, SM3 = three-parameter selection model, TF = Trim and Fill.