

Beyond Overall Effects: A Bayesian Approach to Finding Constraints Across A Collection
Of Studies In Meta-Analysis

Author(s) Redacted¹

¹ Institution(s) Redacted

Author Note

Author Notes redacted

Abstract

Most meta-analyses focus on meta-analytic means, testing whether they are significantly different from zero and how they depend on covariates. This mean is difficult to defend as a construct because the underlying distribution of studies reflects many factors such as how we choose to run experiments. We argue that the fundamental questions of meta-analysis should not be about the aggregated mean; instead, one should ask which relations are stable across all the studies. In a typical meta-analysis, there is a preferred or hypothesized direction (e.g., that violent video games increase, rather than decrease, aggressive behavior). We ask whether all studies in a meta-analysis have true effects in a common direction. If so, this is an example of a stable relation across all the studies. We propose four models: (i) all studies are truly null; (ii) all studies share a single true nonzero effect; (iii) studies differ, but all true effects are in the same direction; and (iv) some study effects are truly positive while others are truly negative. We develop Bayes factor model comparison for these models and apply them to four extant meta-analyses to show their usefulness.

Keywords: meta-analysis, random-effects meta-analysis, Bayesian models, mixed models, order-constrained inference

Beyond Overall Effects: A Bayesian Approach to Finding Constraints Across A Collection Of Studies In Meta-Analysis

Most readers at some point have considered the validity of averages. Sometimes, we may have been asked, “What does this average mean?” or, “Who does this average describe?” We may be quick to gloss over such questions. After all, the average, or sample mean, is a natural measure of the central tendency, and central tendency holds a privileged place in understanding variability.

Yet answers based on naturalness and privilege can be unsatisfying. A better account of the average comes from modeling. A model is an abstract, platonic account that has an irreducible element of uncertainty. According to the model, observations come from a distribution that captures this uncertainty. Part of our goal as analysts is to characterize this distribution. Unlike the data, which are real, the distribution is itself an abstraction (de Finetti, 1974). We often say observations are samples from a distribution. The reader, however, should keep in mind that this saying is somewhat misleading: Although observations are real, the concept of a sample from a distribution is an abstraction.

We may profitably view the sample mean in this context. The sample mean is useful in characterizing this abstract distribution. If we go further and assume that the observations come from a common distribution, say the normal distribution, the sample mean serves as an estimator of another abstraction, a parameter. For the normal, this parameter is called the true mean. Although we use the term “true,” we should be careful to remember that it is not real quantity—rather, it is a mathematical abstraction.¹ Even though parameters are abstractions rather than real, they are nonetheless useful in understanding constraint in data. In this regard, the sample mean is validated as an estimator of a theoretically meaningful parameter in a model.

One area where this validation seems hollow, however, is meta-analysis. The usual goal

¹Some people use the term population mean rather than true mean. The population is an abstraction, for example, the population of all people is an abstract concept not dependent on who is currently alive.

of meta-analysis is to combine several similar studies to draw a common conclusion. This conclusion almost always centers on a grand mean or overall effect. Take, for example, the meta-analysis of Anderson et al. (2010). After an extensive review, these authors concluded the meta-analytic average of the link between violent video game exposure and subsequent aggressive behavior was $r = .21$. Yet, to interpret this meta-analytic mean, we need to posit a distribution over experiments and treat this average as an estimate of a true parameter. The critical problem is this: what does this distribution signify? The distribution surely has something to do violent-video game exposure and aggression, but it also has something to do with how we design, run, and select experiments. In this light, this distribution may be as appropriate for understanding the sociology of how researchers choose experiments as it is for understanding the link between violent video games and aggression. Moreover, even if we generalize from a current set of studies to new sets, these new sets may be run with different design parameters and these differences in design may depend on the results of the previous studies. At the core of the problem, there is no sampling process from which experiments arise, and because of this, the concept of a meta-analytic distribution and meta-analytic means must be treated with much care.

We need not throw out the baby with the bathwater. To make progress, we distinguish between *metric* and *ordinal* properties. The metric properties are the usual real-valued parameters that describe the exact location of the probability mass, including the mean, variance, quantiles, and moments. For the Anderson et al. meta-analysis, the value $r = .21$ is a metric property describing the central tendency of the distribution of effect sizes across studies. For the reasons stated above, we consider metric properties of questionable value as the justification for the distribution they describe is strained.

Ordinal properties, in contrast, are about orderings. We ask whether basic ordering relations hold across all studies. To start, we note that there is almost always an anticipated direction of relations or effects in meta-analysis. For example, if there is an effect of violent video games on aggressive behavior, theory predicts that such violent video games are

positively associated, rather than negatively associated, with aggression. We call this anticipated direction the positive direction, and note that effects may be classified as positive, null, or negative. We propose that although metric properties of distributions across experiments may not be meaningful, ordinal properties of negative, null, and positive are. Here is how: We ask whether all studies in a population of studies have the same ordinal properties.

For example, we may expect that if there is a positive effect between aggression and violent video games, all studies with competent methods and measurements will have a true positive effect. This is not to say that every study will yield a positive sample effect, as some negative sample effects are expected from sample noise. Once this noise is modeled, the resulting parameters may be called *true effects*. They denote the noise-free or population value of the study, and we will use the terms *true* and *truly* throughout to refer to these values as not to confuse them with sample or observed values. The constraint we study is whether all true effects across a class of studies are positive. This all-studies-positive constraint, if it holds, is a strong statement. It means that every experiment in the class has a true positive effect. It is stronger than the usual meta-analytic statement about the averages because it applies to all studies. Likewise, we can also define a strong null constraint—all studies in the class show a true null effect. This null is stronger than the usual null that the average across studies is zero as the average may be zero while constituent studies may be truly positive and negative.

Of course, it may not be that all studies in a corpus have true positive effects or that all have a true null or that all have a true negative effect. Perhaps some studies in the meta-analysis show a true positive effect while others show a true negative effect. This case, should it exist, motivates different considerations. If there is a mix of true positive and true negative effects across studies, it may indicate that the individual studies are measuring disparate phenomena or are confounded by some moderator that is powerful enough to change the sign of the true effect. In this case, researchers may want to study why some

effects are truly positive and others are truly negative.

