

# Mitigating Publication Bias Using Bayesian Stacking

Thomas A. Gibson

December 10, 2021

## 1 Introduction

Results from a meta-analysis may be skewed and unreliable in the presence of publication bias, where the publication or non-publication of a study depends on the statistical significance or magnitude of its results (Rothstein et al., 2006). Statistical methods for publication bias have been designed for sensitivity analysis, testing for the presence/magnitude of publication bias, and calculating bias-corrected parameter estimates. Most methods are either based on the funnel plot or selection models.

Methods based on the funnel plot (Light and Pillemer, 1984) – a scatterplot of effect sizes against their standard errors – inspect the plot’s asymmetry to test or correct for bias. Say we have  $S$  studies indexed by  $i = 1, \dots, S$  and that  $y_i$  and  $v_i = s_i^2$  are their estimated effect sizes and sampling variances. A popular non-parametric test for publication bias (Begg and Mazumdar, 1994) measures the rank correlation between standardized observed effect sizes  $y_i^*$  and the effect sizes’

variances  $v_i$ , where

$$\begin{aligned} y_i^* &= (y_i - \bar{y}) / (v_i^*)^{1/2} \\ \bar{y} &= \left( \sum_j (v_j^{-1}) / y_j \right) / \left( \sum_j v_j^{-1} \right) \\ v_i^* &= v_i - \left( \sum_j v_j^{-1} \right)^{-1}. \end{aligned}$$

Begg and Mazumdar (1994) measure the correlation between pairs  $(y_i^*, v_i)$  with Kendall’s tau, where a symmetric funnel plot would have correlation near zero. Egger’s test (Egger et al., 1997) fits a linear regression of observed standard normal deviates  $\text{SND}_i = y_i / s_i$  against the inverse standard errors  $1/s_i$ , i.e.  $\text{SND}_i = \alpha + \beta \times (1/s_i)$  with the null hypothesis  $H_0 : \alpha = 0$ . Other regression methods (Macaskill et al., 2001; Rücker et al., 2008; Thompson and Sharp, 1999; Peters et al., 2006) are similar to Egger’s test and use regression weights or transformations to improve upon Egger’s test in the presence of heterogeneity or for dichotomous outcomes (Jin et al., 2015). Lin and Chu (2018) develops a measure for the severity of publication bias based on the skewness of standardized deviates. The trim-and-fill method (Duval and Tweedie, 2000) calculates an adjusted mean effect estimate in a series of steps, by 1) estimating the number of missing studies  $k_0$ , 2) “trimming” the smaller studies that are causing funnel plot asymmetry, 3) estimating the true mean effect with the remaining studies, and 4) replacing trimmed studies and their missing counterparts and re-estimating the mean effect and its variance. However, Duval and Tweedie (2000) recommend using trim-and-fill as a sensitivity analysis based on the *potential* number of missing studies, with general guidelines for sensitivity analysis given in Shi and Lin (2019). The trim-and-fill method is the only funnel plot-based method that offers an adjusted mean estimate, and it is not recommended if there is heterogeneity in study effects (Jin et al., 2015).

A second class of methods is based on *selection models*, first described in Hedges

(1984). Let  $Y$  be a random variable representing effect sizes for all studies in a population and let  $\Theta$  be the parameters determining the sampling density  $f(y; \Theta)$ . Selection models assume a biased sampling scheme where the probability of a study being observed (published) is represented by a weight function  $w(y; \lambda)$ , where  $\lambda$ , a scalar or vector parameter, determines how certain studies may be more or less likely to be published. The weighted density for observed effect  $y_i$  is then

$$f^*(y_i; \Theta, \lambda) = \frac{f(y_i; \Theta)w(y_i; \lambda)}{\int f(y; \Theta)w(y; \lambda)dy} \quad (1.1)$$

