A Robust Bayesian Copas Selection Model for Quantifying and Correcting Publication Bias

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Abstract

The validity of conclusions from meta-analysis is potentially threatened by publication bias. Most existing procedures for correcting publication bias assume normality of the between-study heterogeneity. However, this assumption may not be valid, and the performance of these procedures may be highly sensitive to departures from normality. Further, there exist few measures to quantify the magnitude of publication bias based on selection models. In this paper, we address both of these issues. First, we introduce the robust Bayesian Copas (RBC) selection model. This model serves as a default prior that requires minimal problem-specific tuning, offers robustness to strong assumptions about the distribution of heterogeneity, and facilitates automatic inference of the unknown parameters. Second, we develop a new measure to quantify the magnitude of publication bias. Our measure is easy to interpret and takes advantage of the natural estimation uncertainty afforded by the posterior distribution. We illustrate our proposed approach through simulation studies and analysis of real data sets. Our methods are implemented in the publicly available 

R package RobustBayesianCopas.

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1 Introduction

Meta-analysis is a powerful technique for combining statistical evidence from multiple related studies. By synthesizing information from multiple studies, meta-analysis often has higher statistical power and precision than a single study [22]. A standard model in meta-analysis is the random effects model [19, 34], which is specified as

$$y_i = \theta + \tau u_i + s_i \epsilon_i, \quad i = 1, \ldots, n,$$

(1.1)

where $u_i$ and $\epsilon_i$ are independent and distributed as $\mathcal{N}(0,1)$ for all $i = 1, \ldots, n$. In (1.1), $y_i$ is the reported treatment effect for the $i$th study, $\theta$ is the population treatment effect of interest, the $u_i$'s are random effects for the between-study heterogeneity, and the $\epsilon_i$'s are within-study errors, further scaled by each study’s reported standard error $s_i$. The parameter $\tau > 0$ quantifies the amount of between-study heterogeneity.

The validity of meta-analysis is greatly compromised by the potential presence of publication bias, or the tendency for journals to publish studies showing significant results [44, 20]. In the presence of such bias, the studies in the published literature are a biased selection of the research in that area, resulting in biased estimation and misleading inference about $\theta$ [21]. A great deal of effort has gone into developing statistical methods to detect and correct publication bias. Graphical methods, such as the funnel plot, are one popular approach to this problem. Funnel plots assess the asymmetry of a scatter plot of the treatment effects from individual studies against their corresponding precisions. The presence of asymmetry in a funnel plot indicates potential publication bias [9, 39, 38]. Statistical tests to formally detect scatter plot asymmetry, such as regression tests [1, 9, 39, 27] and rank-based tests [8], have also been introduced. Duval and Tweedie [8] further develop a “trim and fill” method for estimating and adjusting for the number and impact of missing studies in meta-analysis.

As an alternative to graph-based methods, selection models have also been developed. Unlike graphical methods, selection models directly address the issue of missing studies. The idea behind this approach is that the observed sample of studies is a biased sample of research done in a particular area, which was produced by a specific selection process. For example, Hedges [16], Givens et al. [13], and Rufibach [36] model the likelihood of a study being selected (i.e. published) as a function of the $p$-value obtained under the hypothesis that there is not a significant treatment effect. Copas and colleagues further introduced a flexible framework in which the probability of selection is modeled as a function of both the effect size and its...
standard error [5, 3, 4, 6]. In addition to correcting for potentially biased estimates of $\theta$ in (1.1), several statistical tests for the Copas selection model have been developed, e.g. goodness of fit tests [4] and score tests [7]. A detailed description of the Copas selection model is provided in Section 2.

There is strong empirical evidence in support of using the Copas selection model for correcting publication bias. Based on 157 meta-analyses with binary outcomes, Schwarzer et al. [37] showed that the Copas selection model gave superior performance over the trim-and-fill method, with better results among the 22 meta-analyses with evidence of selection bias. Carpenter et al. [2] also showed that the Copas selection model gave a clear interpretation in 80 percent of the meta-analyses.

In spite of its benefits, the Copas selection model relies on the assumption that the heterogeneous random effects $u_i, i = 1, \ldots, n$, are distributed as standard normal. This is actually a rather strong assumption, and it cannot be justified using the Central Limit Theorem even when the number of studies is large [18, 23, 43]. In Section 5, we illustrate that the results from selection models that assume normally distributed heterogeneity can be highly sensitive to violations of normality. In addition, existing non-Bayesian inference procedures for the Copas selection model typically rely on asymptotic arguments to construct confidence intervals for the parameters or to perform tests for publication bias [4, 33, 7]. These asymptotic approaches to inference can be potentially problematic in practice, because often times, meta-analysis is performed with a small number of studies, sometimes fewer than five [28]. For example, an analysis of 14,886 meta-analyses from the *Cochrane Database of Systematic Reviews* found that over 90% of meta-analyses featured fewer than 10 studies [42, 24]. Thus, many of the tests developed for graphical approaches or selection models may not have sufficient power for small samples.

Given these issues, Bayesian approaches for correcting publication bias have a distinct advantage. First, Bayesian methods can provide further robustness through a robust prior on the between-study heterogeneity. Second, Bayesian methods automatically allow for nonasymptotic inference about unknown parameters through their marginal posterior distributions. In this work, we introduce the *robust Bayesian Copas selection* (RBC) model which specifically addresses the issue of robustness in the conventional Copas selection model. Unlike previous work on Bayesian selection models, e.g. Mavridis et al. [29], the RBC model also utilizes a default set of noninformative priors on all the unknown parameters. This allows RBC to serve as a good default prior with minimal need for tuning by practitioners.

In standard meta-analysis (1.1) and without addressing the issue of pub-
lication bias, a number of researchers have also raised concerns about the normality assumption for the heterogeneity (see, e.g., [18, 23, 43, 32] and references therein). In [32], the normal assumption on the $u_i$’s in (1.1) is replaced by a skew-normal distribution to provide additional modeling flexibility. In this work, we similarly place heavy-tailed Cauchy priors on the $u_i$’s, except our results are placed within the context of correcting publication bias, not merely standard meta-analysis.

Finally, we are not aware of any methods to quantify publication bias using selection models. For graphical methods, such as the funnel plot, there have been several measures proposed, including Egger’s regression intercept [9] and the skewness of the collected studies’ distribution [25]. See Lin et al. [26] for a more detailed review. However, skewness and asymmetry in funnel plots can arise from causes unrelated to study selection, such as intrinsic correlation between the effect size and standard error [40, 7].