We believe this focus on ordinal properties that are common across all studies matches well with the type of questions researchers are interested in. Do all studies show a true effect in the same direction? Do all studies show a true null effect? Is the effect so heterogeneous that some studies have a true positive and others have a true negative effect? The meta-analytic mean, while convenient, is not helpful in answering these questions. Our goal here is to develop models of these meta-analytic ordinal constraints. We do so and illustrate a variety of patterns in the literature by reanalyzing four extant meta-analyses. One constraint we document is a strong null where all studies have a zero-valued true effect. We find this constraint holds in a reanalysis of Wagenmakers et al. (2016). These authors performed a registered replication of Strack, Martin, & Stepper (1988), who demonstrated a well-cited instance of embodied cognition. A second constraint we document is one where all studies in the meta-analysis are best described as having one true effect. We document this common effect with a reanalysis of a set of studies from Ebersole et al. (2016). These authors replicated a social-psychological phenomenon called moral credentialism (Monin & Miller, 2001) where prejudice is expressed to a greater degree after participants reject overtly sexist statements. A third constraint we document is one where true effects may differ but all are positive. This case comes from a reanalysis of Haaf & Rouder (2017), who reported the results of three extant Stroop experiments. Finally, we document unconstrained variability across studies. This is demonstrated by a reanalysis of Corker, Donnellan, Kim, Schwartz, & Zamboanga (2017), who studied how Big Five personality characteristics varied across different university populations.

Many of the highest visibility developments in meta-analysis today are about accounting for publication bias in computing and testing meta-analytic averages (Assen, Aert, & Wicherts, 2015; Carter, Schonbrodt, Hilgard, & Gervais, 2017; Simonsohn, Nelson, & Simmons, 2014; Stanley & Doucouliagos, 2014). Because we address a more fundamental question—what are the constraints among individual studies—we focus here on basic

development without worrying about publication bias at this juncture.

Constraints Among True Effects

Our main goal is to focus on constraints among the constituent experiments themselves. We first illustrate this focus with a reanalysis of Wagenmakers et al. (2016). Participants were asked to rate how humorous cartoons were while either smiling or pouting. Strack et al. (1988) reported a sizable effect where participants rated the cartoons as more humorous when smiling than when pouting. Wagenmakers et al.’s replication set is comprised of data from 17 independent lab sites who each performed the exact same experiment.

We explicitly model the variability within and between the studies with an ordinary mixed linear model. Let Y_{ijk} denote the rating from the i th site, the j th condition, and the k th participant. For example in the Wagenmakers’ set, there are $I = 17$ studies, two conditions (pout and smile, $j = 1, 2$, respectively), and about 60 replicates per study per condition. The base model is

$$Y_{ijk} = \mu + \alpha_i + x_j\theta_i + \epsilon_{ijk}.$$

Here, μ is a grand mean and α_i is an overall study-specific effect. Studies with higher ratings on average will have greater values of α_i . In this regard, α_i is a study-specific *intercept* parameter. The design element x_j is a condition indicator with $x_j = -1/2$ and $x_j = 1/2$ for pout and smile conditions, respectively. The parameter θ_i is the study-specific effect of the pout/smile manipulation, and it is the main target of inquiry. These parameters may be thought of as study-specific *slopes* as they describe the study-specific change in performance as a function of the manipulation. The term $\epsilon_{ijk} \stackrel{iid}{\sim} \text{Normal}(0, \sigma^2)$ is the usual noise term.

Our critical questions are about θ_i , the effect of the smile/pout manipulation. To address these questions, we place a series of models on θ_i that capture various constraints:

The most constrained model is the *null model*. Here, all of the constituent studies have a true effect of zero, and this model is implemented with the constraint $\theta_i = 0$. Note that

this model is a much stronger null than the usual meta-analytic null where the true grand average is zero; here, both the average and variance of θ_i are zero. Figure 1, left column, provides a graphical representation of the models. Panel A is for the null model. Depicted is the specification of the effect θ_i for two studies. Since θ_i is zero for both studies, the only point with mass is at $(0, 0)$.

The next generalization is what we term a *common effect model*. All constituent studies have the same true value, denoted ν . The constraint is simply $\theta_i = \nu$. This one-effect model captures the assumption of homogeneity sometimes stipulated in fixed-effect meta-analysis (Borenstein, Hedges, Higgins, & Rothstein, 2010). Figure 1B depicts this model. Because of the equality constraint, there is mass only on the main diagonal. If we further constrain ν to be positive, then there is only mass on positive values of this diagonal.

A generalization of the common effect model is to allow the true effects to vary from study-to-study, but to stipulate they have the same direction. For example, it is reasonable to assume that if facial expression affects humor ratings, all studies would show, to some degree, more humorous ratings while smiling than while pouting. Although that degree may vary, and certain factors may lead to smaller effects (less-sensitive measurements, less-susceptible populations, noisier methodology), no study would have a truly negative effect where pouting led to truly higher humor ratings. We call this model the *positive effects* model, and with it we constraint $\theta_i > 0$. For example,

$$\theta_i \sim \text{Normal}_+(\mu_\theta, \sigma_\theta^2),$$

where Normal_+ denotes a normal distribution truncated below at zero. Here μ_θ and σ_θ^2 are population parameter that describe the distribution of effect sizes across studies. Figure 1C shows this model. There is only mass distributed across the quadrant of joint positive effects. Prior settings are needed for μ_θ and σ_θ^2 , and we discuss how we chose these and the effects of these choices on inference subsequently.

Finally, we can relax this positivity constraint:

$$\theta_i \sim \text{Normal}(\mu_\theta, \sigma_\theta^2).$$

This model is termed the *unconstrained model*, and it specifies that true effects may be positive or negative. Figure 1D shows this model, and there is mass across all values of joint effects across participants.

Some readers might be a tad confused that we previously critiqued meta-analytic averages and yet still posit parameter μ_θ , which is the meta-analytic average across studies. The difference, however, is that our focus remains on the collection of θ_i 's and not on μ_θ or σ_θ^2 . In this sense, the experiment-population parameters serve as auxiliary parameters that improve our estimates of the θ_i 's.