and the likelihood function for all observed studies is

$$L(\Theta, \lambda) = \prod_{i=1}^S f^*(y_i; \Theta, \lambda). \quad (1.2)$$

Some models explicitly model the probability of publication for individual studies as a function of their  $p$ -values (Iyengar and Greenhouse, 1988; Hedges, 1992; Givens et al., 1997; Vevea and Hedges, 1995) or as a function of both the effect size and standard error (Copas, 1999; Copas and Shi, 2000, 2001). Hedges (1992) introduced stepped weight functions by dividing the unit interval  $[0, 1]$  into  $K$  segments with  $K-1$  cut points, where studies that have  $p$ -values in different segments have different probabilities of publication. We refer to stepped selection functions by the number of cut points, i.e. a 1-step selection function might have a single cut point at  $p = 0.05$ , or a 2-step function might have cuts at  $p = 0.05, 0.10$ . Earlier selection models were recommended for bias-corrected effect size estimates, and were later recommended only for sensitivity analyses because of identifiability issues in smaller meta-analyses (Veeva and Woods, 2005; Jin et al., 2015). Sensitivity analyses use a grid representing varying levels of publication bias and estimate the mean effect under each assumed scenario. If results do not change much under severe publication bias they are considered robust, and if results do change under mild publication bias they are considered sensitive to publication bias. Bayesian implementations of the

Copas selection model (Mavridis et al., 2013; Bai et al., 2020) have again allowed for estimation of mean effect sizes.

Recent approaches to mitigating publication bias have used Bayesian model averaging (BMA) to consider a set of potential selection functions. Guan and Vandekerckhove (2016) considers four different selection functions, including a no-bias model, an extreme-bias model where results with p-values  $p > \alpha$  are never published, a 1-step function where results with  $p > \alpha$  are published with some probability  $\pi < 1$ , and a model inspired by Givens et al. (1997) where the probability of publication decreases exponentially with  $p$ . The authors only implement the models in a fixed-effects framework. Maier et al. (2020) considers a set of 12 models, using a  $2 \times 2 \times 2$  factorial design with fixed/random effects, a true null/alternative hypothesis, and the presence/absence of publication bias. The authors consider two-step and three-step selection functions based on p-values when publication bias is assumed, where the probability of publication changes at  $p = 0.05$  (two-step) or at both  $p = 0.05$  and  $p = 0.10$  (three-step).

BMA effectively assumes that one of the considered models is the “true” model, which we call the  $\mathcal{M} - closed$  setting. BMA does not perform as well under the  $\mathcal{M} - complete$  or  $\mathcal{M} - open$  settings, where the true data generating mechanism is too complex to implement or to put into a probabilistic framework (Clyde and Iversen, 2013). Multiple issues arise for BMA in these settings, including a) the need to specify prior model probabilities, which makes little sense when we know the true model is not in our list, and b) the model weights from BMA will converge to the 1 for the model “closest” to the true model in terms of Kullback-Leibler divergence, and 0 for all others. Bayesian stacking (Yao et al., 2018, 2021) is a related method that outperforms BMA and solves the above issues by calculating optimal weights using expected log-predictive densities and leave-one-out (LOO) cross validation.

We propose using Bayesian stacking to mitigate publication bias by incorporating multiple different selection models. Copas and Shi (2001) recommends a sensitivity analysis over a grid of possible patterns of publication bias, each of which returns a bias-adjusted mean effect size estimate. A stacked estimate of the mean effect size can be obtained through a weighted average of estimates with the weights coming from Bayesian stacking. Assumed patterns of publication bias that poorly predict the observed data with LOO cross validation will be given little weight. We propose stacking over multiple types of models, including step functions (Hedges, 1992; Vevea and Hedges, 1995) and Bayesian Copas selection models Mavridis et al. (2013); Bai et al. (2020).

## 2 Methods

Say we have  $S$  studies indexed by  $i = 1, \dots, S$ , and each study provides an estimated effect  $y_i$  and an associated standard error  $s_i$ .

