WILEY ECOLOGY

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Journal:	*Ecology*
Manuscript ID	ECY20-1371.R1
Wiley - Manuscript type:	Comment
Date Submitted by the Author:	01-Mar-2021
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Substantive Area:	
Organism:	
Habitat:	
Geographic Area:	
Key words/phrases:	
Abstract:	

An assessment of statistical methods for non-independent data in ecological meta-analyses: Comment

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Running title: Avoid averaging effect sizes per paper

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Key words: meta-regression, Bayesian statistics, Satterthwaite approximation, multilevel modeling, hierarchical models, degrees of freedom

(Introduction)

Recently, Song et al. (2020) conducted a simulation study using different methods to deal with non-independence resulting from effect sizes originating from the same paper – a common occurrence in ecological meta-analyses. The main methods that were of interest in their simulations were: 1) a standard random-effects model used in combination with a weighted average effect size for each paper (i.e., a two-step method), 2) a standard random-effects model after randomly choosing one effect size per paper, 3) a multilevel (hierarchical) meta-analysis model, modelling paper identity as a random factor, and 4) a meta-analysis making use of a robust variance estimation method. Based on their simulation results, they recommend that meta-analysts should either use the two-step method, which involves taking a weighted paper mean followed by analysis with a random-effects model, or the robust variance estimation method.

Song et al.'s simulation results are an important and valuable contribution to the ecological community. However, we disagree with their primary recommendation of calculating a weighted average effect size for each study within a paper for two reasons. First, as we have stated elsewhere (Nakagawa & Santos 2012, Noble et al. 2017), we recommend the use of multilevel meta-analytic models because of improved power and the ability to answer richer biological questions about the drivers underlying variation in published effects. Second, we do not recommend the use of the two-step method with a weighted paper mean because other types of within-study non-independence often co-occur that need to be considered but that are not completely dealt with by Song et al. (2020)'s simulation. We fully agree that a robust variance estimation method is useful, but from Song et al. (2020) paper it would appear to be limited in applicability. However, we show that this method can easily be extended to multilevel meta-analysis, making the best of both worlds.

In this Comment, we overview a previous simulation study with different conclusions to that of Song et al. (2020) and put forward a strong case for why we need to make use of multilevel meta-analysis in the field of ecology. We discuss how the results of this previous simulation, along with our updated simulation results from Song et al. (2020), make different conclusions that show multilevel meta-analysis can perform well when non-independence exists. In our simulations, we demonstrate how a number of additional methods can provide solutions for any increase in Type I error when fitting multilevel meta-analysis models (an issue noted by Song et al., 2020).

Similar Simulations, Different Conclusions

Moeyaert et al. (2017) conducted a similar simulation study to Song et al. (2020) with some minor differences. First, Moeyaert et al. (2017) did not include a condition involving randomly choosing one effect per paper and used the standardized mean difference (aka Cohen's *d* or Hedges' *g*) as their effect size, instead of the log response ratio used by Song et al. (2020) (Hedges et al. 1999). Second, Moeyaert et al. (2017) did not model different correlations within papers (they referred to papers as studies) and heteroscedasticity among papers (different between-paper variances). Finally, Moeyaert et al. (2017) used PROC GLM in SAS 9.3 (SAS Institute Inc, 2011-2014) while Song et al. used R's *metafor* (Viechtbauer 2010) and *robumeta* (Fisher et al. 2017) for multilevel meta-analysis and robust variance estimation, respectively.

Like Song et al. (2020), Moeyaert et al. (2017) found that all of the three methods examined produced unbiased estimates of the overall (meta-analytic) mean. A striking difference was that in Moeyaert et al. (2017), multilevel meta-analyses performed as well as a robust variance estimation method in terms of 95% confidence interval (CI) coverage. In contrast, Song et al. (2020) reported consistently higher Type I error rates (i.e., greater than 5%) for multilevel meta-analyses. The highest Type I error rate of multi-level meta-analysis models achieved across all scenarios was about 8.2% [Mean (Median) Error Rates: 6.42% (6.42%)], which seems marginal in absolute terms, but relative to the nominal rate of 5% constitutes an increase of 64%. Further, Moeyaert et al. (2017) noted that when effect sizes from the same studies are not correlated, the two-step method with a weighted paper mean provided confidence intervals that were too wide (inefficient), which was also the case in Song et al.'s simulation. Based on their results, Moeyaert et al. (2017) recommend both multilevel meta-analysis and robust variance estimation methods but advised against the averaging method.