These four models provide a means of characterizing the ordinal constraint in data. For example, if the null model best describes the data, then the conclusion is that there is no effect for any study. Likewise if the common-effect model best describes the data, we can talk about a unified phenomenon, and, here, the mean becomes meaningful as it characterizes all effect sizes. If the positive model best describes the data, we may note that while there is variation across studies, all index the same basic ordinal relation. It is this relation that is the main constraint in the data. Finally, if the unconstrained model best describes the data, resulting conclusions are nuanced. Perhaps the most prudent course is to wonder about the coherence of the collection of studies—they may index disparate phenomena.

One critical question is which model best describes the obtained data. We address this question in subsequent sections. Before doing so, we take a brief detour to discuss estimation of effects. Although estimation does not provide a calibrated, formal means of assessing the aforementioned constraints, it certainly provides an appropriate informal visualization of these constraints, and therefore, obtaining principled estimates of study effects is consequential.

Estimating True Effects

A standard course to visualizing effects is a *forest plot*, which summarizes the sample effect and corresponding confidence interval for each study or site. Figure 3A is an example from Wagenmakers et al., and it is quite similar to Wagenmakers et al.'s Figure 4. We find that forest plots place too much emphasis on the sample means, which, in the case of meta-analysis, are poor estimates of the true mean.

A sample mean estimate for a certain study relies on the data from that certain study and not on the data from the other studies in the meta-analysis. At first glance, this property may seem reasonable, but since the 1960s, statisticians have known that the data in the other studies may be used to improve the estimate of a particular study's true effect size (Efron & Morris, 1977; Stein, 1956). The estimator for one study's effect size should depend on the data from that study and from the other studies as well. This approach is now standard in hierarchical modeling.

Figure 3B shows the hierarchical estimates from the unconstrained model (filled circles) for Wagenmaker et al.'s data along with associated 95% credible intervals. Notice that the hierarchical estimates are more compact, closer to the meta-analytic average, and have credible intervals that are smaller and more uniform than for the sample mean and CIs. This effect is called regularization, and the notion here is that once the within-study variability is accounted for, the resulting model estimates better show the true variation across studies. There is a large degree of regularization; sample mean estimates are about 3 times as variable as the hierarchical estimates from the unconstrained model. According to this model, about 1/3 of the variation in sample estimates may reflect variation across sites; the other two-thirds may reflect variation within sites. This degree of regularization is meaningful and substantial.

Plots based on sample effects always overstate the variability across the sites. To avoid this overstatement, regularization, whether from frequentist or Bayesian methods, should be used. Sample effects may be plotted, but they should serve as data rather than as a target of

inference. Consequently, confidence and credible intervals should be placed on regularized estimates rather than sample means, and Figure 3B provides an example of such a plot. Fortunately, most researchers are familiar with modern estimation and mixed linear models, and their usage is built into meta-analytic software packages such as `metafor` (Veichtbauer, 2010) and Comprehensive Meta-Analysis.

Evidence for Constraints

Previously, we discussed four theoretically-motivated models of constraint: the null model, the common effect model, the positive effects model, and the unconstrained model. Estimating true values for effects is useful in visualizing data, but it provides no direct and calibrated measure of the evidence for the four models. To provide principled measures of evidence, we use the proper Bayesian approach resulting from Bayes' rule. Rather than providing a formal discourse, which may be found in Jeffreys (1961), Kass & Raftery (1995), and Morey, Romeijn, & Rouder (2016), we provide an informal discussion that we have previously presented in Rouder, Morey, & Wagenmakers (2016) and Rouder (2017). Informally, evidence for models reflects how well they predict data.

The right column of Figure 1 shows the predictions for each of the four models. We consider the relationship between two hypothetical studies that yield sample effects, $\hat{\theta}_1$ and $\hat{\theta}_2$. Possible sample effects for the first experiment are plotted on the x-axis, and possible values for the second experiment are plotted on the y-axis. Each point in the figure represents a possible combination of observed effects. For the null model, the observed effects are predicted to be near (0,0), and this case is shown in Figure 1E. The effect of sampling error is to smear the form of the model.² Figures 1F-H show the predictions for the common effect, positive effects, and unconstrained models, respectively. One aspect of the predictions that is not obvious is the correlation for the positive and unconstrained models. This correlation comes from the hierarchical structure in these models, and is a direct result

²More technically, the predictions are the integral $\int_{\theta} f(Y|\theta)\pi(\theta)d\theta$ where $f(Y|\theta)$ is the probability density of observations conditional on parameter values and $\pi(\theta)$ is the probability density of the parameters.

of variability of the population mean μ_θ . This variability comes from the prior and is discussed further after presenting the applications.

Once the predictions are known, model comparison is simple. All we need to do is note where the data fall. The red dots in the right column denote a hypothetical observed sample effect for both studies. This value is about equal for both studies, and we might suspect that the common effect model does well. To measure how well, we note the density of the prediction. Here, the density is darkest for the common effect model. These densities have numeric values, and we may take the ratio to describe the relative evidence for one model vs. another. For example, the best fitting model in the figure, the common effect model, has a density that is twice the value of that of the positive effects model. Hence, the data are predicted twice as accurately under the common effect model than under the positive effects model. This ratio is the *Bayes factor*, and it serves as the principled measure of evidence for comparing one model to another in the Bayesian framework.

Bayes factors are conceptually straightforward—one simply computes the predictive densities at the observed data. While this computation is conceptually straightforward, it is often inconvenient in practice. The computation entails the integration of a multidimensional integral which is often impossible in closed form and may be slow or inaccurate with numeric methods. To that end, there has been a voluminous literature on how to compute these integrals in mixed settings such as the one here. We follow a fairly general set of specification and computations known to work well. These have been pioneered by Zellner & Siow (1980) and expanded for ANOVA by Rouder, Morey, Speckman, & Province (2012). This development covers comparisons among the null, common effect, and unconstrained models. It does not, however, cover comparisons to the positive effects model. To make these comparisons, we use a different computational approach from Hoijtink and colleagues (Klugkist & Hoijtink, 2007; Klugkist, Kato, & Hoijtink, 2005). The details are provided in Haaf & Rouder (2017).

