Estimating the effect of publication and reporting bias

## Introduction

See word document

## Methods

### Data extraction

All of the large scale replication projects that have been performed in behavioral science research were collected. The original source of each study, test statistics, effect sizes, sample sizes, standard errors, p-values were extracted for each original and replication study. Several of the large scale replication projects did not present the original test statistics and p values (e.g., Many labs 1 and 3). In these cases, these values were manually extracted from the original articles. When sample sizes for original studies were not available they were manually extracted from original articles. When the original and replication effect sizes were not reported as Fisher Z transformed correlation coefficients, effect sizes were converted from test statistics or effect sizes for analysis. In cases where sample sizes were not reported per group, equal sample sizes among groups were assumed to be equal in these estimates. See table one for the number of valid studies extracted from each project. All results are reported in correlation coefficients following {Open Science Collaboration, 2015 #611} in order to present results in a common metric which is likely intuitively understandable and familiar to most psychologists and behavioral researchers.

Three studies which did not report that their findings were indicative of a true effect were excluded from {Open Science Collaboration, 2015 #611}. In some cases in the Nature Science reproducibility projects {Camerer, 2018 #967} multiple replication studies were performed for a single effect. In each of these cases I performed a fixed effects meta-analysis performed using the metafor package {Viechtbauer, 2010 #796} for each study to estimate and the meta-analyitic effect size estiamte was used as the true effect size, and P values, standard errors and sample sizes used in the current study reflect this pooled estimate. This method leads to one study more “replicating” according to the ‘statistical significance in the same direction of the original study’ than was originally reported in the nature science project, where they using the largest performed study instead of a pooled estimate.

In [LOOPR study CITATION], some measures used shorter form version of the original questionnaire, all results presented have been disattenuated using the Spearman-Brown prediction formula and Spearman disattenuation formula to estimate the trait-outcome associations that would be expected if our outcome measure had used the same number of items as the original study (Lord & Novick, 1968). Following the other large scale replication studies, the signs of negative original correlations were set to positive (and the sign of the replication sample were switched too). The experimental philosophy reproducibility project included two original studies which were non-significant (and which were not claimed to provide evidence for the effects under test), these were removed from analysis. Many labs 2 [CITATION] original p values were recalculated from reported summary statistics (i.e., from Cohen’s d). Four studies from this reproducibility project were removed because effect sizes could not be simply derived (the original and replication studies examined a difference in effect sizes seen in different conditions, and the effects were not directly tested against each other), and two additional were excluded because their effect sizes were only available in Cohen’s q.

INSERT TABLE 1 HERE

### Analysis

All analysis was performed in R {R Development Core Team, 2018 #314}. Mean raw differences along with Wald-type 95% confidence intervals around the mean difference, median effect size differences, and raw proportion decreases in effect sizes (i.e., ) were calculated on the Fisher-Z transformed effect sizes. The reported Wald-type confidence intervals do not account for non-independence between effects taken from the same paper, or between studies from the same replication projects. In order to account for this non-independence, multilevel-meta-analysis framework was used. Confidence intervals around binomial proportions are 95% Wilson Score intervals. All difference scores (i.e., proportion changes and mean differences) were calculated using Fisher Z transformed effect sizes. Any studies with missing data (e.g., missing effect sizes or sample sizes for the initial or replication studies) were excluded, and sample sizes are reported alongside each analysis in tables.All analyses were exploratory, and multiple models which were developed are not presented here. See <https://github.com/fsingletonthorn/effectSizeAdjustment> for a git repository with a record of all interim models and for all model code and data, and see <https://osf.io/daj8b> for a preregistration of this project.

#### Multilevel meta-analysis

Meta-analyses were performed using the Metafor package {Viechtbauer, 2010 #796}. In order to obtain a reasonable estimate of the change in effect size between original and replication studies, a multilevel random effects meta-analysis was performed on the difference in Fisher Z transformed correlations between original and replication studies. Standard errors were estimated as , with being the sample size in the original study and being the sample size in the replication study. Empirical Bayes estimates and 95% credible intervals for random effects were calculated following {Robinson, 1991 #999}{Morris, 1983 #1000}. This meta-analysis included random effects for the original study and for the replicaiton project each replication attempt was performed as a part of.

##### Leave one out cross validation

In order to assess whether the main results of this study are sensitive to the inclusion of each of the replication projects and individual findings within each replication project, the models were rerun using leave one out cross validation, excluding both the individual replication attempts and the replication projects one at a time. When leaving out individual studies the range of point estimates (i.e., the difference between the smallest and largest estimate of the difference between original and replication studies) for each of the LOO cross validation models did not exceed more than a Fisher z sore of 0.02. When excluding one replication project at a time, model estimate ranges did not exceed 0.05. See supplementary material [LOO] for a table of the proportion of model estimate p values below .05, and estimate quintiles for each model from the leave on out cross validation on the study and project levels. None of these changes would lead to substantially different conclusions being drawn from the model output.

#### Accounting for null effects

An important question in assessing the degree to which effects are attenuated in this literature is how much this effect is driven by the presence of a subset of null effects (or effects so small as to be effectively null). The average attenuation could be extremely high, and yet this effect be almost entirely driven by the presence of effectively-null effects. This aspect becomes especially important as the sampling of the literature is non-random, meaning it is plausible that some effects were chosen for replication to a greater or lesser extent as it was expected that they may not replicate. In order to account for this issue, three main approaches were taken.

Firstly, original studies were simply excluded using various exclusion criteria, and raw effect size differences calculated and multilevel meta-analysis models re-estimated. The exclusion criteria used are detailed below. Because all of these methods function by removing small effects, no significance testing was performed on the difference between the model estimates estimated decreases after accounting for small or near-null effects. It is certain that, at a population level, all of these actions would lower the size of the observed effect size decrease. The second method of estimating the effect size difference while accounting for the presence of null or effectively null effects was to include the p value of the replication studies as a moderator in the meta-analysis of the effect size differences detailed above. This means that the model estimate, the meta-analytic mean, is the predicted mean effect size decrease assuming a replication p value of 0. The third method of estimating the effect size difference in non-null effects was the a Bayesian mixture model adapted from {Camerer, 2018 #967}.

Multiple exclusion rules were used; excluding studies in which the replication study was not significant, removing statistically equivalent studies found using equivalence testing, and using a cut score from approximate Bayes Factors estimated from the reported correlation coefficient effect sizes. ##### Statistical significance of the replication study

The first method used to exclude likely effectively null effects is to only look at effects that reached statistical significance in the replication study in the same direction as the original effect. This has the issue of meaning that studies which had replication studies which had a true non-null effect are likely to be excluded from this analysis, especially those where the replication study had lower power to detect the true effect size. Especially as in some of the replication projects the sample size in the second study was chosen using a power analysis of the observed effect in the original study {Open Science Collaboration, 2015 #611}, this method is likely to underestimate the amount of effect size exaggeration due to the exclusion of under-powered replications. Original studies which found large effects lead to follow up studies which have smaller sample sizes, and are therefore unlikely to reach statistical significance given a true, non-zero, but smaller effect size.

##### Equivalence tests

A second method we use is to exclude studies from estimates of the amount of effect size decrease based on whether the results of the replication study were statistically equivalent to the null {Lakens, 2017 #214;Lakens, 2018 #951}, or significant in the opposite direction. As a requirement for equivalence testing is that a minimum effect size of interest is selected, we follow one suggestion in {Lakens, 2018 #951} and use the lowest effect size that would be statistically significant to the original study as the smallest effect of interest (assuming an alpha of .05). Equivalence tests were performed used the Fisher Z transformed effect sizes, and approximated the standard errors of each study as , except for studies from {Camerer, 2018 #967} which had more than a single replication attempts, where standard errors are those derived from the meta-analyses that produced the effect size estimate. Equivalence tests were performed using z tests, i.e., assuming a normal sampling distribution. Ideally, a full reanalysis would be performed for each original study using the original statistical test and full access to the original and replication data. However, it was not feasible to extract and reperform full analyses for the over 600 total original and replication studies. As a method of testing how closely this method of approximating standard errors matches the original replication projects results, significance tests for the replication and original studies were performed using this approximation. The results matched the significance or non-significance as reported in the replication projects in every case.

However, the minimum detectable effect was occasionally quite high as original sample sizes were often very small (mean = 0.17, SD = 0.12, 0th, 25th, 50th, 75th and 100th quintiles = [0, 0.1, 0.15, 0.23, 0.74]). This means that original studies were sometimes under-powered to detect even large effects, so this method may exclude studies which have effects the original authors may have considered important, but which they were unlikely to detect, or may have used an experimental design and statistical tests that were more sensitive than the converted correlation coefficient and sample size suggests.

##### Approximate bayes factors

Three different types of Bayes factors were developed for each study using default priors following {Wagenmakers, 2016 #994}. Bayes Factors express the relative evidence for the null hypothesis compared to an alternative model, or equivalently the degree to which a Bayesian observer should update their prior beliefs in response to the receipt of new data in favor of one model or another. If a Bayes factor is greater than one the data is more likely under the alternative hypothesis than under the null hypothesis, and the opposite is true when a Bayes factor is below one. Conventional labels have been proposed, suggesting that Bayes factors between 1 and 3 provide little to no evidence (or ‘anecdotal’ evidence) and Bayes factors from 3-10 provide “substantial” evidence {Jeﬀreys, 1961 #1001}{Wagenmakers, 2016 #994}.