The differences in recommendations between Moeyaert et al. (2017) and Song et al. (2020) may have originated from a well-known issue in linear mixed-effects models, of which multilevel meta-analysis is a special type (Nakagawa & Santos 2012); that is, for linear mixed-effects (multilevel) models, it is difficult to determine the appropriate degrees of freedom, which is required for CI calculations. The SAS procedure used by Moeyaert et al. (2017) implements a method for calculating the degrees of freedom that is more appropriate for smaller sample sizes, while R's *metafor* used by Song et al. (2020) is yet to do so (at the moment, it simply sets the degrees of freedom equal to the total number of effect sizes minus 1). Indeed, Song et al. (2020) suspected this shortcoming by stating "this issue is addressed by adjusting the degrees of freedom... ", but did not explore the possible corrections. If this is the issue, there are several solutions that already exist to correct Type I error rates toward the nominal value. Another potential cause of the difference between Song et al. (2020) and Moeyaert et al. (2017) is that the former modeled heteroscedasticity among papers, while the latter did not. Here, we expand Song et al. (2020)'s simulations to show how currently available tools can resolve many of the issues they identified without the need to resort to averaging methods. Before doing so, we would first like to review the reasons for why, in the past, we have strongly recommend the use of multilevel/hierarchical meta-analytic models over a method that averages multiple effect sizes per paper.

Why Multilevel/Hierarchical Models over Averaging?

Nakagawa and Santos (2012) recommended the use of the following meta-analytic model for datasets which can include effect sizes across different species as well as different papers:

$$y_i = \mu + a_k + s_k + p_j + e_i + m_i, \tag{1}$$

where:

A. y_i is the ith effect size ($i = 1, \ldots, N_{effect\text{-}size}$; the number of effect sizes),

B. μ is the meta-analytic mean,

C. a_k is the phylogenetic effect for the kth species ($k = 1, \ldots, N_{species}$), which is distributed with $\mathrm{N}(0,\sigma_a^2\mathbf{A})$, where **A** is a correlation matrix derived from a phylogenetic tree for species included in a meta-analysis,

D. s_k is the non-phylogenetic (species) effect for the kth species, distributed according to N $(0,\sigma_s^2)$,

E. p_j is the jth paper effect ($j = 1, \ldots, N_{paper}$), distributed according to $\mathrm{N}(0,\sigma_p^2)$,

F. e_i is the ith effect-size specific effect, distributed according to $\mathrm{N}(0,\sigma_e^2)$, and

G. m_i is the ith sampling error effect, distributed according to $N(0,\sigma_i^2)$ where σ_i^2 is the sampling error variance for the ith effect size (note when sampling errors are correlated, a variance-covariance matrix can replace σ_i^2; see below).

Although Song et al. (2012) did not mention phylogenetic non-independence (shown in Equation 1), this issue commonly arises in ecological meta-analysis, and is similar in manner to non-independence due to effects being derived from the same source paper. What is more, it is often important to appropriately take phylogeny into consideration in a meta-analysis (Chamberlain et al. 2012). If we follow the logic of averaging, and we want to avoid using multilevel meta-analysis, we need to average per species. Nakagawa and Santos (2012) put forward three main arguments against averaging (similar arguments were independently put forward by Cheung 2014): 1) the potential loss of statistical power and needlessly large standard errors for the overall effect, 2) the loss of information resulting from not being able to estimate within-paper (within-study) variance, and 3) perhaps most importantly, not being able to estimate ecologically important moderator effects given that aggregation will reduce the information content dramatically (i.e. removes within-species variation in estimated effects).

Both simulation studies suggest the first argument may not apply unless correlations among effect sizes are close to zero. Importantly, Song et al. (2012) discuss two scenarios where dependence among effect sizes could arise: 1) “because they were observed in the same experiment or may have been based on the same subjects” and 2) “even if they arose from separate experiments because experiments likely share common methods, contexts, or other characteristics that influence the effect size”. However, Song et al. (2020) only focused on the latter scenario in their simulation not for the former. For the former, where sampling errors are correlated, we need to use the following formula (Borenstein et al. 2009) to obtain a sampling error variance (or a sampling standard error) to accompany a weighted mean, rather than the fixed-effect model used by Song et al. (2012):

$$\mathrm{var}\left(\frac{1}{n}\sum_{i=1}^{n} y_i\right) = \left(\frac{1}{n}\right)^2\left(\sum_{i=1}^{n}\sigma_i^2 + \sum_{i \neq g}^{n} r_{ig}\sqrt{\sigma_i^2\sigma_g^2}\right) \quad (2),$$