Prior Settings

Bayesian analysis is predicated on specifying prior distributions on parameters. Analysts should be familiar with how these specifications affect model comparison. A few points of context are helpful. It seems reasonable as a starting point to require that if two researchers run the same experiment and obtain the same data, they should reach the same if not similar conclusions. Yet, almost all Bayesians note that priors have effects on inference. To harmonize Bayesian inference with the above starting point, many Bayesian analysts actively seek to minimize these effects by picking likelihoods, prior parametric forms, and heuristic methods of inference so that variation in prior settings have minimal influence (Aitkin, 1991; Gelman, Carlin, Stern, & Rubin, 2004; Kruschke, 2012; Spiegelhalter, Best, Carlin, & Linde, 2002). In the context of these views, the effect of prior settings on inference is viewed negatively; not only is it something to be avoided, it is a threat to the validity of Bayesian analysis.

We reject the starting point above including the view that minimization of prior effects is necessary or even laudable. Rouder et al. (2016) argue that the goal of analysis is to add value by searching for theoretically-meaningful structure in data. Vanpaemel (2010) and Vanpaemel & Lee (2012) provide a particularly appealing view of the prior in this light. Accordingly, the prior is where theoretically important constraint is encoded in the model. In our case, the prior provides the critical constraint on the relations among studies. The choice of prior settings are important because they unavoidably affect the predictions about data for the models (Figure 1). Therefore, these settings necessarily affect model comparison. We think it is best to avoid judgments that Bayes factor model comparisons depend too little or too much on priors. They depend on it to the degree they do. Whatever this degree, it is the degree resulting from the usage of Bayes rule, which in turn mandates that evidence for competing positions are the degree to which they improve predictive accuracy.

When different researchers use different priors, they will reach different opinions about the data. Rouder et al. (2016) argue that this variation is not problematic. They

recommend that so long as various prior settings are justifiable, the variation in results should be embraced as the legitimate diversity of opinion. When reasonable prior settings result in conflicting conclusions, we realize the data do not afford the precision to adjudicate among the positions.

The critical prior specifications are those that define the differences between the models. In our case, the specifications are on μ_θ and σ_θ^2 , the population parameters. Although these parameters are not the primary target of inference, the prior settings on them affect the resulting Bayes factors. A full discussion of the prior structures on these parameters is provided in Haaf & Rouder (2017), and here we review the main issues. The critical settings are the *scale* on μ_θ and σ_θ^2 . The scale on μ_θ calibrates the expected size of the effect. This scale is not a point setting; μ_θ may be free to take on any value that reflects the data. Figure 2A shows a plot of the prior on μ_θ for three different scale settings. In application, we set the scale on μ_θ to be 0.40 in standardized effect size, and this value corresponds to the middle curve in the figure, which is dashed. The other setting is the scale of σ_θ^2 , and this setting calibrates the expected amount of variability in effect size across studies. We chose a value of 0.24 (this is a standard deviation on site-specific standardized effect sizes). The expected variation across sites or studies is 60% of the expected effect size, which seems like a reasonable ratio of scales. Figure 2B shows a plot of the prior on σ_θ for three different scale settings, and the middle one, which is dashed, corresponds to the value we used.

Wagenmakers et al.’s Embodied Cognition

Figure 3B provides the results of the reanalysis of Wagenmakers et al.’s registered replication report. The results from estimation are highly suggestive that there is no effect among any of the studies. The Bayes factor analysis favors the null model. The null is preferred 11-to-1 to the common effect model, the next most preferred model. The strong null is preferred 250-to-1 and 36,000-to-1 to the unconstrained and positive effects models, respectively. Here we see formal support for the strong null model—not only is the *average*

effect nearly zero, but the most parsimonious description among the four models is that *all* studies have a true zero effect.

Above we discussed that these Bayes factors are dependent on prior settings. Our choices of scale for mean and standard deviation are shown as the middle densities in Figure 2. These choices are informed by general knowledge about the field. We have also provided a reasonable range of variation in these choices, and these are indicated by the bracketing densities. We explore the effects of using these bracketing priors, and the resulting Bayes factors are shown in Table 1. There is a fair amount of variability in Bayes factors, and in our opinion, there should be. The range of settings define quite different models with quite different predictions. Nonetheless, there is a fair amount of consistency. For all settings, the ordering of the models remain: the null model is preferred to the common effect model which is preferred to the unconstrained model which is preferred to the positive effects model. This type of sensitivity analysis can always be performed to understand the range of conclusions that may be drawn from the data. In our case, the range is limited to a single ordering.

Ebersole et al.'s Moral Credentialism and Sexism

To show how the meta-analytic Bayes factor model-comparison system works in a more complex example, we re-analyzed a meta-analytic data set from Ebersole et al. (2016). This paper was the result of the *Many Labs 3 Project*, which was designed to assess the replicability of ten effects across several sites and across different periods of the semester. We focus here on one particular effect, *the moral credential effect*, which was originally demonstrated by Monin & Miller (2001).

The Monin and Miller study was designed to assess whether participants were more likely to express prejudiced attitudes when their prior behavior suggested that they were not prejudiced. To manipulate prior behavior, Monin and Miller asked participants to consider sexist statements and endorse those they agreed with and reject those they did not. The key manipulation is whether the statement was worded to describe *most* women or *some* women.

The main notion is that participants would be more likely to reject sexist statements that described most women rather than some women. Participants were randomly assigned to the *most* and *some* condition, with those in the former rejecting more sexist statements than those in the latter. Next, participants read a vignette that described a hiring opportunity at a manufacturing company. Participants rated how much more or less suitable a man would be for the position relative to a woman. The rating scale was a seven-point scale from strong preference for a woman through neutral to strong preference for a man.

The main hypothesis is that participants who previously rejected sexist statements—those who judged sexist statements referring to *most* rather than *some* women—would be more likely to express that men are more suitable than women for the job. Indeed, Monin and Miller report such an effect, and they also report an interaction such that the effect is prevalent for male participants but not for female participants.