In this paper, we develop a new measure for quantifying publication bias based on the Copas selection model. Our measure quantifies the dissimilarity between estimates obtained under the Copas selection model (2.1) and those obtained under a standard meta-analysis model (1.1). A key benefit of our approach is that it not only takes the difference between two point estimates, but it also takes into account the estimation uncertainty afforded by the full posterior distribution. Our measure lies between zero and one, with smaller values indicating negligible publication bias and values close to one indicating a very strong magnitude of publication bias. Thus, our approach has a clear and intuitive interpretation.

The rest of this paper is structured as follows. Section 2 describes the Copas selection model. In Section 3, we introduce the RBC model. In Section 4, we introduce the $D$ measure for quantifying publication bias based on the RBC model. In Section 5, we illustrate the robustness of our approach through simulation studies. In Section 6, we apply the proposed methodology to real data sets. Implementation details for our method and additional empirical studies are provided in the Appendix.

## 2 The Copas Selection Model

The Copas selection model [3, 6] is specified as follows. For all $i = 1, \ldots, n$,

$$y_i | z_i > 0 = \theta + \tau u_i + s_i \epsilon_i,$$

$$z_i = \gamma_0 + \gamma_1/s_i + \delta_i,$$

$$\text{corr}(\delta_i, \epsilon_i) = \rho,$$  

(2.1)
where $u_i, \epsilon_i$ and $\delta_i$ are marginally distributed as $N(0,1)$ and $u_i$ and $\epsilon_i$ are independent. By (2.1), the $i$th study is assumed to be published only if an associated latent variable $z_i$ (also known as the propensity score) is greater than zero. The propensity score, i.e. the propensity to publish, is characterized by two parameters $(\gamma_0, \gamma_1)$. The parameter $\gamma_0$ controls the overall likelihood of a study being published, while $\gamma_1$ characterizes how the chance of publication depends on sample size. In general, $\gamma_1$ is positive so that studies with larger sample sizes are more likely to be published. The reported effects and the propensity scores are assumed to be correlated through $\rho$, which controls how the probability of publication is influenced by the effect size of the study. When publication bias is present, i.e. $\rho \neq 0$, standard meta-analysis will lead to biased estimation of $\theta$. On the other hand, if $\rho = 0$, then there is no publication bias, and the model (2.1) reduces to the standard random effects model (1.1).

For practitioners, the main parameter of interest is the overall treatment effect $\theta$, although there are five total unknown parameters in (2.1). In [6, 33], the unknown parameters $(\theta, \tau, \rho)$ are estimated using maximum likelihood estimation (MLE), conditionally on a given pair $(\gamma_0, \gamma_1)$. Copas and Shi [6] recommend choosing $(\gamma_0, \gamma_1)$ using a grid search. Copas and Shi [4] also developed a goodness-of-fit test for $H_0 : (\gamma_0, \gamma_1) = (a, b)$ for a given choice of values $(a, b)$. On the other hand, Ning et al. [33] assume that the biased data generating mechanism contains an additional latent variable that accounts for the additional unpublished studies. They treat these variables as missing data and develop an EM algorithm to simultaneously obtain the MLEs for $(\theta, \tau, \rho, \gamma_0, \gamma_1)$. Recently, Duan et al. [7] developed a score-based hypothesis test to formally test for the presence of publication bias under the Copas selection model (i.e. testing $H_0 : \rho = 0$).

In the Bayesian framework, Mavridis et al. [29] estimate the parameters in (2.1) by placing noninformative priors on $(\theta, \tau, \rho)$ and informative priors on the lower and upper bounds for $Pr(z_i > 0 | s_i)$, which act as a proxy for priors on $(\gamma_0, \gamma_1)$. To derive informative priors on the bounds for $Pr(z_i > 0 | s_i)$, Mavridis et al. [29] recommend using “both external data and an elicitation process of expert opinion.” However, this may pose potential issues for meta-analyses when such prior information or expertise is difficult or impossible to attain. In our view, it is desirable to devise a default prior that can work well for a variety of problems and that avoids the need for problem-specific tuning by the practitioner. This article thus differs from the work of [29] in several ways. First, we place non-informative priors on $(\gamma_0, \gamma_1)$ directly. Second, unlike [29], we also dispense with the assumption that the random effects are normally distributed. Finally, we introduce a
new measure for quantifying publication bias, an issue which has not been addressed by previous works on selection models under either the Bayesian or the frequentist framework.

3 The Robust Bayesian Copas Selection Model

3.1 The RBC Prior Specification

Let \( y = (y_1, \ldots, y_n)' \), \( u = (u_1, \ldots, u_n)' \), and \( z = (z_1, \ldots, z_n)' \). Our objective is to formulate a robust, default Bayesian model for (2.1) by placing appropriate priors on the unknown parameters. Specifically, we aim to make the priors noninformative so that a default set of hyperparameters will work well for many different problems and situations.

In the RBC model, we first endow the mean effect \( \theta \) in (2.1) with a normal prior,

\[
\theta \sim \mathcal{N}(0, \sigma_\theta^2), \quad (3.1)
\]

where \( \sigma_\theta^2 \) is set to be a large value so that the prior on \( \theta \) is fairly noninformative. As a default, we set \( \sigma_\theta^2 = 10^4 \).

To model the heterogeneity parameter \( \tau \) in (2.1), we endow the variance \( \tau^2 \) with the inverse gamma prior,

\[
\tau^2 \sim \mathcal{IG}(a_\tau, b_\tau), \quad (3.2)
\]

where the hyperparameters \( (a_\tau, b_\tau) \) are set to be small values in order to make the prior on \( \tau^2 \) weakly informative. As discussed earlier, however, this assumption may be inappropriate.

Next, we consider the distribution of the random effects \( u \) in (2.1). In conventional meta-analysis, we have \( u_i \sim \mathcal{N}(0, 1), i = 1, \ldots, n \). If one has strong \textit{a priori} knowledge that the normality assumption holds, then our model can be implemented with standard normal priors on the random effects. As discussed earlier, however, this assumption may be inappropriate. To relax this assumption, we endow each of the \( u_i \)'s with the standard Cauchy prior,

\[
u_i \sim \mathcal{C}(0, 1), \quad i = 1, \ldots, n. \quad (3.3)
\]

The standard Cauchy distribution with density \( f(u) = 1/[\pi(1 + u^2)] \) is equivalent to the Student’s \( t \)-distribution with one degree of freedom. Thus,
it has heavy tails and is appropriate to use in scenarios where the normality assumption may be difficult to justify [18]. In the robust Bayesian modeling literature, the Cauchy distribution is frequently used as an alternative to the normal distribution. See, e.g. [11, 10, 12]. In this paper, we extend its use to selection models in meta-analysis. Because of its heavy tails, the prior (3.3) can help to mitigate the effects of outliers, skewness, and other departures from normality in meta-analysis. At the same time, this prior is also robust in the sense that it gives good estimates even when the random effects \( u \) are truly distributed as standard normal, as assumed by [6]. In our R package RobustBayesianCopas, we provide software to implement our model using either the conventional normal priors or the robust Cauchy priors (3.3) for \( u \). As a default, however, we recommend (3.3).