Two of the developed Bayes Factors ignore the original study and express the relative evidence for and against the point null entirely based on results of the replication study, using a one () and and two tailed () default alternative hypothesis (for details see {Wagenmakers, 2016 #994}). Replication Bayes Factors () were also developed, in which the prior for the replication correlation coefficient is the posterior based on the original research and a flat prior, for details see {Wagenmakers, 2016 #994} and {Verhagen, 2014 #217}. This paper follows the typical notation where the order of the subscripts indicate whether a Bayes Factor represent evidence for the null (, , ) or for the alternative hypothesis (, , ).

The bayes factors presented here were developed using the effect sizes as reported in correlation coefficients, regardless of the original study’s experimental design. Importantly, these Bayes factors differ from those that would normally be developed using the closest Bayesian equivalents to each original replicated study’s analysis, and should be viewed only as a coarse estimate of the degree of evidence provided for and against the null model. See table [bayesFactors] in supplementary materials [Bayes] for a table showing the differences between the values returned by this method compared to those reported in the Bayesian supplement to which were more appropriately calculated {Camerer, 2018 #967}, which demonstrates that the difference can be considerable, especially when the original analysis was unusual. Normally, One of the benefits of Bayes Factors is their continuous and interpretable scale, however in this case these approximate Bayes Factors are used as a heuristic to discard the studies which appear to likely be true (or effectively) null effects. Two different cut scores were used for each type of Bayes factor, discarding studies when Bayes factors suggested that the null model is either more than three times more likely than the alternative model (i.e., when there is more than ‘anecdotal’ evidence that the null is true), or when the alternative model is not at least three times more likely than the null model. A full bayesian treatment of this issue is preseneted in the Bayesian Mixture Model.

#### Simulations to assess exclusion criteria

All methods of excluding studies function by removing studies which have small effect sizes in the replication, so it was a forgone conclusion that the apparent amount of effect size reduction seen will go down as compared to the model which includes all effects. Because of the exploratory nature of the methods used to attempt to remove studies from this literature, a series of simulation studies were performed to assess how accurately the exclusion methods function, and how accurately these methods estimate the amount of effect size attenuation under reasonable assumptions. Simulations took the original effect sizes, estimated a ‘true’ effect size from a normal distribution with a mean of the original effect a standard deviation equal to the standard error of the original study, and reduced this true effect by an attenuation factor of 0 - 1 in steps of 0.1, and set a random proportion of ‘true’ effect sizes to 0 (again a proportion from 0 to 1 in steps of 0.1). Simulations were performed at least 10000 times for each analysis.

Accuracy (i.e., the proportion of studies which were accurately excluded as true negative or null effects, or for equivalence testing the proportion of studies which were at or below the minimum effect size of interest) was assessed under this data generation process in 11958 simulations, showing that accuracy of these methods across all scenarios ranged from 0.75 to 0.84, with SDs of 0.07 to 0.19. See supplementary materials [simulations] table [SM accuracy] for full details on the performed simulations, including a table of the outcomes of these simulations, and heat maps of the mean error over these values. Note that these values are only valid under the simulated specific data generation process, where there is a consistent factor decrease in true effect size, and where the studies which are null are random and independent of the original effect and sample sizes. See supplementary materials [simulation] for a full description of the simulations, heat maps of the mean absolute error at each benchmark and full simulation output tables. The code used in these simulations is available from [OSFOSF.io].

#### Bayesian mixture model

A Bayesian mixture model adapted from {Camerer, 2018 #967} was used to estimate the relative effect sizes of the true positives. This model assumes that the each observed replication effect size comes from one of two components, either from the null hypothesis or from the alternative hypothesis. If the replication effect size is drawn from the null hypothesis, it is modeled to have come from a normal distribution with a mean of 0 and a standard deviation equal to the standard error of the replication study (estimated here as , n being the replication sample size). If the replication effect size comes from the alternative hypothesis, it is assumed to have been drawn from a normal distribution with a standard deviation equal to the standard error of the replication study, and a mean equal to the true sample size. In this case, the true sample size is equal to the original study’s estimated true effect size attenuated by an “attenuation factor”, equal to some value between zero and one and assumed to be equal across all studies. The parameter of interest in this model is the “attenuation factor” (called a deflation factor in {Camerer, 2018 #967}), the degree to which effect sizes are attenuated between original and replication study, as well as the overall rate at which studies are reported assigned to have come from the null hypothesis. This model was estimated using four Markov chains from each of which 100,000 draws were taken (exlcuding a 11,000 draw burn-in period). Trace and density plots for the discussed paramters were assessed and the model appeared to have succesfully converged.

This analysis was performed in JAGS version 4.3.0 {Depaoli, 2016 #1010} using the rjags interface (version 4.8.0; {Plummer, 2018 #1011}). See supplementary materials [“mixture model”] for model code and further analysis details, along with the results of a two adaptations of this model which add a third category of effects which do not decrease as well as another which allowed the alpha rate to differ between replication projects.

## Results

### Raw decreases in effect sizes

Looking at the 314 replications for which both original and replication effect sizes were available, the effect size seen in the replication study was lower than that seen in the original study in 227 articles, 72% of those included. The average effect size for original studies was 0.38, and the mean effect size for replication studies was 0.27. There was an average decrease of r = -0.13 (Wald-type 95% CI [-0.16, -0.1]). Notably, this represents an average decrease in effect sizes from the original to the replication study of -29.44%. See Table 2 for a more comprehensive list of descriptives on the effect size differences seen, and figure 1 for a scatterplot of the replication effect sizes plotted against the original studies’.

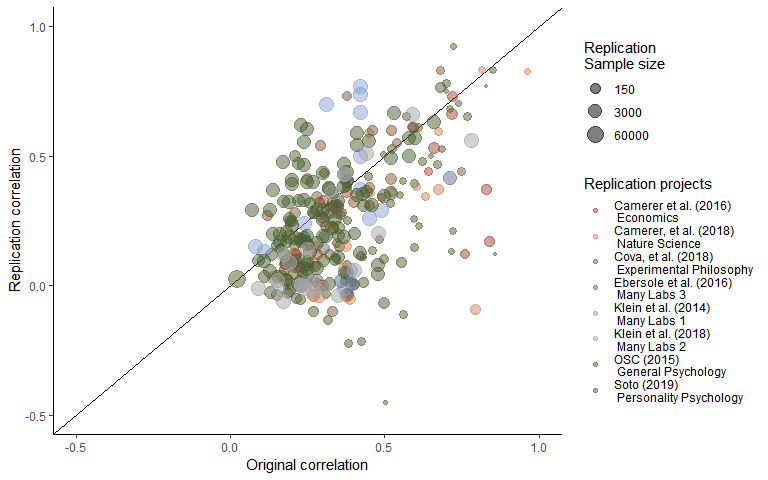


Figure 1. A scatterplot of replication study effect sizes (in correlation coefficients) plotted against original study effect sizes. Points which fall on the the solid, diagonal line represent replication effect sizes equal to the original effect sizes. Point size represents (the log) of the number of participants in the replication study, and the color of the points shows which replication project each effect size pair was from.

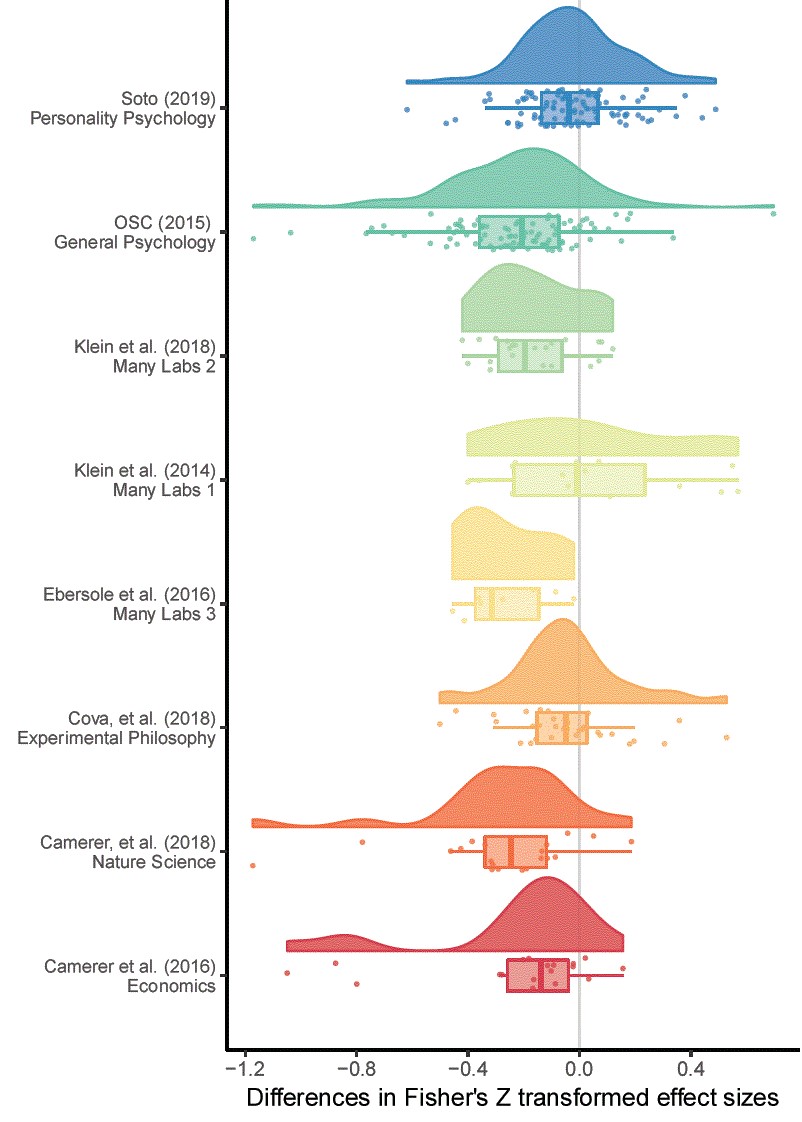


Figure 2. A raincloud plot of the change in effect sizes (here Fisher Z scores) from the original to the replication study by the replication project that the replication study was performed as a part of.