We specify four critical parameters for each site. There is a site-specific intercept parameter, denoted α_i for the i th site. This parameter denotes overall rated suitability of men vs. women for the hypothetical job opportunity. Variation in this parameter across sites accounts for variation of overall expression of gender prejudice. There are three slope parameters to describe the effects. One is a site-specific gender-of-rater effect parameter, denoted θ_{gi} . The gender-of-rater effect is whether male participants rate men candidates higher than female participants rate men candidates. We refer to this effect as the gender effect for brevity. The remaining two parameters represent a moral credential effect—do participants express more prejudice if they were in the *most*-women condition previously? Because Monin and Miller reported moderation of this moral credential effect by gender, we used separate site-specific parameters for male and female participants, denoted θ_{mi} and θ_{wi} , respectively. This parameterization is well-suited for assessing the question whether any credential effect is stronger for men than for women.

We start with an unconstrained model where all four site-specific parameters are free

to vary subject to a hierarchical structure as used above.³ These hierarchical structures lead to regularization, and the resulting estimates for the slope effects are shown in Figure 4. From these estimates several trends are evident. From Figure 4A, there is an overall tendency to judge men, as compared to women, as more suitable for the job. This tendency seems not to vary among the sites. This tendency is a function of the gender of the rater: as compared to female participants, male participants are more likely to rate men higher than women. The gender effect seems to be stable across sites. Finally, there is a small credential effect for both men and women.

The figure alone does not lead to calibrated inference. There are many possible models corresponding to the placement of null, common effect, positive effects, and unconstrained structures jointly on the four site-specific variables α , θ_g , θ_m , and θ_w .

Table 2 shows a comparison of a preferred model, labeled *Common Site + Common Gender + Common Credential*, versus similar alternatives. Perhaps the most theoretically similar alternative is the model where there is only a common credential effect for male participants and none for female participants. This model, labeled *Common Site + Common Gender + Common Men Credential*, fares worse than the above model by a Bayes factor of 50, indicating that there is a credential effect for participants of both genders. Likewise, a model with separate credential effects for men and women, labeled *Common Site + Common Gender + Common 2 Credentials* also fares worse, though not as extremely. Table 2 also shows that common gender and credential effects are strictly necessary to predict the data. Removing either results in a drastically lower Bayes Factor value.

We also consider more complex models by adding in positive and unconstrained site-specific effects in intercept, gender and credentials. Adding positive variation to the intercept produced a slightly better Bayes factor value than the preferred model (1-to-0.7).

³A formal statement of the unconstrained model is as follows. Let $Y_{ijk\ell}$ denote the ℓ th replicate for the i th site, j th gender-of-rater ($j = 1, 2$), and k th credential condition ($k = 1, 2$). The model is given by $Y_{ijk\ell} \sim \text{Normal}(\mu_{ijk}, \sigma^2)$, where $\mu_{ijk} = \alpha_i + u_j\theta_{gi} + m_{jk}\theta_{mi} + w_{jk}\theta_{wi}$. Here $u_j = -.5, .5$ is an indicator that encodes the gender of the rater; $m_{jk} = 0, 1$ is an indicator that is 1 if the rater is a man and the condition is credentialed (most statements) and 0 otherwise; $w_{jk} = 0, 1$ is an indicator that is 1 if the rater is a woman and the condition is credentialed (most statements) and 0 otherwise.

This modest Bayes factor indicates that there is only equivocal evidence as to whether the prejudice against women is constant or variable across sites. Without firm evidence for variation, we prefer to use the common intercept form as our preferred comparison model for its simplicity. We also ran the Bayes factor model comparison statistics for the range of reasonable prior settings. The findings above held constant across this range with one notable exception. The conclusion about variability in the intercept depended markedly on the prior settings. When smaller effects are expected, the positive intercepts model is favored; when larger effects are expected, the common intercept model is favored. Hence, the data are not evidential enough to make statements about the variability in the intercept across sites.

In summary, we find a gender-of-rater prejudice effect and a moral credential effect. Further, we find there were no differences across the sites in these effects. Finally, the moral credential effect was the same for both men and women participants. We are unable to learn from the data whether overall prejudice varied across sites.

Haaf and Rouder’s Stroop-Effect Analysis

The above two analyses favored models where there was a single common effect across the sites for the critical slope effects. In some sense, this result is not too surprising as these meta-analyses come from carefully planned replication studies. Each of the constituent studies, which are from different sites, followed the same procedures. Hence, the homogeneity of the effects across the sites is plausible. In the next two analyses, we highlight cases where this homogeneity is not favored. Models with heterogeneity best describe the data.

Haaf & Rouder (2017) developed the models we use here for repeated-measure tasks. In these tasks, several participants each performed several trials in one of two conditions. Haaf and Rouder analyzed three different Stroop experiments, each independently. We analyze the same data here meta-analytically. For each participant in each experiment, we calculate two scores: a mean response time across all trials in the congruent condition, and a mean response time across all trials in the incongruent condition. Note that this meta-analysis is

that of a within-subject manipulation. All participants provide a score in each condition.

We analyze the data with the four basic meta-analytic models: the strong null model that there is no Stroop effect in any study; the common effect model that there is a single, common true Stroop effect for all studies; the positive effects model that true Stroop effects for all studies are in the usual direction; and the unconstrained model where true Stroop effects across studies may have different directions. These four models may be adapted in a straightforward manner for within-subject designs.⁴ The only complication is reconsideration of the prior settings on scale, and this reconsideration reflects the increased resolution of within-subject designs to detect variation. To set a scale on overall effects we need to consider the size of the effect in individuals. In our experience, response times on repeated trials for the same individual vary about 300 ms in standard deviation. In these experiments, there are about 100 trials per individual per condition. These two facts combined imply that the per-individual-per-condition sample mean has about 30 ms in variation. Whereas these sample means serve as data in analysis, we can ballpark the value of σ at 30 ms. Now, we expect Stroop effects on the order of 50 ms. The implication is that the scale on μ_θ in these designs is about 50/30 or 1.6. We also expected that if there was true variation in the effect across sites, it might be 20 ms or so in standard deviation. This yields a scale for σ_θ at 20/30 or .67. We used these values in analysis.

The first task is plotting the estimates of the Stroop effect from the unconstrained model. These estimates are shown with corresponding 95% credible intervals in Figure 5. There is very little shrinkage here. Because of the massively-repeated character of the within-subjects experimental design, there is far less sample noise to regularize.