We note that we choose to model only the between-study heterogeneity with the Cauchy distribution and not the within-study random errors \( \epsilon_i \). This is because there is rarely enough information in the sample of collected studies for the meta-analysis practitioner to model the within-study errors for any individual study. On the other hand, the sample of collected studies typically does contain enough information to model the between-study heterogeneity.

Next, we endow the correlation parameter \( \rho \) in (2.1) with the noninformative uniform prior,

\[
\rho \sim U(-1, 1). \tag{3.4}
\]

Finally, we consider the priors for \( \gamma_0 \) and \( \gamma_1 \) in (2.1), which control the probability of publication. We will ultimately place noninformative uniform priors on these two quantities. To determine appropriate values for the hyperparameters in the priors on \((\gamma_0, \gamma_1)\), we first note that for some values \((P_{\text{low}}, P_{\text{high}})\) between zero and one, our model should satisfy

\[
0 \approx P_{\text{low}} \leq \Pr(z_i > 0| s_i) \leq P_{\text{high}} \approx 1, \quad i = 1, \ldots, n.
\]

Letting \(s_{\text{min}}\) and \(s_{\text{max}}\) denote the smallest and largest reported standard errors respectively, Mavridis et al. [29] showed that when \( \gamma_1 \geq 0 \), the above inequality translates to

\[
\Phi^{-1}(P_{\text{low}}) \leq \gamma_0 + \frac{\gamma_1}{s_{\text{max}}} \leq \gamma_0 + \frac{\gamma_1}{s_{\text{min}}} \leq \Phi^{-1}(P_{\text{high}}),
\]

where \( \Phi^{-1} \) denotes the inverse cumulative distribution function (cdf) for the standard normal density. Since the standard normal density places most of its mass in the interval \((-2, 2)\), this suggests the following priors for \((\gamma_0, \gamma_1)\):

\[
\gamma_0 \sim U(-2, 2), \tag{3.5}
\]

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and
\[ \gamma_1 \sim \mathcal{U}(0, s_{\text{max}}). \] (3.6)
This ensures that most of the mass for the \( z_i \)'s will lie between \((-2, 3)\), leading to selection probabilities from 2.5% to 99.7%. As noted earlier, our prior specification (3.5)-(3.6) differs from the Bayesian selection model introduced by Mavridis et al. [29], who placed informative priors on the lower and upper bounds of the selection probabilities \( \Pr(z_i > 0 | s_i), i = 1, \ldots, n \). Here, we place noninformative priors on \((\gamma_0, \gamma_1)\) directly, with the primary aim of avoiding the need to perform problem-specific tuning of hyperparameters.

### 3.2 Inference Under the RBC Model

Under the independent priors (3.1)-(3.6) on \((\theta, u, \tau, \rho, \gamma_0, \gamma_1)\), the RBC model produces a posterior distribution over these unknowns. Using MCMC, we can easily approximate the marginal posteriors \( \pi(\theta | y) \), \( \pi(\tau | y) \), \( \pi(\rho | y) \), \( \pi(\gamma_0 | y) \), and \( \pi(\gamma_1 | y) \). We can then use these marginal densities to construct nonasymptotic posterior credible intervals for each of these parameters. This allows us to automatically quantify uncertainty in a coherent manner, in addition to obtaining point estimates using either the posterior mean or median. Section A of the Appendix provides the full details of the MCMC implementation for the RBC model.

Rather than conducting statistical tests for \((\gamma_0, \gamma_1)\) (as in [4]) or \(\rho\) (as in [7]), inference about these parameters can also be conducted directly through their marginal posteriors. Instead of testing \( H_0 : \rho = 0 \), for instance, the posterior \( \pi(\rho | y) \) can be used to deduce the presence of non-negligible publication bias. For example, as shown in the two plots on the left of Figure 4, the posteriors \( \pi(\rho | y) \) are peaked around \( \rho = 0.5 \) and \( \rho = 0.9 \) respectively, suggesting non-negligible publication bias. On the other hand, if \( \pi(\rho | y) \) is concentrated near zero, this suggests that there is negligible publication bias. Although the marginal posterior cannot be used to formally test if \( H_0 : \rho = 0 \) is true, we view uncertainty quantification for \( \rho \) as a more critical task. Moreover, we can still infer if \( \rho \approx 0 \) from the posterior density \( \pi(\rho | y) \).

The \( D \) measure for quantifying publication bias that we will introduce in Section 4 can also be used to infer if \( \rho \approx 0 \).
4 Quantifying Publication Bias with the RBC Model

4.1 The $D$ Measure

Apart from inference about $\theta$, we may be interested in quantifying the magnitude of publication bias. To the best of our knowledge, this issue has not been addressed before for selection models, although there exist several procedures based on funnel plots [26]. Since the Copas selection model (2.1) explicitly models the selection mechanism, a natural measure for quantifying publication bias is the dissimilarity between the posterior of $\theta$ under the standard random effects model (1.1) (i.e. fixing $\rho = 0$ in (2.1)) and the posterior for $\theta$ under the RBC model where $\rho$ is also estimated from the data.

Let $\pi_{rbc} := \pi_{rbc}(\theta|y)$ be the posterior for $\theta$ under the complete RBC model with priors (3.1)-(3.6). Let $\pi_{\rho=0} := \pi_{\rho=0}(\theta|y)$ be the posterior for $\theta$ under the RBC model where we a priori fix $\rho = 0$. When $\rho = 0$, the posterior $\pi(\theta, \tau^2, u|y)$ does not depend on $(z, \gamma_0, \gamma_1)$, and thus, it is the same as the posterior distribution under the standard random effects model (1.1) with only priors (3.1)-(3.3) on $(\theta, \tau^2, u)$.