### Excluding null results

Looking at the 220 replications in which the replication study was statistically significant 0.7, the average effect for original studies was 0.4, and the mean effect size for replication studies was 0.38. There was an average decrease of r = -0.02 (Wald-type 95% CI [-0.05, 0, an average decrease of 3.49%.

Excluding studies which were not statistically significant is likely to lead to an underestimate of the degree of effect size attenuation, as this exclusion rule will lead to the exclusion of under-powered replication studies as well as studies which are likely to be true null effects. In order to avoid this issue, equivalence tests were performed, meaning that the studies which are not-statistically equivalent to the null are included (using a bound of equivalence equal to the minimum detectable effect in the original study). This method is an attempt to not exclude the non-diagnostic replication studies, studies which are not statistically significant but which do not suggest that the null hypothesis is true. Using these method, 237 replications were not statistically equivalent to the null, 77.7% of studies for which equivalence tests could be performed. The average effect size in the original non-equivalent studies was 0.41, compared to a mean effect size for replication studies of r = 0.35. This is a mean decrease of r = -0.07 (Wald-type 95% CI [-0.1, -0.04, an average decrease of -6.65%.

The results of the various Bayes Factors analyses generally support the results of the analysis removing statistically equivalent studies. Using this method, 177 to 232 replications were included, 58.22 to 76.32% of studies for which Bayes Factors tests could be estimated. See table 2 for full output.

Table 2. Differences between original and replication studies. All calculations were performed on Fisher’s Z transformed correlations and back-transformed into correlation coefficients for interpretability.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | n included | n criteria calculable for | Mean original ES | Median original ES | Mean replication ES | Median replicaiton ES | Mean ES difference | 95% CI LB Mean ES Change | 95% CI UB Mean ES Change | Median ES difference | SD difference | Mean proportion change | Median proportion change |
| Overall | 314 | 314 | 0.38 | 0.33 | 0.27 | 0.20 | -0.13 | -0.16 | -0.10 | -0.11 | 0.25 | -0.29 | -0.35 |
| StatisticalSignificance | 220 | 314 | 0.40 | 0.35 | 0.38 | 0.32 | -0.02 | -0.05 | 0.00 | -0.04 | 0.20 | 0.03 | -0.07 |
| Nonequivalence | 237 | 305 | 0.41 | 0.35 | 0.35 | 0.30 | -0.07 | -0.10 | -0.04 | -0.06 | 0.24 | -0.07 | -0.16 |
| BF0RepBelow3 | 220 | 303 | 0.40 | 0.34 | 0.37 | 0.32 | -0.04 | -0.06 | -0.01 | -0.05 | 0.20 | -0.01 | -0.13 |
| BFRep0Above3 | 186 | 303 | 0.41 | 0.35 | 0.40 | 0.36 | -0.01 | -0.04 | 0.02 | -0.01 | 0.20 | 0.09 | -0.05 |
| BF01Below3 | 221 | 304 | 0.42 | 0.36 | 0.36 | 0.32 | -0.06 | -0.10 | -0.03 | -0.05 | 0.25 | -0.04 | -0.13 |
| BF10Above3 | 177 | 304 | 0.41 | 0.35 | 0.40 | 0.35 | -0.01 | -0.05 | 0.02 | -0.01 | 0.20 | 0.08 | -0.04 |
| BF0PBelow3 | 232 | 304 | 0.42 | 0.35 | 0.36 | 0.31 | -0.07 | -0.10 | -0.03 | -0.05 | 0.24 | -0.04 | -0.14 |
| BFP0Above3 | 186 | 304 | 0.41 | 0.35 | 0.40 | 0.35 | -0.01 | -0.04 | 0.02 | -0.01 | 0.21 | 0.08 | -0.05 |

### Multilevel model

The model including all data estimates a -0.14 (95% CI [-0.2, -0.07]) point decrease in effect sizes from the original to replication studies in correlation coefficient terms. This is represents a change equivalent to -34.34 (95% CI [-50.79%, -17.88%]) of the mean effect size in the original studies (r = 0.36).

Looking at there was more variance attributable to the article (i.e., the original article) than too the project ( = 0.02 compared to = 0.01). QE tests of heterogeneity suggest that there is a large amount of unexplained heterogeneity, QE(304) = 3527.86, p < .001.

Table [nice mod sum]. Model output from a multilevel random effects meta-analysis of the difference between original and replication effect sizes, with random effects for the project (i.e., which large scale replication project the replication was a part of) and the original (i.e., replicated) article or effect.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.14 | -0.21 | -0.07 | 0.03 | < .001 |  |
|  |  |  |  |  | Project variance = 0.007, n = 8 |
|  |  |  |  |  | Article variance = 0.025, n = 228 |
|  |  |  |  |  | QE(304) = 3527.86, p < .001 |

Table [BLUP]. Empirical Bayes estimates and 95% credible intervals for random effects, which contain the true value with 95% confidence assuming that the studies are a random sample from a population with normally distributed average effect size difference.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Standard Error | 95% PI lower bound | 95% PI upper bound |
| Camerer et al. (2016) Economics | -0.06 | 0.05 | -0.15 | 0.04 |
| Camerer, et al. (2018) Nature Science | -0.07 | 0.05 | -0.17 | 0.03 |
| Cova, et al. (2018) Experimental Philosophy | 0.08 | 0.04 | -0.01 | 0.17 |
| Ebersole et al. (2016) Many Labs 3 | -0.06 | 0.06 | -0.17 | 0.05 |
| Klein et al. (2014) Many Labs 1 | 0.11 | 0.05 | 0.01 | 0.21 |
| Klein et al. (2018) Many Labs 2 | -0.03 | 0.05 | -0.12 | 0.06 |
| OSC (2015) General Psychology | -0.05 | 0.04 | -0.12 | 0.03 |
| Soto (2019) Personality Psychology | 0.07 | 0.04 | -0.01 | 0.15 |

The model was re-estimated using each the subsets of studies, excluding studies based on the exclusion criteria detailed above. See table [all model output] for the model estimates from each model. The estimates of the proportion of variance attributable to the article or replication project level did not change considerably in any of these models. There is a notable reduction in the estimated effect sizes under these different selection criteria, with estimates of the amount of effect size decrease from r = -0.04 to -0.09, representing 8.95% to 22.31% of the average effect in the original studies.

However, it is important to emphasize the degree of uncertainty in these results. For example, taking the highest effect size decrease using any of the exclusion criteria, estimating the decrease using only the results of the 228 experiments which did not provide have a of greater than 3 (i.e., which did not have at more than “anecdotal” evidence for the null hypothesis compared to the one sided alternative hypothesis), showed that an estimated decrease of summarize r = -0.09, 95% CI [-0.16, -0.02]. Looking at the smallest estimated effect size difference under any exclusion criteria on the other hand, running the multilevel meta-analysis on just the results of the 186 experiments which had a of three or more (i.e., which had a replication Bayes factor which showed more than ‘anecdotal’ evidence for the alternative hypothesis), showed an estimated decrease of -0.04, 95% CI [-0.09, 0.02]. This is equivalent to a decrease of -8.95% of the average original effect size, 95% CI [-23.47, 5.57].

See supplementary materials [all exclusion Cartier output] for full model output and scatter plots of the data-set using each exclusion rule.

##### Table [all model output]

The number of studies included in each model, and the estimated correlation coefficient decrease from each model. Models were estimated using Fisher Z transformed correlation coefficients and back transformed for interpretability. Percentage attenuation give the percentage attenuation this effect size difference would as a percentage for the the mean original effect size.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Inclusion rule | Model N | Model Estimate | 95% CI lb | 95% CI ub | Estimated % attenuation | LB % attenuation | UB % attenuation |
| All studies | 305 | -0.14 | -0.20 | -0.07 | -34.3 | -51 | -17.88 |
| Statistically significant | 195 | -0.05 | -0.12 | 0.01 | -13.2 | -29 | 2.67 |
| Non-equivalent | 235 | -0.08 | -0.15 | -0.01 | -20.5 | -38 | -2.58 |
| BF0P < 3 | 228 | -0.09 | -0.16 | -0.02 | -22.3 | -40 | -4.50 |
| BFP0 > 3 | 182 | -0.05 | -0.11 | 0.02 | -12.0 | -28 | 3.79 |
| BF01 < 3 | 217 | -0.09 | -0.16 | -0.01 | -21.5 | -39 | -3.67 |
| BF10 > 3 | 173 | -0.05 | -0.11 | 0.02 | -12.0 | -28 | 4.33 |
| BF0Rep < 3 | 220 | -0.06 | -0.12 | 0.00 | -14.5 | -29 | 0.01 |
| BFRep0 > 3 | 186 | -0.04 | -0.09 | 0.02 | -8.9 | -23 | 5.57 |

### Including replication p values as a moderator

Including the p value of the replication study as a moderator leads to similar conclusions to the models with exclusions, with an estimated effect size decrase of r = -0.08, 95% CI [-0.14, -0.02]. This represents a decrease of -20.17 (95% CI 95% CI [-34.28, -6.06]) of the average original effect size. The projects and article level differences are functionally identical to the model that does notinclude replication p values as a moderator.