where y_i is the ith effect size ($i = 1, \ldots, n$ and $g = 1, \ldots, n$, where n is the number of effect size within a paper to be combined), σ_i^2 and σ_g^2 are the sampling error variances for y_i and y_g, and r_{ig} is the correlation between the sampling errors of y_i and y_g (note that one can use the function, *aggregate* in *metafor* to calculate a weighted mean and accompanying sampling variance as in Equation 2). We believe that both types of non-independence frequently co-occur and need to be accounted for. For the multilevel meta-analysis, we can model the variance-covariance matrix of the sampling errors for the former type of non-independence as well as model a random effect for paper, although r_{ig} is often not known and needs to be assumed (detailed in Noble et al. 2017; see also, Lajeunesse, 2009; 2011. Further, beyond these two types of multilevel meta-analytic models we can model different sources of non-independence (e.g., phylogenetic relatedness and species relatedness not due to phylogeny; see Equation 1) simultaneously and flexibly, although more data is required for more complex models (Nakagawa and Santos 2012).

The loss of information is a more serious issue, especially the loss of moderator information. The high heterogeneity observed in ecological meta-analyses (Senior et al. 2016) often implies that ecologists must use meta-regression models, which use moderators (or ‘predictors’) to explain variation among effect sizes. In many cases, meta-regression models are likely to be more useful and informative in ecology than simple meta-analytic models (Gurevitch et al. 2017). Indeed, meta-regression can provide us with review- or synthesis-generated evidence which cannot be obtained via single studies (Nakagawa et al. 2017). If we extend Song et al. (2020)'s recommendation of not using multilevel meta-analyses to 'multilevel meta-regression', this would severely limit our ability to test moderator effects. For example, it is common to obtain separate effect sizes for males and females from one paper. If we aggregate these effect sizes per paper then we would not be able to test sex-specific effects, which runs counter to recent movements to test ubiquitous sex effects (Tannenbaum et al. 2019; Zajitschek et al. 2020).

Solutions for Type I Errors in Multilevel Meta-analysis without the Need for Averaging

Alongside the methods (referred to as Methods 1-5) used by Song et al. (2020), we explored four further methods that are known to overcome the slight excess in Type I error rates observed when using multi-level meta-analytic models. Our simulations reproduced the simulations by Song et al. (2020) but added: 1) a simple correction to the degrees of freedom used to calculate the overall effect size confidence intervals. This involved simply using one less than the total number of papers instead of the typical degrees of freedom that uses the total number of effect sizes (i.e., df = total papers – 1); 2) a Satterthwaite approximation to the effective degrees of freedom, which is commonly applied in the linear mixed effect model literature (Satterthwaite, 1946); 3) a second cluster-robust estimation method implemented in the *clubSandwich* package in R (Pustejovsky, 2020) that uses a bias-reduced linearization method (Pustejovsky and Tipton, 2018). The R package *clubSandwich* uses a similar robust-variance estimation method as *robumeta* (Fisher et al. 2017) used in Song et al. (2020), but can be applied to *metafor's rma.mv* model objects; and 4) a Bayesian modelling approach that uses an MCMC algorithm (using the R package *MCMCglmm* – Hadfield, 2010), instead of restricted maximum likelihood (REML) estimation, as MCMC algorithms are known to have robust coverage, albeit are slightly conservative with small sample sizes (Pappalardo et al. 2020). We also explored other modelling approaches, but present these four as they are simple solutions that can be easily implemented. We focus exclusively on coverage / error rates given that bias was unaffected by the different modelling approaches in Song et al. (2020)'s simulations. For each method (the five existing methods from Song et al. 2020) plus the four new approaches we describe above, we ran 5,000 iterations across all the scenarios detailed in Song et al. (2020). An updated set of scripts from Song et al. (2020), including a coding correction, that implements these new methods can be found at https://(Fisher et al. 2017).

Our new simulation results (Figure 1) show that the four proposed solutions perform quite well across all the scenarios described by Song et al. (2020). The overall performance of each method for each specific simulation scenario is provided in Figure 1B, which reproduces Figure 3 (Experiment 1 and 2) from Song et al. (2020). Overall, the simple approaches we implemented corrected the excess in Type I error rates in the multi-level meta-analytic models implemented in *metafor* (Figure 1A). In particular, Bayesian methods, while having inflated Type II error under small sample situations, perform extremely well across a variety of conditions (Figure 1A and B), with average Type I error rates converging on the 5% level but being slightly conservative overall [Mean (SD) = 4.82% (0.0053)]. A Satterthwaite approximation to the effective degrees of freedom also performs quite well under a variety of conditions as expected [Figure 1A & B – 5.02% (0.0046)]; even the simplest degrees of freedom correction that uses total papers minus one performs quite well [Figure 1A & B – 5.39% (0.0059]. Considering these results above, and the ease of implementation, we recommend fitting a multilevel model with a robust variance estimator because it can easily be applied to multilevel-meta-analytic models in *metafor*. Also, one can certainly use Bayesian modelling, as long as the dataset is large enough (e.g., > 100 effect sizes). A step-by-step guide to implement both of these methods can be found at https://github.com/daniel1noble/ecology_comment.