If $\rho = 0$ in (2.1), then there is no publication bias, and the estimates for $\theta$ under the standard meta-analysis model (1.1) and the Copas selection model (2.1) are theoretically the same. Thus, the density $\pi_{\rho=0}(\theta|y)$ can be interpreted as the posterior for $\theta$ before bias correction. On the other hand, if $\rho \neq 0$ in (2.1), then the estimate of $\theta$ under (1.1) is a biased estimate, whereas the estimate for $\theta$ under (2.1) corrects this bias. The density $\pi_{rbc}(\theta|y)$ is therefore the posterior after bias correction. Thus, the dissimilarity between $\pi_{\rho=0}(\theta|y)$ and $\pi_{rbc}(\theta|y)$ allows us to quantify the magnitude of publication bias. If publication bias is negligible (i.e. the true $\rho$ is close to zero), then the posteriors for $\theta$ before and after bias correction will be very similar to each other.

To utilize the posterior $\pi(\theta|y)$ in our quantification of publication bias, we propose using the Hellinger distance between $\pi_{rbc}$ and $\pi_{\rho=0}$. The Hellinger distance between two densities $f(x)$ and $g(x)$ is defined as

$$H(f, g) = \left[1 - \int \sqrt{f(x)g(x)}dx\right]^{1/2}.$$  \hspace{1cm} (4.1)

The Hellinger distance is symmetric and is bounded by zero and one. The magnitude of the Hellinger distance also has a clear interpretation. Values close to zero indicate that $f$ and $g$ are nearly identical distributions, while values close to one indicate that the majority of the probability mass in $f$ does not overlap with that of $g$. 
In the present context, we may estimate the posterior for $\pi_{rbc}$ and $\pi_{\rho=0}$ by using MCMC samples of $\theta$ (after a burn-in period) to obtain kernel density estimates, $\hat{\pi}_{rbc}$ and $\hat{\pi}_{\rho=0}$. We then use numerical integration to estimate the Hellinger distance (4.1) between $\hat{\pi}_{rbc}$ and $\hat{\pi}_{\rho=0}$. In short, our measure for publication bias, based on the full posterior, is

$$D = H (\hat{\pi}_{rbc}(\theta|y), \hat{\pi}_{\rho=0}(\theta|y)) .$$

Small values of $D$ ($D \approx 0$) indicate a small or negligible magnitude of publication bias, while larger values of $D$ ($D \approx 1$) indicates a strong magnitude of publication bias. We note that $D$ can also be used to quantify the publication bias in the heterogeneity parameter $\tau$ by computing the Hellinger distance between $\pi_{rbc}(\tau|y)$ and $\pi_{\rho=0}(\tau|y)$. However, as meta-analysis practitioners are mainly interested in the treatment effect, we focus on $\theta$.

Figure 1 illustrates the benefits of using $D$ as a measure of publication bias magnitude. These were taken from two simulations in the empirical study in Appendix B where the random effects $u_i, i = 1, \ldots, n$, are distributed as $t_3$. In the top panel, we have plotted the posterior $\pi_{rbc}(\theta|y)$ (the solid line) against the posterior $\pi_{\rho=0}(\theta|y)$ (the dashed line) when $\rho = 0.02$ (or very low publication bias). We see that there is significant overlap between the two distributions, and thus, $D = 0.028$. On the other hand, we see in the bottom panel that when $\rho = 0.98$ (i.e. substantial publication bias), $\pi_{rbc}(\theta|y)$ and $\pi_{\rho=0}(\theta|y)$ give more distinctive estimates of $\theta$. Moreover, $\pi_{rbc}(\theta|y)$ gives greater uncertainty about $\theta$ than $\pi_{\rho=0}(\theta|y)$, since the posterior is for $\pi_{\rho=0}(\theta|y)$ is taller and thinner. Here, we obtain $D = 0.78$.

Since the magnitude of $D$ usually depends on the magnitude of the correlation parameter $\rho$, one may wonder what the advantage of using $D$ is over simply using the posterior $\pi(\theta|y)$ to quantify publication bias. In our view, $D$ is a more intuitive measure because it directly characterizes the amount of publication bias in the mean treatment effect $\theta$. As shown in Figure 1, $D$ quantifies how much the posterior $\pi(\theta|y)$ changes after a bias correction has been made by the RBC model.

Unlike measures based on funnel plot asymmetry, such as skewness [25], our proposed $D$ measure cannot determine the direction of the potential publication bias. However, our approach has several advantages. First, as a divergence measure between two probability distributions, $D$ automatically takes into account the estimation discrepancy and the variability in $\theta$. Second, since $D$ is always bounded between zero and one, it has a clear interpretation. Finally, our measure quantifies the change in $\pi(\theta|y)$ that can be solely attributed to selection bias (or how much the posterior changes because of $\rho$), whereas asymmetry may be due to factors unrelated to selection,
such as methodological differences between studies [40]. If the direction of the bias is of particular interest, the practitioner can examine scatter plots or the sign (positive or negative) of the sample skewness of the standardized
deviates $d_i = (y_i - \hat{\theta})/\sqrt{s_i^2 + \hat{\tau}^2}$, $1, \ldots, n$, where $(\hat{\theta}, \hat{\tau})$ are point estimates under the usual random effects model (1.1) [25, 31].

Figure 1: The posterior distributions $\pi_{rbc}(\theta|y)$ (solid line) and $\pi_{\rho=0}(\theta|y)$ (dashed line) from two experiments where the true random effects $u_i$, $i = 1, \ldots, n$, are distributed as $t_3$. In the top panel, the true $\rho = 0.02$ and $D = 0.028$. In the bottom panel, the true $\rho = 0.98$ and $D = 0.78$. 
4.2 Interpreting the $D$ Measure

The posteriors $\pi_{rbc}(\theta|y)$ and $\pi_{\rho=0}(\theta|y)$ are analytically intractable and therefore have to be approximated using MCMC. Using kernel density estimation and numerical integration to evaluate the Hellinger distance (4.1) also introduces some approximation error. Due to these approximations, we will not, in general, be able to obtain $D = 0$ (which would indicate the complete absence of publication bias, or that $\pi_{rbc}(\theta|y)$ and $\pi_{\rho=0}(\theta|y)$ are identical). However, even MLE approaches to estimating the parameters in (2.1) and (1.1) are typically unable to produce exactly identical estimates for $\theta$, because we need to perform numerical optimization on two different likelihood functions. We believe it is much more important to determine whether publication bias is negligible, as opposed to completely absent.