### 2.1 Selection models based on p-values

The first selection models for publication bias assumed the selection process was based solely on  $p$ -values. Here we consider a subset of  $p$ -value-based models that split the unit interval  $[0, 1]$  into  $K$  sub-intervals, where studies with  $p$ -values that fall into different intervals have different probabilities of publication (Hedges, 1992; Vevea and Hedges, 1995; Vevea and Woods, 2005). The data model is that of a standard random effects meta-analysis: let  $y_1, \dots, y_S$  be observed effect sizes with

associated standard errors  $s_i$ . We model the observed effects as

$$y_i|\theta_i \sim N(\theta_i, s_i^2) \quad (2.1)$$

$$\theta_i|\theta, \tau^2 \sim N(\theta, \tau^2) \quad (2.2)$$

where  $\theta_i$  represent random study effects normally distributed around global mean  $\theta$  and with variance  $\tau^2$ . Here we combine the study-specific standard errors  $s_i$  and the between-study variability  $\tau^2$  into a single residual so that

$$y_i|\theta, \tau^2 \sim N(\theta, s_i^2 + \tau^2). \quad (2.3)$$

We then define a stepped weight function  $w(\cdot)$ , where  $w(p)$  represents the probability that a study with  $p$ -value  $p$  is observed. Dividing the unit interval into  $K$  sub-intervals with descending endpoints  $a_k$  in which the weight function  $w(p)$  is constant, we have that

$$w(p_i) = \begin{cases} \omega_1 & \text{if } a_1 < p_i < 1 \\ \omega_j & \text{if } a_j < p_i < a_{j-1} \\ \omega_K & \text{if } 0 < p_i < a_{K-1} \end{cases} \quad (2.4)$$

where  $a_0 = 1$  and  $a_K = 0$ . Say  $\boldsymbol{\omega} = (\omega_1, \dots, \omega_K)$ . We then have that the likelihood contribution for each observation  $y_i$  given  $\theta$ ,  $\tau^2$  and weight function  $w(\cdot)$  is

$$f(y_i|\theta, \tau^2, \boldsymbol{\omega}) = \frac{\phi(y_i; \theta, \tau^2 + s_i^2) \times w(p_i)}{\int \phi(x; \theta, \tau^2 + s_i^2) \times w(1 - \Phi(x/2))dx}, \quad (2.5)$$

where  $\phi(x)$  and  $\Phi(x)$  represent the standard normal probability density and cumulative density functions, respectively. Maier et al. (2020) place a ‘‘cumulative-Dirichlet’’ prior distribution on the weights  $\boldsymbol{\omega}$ , which effectively means placing a symmetric Dirichlet prior on an auxiliary parameter  $\tilde{\boldsymbol{\omega}} \in (0, 1)^K$  and taking the

cumulative sum

$$\begin{aligned}\tilde{\omega} &\sim \text{Dirichlet}(\text{rep}(1, K)) \\ \omega &= \text{cumulative-sum}(\tilde{\omega}).\end{aligned}\tag{2.6}$$

This restricts  $\omega$  so that the  $K$  intervals in (2.4) have increasing probability of publication with decreasing  $p$ -values, and  $\omega_K = 1$ . The symmetric Dirichlet prior on  $\tilde{\omega}$  leads to prior means  $(\frac{1}{K}, \frac{2}{K}, \dots, 1)$  for  $\omega$ . Restricting  $\omega_K = 1$  means each other  $\omega_j$  represents the probability of publication for a study in interval  $j$  relative to the probability of publication in the lowest interval. We consider a range of possible structures for the weight function  $w(p)$  by varying both the number of intervals  $K$  and the choice of cut-points  $a_j$ .