Conclusion

We appreciate the thorough simulations conducted by Song et al. (2020) in an attempt to better understand the ways in which meta-analysts can overcome one of the most common challenges of meta-analysis; dealing with non-independent effect sizes. While we agree with their recommendation of using robust variance estimation methods (with caveats), we disagree with their recommendation that averaging effect sizes within studies is a solution. While we recognise that there may be times when averaging effect sizes is easier (e.g., when there are very few studies with repeated effects), one most likely needs to use Equation 2 above, not the method of averaging suggested by Song et al. (2020). Regardless, averaging effect sizes within studies comes with a number of significant disadvantages that include: 1) not being able to control for additional sources of non-independence, such as phylogenetic non-independence, which will be commonplace in ecological meta-analyses and 2) not being able to understand the drivers of effect size heterogeneity given that moderator information, which could be included in meta-regression models, is lost. As we have shown, there are a number of very simple, and easily implemented solutions to correct any inflated Type I error rates to their nominal level. Indeed, even robust variance estimators can readily be incorporated into multilevel meta-analytic models, which we recommend ecologists employ. Ignoring these elements prevents meta-analysts from answering a richer set of biologically relevant questions about the drivers underlying effect size variability. As such, we argue strongly against averaging effect sizes within a paper whenever possible.

Acknowledgement

We thank James Pustejovsky for his advice on the robust variance estimator implemented in *clubSandwich*, and also three anonymous reviewers whose comments improved our manuscript. SN and DWAN are supported by an ARC (Australian Research Council) Discovery grant (DP200100367). AMS is supported by an ARC fellowship (DE180101520).

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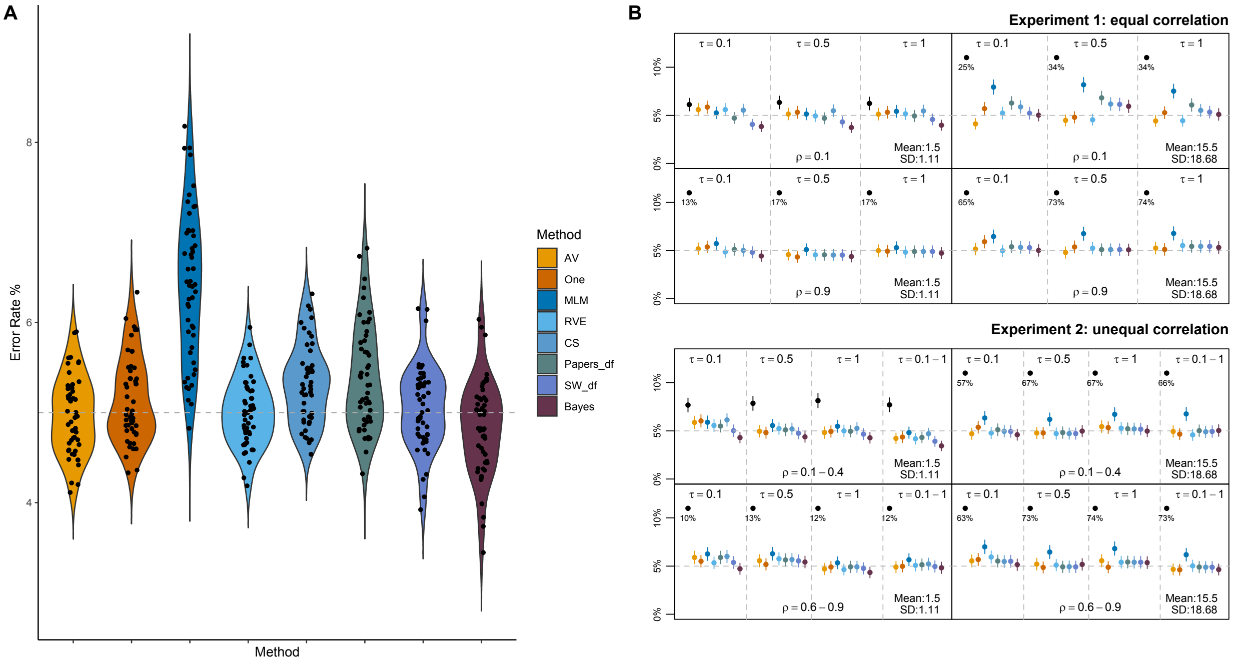
Figure captions