We recommend the following rules of thumb for interpreting $D$.

| Range       | Interpretation                  |
|-------------|---------------------------------|
| $0.0 \leq D \leq 0.25$ | Negligible publication bias     |
| $0.25 < D \leq 0.5$   | Moderate publication bias       |
| $0.5 < D \leq 0.75$   | High publication bias           |
| $0.75 < D \leq 1.0$   | Very high publication bias      |

As demonstrated by our analysis of real data sets in Section 6 and an empirical study of 2000 simulated meta-analyses detailed in Appendix B, these guidelines are often reasonable in practice. Nevertheless, we caution that the actual value of $D$ may vary depending on many factors, such as the magnitudes of $\gamma_0$, $\gamma_1$, and $\tau$ in (2.1), or the magnitude and direction of the reported effect sizes $y_i$, $i = 1, \ldots, n$. Therefore, our recommendations for interpreting $D$ above should be used as rough guidelines, and “acceptable” or “unacceptable” values for $D$ should be determined within the context of the problem being studied. We also recommend that practitioners examine plots of $\pi_{rbc}(\theta|y)$ against $\pi_{\rho=0}(\theta|y)$ (such as the ones in Figures 1 and 4) to visualize the extent of the bias correction made by the RBC method.

5 Evaluation of the Robustness of the RBC Model

5.1 Methodology

We evaluated the robustness of the RBC method under a variety of distributions for the heterogeneity. We are mainly concerned with how sensitive
our method’s performance is to departures from the standard normality assumption for $u$. For a detailed simulation of the $D$ measure (4.2), we refer readers to Appendix B. We compared four selection models, benchmarked against the standard meta-analysis model.

1. RBC: the complete model with priors (3.1)-(3.6) on $(\theta, \tau, u, \rho, \gamma_0, \gamma_1)$ under (2.1);

2. RBC-conv: the RBC model for conventional meta-analysis with standard normal errors for the random effects $u$;

3. Copas: the original (frequentist) Copas selection model (2.1);

4. CLS: the Copas-like selection model of [33]; and

5. SMA: the standard meta-analysis model (1.1) that does not account for publication bias.

RBC-conv, Copas, CLS, and SMA all assume that the heterogeneity is normally distributed. In particular, the RBC-conv model uses the same priors on $(\theta, \tau, \rho, \gamma_0, \gamma_1)$ as those for RBC, but replaces the Cauchy priors (3.3) on $u$ with normal priors $N(0, 1)$. For RBC and RBC-conv, we ran the Gibbs sampling algorithms described in Appendix A for 20,000 iterations, discarding the first 10,000 samples as burn-in. We used the posterior mean for $\pi(\theta|y)$ as the point estimate for $\theta$. The posteriors for $\theta$ were also used to obtain 95% nonasymptotic posterior credible intervals for $\theta$.

The Copas selection model was implemented using the R function `copas` in the R package metasens and uses a grid search for tuning $(\gamma_0, \gamma_1)$. We bootstrapped the residuals to obtain an estimate of the standard error (s.e.) of $\theta$. The CLS model uses an EM algorithm to compute the MLEs for $(\theta, \tau, \rho, \gamma_0, \gamma_1)$ simultaneously. To estimate the s.e.’s for $\theta$ under CLS, we used the inverse Hessian matrix. For both Copas and CLS, we constructed the 95% confidence intervals as $\hat{\theta} \pm 1.96 \times \text{s.e.}(\hat{\theta})$. The SMA method uses MLE to obtain estimates for $(\theta, \tau)$ under model (1.1) without accounting for publication bias. Similarly to CLS, we used the inverse Hessian matrix to estimate standard errors and 95% confidence intervals for SMA. Functions to implement CLS and SMA are provided in the R package RobustBayesianCopas.

We considered four simulation settings for true distribution of the random effects $u_i, i = 1, \ldots, n$, in (2.1):

- **Experiment 1** (heavy-tailed): $u_i \sim t_3$;

- **Experiment 2** (standard normal): $u_i \sim N(0, 1)$;
• **Experiment 3** (several outliers): \( u_i \sim 0.15N(-4, 0.2) + 0.85N(0, 1); \) and

• **Experiment 4** (skewed right): \( u_i \sim \text{ALD}(0.5, 0.3) \), where \( \text{ALD}(\sigma, \kappa) \) denotes the asymmetric Laplace distribution with scale \( \sigma > 0 \) and asymmetry parameter \( \kappa \in (0, 1) \).

In Figure B.2 of Appendix B, we provide a plot for these four different distributions for the random effects.

### 5.2 Simulation Results

For our synthetic experiments, we simulated a meta-analysis of \( n = 30 \) studies under the model (2.1). We generated the within-study standard errors \( s_i, i = 1, \ldots, n \), from \( U(0.2, 0.8) \). We set \( \theta = 0.3, \tau = 0.5, \gamma_0 = -1, \) and \( \gamma_1 = 0.4 \). We varied the correlation \( \rho \in \{0, 0.3, 0.6, 0.9\} \), so that we could evaluate the methods in Section 5.1 under varying degrees of publication bias. For the four experiments detailed in Section 5.1, we repeated this for 100 replications and computed the average bias, \( \hat{\theta} - \theta \), and the coverage probability (CP) (or the proportion of times the 95\% posterior credible or confidence intervals contained \( \theta \)).

Figure 2 shows the average bias and CP for Experiment 1 (heavy-tailed heterogeneity) and Experiment 2 (standard normal heterogeneity) for the five methods we described in 5.1. In Experiment 1, the RBC method had the lowest bias and the highest coverage. In Experiment 2, RBC-conv had the lowest bias and highest CP, which is to be expected because RBC-conv correctly specified the normal distribution for the random effects. However, the default RBC method with Cauchy priors on the random effects performed very similarly to the other selection methods, with nearly the same amount of bias. Moreover, the default RBC model with Cauchy priors on \( u \) maintained excellent coverage even when \( u \) is truly distributed as standard normal. Unsurprisingly, SMA had the highest bias and the lowest CP as \( \rho \) increases, because SMA fails to take into account the publication bias.