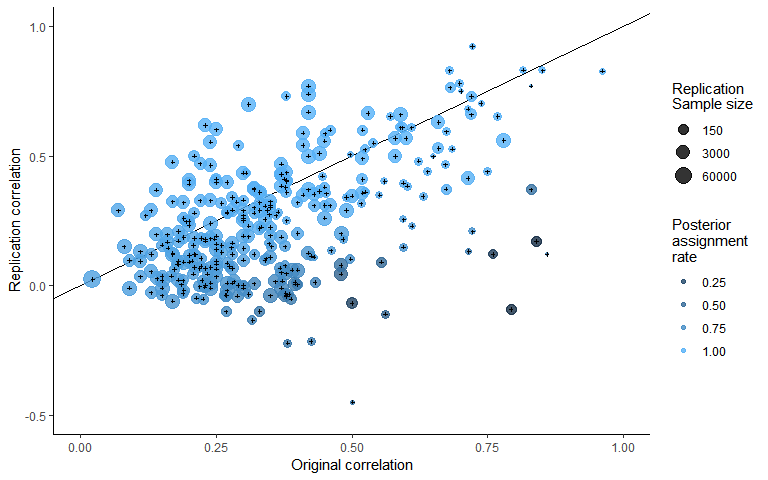
Table [moderators]. Multilevel meta-regression results including

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| Estimate | -0.082 | -0.14 | -0.024 | 0.029 | 0.005 |  |
| p value | -0.327 | -0.40 | -0.256 | 0.036 | < .001 |  |
|  |  |  |  |  |  | Project variance = 0.005, n = 8 |
|  |  |  |  |  |  | Article variance = 0.021, n = 228 |
|  |  |  |  |  |  | QE(304) = 3143.78, p < .001 |

### Mixture model results

The main targets for inference are threefold. First, every individual effect is associated with aparticular probability that it originates from the alternative hypothesis instead of the null hypoth-esis; we term this the posterior assignment rate. Second,’is the overall rate with which studiesare assigned to the alternative hypothesis; we term this the true positive rate. Third, as mentionedabove,is the effect size deflation factor

A total of 305 effects were included in the mixture model. This model estimates that of studies are drawn from non-null effects, and that the average attenuation factor is 0.19 with a 95% highest probability density interval of []. Notably, this model allows for true effect sizes to be estimated as being extremely low or near zero due to sampling variability alone, and % of the estimated true effect sizes are below an r of .1. Figure [mixture model], shows the original effect sizes plotted against replication effect sizes. weighted by sample size, along with the posterior assingment rate. The colouring in this plot indicates the proportion of times each effect was assinged to the alternative hypothesis. As was seen and pointed out in the first use of this model in {Camerer, 2018 #967}, values close to the diagonal are reliably assigned to the alternative hypothesis whereas effects far below the diagonal are more repliably assigned to the null hypothesis.

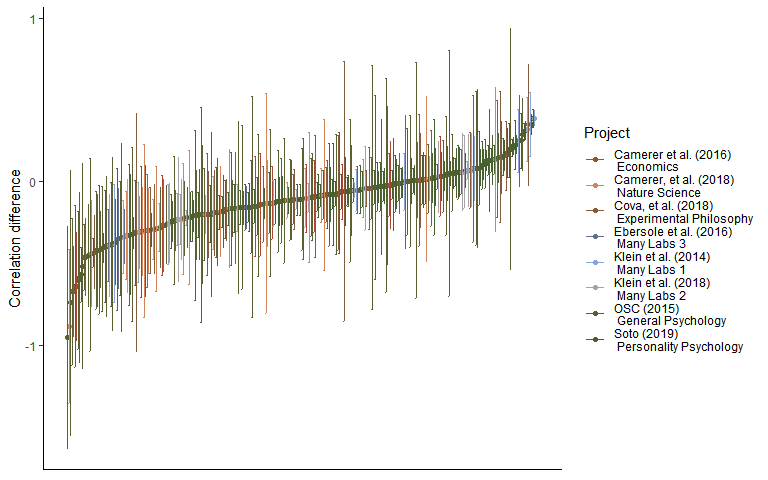


###### Figure [mixture model]. A scatterplot of replication study effect sizes (in correlation coefficients) plotted against original study effect sizes, colored by the posterior assignment rate, the proportion of times each study was assigned to the alternative hypthesis. Points which fall on the the solid, diagonal line represent replication effect sizes equal to the original effect sizes. Point size represents (the log) of the number of participants in the replication study.

## Discussion

Overall, there was an average decrease in correlation coefficient terms of -0.13, approximately equal to a Cohen’s d difference of -0.26. On average, replication sample sizes were 30% smaller in replication studies than they were in original studies, a considerable decrease. In looking at the results of the multilevel meta-analysis including all data, there is an estimated -0.14 correlation coefficient decrease (95% CI [-0.2, -0.07]), equivalent to a -0.28 point Cohen’s d decrease (95% CI [-0.41, -0.14]), or an estimated decrease of -34.34 (95% CI [-50.79%, -17.88%]) of the mean effect size in the original studies (a Fisher Z equal to r = 0.38).

These results also provides preliminary estimates of the degree of decrease from original to replication effect size when the effect size is a true non-zero effect. Taking a simple mean of the mean differences seen across the exclusion methods, there is an -0.04 point change in correlation coefficient terms from the original to replication effect size, or an average decrease of just -1.5%. The results from the multilevel models also support this idea, and highlight the degree of uncertainty in this result. Although all model estimates show a lower effect size decrease when attempting to exclude null (or effectivly null) results, the confidence intervals for all results extend from a decrease of -44.39% of the average original correlation coefficient, to an increase of 6.22%. More data is required to more precisely estimate the degree to which effect size attenuation is driven by the presence of null effects.

 Figure x. A catapillar plot of the effect size difference between original and replication study effect sizes ordered by magnitude, error bars are 95% confidence intervals.

#### Limitiations:

None of the projects included in this analysis were true random selections from the literature, and it is possible that the pattern in the selected sample may be different that that which would be seen in the literature overall. All of the methods that were used to the replication studies which were null-or-effectively were bound to decrease the amount of effect size decrease that is seen. At worst, they could be seen as just removing the studies which happened to find low effects as opposed to removing all the true null hypotheses. However, this preliminary analysis does provide suggestive evidence that the degree of effect size attenuation that is seen may be largely attributed to the presence of effectively-null results, and that the overall. The current study also cannot distinguish between heterogeneity (i.e., effect sizes that are different under different scenarios) and effect size scenario. However, it seems reasonable to except in that effect size heterogeneity should lead to symmetrical effect size differences under most scenarios.

#### Future directions

This analysis also shows that there is a degree of heterogeneity between replication projects and studies. However, this analysis did not examine in detail the possible differences in the effect of publicaiton and report bias differ ammong fields of behavioral sciences research. Future analyses of this growing body of replication studies may be able to examine these issues in more depth as future projects examine studies across areas of reserach and . Additionally, the approaches used here to estimating the effect of publication bias without the influence of the likely-or-effectively null studies relies on dichotomising the evidence and discarding those that do not reach a given criterion. Here, we have attempted to mitigate this issue by using varied classification methods, however another approach could be to explicitly model the full data generation process using, for example, an approach similar to the Bayesian Mixture in the supplementary analysis of {Camerer, 2018 #967}.

### Conclusion

These results highlight some major issues in the psychological research literature. Looking at the raw average proportion decrease, -29%, or the results of the multilevel model, an r =-0.14 (95% CI [-0.2, -0.07]) average decrease, differences which would make a considerable difference in most research scenarios. Researchers reading the literature should be aware of this large discrepancy, and plan their future experiments accordingly. Researchers who wish to ensure that they do not perform experiments that are unlikely to detect real effects should be aware that their experiments are likely to be under-powered if they plan their sample sizes using the effect size reported in a previous experiment. As a heuristic, researchers could follow the advice given in {Camerer, 2018 #967} and plan their experiments assuming that the original effect size is 50% of its reported value, a value matched by the more extreme 95% confidence interval of the estimated amount of effect size decrease using the multilevel meta-analytic framework as a percentage of the average effect size seen in the original studies.