Bayes factor analysis reveals that the positive model is most preferred. It is preferred

⁴A formal statement of the unconstrained model is as follows. Let N denote the total number of participants across all the studies, and let $j = 1, \dots, N$ index these participants. Let i_j be the study that the j th participant is in. Let Y_{jk} denote the response time for the j th participant in the k th Stroop condition ($k = 1, 2$). The model is given by $Y_{jk} \sim \text{Normal}([\alpha_j^* + \alpha_{i_j} + x_k[\theta_j^* + \theta_{i_j}], \sigma^2)$. Here $x_k = 0, 1$ is an indicator that encodes the Stroop condition. Parameters α_i and θ_i are study-specific intercept and effect parameters; parameters α_j^* and θ_j^* are participant-specific deviations from study-specific parameters. The null, common-effect, and positive models are placed on θ_i , the site-specific effect parameters.

by a factor of 3.6-to-1 over the unconstrained model, by a factor of 10^{11} -to-1 over the common-effect model, and by a factor of 10^{46} -to-1 over the null model.

Corker et al's Stability of the Big Five Personality Traits

In the preceding three analyses, the models favored were the null, the common effect, and the positive effects models. We have yet to find a meta-analysis where the unconstrained model is preferred to the positive effects model. We suspect, in fact, that such circumstances are rare in the literature for well-defined phenomena.

In this section, we reanalyze a recent meta-analysis from Corker et al. (2017) who examined the stability of personality data from 30 sites. Their main question is whether the Big Five traits are stable across different university populations. Big Five traits are measured as Likert scale ratings of endorsement of certain statements, and each individual is given a score that ranges from 1 to 5 for each characteristic. Stability across sites means that the average across people for a particular trait does not vary across sites. One might hope *a priori* that site averages do not truly vary as such variation may complicate personality research.

One feature of the Corker et al. application is that there is no concept of a true zero, nor are there positive and negative effects. For this application we focus on models with and without variability across sites. Corker et al. use a mixed linear model analysis to assess the variability across sites and to test whether certain covariates, when included, account for this variability. Their work is exemplary and they highlight the two themes promoted here: (i). that estimates should be regularized by models, and (ii). that model comparison and selection is the primary approach to formally address questions about constraints in data. Their approach, frequentist mixed modeling, at least in this application, is similar in spirit to our Bayesian mixed modeling. Therefore we refit their data as a demonstration that our approach yields similar conclusions to standard mixed models in cases where order constraints are not relevant.

To estimate personality traits among labs, we develop a random slope and intercept estimation model where there are site-specific intercept parameters and site-specific slope parameters for each personality trait. For each lab there is a site-specific intercept denoting on average how people in that lab score across all five factors. If participants in one lab tend to endorse higher ratings than in another, the intercept is higher for the first than for the second. There are also five site-specific personality-characteristic parameters; these are denoted θ_{ij} , where i indexes the site and j indexes the personality characteristic $j = 1, \dots, 5$.

The personality parameters are the target of interest. There are two theoretical positions: one where the distribution of personality traits is common across sites and another where the distribution indeed varies across sites. We take the common-effect position first. We constrain $\theta_{ij} = \nu_j$, where ν_j is a constant that describes how much of the j th characteristic there is in the population. To add heterogeneity across sites⁵, we simply distribute these parameters: $\theta_{ij} \sim \text{Normal}(\nu_j, \delta_j)$. Here δ_j is the variability across the j th trait.

Figure 6 shows the estimates of θ from the unconstrained model. As can be seen, there is a fair amount of variability for each of the personality characteristics.

There are several approaches to specifying families of models for comparison. We highlight what we consider to be an appropriate minimalist approach based on the comparison among three models. The simplest of these models has slopes and intercepts do not vary across labs, the second model has intercepts that vary but slopes do that not, and the third model has intercepts and all five slope parameters that vary across labs.

The results are as follows: The common intercept and slope model is least compatible with the data. It is dominated by the unconstrained intercept and common slope model (Bayes factor of about 10^{39} -to-1), which is in turn dominated by the unconstrained intercept

⁵A formal statement of the models are as follows. Let Y_{ijk} denote the k th participants score on the j th characteristic in the i th site. The model is given by $Y_{ijk} \sim \text{Normal}(\alpha_i + \theta_{ij}, \sigma^2)$ where α_i are site-specific intercepts and θ_{ij} are defined above. In the common-effect model, the constraint $\theta_{ij} = \nu_j$ guarantees identifiability. In the unconstrained model, the constraint $\theta_{ij} \sim \text{Normal}(\nu_j, \delta_j)$ is sufficient to guarantee identifiability in this context (Rouder et al., 2012).

and unconstrained slope model (Bayes factor of about 10^{48} -to-1). These staggering values remain staggering across reasonable variation in prior settings.

The alternative approach, perhaps a maximalist approach, is to specify all possible submodels of the unconstrained intercept and slopes model. Accordingly, we include models where some traits vary across sites while others do not. An example of such a model is where *agreeableness* and *openness* vary across sites, but *conscientiousness*, *extraversion*, and *neuroticism* are constant. We have avoided such models because we have no theoretical basis for testing why some but not other traits vary across sites. Hence, to us, assessing all these models is not a well-motivated inferential question. We prefer to reserve testing (through Bayes factor model comparison) for cases where models have immediate theoretical interpretations, as they do for the above three models.

Even when testing is inappropriate, we may still report estimates of the variability of the characteristics across the sites. Figure 7 shows the credible intervals on the standard deviation of personality ratings across sites. As can be seen, the degree of variability is fairly stable across the characteristics. This usage of Bayes factor assessment for theoretically important positions along with estimation for exploration of new phenomena is broadly useful.

General Discussion

In this paper, we seek to redefine the fundamental question of meta-analysis. Traditionally, inferences in meta-analysis are performed using the mean and CIs. These are properties that help the analyst understand the distribution of outcomes across a population of experiments. Yet, we argue this distribution is not well defined, and properties like mean reflect not only the phenomena under consideration but how we as a community chose to study it. Moreover, this distribution is artificial as there is no random sampling process for choosing design parameters for individual studies.