The advantage of the RBC method over the other methods becomes even more pronounced when there is heavy departure from normality for the heterogeneity. We see this in our results for Experiment 3, where \( u \) follows a mixture of normal distributions that results in several outliers, and in Experiment 4, where the distribution of \( u \) is skewed right. Figure 3 shows the average bias and CP for Experiment 3 (several outliers) and Experiment 4 (skewed right) for the five methods we described in 5.1. Under these scenarios, RBC not only had lower bias, but it also gave significantly better
Figure 2: The average bias and coverage for Experiment 1 (heavy-tailed random effects) and Experiment 2 (standard normal random effects) for the methods: RBC (○), RBC-conv (△), Copas (◊), CLS (□), and SMA (▽). In Experiment 1, RBC had the lowest bias and the highest CP. In Experiment 2, RBC-conv had the lowest bias and the highest CP.

coverage than the other methods. Our results illustrate that the default RBC method is much less sensitive to the presence of outliers or skewness of the heterogeneity. We also note that even though RBC-conv resulted in higher average bias, its CP was still better than Copas, CLS, or SMA. This suggests that for selection models, Bayesian posterior credible intervals can often produce better uncertainty quantification than frequentist confidence intervals constructed using asymptotic arguments or bootstrapping.
Figure 3: The average bias and coverage for Experiment 3 (several outliers) and Experiment 4 (skewed right) for the methods: RBC (○), RBC-conv (△), Copas (♦♦♦), CLS (□□□), and SMA (▽). In these experiments, RBC had lower bias and much higher CP than the other methods. This demonstrates that RBC is the most robust to departures from normality.

6 Real Data Applications

6.1 Relationship Between Second-Hand Tobacco Smoke and Lung Cancer

We first applied the proposed RBC method to a meta-analysis of studies on the relationship between second-hand tobacco smoke and lung cancer. Hackshaw et al. [14] previously analyzed the results from 37 studies that
Figure 4: Results from our real data examples. The top-left panel plots the posterior distribution $\pi(\rho|y)$ for the meta-analysis on the risk of developing lung cancer from second-hand smoke. The top-right panel plots the posterior distributions for the log-odds ratio of developing lung cancer, $\pi_{rbc}(\theta|y)$ (solid line) and $\pi_{\rho=0}(\theta|y)$ (dashed line). In the bottom-left panel, we plot the posterior distribution $\pi(\rho|y)$ for the meta-analysis on antidepressants. In the bottom-right panel, we plot the posterior distributions for the mean improvement in depression symptoms, $\pi_{rbc}(\theta|y)$ (solid line) vs. $\pi_{\rho=0}(\theta|y)$ (dashed line).

evaluated the risk of developing lung cancer in women who were lifelong non-smokers but whose husbands smoked, compared to women whose husbands had never smoked. In particular, Hackshaw et al. [14] fit a random effects meta-analysis model (1.1), resulting in a pooled odds ratio (OR) of 1.24 and a 95% confidence interval of (1.13, 1.36). Hackshaw et al. [14] concluded that married, non-smoker women who were exposed to secondhand smoke by their smoker husbands were 24% more likely to develop lung cancer than those whose husbands did not smoke.

Previous analysis of this data by [33] suggested some evidence of publication bias. We used the RBC model to estimate $\theta$, the log-odds ratio for developing lung cancer. We first performed inference about the presence of publication bias using the posterior distribution for $\pi(\rho|y)$. The top-left
panel of Figure 4 shows that $\pi(\rho|y)$ is concentrated about 0.5, with a posterior median of $\hat{\rho} = 0.42$. This suggests the presence of publication bias. Note that for $\rho$, we use the posterior median as a point estimate rather than the mean, since the posterior for $\pi(\rho|y)$ is often skewed (and hence the posterior mean is heavily influenced by a few extreme values near $-1$ and $1$). While the posterior $\pi(\rho|y)$ is useful for assessing the presence of publication bias, it is not as informative as the $D$ measure in quantifying how much the posterior $\pi(\theta|y)$ changes once we have corrected publication bias.

Next, we estimated $\theta$. The top-right panel of Figure 4 displays the posterior distribution for $\pi_{rbc}(\theta|y)$ (solid line) against the posterior for $\pi_{\rho=0}(\theta|y)$ (dashed line). We computed $D = 0.30$, which suggests a moderate magnitude of publication bias. In order to compare our results to those of [14], we computed the odds ratio as $\exp(\hat{\theta})$, where $\hat{\theta}$ is the posterior mean for $\pi_{rbc}(\theta|y)$. For uncertainty quantification, we took the 95% posterior credible interval $(\exp(\theta_L), \exp(\theta_U))$, where $(\theta_L, \theta_U)$ is the 95% equal-tailed posterior credible interval for $\theta$. The RBC model gave a posterior mean OR of 1.19, with a 95% credible interval of (1.03, 1.35). In short, our analysis suggests that married, non-smoker women who were exposed to second-hand smoke by their husbands still had a significant risk of developing lung cancer, albeit a slightly lower risk than previously concluded (i.e. about 19% more likely, as opposed to 24% more likely [14]).

6.2 The Efficacy of Antidepressants

Although antidepressents are among the world’s most widely prescribed drugs, there has been considerable controversy about their effectiveness. In 2008, Turner et al. [41] presented a comparison of effectiveness data on depressants published in journals with the corresponding results from trials submitted to the Food and Drug Administration (FDA) between 1987 and 2004 for licensing. Turner et al. [41] found evidence of bias towards results favoring active intervention. In particular, there were 73 studies with results as reported to the FDA (74 originally but two of them were subsequently combined), but only 50 (69%) of these studies were subsequently published.

We applied the RBC model to the meta-analysis of these 50 published studies. In these studies, the outcome $\theta$ is a quantitative measure for improvement in depression symptoms. Since studies reported their outcomes on different scales, effect sizes were all expressed as standardized mean differences estimated by Hedges’ $g$, accompanied by corresponding variances [30, 15]. This data set is available in the R package RobustBayesianCopas.

We first used the RBC model to perform inference about $\rho$. The bottom-
left panel of Figure 4 displays the posterior distribution for \( \pi(\rho | y) \). We see that \( \pi(\rho | y) \) is highly concentrated on large values, with a posterior median of \( \hat{\rho} = 0.88 \), which suggests very strong publication bias.

Next, we considered estimates for \( \theta \) under the RBC model, compared to those obtained from a standard meta-analysis (1.1). Under the standard model, we estimated the MLE \( \hat{\theta}_{mle} = 0.41 \) with a 95% confidence interval of \((0.36, 0.46)\). The posterior mean effectiveness under the RBC model, on the other hand, was only \( \hat{\theta}_{rbc} = 0.25 \) with a 95% posterior credible interval of \((0.17, 0.37)\). Our results suggest that the mean improvement in depression symptoms from antidepressents may be lower than previously reported.

The bottom-right panel of Figure 4 displays \( \pi_{rbc}(\theta | y) \) (solid line) against \( \pi_{\rho=0}(\theta | y) \) (dashed line). This plot shows that once we have corrected for the publication bias with the RBC model, we obtain significantly lower estimates of \( \theta \) with greater uncertainty and very little overlap with the non-bias-corrected posterior. We computed \( D = 0.95 \), indicating a very high magnitude of publication bias. The contrast between the two plots on the right in Figure 4 shows that \( D \) is a very useful measure for quantifying uncertainty bias.