This study also provides preliminary evidence that a large amount of this decrease my be accounted for by the presence of effect which are close to or effectively nulls. Future research is necessary to quantify the degree of effect size attenuation expected given that a real effect was under examination experiment has been performed, as the current experiment suggests that the degree of attenuation is between a negligibly small to quite large negative decrease (e.g., the confidence intervals of the multilevel meta-analyses extend from a small positive effect to an effect equal to 40% of the average original effect size). However, in the current sample it the degree of attenuation seen in studies after discounting

## Supplementary material

### Approximate bayes factors comparison

A comparison of the results of the Bayes Factors as estimated here and as reported in {Camerer, 2018 #967} shows that they agree with each other in approximate magnitude and direction for the most part, although there are some notable discrepancies. See Table SM1 for the Bayes factors reported in {Camerer, 2018 #967} and those reported in the current paper. The only large discrepancy included is seen in Balafoutas and Sutter (2012) in which the Bayes Factor reported in {Camerer, 2018 #967} was based on a hypothesis test of ordered binomial probabilities, making it difficult to appropriately convert into a correlation coefficient, and likely accounting for the large difference.

Table SM1. One-sided and () and replication () Bayes Factors for as reported in {Camerer, 2018 #967} and as estimated in the current paper, along with the reported correlation coefficients and sample sizes from the orig final and replication studies.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Article | Original\_r | Original\_N | Replication\_r | Replication\_n | Camerer\_et\_al.\_BFP0 | Camerer\_et\_al.\_BFRep0 | BFrep0 | BF0plus | BF01 |
| Ackerman et al. (2010), Science | 0.27 | 54 | 0.09 | 858 | 5.4e-01 | 3.1e-01 | 2.6e+00 | 2.1e+00 | 1.0e+00 |
| Aviezer et al. (2012), Science | 0.96 | 15 | 0.83 | 14 | 4.5e+02 | 5.7e+01 | 2.3e+02 | 2.7e+02 | 1.4e+02 |
| Balafoutas and Sutter (2012), Science | 0.28 | 72 | 0.15 | 243 | 4.2e+00 | 4.3e+00 | 4.1e+00 | 2.1e+00 | 1.1e+00 |
| Derex et al. (2013), Nature | 0.52 | 51 | 0.36 | 65 | 3.1e+03 | 3.7e+03 | 3.3e+01 | 2.2e+01 | 1.1e+01 |
| Duncan et al. (2012), Science | 0.67 | 15 | 0.37 | 128 | 2.7e+03 | 2.5e+03 | 2.0e+03 | 2.3e+03 | 1.2e+03 |
| Gervais and Norenzayan (2012), Science | 0.29 | 57 | -0.04 | 755 | 6.0e-02 | 3.0e-02 | 3.0e-02 | 2.0e-02 | 9.0e-02 |
| Gneezy et al. (2014), Science | 0.22 | 178 | 0.18 | 407 | 2.3e+02 | 4.9e+02 | 4.7e+02 | 1.1e+02 | 5.7e+01 |
| Hauser et al. (2014), Nature | 0.82 | 40 | 0.83 | 22 | 2.9e+03 | 1.0e+04 | 1.0e+05 | 2.5e+04 | 1.2e+04 |
| Janssen et al. (2010), Science | 0.63 | 63 | 0.34 | 42 | 5.9e+00 | 0.0e+00 | 1.9e+00 | 4.2e+00 | 2.1e+00 |
| Karpicke and Blunt (2011), Science | 0.60 | 40 | 0.38 | 49 | 1.5e+01 | 1.2e+01 | 1.4e+01 | 1.3e+01 | 6.5e+00 |
| Kidd and Castano (2013), Science | 0.27 | 86 | -0.04 | 999 | 5.0e-02 | 1.0e-02 | 1.0e-02 | 2.0e-02 | 8.0e-02 |
| Kovacs et al. (2010), Science | 0.45 | 24 | 0.59 | 95 | 5.6e+07 | 1.3e+08 | 8.7e+07 | 5.4e+07 | 2.7e+07 |
| Lee and Schwarz (2010), Science | 0.39 | 40 | -0.05 | 409 | 8.0e-02 | 1.0e-02 | 2.0e-02 | 3.0e-02 | 1.1e-01 |
| Morewedge et al. (2010), Science | 0.45 | 32 | 0.35 | 89 | 8.7e+01 | 1.6e+02 | 1.6e+02 | 8.1e+01 | 4.0e+01 |
| Nishi et al. (2015), Nature | 0.20 | 200 | 0.12 | 480 | 7.0e+00 | 7.8e+00 | 8.4e+00 | 2.9e+00 | 1.4e+00 |
| Pyc and Rawson (2010), Science | 0.38 | 36 | 0.15 | 438 | 6.8e+00 | 4.0e+00 | 1.7e+01 | 1.6e+01 | 8.0e+00 |
| Ramirez and Beilock (2011), Science | 0.79 | 20 | -0.09 | 105 | 1.4e-01 | 0.0e+00 | 0.0e+00 | 7.0e-02 | 1.9e-01 |
| Rand et al. (2012), Nature | 0.14 | 343 | 0.03 | 3150 | 1.4e-01 | 1.0e-01 | 1.3e-01 | 1.3e-01 | 7.0e-02 |
| Shah et al. (2012), Science | 0.27 | 56 | -0.04 | 897 | 7.0e-02 | 4.0e-02 | 4.0e-02 | 2.0e-02 | 8.0e-02 |
| Sparrow et al. (2011), Science | 0.37 | 69 | 0.07 | 338 | 1.5e-01 | 3.0e-02 | 6.0e-02 | 2.6e-01 | 1.5e-01 |
| Wilson et al. (2014), Science, | 0.67 | 30 | 0.59 | 39 | 6.0e+02 | 1.9e+03 | 1.9e+03 | 8.3e+02 | 4.2e+02 |

### Plots and multilevel model output of the relationship between original and replication correlation coefficents using varied exclusion criteria

The following output shows scatter plots and model output for all of the multilevel meta-analyses performed using the varied exclusion criteria explained in the main text.

Table SM2. Multilevel meta-analysis model estimates and random effects for all data.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.14 | -0.21 | -0.07 | 0.03 | < .001 |  |
|  |  |  |  |  | Project variance = 0.007, n = 8 |
|  |  |  |  |  | Article variance = 0.025, n = 228 |
|  |  |  |  |  | QE(304) = 3527.86, p < .001 |

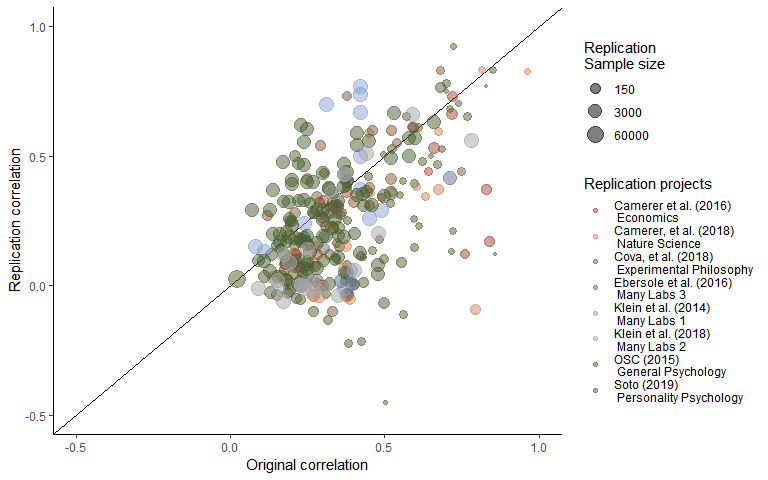


Figure SM1. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including all data.

Table SM3. Multilevel meta-analysis model estimates and random effects including only statistically significant replications.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.05 | -0.12 | 0.01 | 0.03 | 0.1 |  |
|  |  |  |  |  | Project variance = 0.006, n = 8 |
|  |  |  |  |  | Article variance = 0.019, n = 129 |
|  |  |  |  |  | QE(194) = 2706.56, p < .001 |

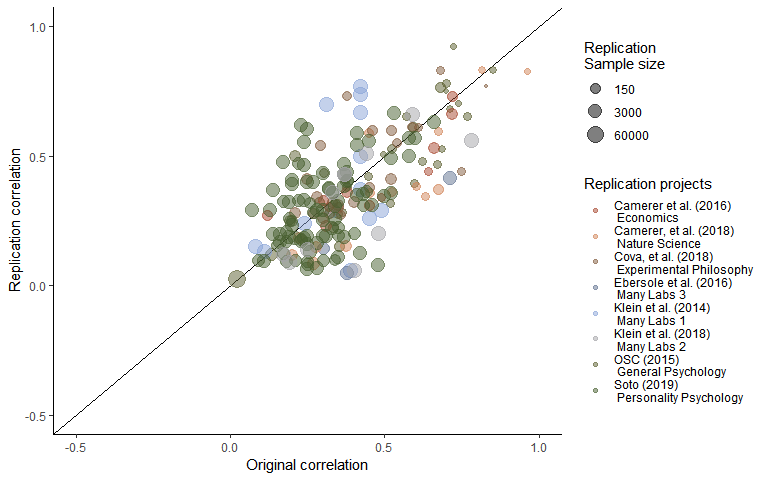


Figure SM2. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including only statistically significant replications.