Here, we suggest focusing on basic ordinal properties that may be shared in common

among all studies in a class. Our null model stipulates that no study shows an effect. Our common effect model predicts that all studies have the same common effect. Our positive effects model relaxes this prediction, stipulating the effect may vary in size, but not in sign, across studies. We also leave room for the unconstrained case where some studies show an effect in one direction and others in the opposite direction. This unconstrained model, if favored, suggests substantial differences between studies, such that certain methods, measures, or populations appear to change the sign of the effect. For laboratory phenomena, success of this unconstrained model should be cause for careful scrutiny, as even the sign of the effect cannot be predicted in advance.

Advantages and Limitations in Bayesian Analysis

The current development is made within the Bayesian framework. There are a number of reasons we use the Bayesian framework, but perhaps the most compelling one is that we know of no comparable frequentist development for the positive-effects model. This model is comprised by placing order constraints on the true values for each of many studies. Placing a single order constraint on a linear model is well understood (Robertson, Wright, & Dykstra, 1988), but placing tens or hundreds of them (one per study) simultaneously is not. To our knowledge, although there is a voluminous frequentist literature on order-constrained inference (Silvapulle & Sen, 2011), there are no frequentist tests or model comparison strategies for the positive effects model vs. the unconstrained model. Fortunately, order-constrained inference is straightforward in the Bayesian framework (Gelfand, Smith, & Lee, 1992; Klugkist et al., 2005), and the basic machinery generalizes gracefully for consideration of many order constraints simultaneously (Haaf & Rouder, 2017). Indeed, Bayesian inference has become popular in statistics because it is tractable in many cases where frequentist inference is not.

Coarsely speaking, there are two prominent camps or points-of-view in Bayesian analysis in psychological science. The first camp is the *estimation camp*, and it is

popularized by John Kruschke and colleagues (Kruschke, 2012; Kruschke & Liddell, 2017). Here, the goal is to estimate parameters of interest, and from these estimates, draw conclusions about the likely relations in the data. The other camp is the *model comparison* camp, and it is popularized by the Bayes factor approach (Myung & Pitt, 1997; Rouder, Speckman, Sun, Morey, & Iverson, 2009; Wagenmakers, 2007). Practitioners follow Bayes rule to derive predictions for models under consideration and compare models by comparing their predictions. The critical questions here, “are all studies null,” or “are all studies positive,” are best answered by model comparison. It is unclear what target parameter of interest one would estimate to assess whether the positive model holds vs. its competitors.

One of the key properties we have tried to emphasize in our discourse are the limitations of testing with Bayes factor model comparison. We view testing as a powerful tool that must be wielded with expertise, wisdom, and restraint. Researchers should have well-conceived questions that are well-instantiated in well-specified models. Not all model comparisons are helpful and some are even misleading. For example, we decided to not test variability across each of the Big Five personality characteristics separately because we were unsure of the theoretical ramifications of the results.

Another limitation with Bayesian model comparison comes from considerations in specifying the prior. We expect analysts to differ in their choices, though these differences should fall in a range of reasonable values rather than be arbitrarily broad. Restraint is practiced when we respect this range. In our case, for example, we were unable to assess whether or not there was variation in prejudice toward women across sites in Ebersole et al’s data set. The conclusion depended too heavily on how much variation one expected, and different reasonable values resulted in qualitatively different conclusions. The most prudent course was to note that the question could not be answered with the data in hand.

Future Directions

We view the development here as only a first step in implementing this ordinal approach where we ask what is common among a population of studies. There are many possible extensions that would increase the usefulness of this approach. One extension is to account for the role of moderators and other covariates in assessment. We may still assess whether all studies are positive or null or varied even when demographics and other covariates are accounted for. Another extension is to expand the models of incoherent phenomena. Incoherent phenomena are those where some studies yield truly negative effects while other studies yield truly positive effects. For these cases, we can stipulate three classes of studies: those that are negative, null, and positive, and we can model the distribution of these studies as a three-component mixture. Each study then has a probability of being in each class. Moreover, we can assess whether this more flexible model better accounts for the data than the four presented. Haaf & Rouder (submitted) have started making progress on these incoherent mixture models. A third extension is to model publication bias. Guan & Vandekerckhove (2016) provide a new model-based approach, and their treatment of publication bias may conceivably be incorporated into our meta-analytic models.

We hope this new approach to meta-analysis proves timely and topical.

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Table 1

Mean	SD	Null-to-Common	Null-to-Unconstrained	Null-to-Positive
0.40	0.24	11.3-to-1	261.1-to-1	47173.7-to-1
0.40	0.40	11.3-to-1	1964.3-to-1	2689151.6-to-1
0.40	0.12	11.4-to-1	52.8-to-1	1620.3-to-1
0.80	0.48	22.2-to-1	9929.5-to-1	Inf-to-1
0.80	0.80	22.3-to-1	371027.3-to-1	Inf-to-1
0.80	0.24	21-to-1	504.4-to-1	149297.3-to-1
0.20	0.12	5.8-to-1	27.1-to-1	630.7-to-1
0.20	0.20	5.8-to-1	78.1-to-1	14582.6-to-1
0.20	0.06	5.8-to-1	12.8-to-1	82.9-to-1

Note. Infinite values exceed our machine precision of 10^304

Table 2

Model	Bayes Factor
Common Site + Common Gender + Common Credential	1-to-1
Common Site + Common Gender + Common Men Credential	1-to-50.6
Common Site + Common Gender + Common 2 Credentials	1-to-6.3
Common Site + Common Gender	1-to-101.7
Common Site + Common Credential	1-to-26977.6
Positive Site + Common Gender + Common Credential	1-to-0.8
Unconstrained Site + Common Gender + Common Credential	1-to-4.3
Common Site + Positive Gender + Common Credential	1-to-4.5
Common Site + Common Gender + Positive Credential	1-to-12
Common Site + Common Gender + Unconstrained Credential	1-to-Inf
Common Site + Unconstrained Credential + Common Credential	1-to-3.3