6.3 The Prevalence of Publication Bias

Though the RBC model has shown promising performance in simulation studies and the meta-analyses done in Sections 6.1 and 6.2, one may be interested in assessing how prevalent the issue of publication bias is across multiple meta-analyses. Similarly, Higgins et al. [17] developed Cochrane’s \( I^2 \) measure as a measure of consistency of the results of studies in meta-analyses. Higgins et al. [17] evaluated the performance of \( I^2 \) on 509 meta-analyses of dichotomous outcomes in the Cochrane Database of Systematic Reviews.

Inspired by this, we computed the \( D \) measure for the overall treatment effect \( \theta \) for a set of 1500 randomly selected meta-analyses of dichotomous outcomes from the Cochrane Database of Systematic Reviews where each meta-analysis contained at least eight studies. The number of studies in these meta-analyses varied from \( n = 8 \) to \( n = 135 \). Figure 5 shows the empirical histogram for the \( D \) measure. We found that 984 (65.6%) of these meta-analyses had negligible publication bias \((0 \leq D \leq 0.25)\), 411 (27.4%) had moderate publication bias \((0.25 < D \leq 0.5)\), 91 (6.1%) had high publication bias \((0.5 < D \leq 0.75)\), and 14 (0.9%) had very high publication bias \((0.75 < D \leq 1)\).
7 Discussion

In this paper, we have introduced the robust Bayesian Copas (RBC) selection model for correcting publication bias in meta-analysis. Our method combines robust Cauchy priors on the heterogeneity $u$ with a set of default, noninformative priors on all the unknown parameters ($\theta, \tau, \rho, \gamma_0, \gamma_1$) in the Copas selection model (2.1). This affords us greater modeling flexibility, avoids the need for problem-specific tuning of hyperparameters, and facilitates nonasymptotic inference. We also introduced the $D$ measure (4.2) for quantifying the magnitude of publication bias. Specifically, $D$ quantifies the amount of dissimilarity between a standard random effects meta-analysis (1.1) and a meta-analysis done with the Copas selection model (2.1). We illustrated that our method performs very well in a variety of simulation and real data settings. We have provided an R package RobustBayesianCopas to implement our method, which can be found on the Comprehensive R Archive Network (CRAN).

In this paper, we have focused only on univariate meta-analysis. However, there is an increasing need to explore multivariate and network meta-
analysis methods, which simultaneously analyze multiple treatments or comparisons between multiple treatments. See e.g. [35, 22] for a review of different motivating applications and methods. For multivariate and network meta-analyses, the presence of publication bias will also lead to biased estimates of the treatment effects. In future work, we will extend the RBC model to multivariate and network settings.

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A Implementation Details for the RBC Model

We first describe how to implement the full RBC model described in Section 3 with the priors (3.1)-(3.6) on \((\theta, \tau^2, \mathbf{u}, \rho, \gamma_0, \gamma_1)\). Our model is implemented using the JAGS software and is available in the publicly available R package RobustBayesianCopas.

Let \(\mu_i = \theta + \tau u_i, i = 1, \ldots, n\), and let \(\mu = (\mu_1, \ldots, \mu_n)'\). An alternative way to jointly write model (2.1) is then

\[
\begin{pmatrix} y_i \\ z_i \end{pmatrix} \sim \mathcal{N}_2 \left( \left( \begin{array}{c} \mu_i \\ \gamma_0 + \gamma_1/s_i \end{array} \right), \left( \begin{array}{cc} s_i^2 & \rho s_i \\ \rho s_i & 1 \end{array} \right) \right) \mathbf{1}_{z_i > 0}, \quad i = 1, \ldots, n, \quad (A.1)
\]

where \((y_i, z_i)'\) is a truncated bivariate normal distribution. To sample from \((y_i, z_i)\) in (A.1), we follow the approximation introduced in [29], where we first sample \(z_i \sim \mathcal{N}(\gamma_0 + \gamma_1/s_i, 1)\mathbf{1}_{z_i > 0}\), and then we sample \(y_i | z_i \sim \mathcal{N}(\mu_i + \tau u_i, \sigma^2)\).
\[ \rho s_i(z_i - \gamma_0 - \gamma_1/s_i), s_i^2(1 - \rho^2)) \text{.} \] With this approximation for (A.1) and the reparametrization of our model in terms of \( \mu \), we can easily implement a Gibbs sampler.

Under the reparametrization \( \mu_i = \theta + \tau u_i, i = 1, \ldots, n \), in model (2.1) and using the approximation of the truncated bivariate normal density (A.1) by [29] to sample \((y_i, z_i), i = 1, \ldots, n\), our (approximate) model is:

\begin{align*}
  y_i | z_i & \sim \mathcal{N}(\mu_i + \rho s_i (z_i - \gamma_0 - \gamma_1/s_i), s_i^2(1 - \rho^2)), \quad i = 1, \ldots, n, \\
  z_i & \sim \mathcal{N}(\gamma_0 + \gamma_1/s_i, 1)_{z_i > 0}. \quad (A.2)
\end{align*}

Since the Cauchy distribution belongs to the location-scale family, the induced prior on \( \mu_i \) under (3.3) is \( \mu_i \sim \mathcal{C}(\theta, \tau_0), i = 1, \ldots, n \). That is, \( \mu_i \) is a generalized Cauchy distribution with mean \( \theta \) and scaling parameter \( \tau_0 \).

The density of \( \mathcal{C}(\theta, \tau_0) \) is

\[ f(x) = \frac{1}{\pi \tau_0 (1 + (x - \theta)^2/\tau_0^2)}. \]

Noting that \( \mathcal{C}(\theta, \tau_0) \) can be rewritten as a scale-mixture density i.e. \( \mu_i | \lambda^2 \sim \mathcal{N}(\theta, \lambda^2 \tau_0^2), \lambda^2 \sim \mathcal{IG}(1/2, 1/2) \), our induced prior hierarchy under the RBC model (3.1)-(3.6) is:

\begin{align*}
  \mu_i & \sim \mathcal{N}(\theta, \lambda^2 \tau_0^2), \quad i = 1, \ldots, n, \\
  \theta & \sim \mathcal{N}(0, \sigma_\theta^2), \\
  \lambda^2 & \sim \mathcal{IG}(1/2, 1/2), \\
  \tau_0^2 & \sim \mathcal{IG}(a_\tau, b_\tau), \\
  \rho & \sim \mathcal{U}(-1, 1), \\
  \gamma_0 & \sim \mathcal{U}(-2, 2), \\
  \gamma_1 & \sim \mathcal{U}(0, s_{\text{max}}). \quad (A.3)
\end{align*}

From (A.2)-(A.3), it is clear that the parameters \( (z, \mu, \theta, \lambda^2, \tau_0^2, \gamma_0, \gamma_1) \) in our Gibbs sampling algorithm can be updated in closed form. In particular, the full conditional for each \( z_1, \ldots, z_n \) is a truncated normal density, the full conditionals for \( \mu_1, \ldots, \mu_n, \theta, \gamma_0, \) and \( \gamma_1 \) are normal densities, and the full conditionals for \( \lambda^2 \) and \( \tau_0^2 \) are inverse-gamma densities. To update \( \rho \) at each iteration, we can use either slice sampling or Metropolis-Hastings with a proposal density bounded between \((-1, 1)\), e.g. a rescaled beta density whose mode is the previous MCMC draw for \( \rho \).