Figure 1 – A) Density distribution of average Type I error rates (%) across all 51 scenarios simulated by Song et al. (2020). The first four methods reproduce Song et al. (2020)'s simulations and include: "One" = Choosing a single effect size; "AV" = two-step method that averages effects within a study; "MLM" = Multi-level meta-analytic model; "RVE" = Robust variance estimation method with *robumeta*. In addition to these, we implemented four new methods to correct the slight increase in Type I error rates for the MLM method. These included: "CS" = club sandwich robust variance estimation; "Papers_df" = degrees of freedom equal to the total number of papers minus one to adjust confidence intervals from MLM; "SW_df" = Satterthwaite degrees of freedom to adjust the confidence intervals of the MLM, and "Bayes" = Bayesian estimation methods. See details in text. Raw error rates across all simulated scenarios described by Song et al. (2020) are depicted by black points. Grey dashed line represents the nominal 5% error rate. Note that the method ignoring non-independence is not included here (see Figure S1). B) Average Type I error rates (%) across a sub-sample of scenarios simulated by Song et al. (2020). Note that the sub-sample of simulation scenarios matches those presented in Song et al. (2020) and does not include all 51 simulation scenarios presented in panel A. Colors match methods described in panel A, except we also present the original Method 1 as denoted in black, which completely ignores non-independence.


A
Error Rate %
8
6
4
Method
Method
AV
One
MLM
RVE
CS
Papers_df
SW_df
Bayes
B
Experiment 1: equal correlation
τ = 0.1
τ = 0.5
τ = 1
10%
5%
0%
25%
34%
34%
ρ = 0.1
Mean:1.5
SD:1.11
Mean:15.5
SD:18.68
13%
17%
17%
65%
73%
74%
ρ = 0.9
Experiment 2: unequal correlation
τ = 0.1 – 1
57%
67%
67%
66%
ρ = 0.1 – 0.4
10%
13%
12%
12%
63%
73%
74%
73%
ρ = 0.6 – 0.9

Dear Prof Conn

Please find our revision of “An assessment of statistical methods for non-independent data in ecological meta-analyses”. We would like to thank all the referees for their insightful and constructive comments. We have provided point-by-point replies below to all the referee comments. The changes we have made have greatly improved our paper. We hope this version is now acceptable for the publication in Ecology.

Best wishes,

Shinichi Nakagawa on behalf of all the co-authors

01-Feb-2021

Dear Dr. Nakagawa:

Thank you very much for submitting your manuscript "An assessment of statistical methods for non-independent data in ecological meta-analyses: Comment" ECY20-1371 to Ecology. I have now received three reviews on this comment (including the author of the original article). All three authors were positive about your work; we are thus willing to consider a revised version for publication in the journal, assuming that you are able to modify the manuscript according to the recommendations.

Your revisions should address the specific points made by each reviewer.

To submit your revised manuscript, log into https://mc.manuscriptcentral.com/ecology and enter your Author Center. You will find your manuscript title listed under "Manuscripts with Decisions." Under "Actions," click on "Create a Revision." Your manuscript number has been appended to denote a revision. Please DO NOT upload your revised manuscripts as a new submission.

When submitting your revised manuscript, you will be able to respond to the comments made by each reviewer in the space provided. You can use this space to document any changes you make to the original manuscript. In order to expedite the processing of the revised manuscript, please be as specific as possible in your response.

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Because we are trying to facilitate timely publication of manuscripts submitted to Ecology, your revised manuscript should be uploaded as soon as possible. Please complete the revision within the next six weeks.

Once again, thank you for submitting your manuscript to Ecology and I look forward to receiving your revision.

Sincerely,

Dr. Paul Conn

Subject Matter Editor, Ecology
paul.conn@noaa.gov

Reviewer(s)' Comments to Author:

Reviewer: 1

I appreciate Nakagawa et al.'s timely and insightful comments on our recent paper. The discussion on the advantages and disadvantages of various methods we explored and the methods to address inflated type I error rates in hierarchical models would be of great value to meta-analysts. I thus advocate for the publication of this comment.

This comment mainly discussed two issues related to our paper. First, I agree with the assessment that the two-step method using a weighted mean from each paper has limitations. As the authors' noted, it cannot be used when the meta-analysis model contains covariates whose values/levels vary within a paper. It also cannot address non-independence caused by phylogeny because all observed effect sizes will be non-independent, and one cannot identify a group from which a weighted mean effect size should be calculated. We in fact made a brief mention of this issue in our originally submitted paper but elected not to include it in the revision based on page limits and the confusion it caused a reviewer. I thus believe the discussion on the limitation of this method in the comment is very useful.

Reply 1: We very much appreciate this supportive comment.