Table SM4. Multilevel meta-analysis model estimates and random effects including studies which are not statistically equivalent to the null, using equivalence bounds set as the minimum effect size that would have been statistically significant in the original study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.08 | -0.16 | -0.01 | 0.04 | 0.02 |  |
|  |  |  |  |  | Project variance = 0.008, n = 8 |
|  |  |  |  |  | Article variance = 0.025, n = 167 |
|  |  |  |  |  | QE(234) = 3023.83, p < .001 |

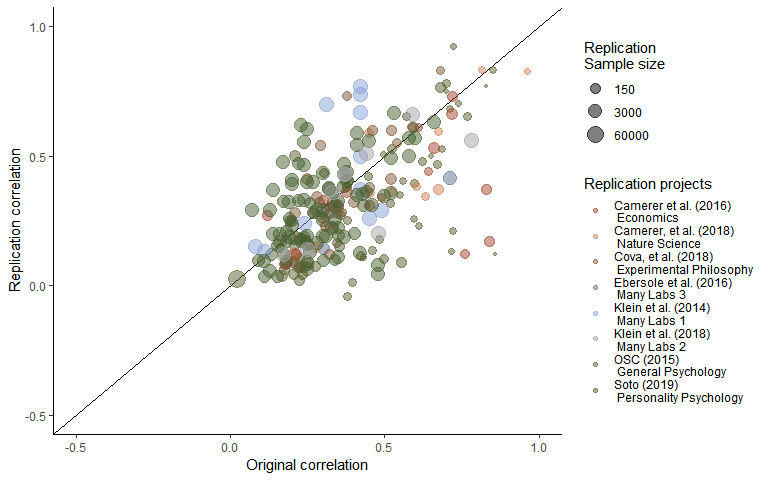


Figure SM3. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including studies which are not statistically equivalent to the null, using equivalence bounds set as the minimum effect size that would have been statistically significant in the original study.

Table SM5. Multilevel meta-analysis model estimates and random effects for studies with < 3.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.09 | -0.16 | -0.01 | 0.04 | 0.02 |  |
|  |  |  |  |  | Project variance = 0.008, n = 8 |
|  |  |  |  |  | Article variance = 0.026, n = 151 |
|  |  |  |  |  | QE(216) = 2867.77, p < .001 |

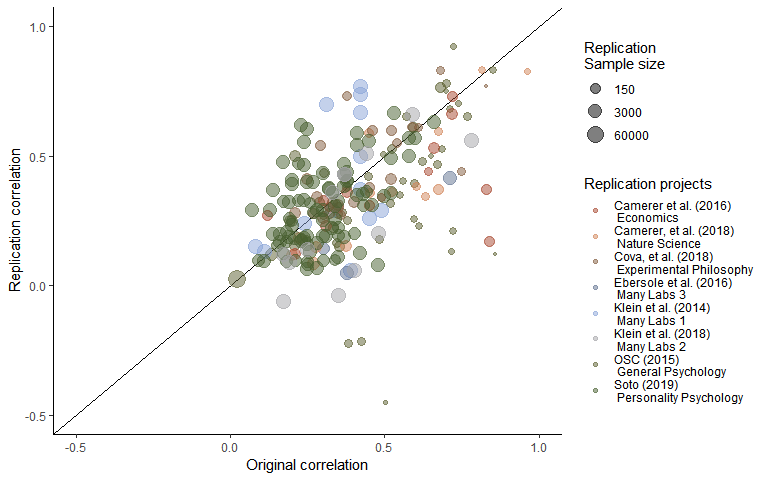


Figure SM4. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including only studies with < 3.

Table SM6. Multilevel meta-analysis model estimates and random effects for studies with > 3.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.05 | -0.11 | 0.02 | 0.03 | 0.15 |  |
|  |  |  |  |  | Project variance = 0.006, n = 8 |
|  |  |  |  |  | Article variance = 0.021, n = 115 |
|  |  |  |  |  | QE(172) = 2516.9, p < .001 |

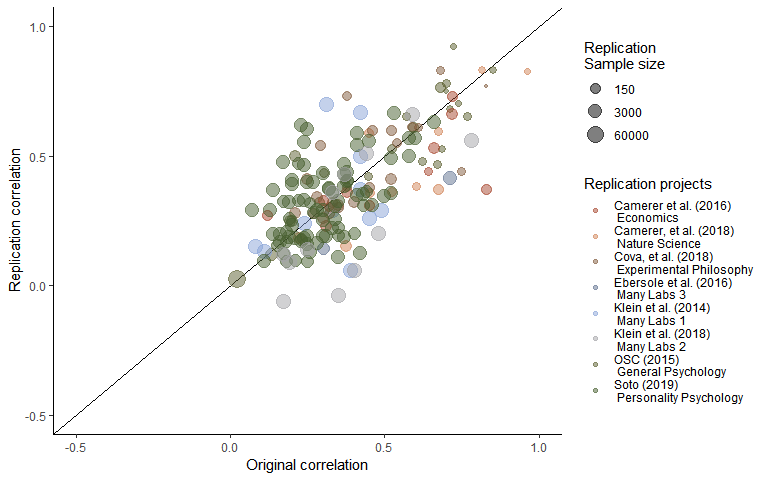


Figure SM5. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including only studies with > 3.

Table SM7. Multilevel meta-analysis model estimates and random effects for studies with < 3.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.09 | -0.16 | -0.02 | 0.04 | 0.01 |  |
|  |  |  |  |  | Project variance = 0.008, n = 8 |
|  |  |  |  |  | Article variance = 0.025, n = 161 |
|  |  |  |  |  | QE(227) = 2885.86, p < .001 |

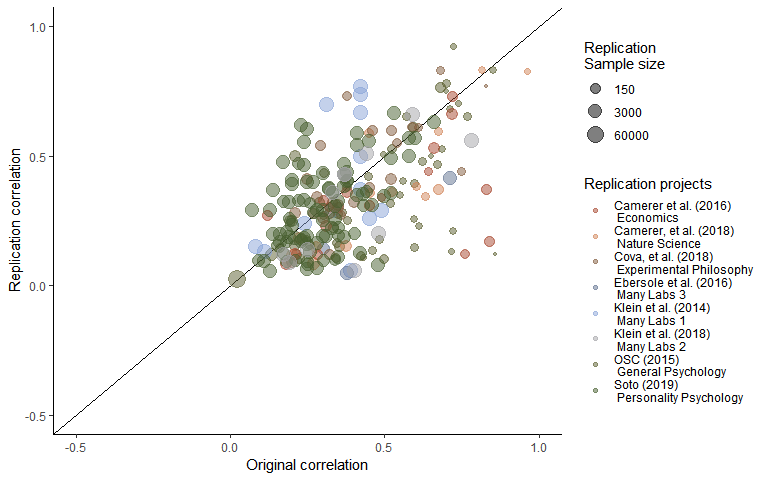


Figure SM6. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including only studies with < 3.

Table SM8. Multilevel meta-analysis model estimates and random effects for studies with

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.05 | -0.11 | 0.02 | 0.03 | 0.14 |  |
|  |  |  |  |  | Project variance = 0.005, n = 8 |
|  |  |  |  |  | Article variance = 0.024, n = 120 |
|  |  |  |  |  | QE(181) = 2675.47, p < .001 |

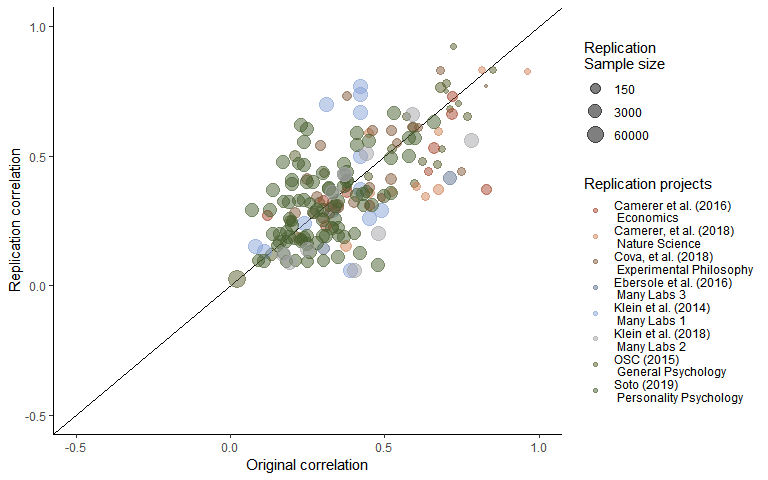


Figure SM7. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including studies with

Table SM9. Multilevel meta-analysis model estimates and random effects for [!]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.04 | -0.09 | 0.02 | 0.03 | 0.23 |  |
|  |  |  |  |  | Project variance = 0.004, n = 8 |
|  |  |  |  |  | Article variance = 0.017, n = 126 |
|  |  |  |  |  | QE(185) = 2457.39, p < .001 |

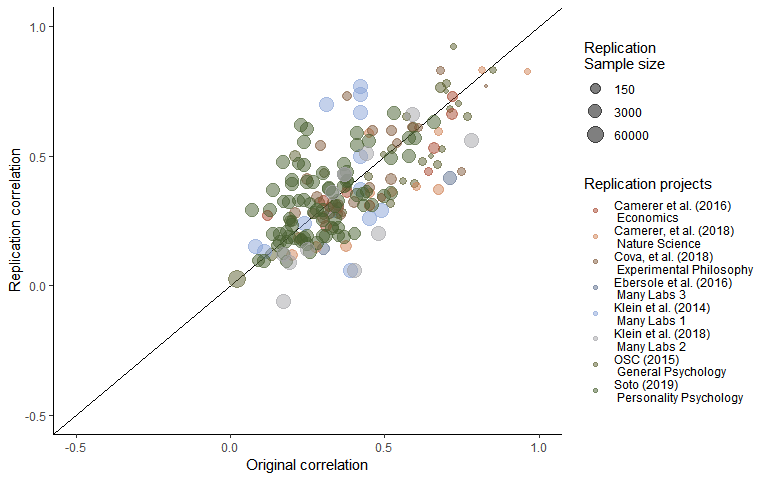


Figure SM8. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including studies with