The R package RobustBayesianCopas also provides a Gibbs sampler to sample from the posterior, \( \pi_{\rho=0}(\cdot|y) \), i.e. the RBC model when \( \rho \) is a priori fixed at \( \rho = 0 \). Since the observed treatment effects \( y \) are independent of the propensity scores \( z \) in (2.1) when \( \rho = 0 \), we do not need to estimate \( (z, \rho, \gamma_0, \gamma_1) \), and the model (2.1) reduces to the standard random effects model (1.1),

\[ y_i \sim \mathcal{N}(\mu_i, s_i^2), \quad i = 1, \ldots, n. \quad (A.4) \]
To summarize briefly, we randomly simulated 2000 meta-analyses, each with

![Plot of D against ρ](image)

Figure B.1: Plot of the D measures against the true ρ for 2000 simulated
meta-analyses.

As before, μ_i ∼ C(θ, τ) for all i = 1, . . . , n. Using the scale-mixture representation of the generalized Cauchy distribution, we now only need to place priors on (μ, θ, λ^2, ρ^2) as follows:

\[ μ_i \sim N(θ, λ^2τ^2), \quad i = 1, . . . , n, \]
\[ θ \sim N(0, σ_θ^2), \]
\[ λ^2 \sim IG(1/2, 1/2), \]
\[ ρ^2 \sim IG(a_ρ, b_ρ). \]  \hspace{1cm} (A.5)

From (A.4)-(A.5), all the parameters (μ, θ, λ^2, ρ^2) can be updated in closed form, conditional on the others, in the Gibbs sampler.

B Empirical Study for the D Measure

We use an empirical study to justify our rules of thumb for interpreting the D measure (4.2) given in Section 4.2 of the main manuscript are reasonable. To summarize briefly, we randomly simulated 2000 meta-analyses, each with different numbers of studies n, different values for (θ, τ, ρ, γ_0, γ_1), and different distributions for the random effects u. To ensure that we covered a wide range of values for ρ, we simulated 100 observations for ρ in each of the 20 intervals (-1, -0.9], (-0.9, 0.8], . . . , (0.8, 0.9], and (0.9, 1).

Figure B.1 plots D against ρ for our empirical study. Figure B.1 confirms that larger values of |ρ| are correlated with larger values of D, whereas
values of \( \rho \) close to zero correspond to smaller values of \( D \). For values of \( \rho \in (-0.1, 0.1) \), \( D \) is generally less than 0.25. For values of \( \rho \in (-0.5, 0.5) \), most values of \( D \) are less than 0.5.

We used the below steps to generate the 2000 meta-analyses for our empirical study:

1. Generate 100 values of \( \rho \) in each of the intervals \((-1, -0.9], (-0.9, 0.8], \ldots, (0.8, 0.9], \) and \((0.9, 1)\).

2. For each of the 2000 \( \rho \)'s:
   
   (a) Sample the meta-analysis size \( n \) uniformly from \( \{8, 9, \ldots, 50\} \) and generate the within-study standard errors \( s_i, i = 1, \ldots, n \), from \( U(0.2, 0.8) \).
   
   (b) Randomly generate \( \theta \sim U(-2, 2), \tau \sim U(0.1, 1.5), \gamma_0 \sim U(-1.5, 1.5), \) and \( \gamma_1 \sim U(0, 0.9) \).

   (c) Randomly choose one of the four distributions for the heterogeneity \( u \) used in the experiments in Section 5.1 of the main manuscript and depicted in Figure B.2.

   (d) Generate the observed treatment effects according to the Copas selection model, with the given \( (\theta, \tau, \rho, \gamma_0, \gamma_1) \) and choice of distribution for \( u \).

   (e) Compute the posteriors \( \pi_{rbc}(\theta|y) \) and \( \pi_{\rho=0}(\theta|y) \) and the \( D \) measure.

We caution that while we expect for \( D \) to generally follows the v-shape given in Figure B.1 (i.e. \( D \) increases as \(|\rho|\) increases), the actual magnitude of \( D \) shows considerable variability in each of the intervals \((-1, 0.9], (-0.9, -0.8], \ldots, (0.9, 1)\). This is likely because \( D \) also depends on things such as the magnitudes of \( (\gamma_0, \gamma_1, \tau) \) or the magnitude and direction of the effect sizes \( y_i, i = 1, \ldots, n \). Therefore, we reiterate that our recommendations for interpreting \( D \) in Section 4.2 should be used as rough guidelines, and it is best for \( D \) to be interpreted within the context of the problem being studied. Nevertheless, our empirical results and Figure B.1 offer some empirical evidence that our chosen guidelines for interpreting the magnitude of publication bias are reasonable.

To determine the rules of thumb for interpreting \( D \) given in Section 4.2 of the main manuscript, we looked at the empirical histograms for \( D \) for \( \rho \in (-0.1, 0.1) \) and \( \rho \in (-0.5, 0.5) \), given in Figure B.3. When \( \rho \in (-0.1, 0.1) \), we see that \( D \) is usual less than 0.25. When \( \rho \in (-0.5, 0.5) \), we see that \( D \) is
Figure B.2: Plots of the four distributions for the random effects considered in our experiments.

usually less than 0.5. Based on these empirical histograms, we recommend using the following guidelines: $D \leq 0.25$ means negligible publication bias, $0.25 < D \leq 0.5$ means moderate publication bias, and $D > 0.5$ means high publication bias.
Figure B.3: The empirical histograms for the $D$ measure when $\rho \in (-0.1, 0.1)$ in the left panel, and when $\rho \in (-0.5, 0.5)$ in the right panel.