## 2.2 Copas selection model

The Copas selection model (Copas, 1999; Copas and Shi, 2000, 2001) assumes that the selection mechanism for publication depends study effects  $y_i$  and associated standard errors  $s_i$  instead of  $p$ -values. The data model is

$$y_i = \theta_i + s_i \epsilon_i \tag{2.7}$$

$$z_i = \gamma_0 + \frac{\gamma_1}{s_i} + \delta_i \tag{2.8}$$

$$\theta_i \sim N(\theta, \tau^2) \tag{2.9}$$

where  $\theta_i$  is again study  $i$ 's true effect,  $\theta$  is the global mean effect, and  $\tau^2$  describes between-study heterogeneity. The latent factor  $z_i$  models the publication process, where study  $i$  is selected (published) only if  $z_i > 0$ . The parameter  $\gamma_0$  controls the baseline probability of publication, and  $\gamma_1$  defines the relationship between the observed standard deviation  $s_i$  and the probability of publication. Usually  $\gamma_1$  is assumed to be positive, so that studies with smaller standard errors are more likely

to be published. The random effects  $(\epsilon_i, \delta_i)$  are modeled as bivariate normal

$$\begin{pmatrix} \epsilon_i \\ \delta_i \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix} \right) \quad (2.10)$$

where  $\text{corr}(\epsilon_i, \delta_i) = \rho$  measures how the probability of selection changes with observed effect sizes.

Interpretation of the parameters  $(\gamma_0, \gamma_1, \rho)$  can be difficult. The marginal probability that a study with standard error  $s_i$  is published is

$$P(z_i > 0 | s_i) = \Phi(\gamma_0 + \frac{\gamma_1}{s_i}).$$

Thus, if  $\gamma_0$  is large and positive then all studies are published with high probability regardless of the value of  $s_i$ . We restrict  $\gamma_1$  to be positive under the assumption that larger studies are more likely to be published for various reasons (e.g. more funding, quality of writing, etc.). Larger values of  $\gamma_1$  lead to larger differences in publication probabilities for studies with different standard errors. The correlation parameter  $\rho$  is the main driver in how unadjusted estimates of  $\theta$  are biased from the truth. If  $\rho = 0$ , then the selection process does not depend on observed effect sizes and unadjusted estimates are unbiased. Positive values of  $\rho$  indicate that observed effects  $y_i$  influence the selection process such that larger values of  $y_i$  (relative to their true mean  $\theta_i$ ) are being selected for, while negative values of  $\rho$  would show selection favoring larger negative values of  $y_i$ .

We consider two Bayesian adaptations of the Copas model (Mavridis et al., 2013; Bai et al., 2020), which put prior distributions on all parameters including  $\gamma_0$  and  $\gamma_1$ . Mavridis et al. (2013) instead places priors on the lower and upper bounds for the probability of publication,  $P_{\text{low}}$  and  $P_{\text{high}}$ , as

$$\begin{aligned} P_{\text{low}} &\sim \text{Uniform}(L_1, L_2) \\ P_{\text{high}} &\sim \text{Uniform}(U_1, U_2), \end{aligned} \quad (2.11)$$



where  $(L_1, L_2)$  and  $(U_1, U_2)$  represent plausible ranges for the probability of publication for the studies with the largest and smallest standard errors, respectively. They then transform  $(P_{\text{low}}, P_{\text{high}})$  to  $(\gamma_0, \gamma_1)$  with a 1-to-1 transformation using

$$\begin{aligned}\gamma_0 + \frac{\gamma_1}{s_{\text{max}}} &= \Phi^{-1}(P_{\text{low}}) \\ \gamma_0 + \frac{\gamma_1}{s_{\text{min}}} &= \Phi^{-1}(P_{\text{high}})\end{aligned}\tag{2.12}$$

where  $s_{\text{min}}$  and  $s_{\text{max}}$  are the smallest and largest observed standard errors in the sample of  $S$  studies. Bai et al. (2020) place priors directly on  $\gamma_0$  and  $\gamma_1$  as

$$\begin{aligned}\gamma_0 &\sim \text{Uniform}(-2, 2) \\ \gamma_1 &\sim \text{Uniform}(0, s_{\text{max}}).\end{aligned}\tag{2.13}$$

They reason that this range of values allows for selection probabilities between 2.5% and 99.7% by restricting most of the mass for latent variables  $z_i$  to the range  $(-2, 3)$ . Priors (2.13) are meant to be default prior distributions, while (2.11) may require more problem-specific tuning, and the two priors lead to surprisingly different posterior distributions for the mean parameter  $\theta$ .