Table SM10. Multilevel meta-analysis model estimates and random effects for studies with

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Estimate | 95% CI LB | 95% CI UB | SE | p | Random effects |
| -0.06 | -0.12 | 0 | 0.03 | 0.05 |  |
|  |  |  |  |  | Project variance = 0.005, n = 8 |
|  |  |  |  |  | Article variance = 0.016, n = 159 |
|  |  |  |  |  | QE(219) = 2532.44, p < .001 |

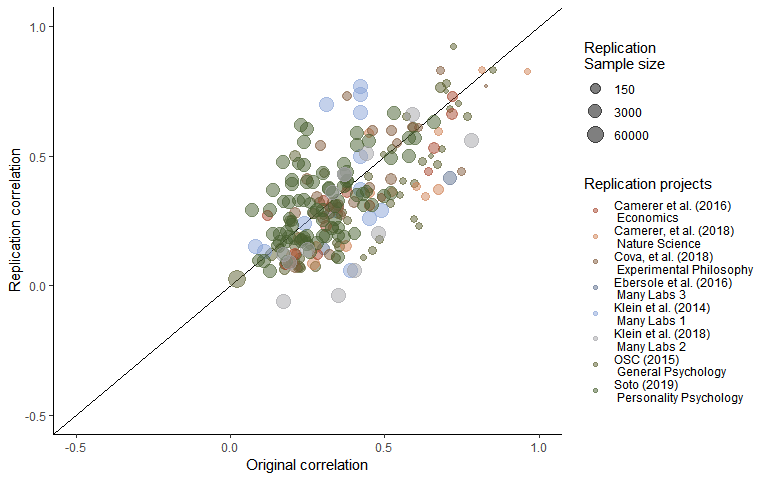


Figure SM9. Scatter plot of replication effect sizes (in correlation coefficients) plotted against original effects including studies with

### Simulation of removal methods

In order to assess whether the methods that were used to estimate the proportion change in studies excluding null results develop reasonable estimates, a series of simulations were performed. Simulations took as a starting point the observed effects in the original studies, estimating a true effect from these original results based on the Fisher Transformed ES standard error (i.e., estimating the true effect of each original study assuming a normal distribution with a mean of the original effect and a standard deviation of the standard error), and applying an attenuation factor (i.e., the proportion by which the true effect is reduced between initial and replication studies). Simulations were performed on attenuation factors from 0 to 1 in steps of .1. Simulation studies also varied the number of true effects, also varying between 0 and 1 in steps of .1, setting some studies to have true effect sizes of 0 randomly.

These simulations assumed that the probability of each study being a true null results was unrelated to the original effect size, sample size, source or original paper. See Table [all estimates output] for a table of how each method functions under each set of parameter values, along with the number of simulations that make up each value. See Plots [simulation] - [simulation] for heat maps of the root mean square error (RMSE), the mean absolute error (MAE) and average error are reported below in tables for all models. See table [simulation output] for a table of each method’s root mean square error (RMSE), the mean absolute error (MAE) and average error using each exclusion rule.

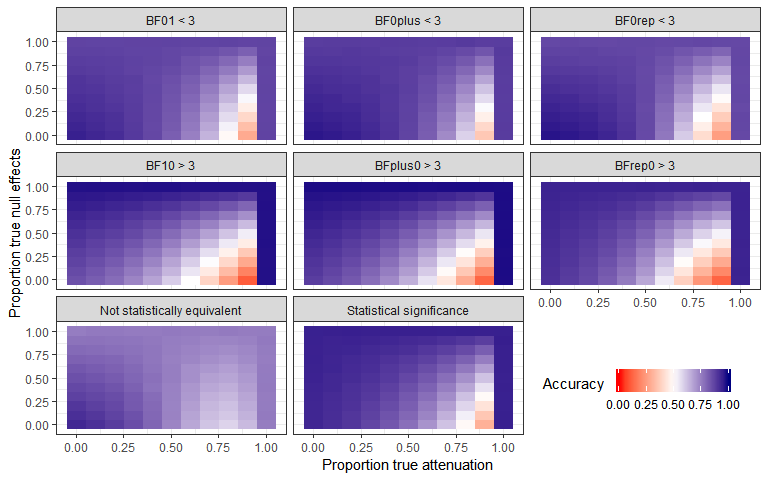


Figure [accuracy of cut scores]. The proportion of studies correctly classified in 11958 simulations of the accuracy of cut scores under varied true proportions of attenuation and proportion of effects which are true nulls.

Table [accuracy plot]

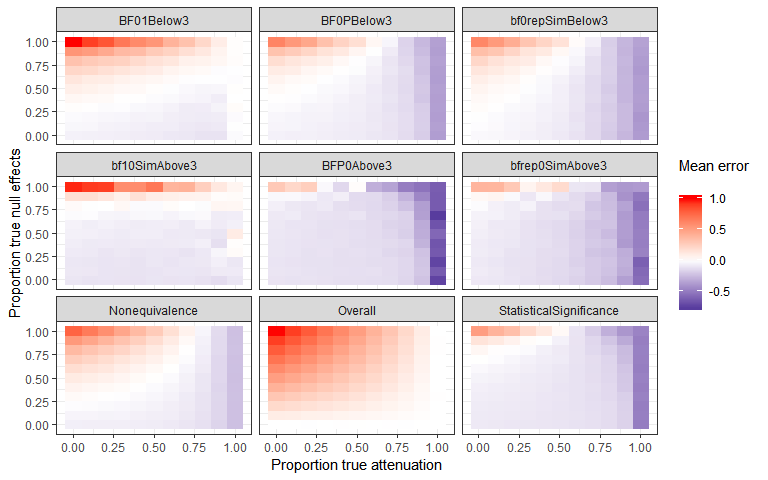
|  |  |  |
| --- | --- | --- |
| Data inclusion rule | Accuracy | Accuracy SD |
| Not statistically equivalent | 0.75 | 0.074 |
| Statistical significance | 0.84 | 0.135 |
| BF01 < 3 | 0.81 | 0.127 |
| BF10 > 3 | 0.78 | 0.127 |
| BFplus0 > 3 | 0.81 | 0.188 |
| BF0plus < 3 | 0.84 | 0.113 |
| BFrep0 > 3 | 0.78 | 0.190 |
| BF0rep < 3 | 0.81 | 0.144 |

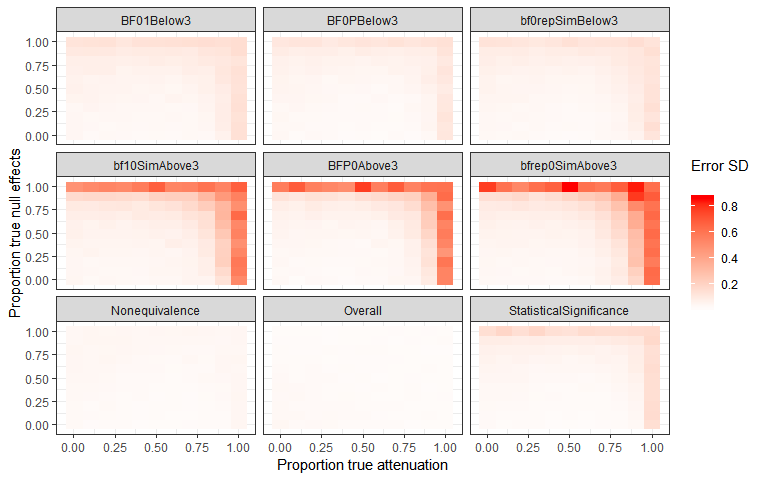
Additionally, simulations were performed using the same data-generation method to estimate the accuracy of the raw methods of estimating the simulated true proportion decrease under these different scenarios. Looking the mean proportion of effect size attenuation in the study, the results of the simulation study suggest that none of these methods for removing effect sizes lead to particularly accurate estimates of the true mean proportion error or the true average reduction in effect sizes in extreme circumstances. The simulation studies show Mean Absolute Errors (MAE) of between 0.13 and 0.25 for estimates of the proportion of attenuation seen, with error standard deviations of between 0.18 and 0.35, compared to a MAE of 0.25 when not removing any studies (error SD = 0.24). However, at reasonable levels of attenuation and proportion of null effects being correct, the simulations suggest that these methods are more accurate. For example, excluding simulations with a proportion of null results or attrition of .8 or greater, these methods have a MAE range of between 0.06 and 0.12, error SDs of 0.04 to 0.08, compared to MAE of 0.23 when not excluding any studies (error SD = 0.18).