Second, the authors presented several solutions to address the issue of inflated type I error rates in hierarchical models. These solutions have been rarely discussed in the meta-analysis literature, and therefore provide an extremely valuable contribution. I do not necessarily agree with the view implied in the comment that an 8% error rate can always be considered a small departure from a nominal 5% rate. While some may consider 8% error rate at the 5% significance level to be acceptable, others may view the 60% increase in error rate problematic. It depends on the analyst's tolerance of error. I am afraid that some readers of this comment might take away from the presentation that there is no real need to address the inflated type I error rates of hierarchical models. This is likely a topic I would address in a reply depending on the final presentation in this comment.

Reply 2: This is an important point and we certainly do not want to our readers to think this is a trivial problem. Therefore, we deleted the following sentences:

"It is important to emphasize that variation in error rates across all methods was rather small (varying between ~ 3.44–8.20%), suggesting that any problem in not accounting for non-independence, even if just using multi-level models, will be fairly small."

"any inflated Type I error rates are fairly small when using multi-level models, but we also show that…"

We have also revised the following sentence:

"The highest Type I error rate of multi-level meta-analysis models achieved across all scenarios was about 8.2% [Mean (Median) Error Rates: 6.42% (6.42%)], which seems marginal in absolute terms, but relative to the nominal rate of 5% constitutes an increase of 64%."

Below, I list a few detailed suggestions for the authors' consideration.

Line 119: I don't think one can use the "paper mean" method in this situation. When there is dependence caused by phylogeny, all observed effect sizes will be correlated with the strength of correlation determined by the phylogenetic relationships. Averaging effect size from the same species addresses only part of this problem. For example, if species A and B are closely related to each other but only distantly related to species C, we still cannot treat the average effect sizes for species A, B, and C as independent in the meta-analysis. The phylogenetic non-independence still exists.

Reply 3: Many thanks for pointing this out. We have now fixed this sentence to say:

"If we follow the logic of averaging, and we want to avoid using multilevel meta-analysis, we need to average over species." (deleted "after averaging over a study")

Line 129: The authors are correct that we only considered dependence arising from correlated among-study random effect. But we did not fail to note the possibility of correlated sampling error. We explicitly stated that we only considered the dependence from among-study random effect because correlated sampling error can often be recognized from the experimental design of the primary literature and be explicitly modeled in meta-analysis (second paragraph after equation 4).

Reply 4: We apologise for this wording error. We have now deleted the relevant section with some minor edits.

Line 139: Equation 2 is the variance of the arithmetic mean, not the weighted mean. In addition, equation 2 for the variance of the arithmetic mean is incorrect. It should be

$$\mathrm{var}\left(\frac{1}{n}\sum y_i\right) = \left(\frac{1}{n}\right)^2 \left(\sum_{i \neq g} r_{ig}\sqrt{\sigma_i^2 \sigma_g^2}\right) + \left(\frac{1}{n}\right)^2 \sum_{i=1}^{n} \sigma_i^2$$

Reply 5: Many thanks to referee 1 for pointing out our mistake! The equation is now fixed.

Line 164: The results suggest that all four methods work well to eliminate inflated error rates in hierarchical models. A brief discussion on how to choose among the four methods could be a useful practical guide for analysts.

Reply 6: We have made some recommendations based on 2 things: 1) our simulation results and 2) how easy it is to implement. We now added:

"Considering these results above, and the ease of implementation, we recommend fitting a multilevel model with a robust variance estimator. Also, one can certainly use Bayesian modeling, as long as the dataset is large enough (e.g., > 100 effect sizes). A step-by-step guide to implement both of these methods can be found at https://github.com/daniel1noble/ecology_comment."

Figure 1: While the figure shows the general magnitude of deviation from the desired error rate, the distribution of the error rates is not particularly useful in my opinion. Because the error rate is scenario dependent, the distribution is largely determined by the choice of parameters and non- independence patterns. A violin plot that presents the error rates as distributions does not highlight the fact that error rates could be consistently high under certain scenarios. I think Figure S1 would be a more informative figure.

Reply 7: This is a fair point. We choose to provide an overall snapshot across all simulation scenarios focusing mainly on the method performance because we wanted to show that, on average, across all these simulations, the new methods perform fairly similar. However, we understand that the utility of a given method will depend on the specific simulation parameters. Hence, we have now combined Figure 1 and Figure S1, into a two-panel figure.

Reviewer: 2

Comments to the Author
Although I sometimes work in the area of meta-analysis with non-independent data, I had not yet read the Song (2020) paper before reviewing this manuscript by Nakagawa et al. Having now read the Song paper, I fully appreciate and support the analysis and conclusions put forth by Nakagawa et al in this manuscript. I also want to thank and commend the authors for the professional tone of their critique of the Song paper's conclusions. Such commentary and professional level of discourse is most welcome in the scientific literature. In addition, the paper strikes a nice balance between big-picture ideas and technical details, with full reproducibility possible using the provided code.