### 2.3 Bayesian stacking

We use  $\mathcal{M}$ -open to refer to the setting in which our list of candidate models does not include the true data generating mechanism (Bernardo and Smith, 2009). Bayesian stacking (Yao et al., 2018) is an alternative to BMA that has superior performance in the  $\mathcal{M}$ -open setting. If we have  $K$  candidate models, the goal is to find the set of optimal weights  $w \in \mathcal{S}_1^K$ ,  $\mathcal{S}_1^K = \{w \in [0, 1]^K : \sum_{k=1}^K w_k = 1\}$ , that maximizes a score  $S$  comparing weighted predictive distributions  $p_k(\tilde{y}|y, M_k)$  to the true distribution  $p_t(\tilde{y}|y)$ . Rather than requiring holdout data  $\tilde{y}$  and Yao et al. (2018) replace  $p(\tilde{y}|y)$  with observed values  $y_i$  and replace  $p(\tilde{y}|y, M_k)$  with its corresponding leave-one-out (LOO) predictive distribution  $\hat{p}_{k,-i}(y_i) = \int p(Y_i|\theta_k, M_k)p(\theta_k|y_{-i}, M_k)d\theta_k$ , where

$M_k$  is model  $k$ ,  $k = 1, \dots, K$ , and  $\theta_k$  are the parameters in model  $k$ . The authors recommend the logarithmic scoring rule, which reduces the stacking problem to solving for weights  $w$  in

$$\max_{w \in \mathcal{S}_1^K} \frac{1}{n} \sum_{i=1}^n \log \sum_{k=1}^K w_k p(y_i | y_{-i}, M_k) \quad (2.14)$$

via optimization. Instead of refitting each model  $n$  times to obtain LOO distributions  $p_k(y_i | y_{-i} M_k)$ , Yao et al. (2018) use Pareto smoothed importance sampling (PSIS) (Vehtari et al., 2017) to obtain approximations.

After stacking weights  $w$  have been optimized, the stacked posterior distribution of  $\theta$  can be obtained by taking  $w_k \times T$  samples from each model  $k$ 's posterior distribution  $p(\theta | y)$  for a total of  $T$  posterior samples.

Implementation of Bayesian stacking can be done using the R package ‘loo’.

## 2.4 Stacking selection models for publication bias

It would be naive to think that either the stepped selection functions in Section 2.1 or the Copas models in Section 2.2 represent the true data generating mechanism for publication bias. As Bayesian stacking is designed to perform well in the event that our model list does not contain the true model, we propose stacking over a variety of stepped selection functions and Copas models to obtain a more robust posterior distribution for the mean parameter  $\theta$ . We fit both Bayesian Copas selection models (Mavridis et al., 2013; Bai et al., 2020) and a set of stepped selection models with varying numbers of steps. As a default, we use a 1-step function with the step at  $p = 0.05$ , a two-step function with steps at  $p = (0.05, 0.10)$ , and a three-step function with steps  $p = (0.05, 0.10, 0.20)$ .

We fit the Copas models in JAGS (Plummer et al., 2003) as there is a straight-

forward Gibbs sampling routine. Writing model (2.7) - (2.9) as

$$\begin{pmatrix} y_i \\ z_i \end{pmatrix} \sim N \left( \begin{pmatrix} \theta \\ u_i \end{pmatrix}, \begin{pmatrix} \tau^2 + s_i^2 & \rho s_i \\ \rho s_i & 1 \end{pmatrix} \right) \mathbb{1}_{z_i > 0} \quad (2.15)$$

we see that we can first sample  $z_i$  from a truncated normal  $z_i \sim N(u_i, 1) \mathbb{1}_{z_i > 0}$ , and then sample  $y_i | z_i \sim N(E(y_i | z_i), \text{Var}(y_i | z_i))$  where  $E(y_i | z_i) = \theta + \rho s_i(z_i - u_i)$  and  $\text{Var}(y_i | z_i) = \tau^2 + s_i^2(1 - \rho^2)$ . We also need to extract the log-likelihood for each observation  $(y_i, s_i)$  in order to stack models. The model construction leads to a simple form for the log-likelihood