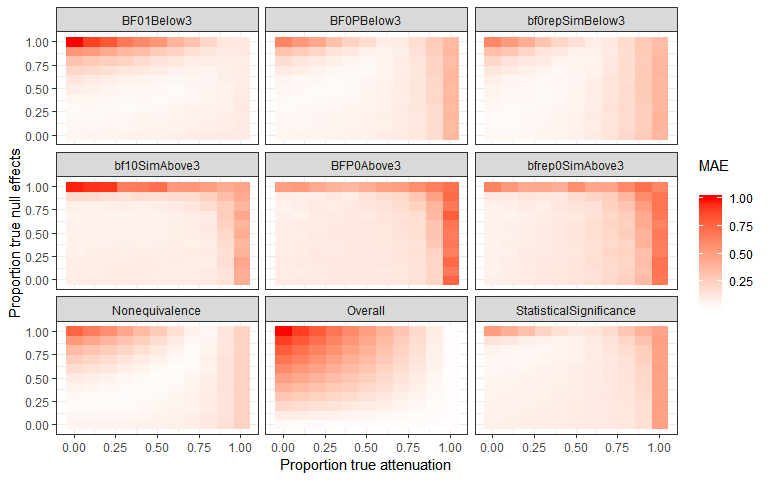
Note that these values are only valid under a specific data generation process, where there is a consistent factor effect size decrease, and where the studies which are null are random and independent of the original effect and sample sizes. See Table [simulation output] for the mean squared error (MSE), root mean square error (RMSE), mean absolute error (MAE), mean error (i.e., the average difference between the estimated proportion of effect size attenuation and the simulated amount of effect size attenuation), the error standard deviation, (i.e., the SD of the error scores for each simulation) across the parameter space, and figures 10 to 13 for heat-plots of the simulation mean error, mean absolute error and error SD across simulation conditions. The code used in these simulations is available from [OSFOSF.io].

heat maps of the mean absolute error at each benchmark and full simulation output tables. Table [simulation output]. The number of simulations for each subsample, the mean squared error (MSE), root mean square error (RMSE), mean absolute error (MAE), mean error (i.e., the average difference between the estimated proportion of effect size attenuation and the simulated amount of effect size attenuation), the error standard deviation, (i.e., the SD of the error scores for each simulation).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Subsample | nSims | MSE | Mean Error | RMSE | MAE | Error SD |
| BF01Below3 | 10101 | 0.05 | 0.08 | 0.23 | 0.14 | 0.22 |
| BF0PBelow3 | 10101 | 0.04 | -0.06 | 0.19 | 0.13 | 0.18 |
| bf0repSimBelow3 | 10101 | 0.04 | -0.06 | 0.21 | 0.15 | 0.20 |
| bf10SimAbove3 | 10101 | 0.11 | 0.00 | 0.32 | 0.19 | 0.32 |
| BFP0Above3 | 10101 | 0.13 | -0.18 | 0.36 | 0.22 | 0.32 |
| bfrep0SimAbove3 | 10101 | 0.15 | -0.17 | 0.39 | 0.25 | 0.35 |
| Nonequivalence | 14232 | 0.04 | 0.02 | 0.19 | 0.13 | 0.19 |
| Overall | 14232 | 0.12 | 0.25 | 0.35 | 0.25 | 0.24 |
| StatisticalSignificance | 14232 | 0.05 | -0.12 | 0.21 | 0.15 | 0.18 |







### LOO Cross validation output

# Table [LOO cross validation output](#loo-cross-validation-output).

0th, 25th, 50th, 75th and 100th percentiles from leave one out cross validation for each multilevel model, excluding one original article at a time, including only the sample indicated in “subsample”.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Subsample | Proportion significant | Minimum estimate | 25th percentile | Median | 75th percentile | Maximum estimate |
| bf01<3 | 1.00 | -0.09 | -0.09 | -0.09 | -0.09 | -0.08 |
| bf0plus<3 | 1.00 | -0.10 | -0.09 | -0.09 | -0.09 | -0.08 |
| bf0Rep<3 | 1.00 | -0.10 | -0.09 | -0.09 | -0.09 | -0.08 |
| bf10>3 | 0.00 | -0.06 | -0.05 | -0.05 | -0.05 | -0.04 |
| bfplus0>3 | 0.00 | -0.06 | -0.05 | -0.05 | -0.05 | -0.04 |
| bfRep0>3 | 0.98 | -0.07 | -0.07 | -0.07 | -0.07 | -0.05 |
| Significant in same direction | 0.01 | -0.06 | -0.05 | -0.05 | -0.05 | -0.04 |
| All studies included | 1.00 | -0.15 | -0.14 | -0.14 | -0.14 | -0.13 |

#### Table [LOO cross validation output](#loo-cross-validation-output).

0th, 25th, 50th, 75th and 100th percentiles from leave one out cross validation for each multilevel model, excluding one replication project at a time, including only the sample indicated in “subsample”.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Subsample | Proportion significant | Minimum estimate | 25th percentile | Median | 75th percentile | Maximum estimate |
| bf01<3 | 0.56 | -0.11 | -0.10 | -0.08 | -0.08 | -0.07 |
| bf0plus<3 | 0.89 | -0.11 | -0.10 | -0.09 | -0.08 | -0.07 |
| bf0Rep<3 | 1.00 | -0.11 | -0.10 | -0.08 | -0.08 | -0.06 |
| bf10>3 | 0.00 | -0.07 | -0.06 | -0.04 | -0.04 | -0.03 |
| bfplus0>3 | 0.11 | -0.07 | -0.06 | -0.04 | -0.04 | -0.03 |
| bfRep0>3 | 0.33 | -0.09 | -0.08 | -0.06 | -0.06 | -0.04 |
| Significant in same direction | 0.11 | -0.07 | -0.06 | -0.05 | -0.04 | -0.03 |
| All studies included | 1.00 | -0.16 | -0.15 | -0.14 | -0.13 | -0.13 |

### Bayesian Mixture Model

Three versions of the Bayesian mixture model were developed. The main mixture model presented in text presents the model developed by of Camerer, 2018 (see <https://osf.io/xhj4d/> for their detailed description of this model). Two extensions of this model were developed and tested. The first extension allowed for the attenuation factor to differ by effect size. except in that it allows for different replication projects to have different attenuation factors. All priors are chosen to be uninformative.

First, this is the original model from {Camerer, 2018 #967}. This has the issue of constraining all effect size attenuation factor factors to a single value.

model{  
# Mixture Model Priors:  
alpha ~ dunif(0,1) # flat prior on slope for predicted effect size under H1  
tau ~ dgamma(0.001,0.001) # vague prior on study precision  
phi ~ dbeta(1, 1) # flat prior on the true effect rate  
# prior on true effect size of original studies:  
for (i in 1:n){  
trueOrgEffect[i] ~ dnorm(0, 1)  
}  
# Mixture Model Likelihood:  
for(i in 1:n){  
clust[i] ~ dbern(phi)# extract errors in variables (FT stands for Fisher-transformed):  
orgEffect\_FT[i] ~ dnorm(trueOrgEffect[i], orgTau[i])  
repEffect\_FT[i] ~ dnorm(trueRepEffect[i], repTau[i])  
trueRepEffect[i] ~ dnorm(mu[i], tau)  
# if clust[i] = 0 then H0 is true; if clust[i] = 1 then H1 is true and  
# the replication effect is a function of the original effect:  
mu[i] <- alpha \* trueOrgEffect[i] \* equals(clust[i], 1)  
# when clust[i] = 0, then mu[i] = 0;  
# when clust[i] = 1, then mu[i] = alpha \* trueOrgEffect[i]  
 }  
}

The expanded model includes an alpha parameter, an effect size attenuation factor, for each included study.

model{  
# Mixture Model Priors:  
tau ~ dgamma(0.001,0.001) # vague prior on study precision  
phi ~ dbeta(1, 1) # flat prior on the true effect rate  
  
# prior on alpha, the effect size attenuation value   
for(i in 1:nSource){  
alpha[i] ~ dunif(0,1) # flat prior on attenuation factor for each replication project  
}  
  
# prior on true effect size of original studies:  
for (i in 1:n){  
trueOrgEffect[i] ~ dnorm(0, 1) # Normal prior on the original effect size   
}  
  
# Mixture Model Likelihood:  
for(i in 1:n){  
clust[i] ~ dbern(phi)  
orgEffect[i] ~ dnorm(trueOrgEffect[i] , orgTau[i]) #   
repEffect[i] ~ dnorm(trueRepEffect[i] , repTau[i])   
trueRepEffect[i] ~ dnorm(mu[i], tau)  
  
# if clust[i] = 0 then H0 is true; if clust[i] = 1 then H1 is true and  
# the observed replication effect is a function of the original effect:  
mu[i] <- (alpha[source[i]] \* trueOrgEffect[i] \* equals(clust[i], 1))  
# when clust[i] = 0, then mu[i] = 0;  
# when clust[i] = 1, then mu[i] = alpha \* trueOrgEffect[i]  
 }  
}

This later model allows for all of the replication effect sizes attenuation factors to differ by replication project.

### Supplementary materials [meta-moderaters]

Two methods were used to normalize the distribution of the p values, the Tukey-Freeman double Arcsine transform {Miller, 1978 #744}, and the The Ordered Quantile normalization transformation {Peterson, 2018 #1009}. Residual normality appeared to approximately hold in all cases, and as the results for all methods were functionally identical to those derived from those without any transformation only the raw results are presented in the main text. See supplementary materials [meta-moderators] for the results of the model with normalized predictors.

{Camerer, 2018 #967}’s model was adapted to allowed the amount of effect size attenuation to vary by replication project, as it is expected that these different projects will have different amounts of effect size attenuation, and as the differences are interesting in of themselves.