Reply 8: We very much appreciate this supporting comment.

My only suggested revision to the manuscript I reviewed is that the authors should clarify where the "51" number came from in the number of scenarios referred to in Figure 1 (and Figure S1). No matter how I counted the simulation settings considered in the Song paper, I couldn't get to 51.

Reply 9: Thanks for this comment. Yes, this is confusing, but 51 is correct. However, we understand why the reviewer may have been confused because not all simulations are presented in the figures described by Song et al. (2020). The reason for this is that their figures only present a subset of results – as they indicate in their paper (taken from Song et al.: "For clarity of presentation, the figures contain a representative subset of results. Full results can be found in Appendix S1: Figs. S3 and S4.").

Nonetheless, to be clear about how we arrived at this number one needs to consider all the simulation settings across the following R scripts: "EqualStudy.R", "UnequalStudy.R." And "UnequalStudy_Vary_Tau.R". If we do this, we arrive at 27, 18 and 6, respectively; for each file (i.e., see the contents of the "param" object). Hence, 51 scenarios, as is presented in Figure 1. We only present a subset of scenarios that match those presented by Song et al. (2020) in Figure 1 to keep this consistent with their figure 3.

We have now made this point clearer by adding a sentence to the figure legends that indicate why this discrepancy appears to exist:

"Note that the sub-sample of simulation scenarios matches those presented in Song et al. (2020), and does not include all 51 simulation scenarios presented in panel A."

Reviewer: 3

Comments to the Author
I don't necessarily disagree with Nakagawa et al. comment on Song et al. recent paper, I too thought Song's conclusions to be rigid – especially in terms of advocating for 2-step pooling of effects prior to synthesis. Clearly if the opportunity arises, I would always advocate modelling covariances when possible. However, the challenges with Nakagawa's recommendations are that they require significant overhead in terms structuring covariance of effect sizes to model multiple levels of non-independence (e.g., separate covariance matrices to model independence within each study, phylogenetic correlations, etc.). Do most ecologists really want to take the modelling this far just to get slight gains in coverage?

Reply 10: We did not discuss how easy it is to implement our method compared with that of Song et al. (2020). We address this point at our Reply 13.

I don't know the answer to that, but here's an example of a semi-unrealistic modelling approach. One of the points that Nakagawa emphasizes is a gap in Song's simulation that excluded models of non-independence structured with equation 2 -- which includes r-ig, the correlation between sampling variances. In a phylogenetic context, I think Lajeunesse (2009) applied that equation and so r-ig can be derived from phylogenetic correlations, but other forms of non-independence there is no way to know what r-ig should be.

Reply 11: This is an important point which we did not discuss. We added below to point this out in our revised manuscript:

"For the multilevel meta-analysis, we can model the variance-covariance matrix of the sampling errors for the former type of non-independence as well as model a random effect for paper, although rig is often not known and need to be assumed (detailed in Noble et al. 2017; see also, Lajeunesse, 2009; 2012)."