$$\begin{aligned} L(\theta, \tau^2, \rho, \gamma_0, \gamma_1) &= \sum_{i=1}^S \log[p(y_i | z_i > 0, s_i)] \\ &= \sum_{i=1}^S \log \left[ \frac{p(z_i > 0 | y_i, s_i) f(y_i)}{p(z_i > 0 | s_i)} \right] \\ &= \sum_{i=1}^S \log(\phi(y_i; \theta, \tau^2)) - \log \Phi(u_i) + \log \Phi(v_i) \end{aligned} \quad (2.16)$$

where  $\phi(y_i; \theta, \tau^2)$  represents the density at the point  $y_i$  of a normal distribution with mean  $\theta$  and variance  $\tau^2$ ,  $\Phi(\cdot)$  represents the standard normal cumulative density function, and

$$\begin{aligned} u_i &= \gamma_0 + \frac{\gamma_1}{s_i} \\ v_i &= \frac{u_i + \tilde{\rho}_i \frac{y_i - \theta}{\sqrt{\tau^2 + s_i^2}}}{\sqrt{(1 - \tilde{\rho}_i^2)}} \\ \tilde{\rho}_i &= \frac{s_i}{(\tau^2 + s_i^2)^{1/2}} \rho. \end{aligned}$$

We fit the stepped selection models in Stan (Gelman et al., 2015) because of the ability to easily code the custom probability distribution (2.5).

### 3 Simulation

We assess model performance using bias, 95% interval coverage, 95% interval length, and root-mean squared error (RMSE). We use a factorial design with  $\theta = (0, 0.4)$  and  $\tau = 0.2$ , sample  $S = 30, 60, 100$  values  $s_i$ ,  $i = 1, \dots, S$  from a  $\text{Uniform}(0.2, 0.8)$  distribution as study-specific standard errors, and sample  $\theta_i \sim N(\theta, \tau^2)$  or  $\theta \sim t(\theta, \tau^2, df = 4)$  as true study effects. We then sample  $y_i \sim N(\theta_i, s_i^2)$  as observed study effects. Because we propose stacking models when the true model is not in our list, we use several complex selection mechanisms that endow each study  $i$  with a probability  $\alpha_i$  of being observed as  $f(y_i, s_i, p_i)$ , where  $p_i = 2 \times (1 - \Phi(|y_i|/s_i))$  and a selection indicator for each study  $i$  is drawn from  $\text{Bernoulli}(\alpha_i)$ .

### References

- Bai, R., Lin, L., Boland, M. R., and Chen, Y. (2020). A robust bayesian copas selection model for quantifying and correcting publication bias. *arXiv preprint arXiv:2005.02930*.
- Begg, C. B. and Mazumdar, M. (1994). Operating characteristics of a rank correlation test for publication bias. *Biometrics* pages 1088–1101.
- Bernardo, J. M. and Smith, A. F. (2009). *Bayesian theory*, volume 405. John Wiley & Sons.
- Clyde, M. and Iversen, E. S. (2013). Bayesian model averaging in the m-open framework. *Bayesian theory and applications* **14**, 483–498.
- Copas, J. (1999). What works?: selectivity models and meta-analysis. *Journal of the Royal Statistical Society: Series A (Statistics in Society)* **162**, 95–109.

- Copas, J. and Shi, J. Q. (2000). Meta-analysis, funnel plots and sensitivity analysis. *Biostatistics* **1**, 247–262.
- Copas, J. and Shi, J. Q. (2001). A sensitivity analysis for publication bias in systematic reviews. *Statistical methods in medical research* **10**, 251–265.
- Duval, S. and Tweedie, R. (2000). Trim and fill: a simple funnel-plot–based method of testing and adjusting for publication bias in meta-analysis. *Biometrics* **56**, 455–463.
- Egger, M., Smith, G. D., Schneider, M., and Minder, C. (1997). Bias in meta-analysis detected by a simple, graphical test. *Bmj* **315**, 629–634.
- Gelman, A., Lee, D., and Guo, J. (2015). Stan: A probabilistic programming language for bayesian inference and optimization. *Journal of Educational and Behavioral Statistics* **40**, 530–543.
- Givens, G. H., Smith, D., and Tweedie, R. (1997). Publication bias in meta-analysis: a bayesian data-augmentation approach to account for issues exemplified in the passive smoking debate. *Statistical Science* **12**, 221–250.
- Guan, M. and Vandekerckhove, J. (2016). A bayesian approach to mitigation of publication bias. *Psychonomic bulletin & review* **23**, 74–86.
- Hedges, L. V. (1984). Estimation of effect size under nonrandom sampling: The effects of censoring studies yielding statistically insignificant mean differences. *Journal of Educational Statistics* **9**, 61–85.
- Hedges, L. V. (1992). Modeling publication selection effects in meta-analysis. *Statistical Science* **7**, 246–255.

- Iyengar, S. and Greenhouse, J. B. (1988). Selection models and the file drawer problem. *Statistical Science* pages 109–117.
- Jin, Z.-C., Zhou, X.-H., and He, J. (2015). Statistical methods for dealing with publication bias in meta-analysis. *Statistics in medicine* **34**, 343–360.
- Light, R. J. and Pillemer, D. B. (1984). Summing up: the science of reviewing research.
- Lin, L. and Chu, H. (2018). Quantifying publication bias in meta-analysis. *Biometrics* **74**, 785–794.
- Macaskill, P., Walter, S. D., and Irwig, L. (2001). A comparison of methods to detect publication bias in meta-analysis. *Statistics in medicine* **20**, 641–654.
- Maier, M., Bartoš, F., and Wagenmakers, E.-J. (2020). Robust Bayesian meta-analysis: Addressing publication bias with model-averaging.
- Mavridis, D., Sutton, A., Cipriani, A., and Salanti, G. (2013). A fully bayesian application of the copas selection model for publication bias extended to network meta-analysis. *Statistics in medicine* **32**, 51–66.
- Peters, J. L., Sutton, A. J., Jones, D. R., Abrams, K. R., and Rushton, L. (2006). Comparison of two methods to detect publication bias in meta-analysis. *Jama* **295**, 676–680.
- Plummer, M. et al. (2003). Jags: A program for analysis of bayesian graphical models using gibbs sampling. In *Proceedings of the 3rd international workshop on distributed statistical computing*, volume 124, pages 1–10. Vienna, Austria.
- Rothstein, H. R., Sutton, A. J., and Borenstein, M. (2006). *Publication bias in meta-analysis: Prevention, assessment and adjustments*. John Wiley & Sons.

- Rücker, G., Schwarzer, G., and Carpenter, J. (2008). Arcsine test for publication bias in meta-analyses with binary outcomes. *Statistics in Medicine* **27**, 746–763.
- Shi, L. and Lin, L. (2019). The trim-and-fill method for publication bias: practical guidelines and recommendations based on a large database of meta-analyses. *Medicine* **98**,.
- Thompson, S. G. and Sharp, S. J. (1999). Explaining heterogeneity in meta-analysis: a comparison of methods. *Statistics in medicine* **18**, 2693–2708.
- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical bayesian model evaluation using leave-one-out cross-validation and waic. *Statistics and computing* **27**, 1413–1432.
- Vevea, J. L. and Hedges, L. V. (1995). A general linear model for estimating effect size in the presence of publication bias. *Psychometrika* **60**, 419–435.
- Vevea, J. L. and Woods, C. M. (2005). Publication bias in research synthesis: sensitivity analysis using a priori weight functions. *Psychological methods* **10**, 428.
- Yao, Y., Pirš, G., Vehtari, A., and Gelman, A. (2021). Bayesian hierarchical stacking. *arXiv preprint arXiv:2101.08954* .
- Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018). Using stacking to average bayesian predictive distributions (with discussion). *Bayesian Analysis* **13**, 917–1007.