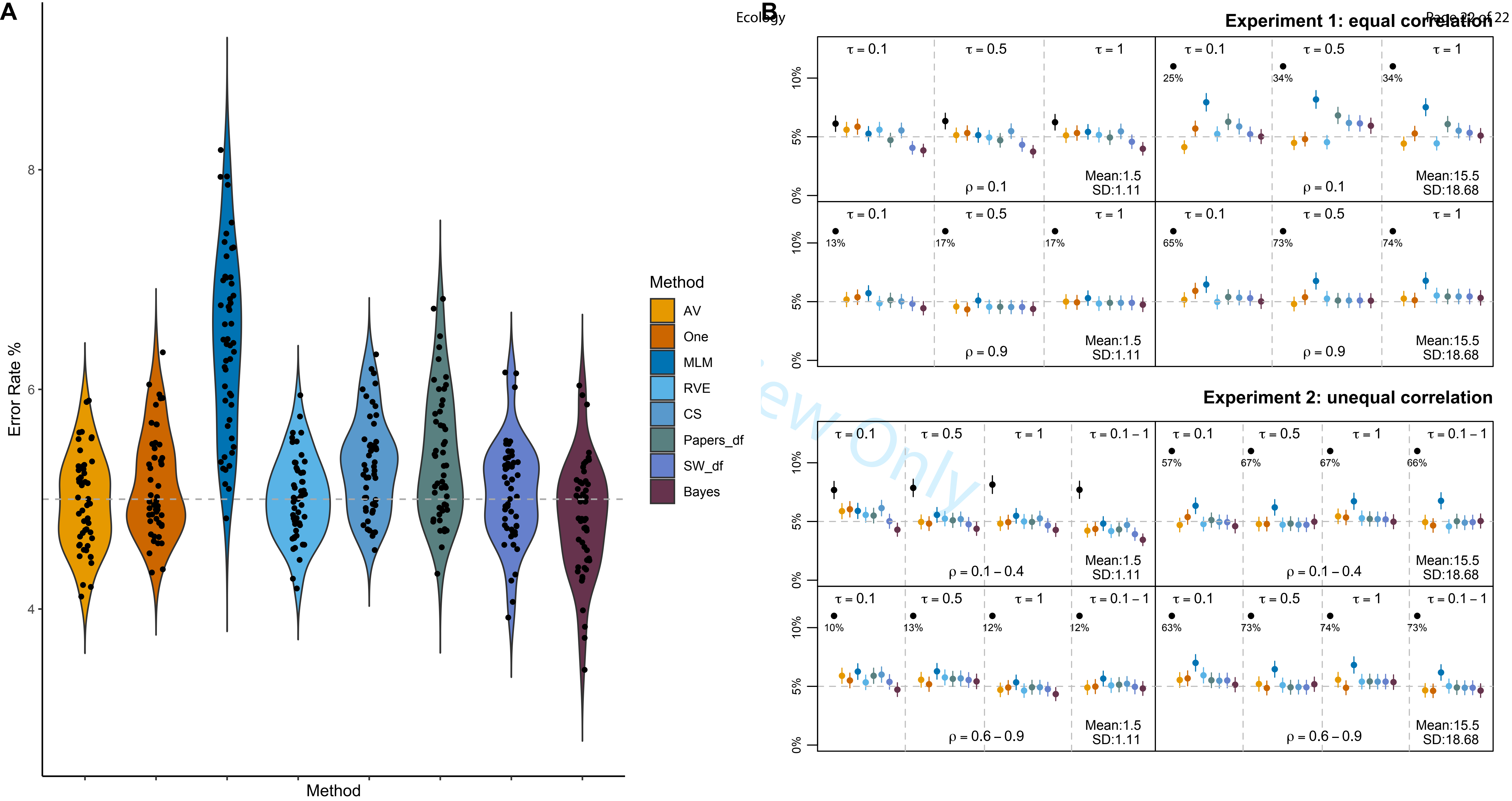
Robust methods are meant to side-step these unknowns, but there is often little discussion on what new assumption are made when applying these tools. Pooling effects prior to analyses is also another side-step to these unknowns – but at least it's straightforward, and relative to other practices does reasonably well (as shown by both Song and Nakagawa), if you balance out the crudeness and the low overhead in terms of modelling.

Reply 12: The referee is correct about the robust method, and we show we can use this method with multilevel models, which, we believe, will be more useful for ecologists. Incipiently, we believe that ecologists are very capable and often quantitatively minded. More relevantly, we have added a comment on how easily pooling can be implemented:

"(note that one can use the function, *aggregate* in *metafor* to calculate a weighted mean and accompanying sampling variance as in Equation 2)."

I'm ok with this comment, and I see no issues with the tools presented, they're cool, I just wished it offered some hands-on discussion on how a non-technically savvy ecologist would apply these tools. I fear Song's approach will resonate with many ecologists, not because it's the best approach, but because it's a simple solution to complex problem. Nakagawa's recommendations, however, are practically the opposite, model everything simultaneously overlooking the fact that it's technically not easy-breezy to achieve.

Reply 13: This comment is a fair criticism. Therefore, we now provide a tutorial, as a supplement, where we take the reader through the modelling process we are advocating. With this, we believe that more readers will try what we suggest, which we believe, ultimately is more appropriate. Given that mixed modelling is very popular, and routinely used among ecologists, what we show will not be very challenging for many ecologists (e.g., we can achieve what we suggest by just using a few lines of code).


A
Error Rate %
8
6
4
Method
Method
AV
One
MLM
RVE
CS
Papers_df
SW_df
Bayes
B
Experiment 1: equal correlation
τ = 0.1
τ = 0.5
τ = 1
10%
5%
0%
25%
34%
34%
ρ = 0.1
Mean:1.5
SD:1.11
Mean:15.5
SD:18.68
13%
17%
17%
65%
73%
74%
ρ = 0.9
Experiment 2: unequal correlation
τ = 0.1 – 1
57%
67%
67%
66%
ρ = 0.1 – 0.4
10%
13%
12%
12%
63%
73%
74%
73%
ρ = 0.6 – 0.9