Note. Infinite values exceed our machine precision of 10^{304}

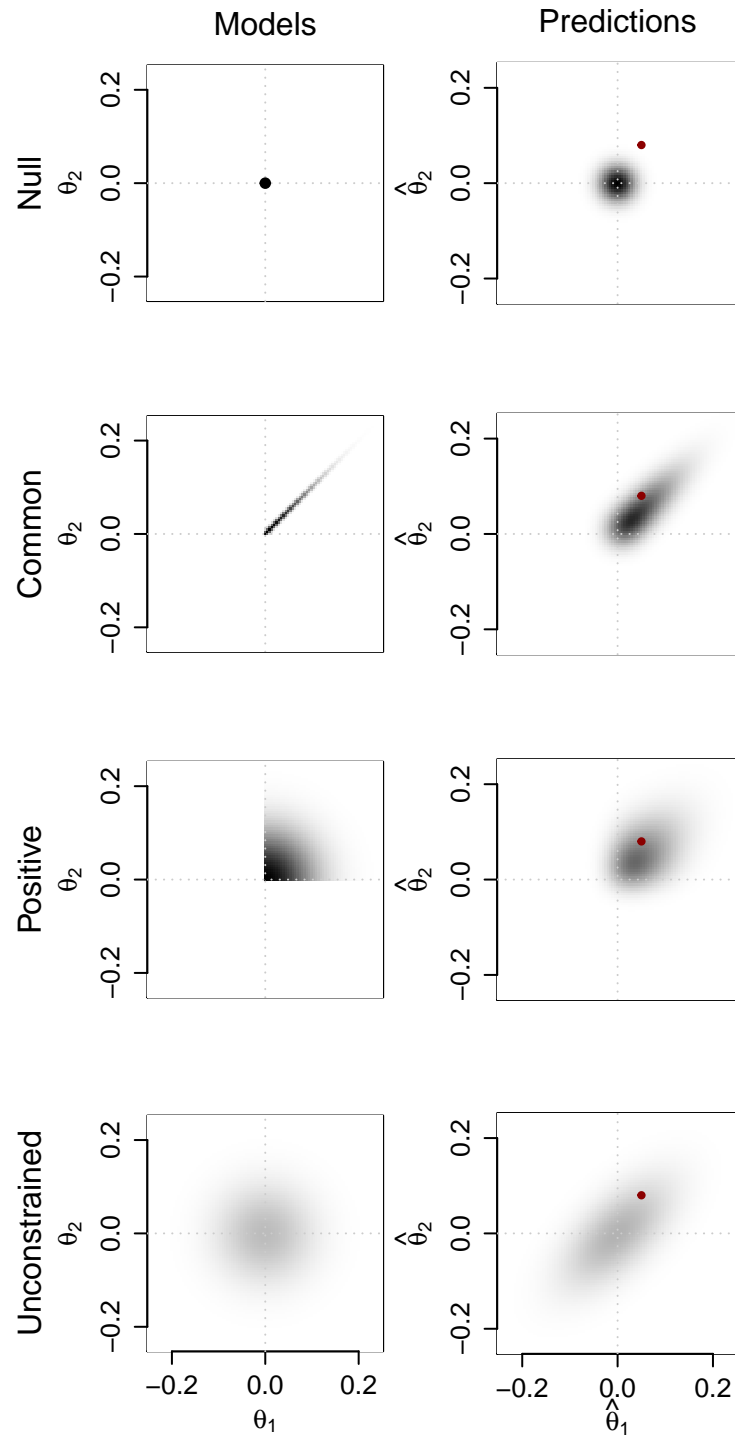


Figure 1. The four meta-analytic models as shown for two hypothetical studies. The left column shows the specifications; the right column shows the resulting predictions on observed effects.

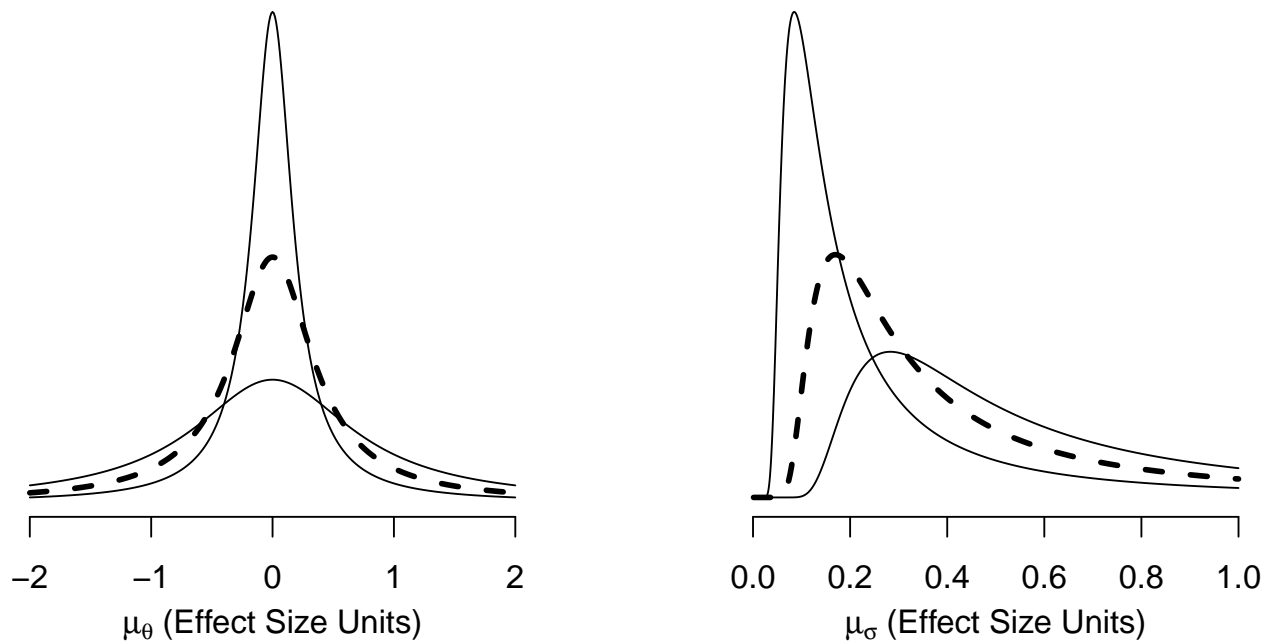


Figure 2. Prior distributions on critical parameters for different scale settings. **A** Priors for μ_θ with scale factors that range from 0.20 to 0.80. Our choice is the dashed curve for scale value of 0.40. **B.** Priors for σ_θ with scale factors that range from 0.12 to 0.48. Our choice is the dashed curve for scale value of 0.24.

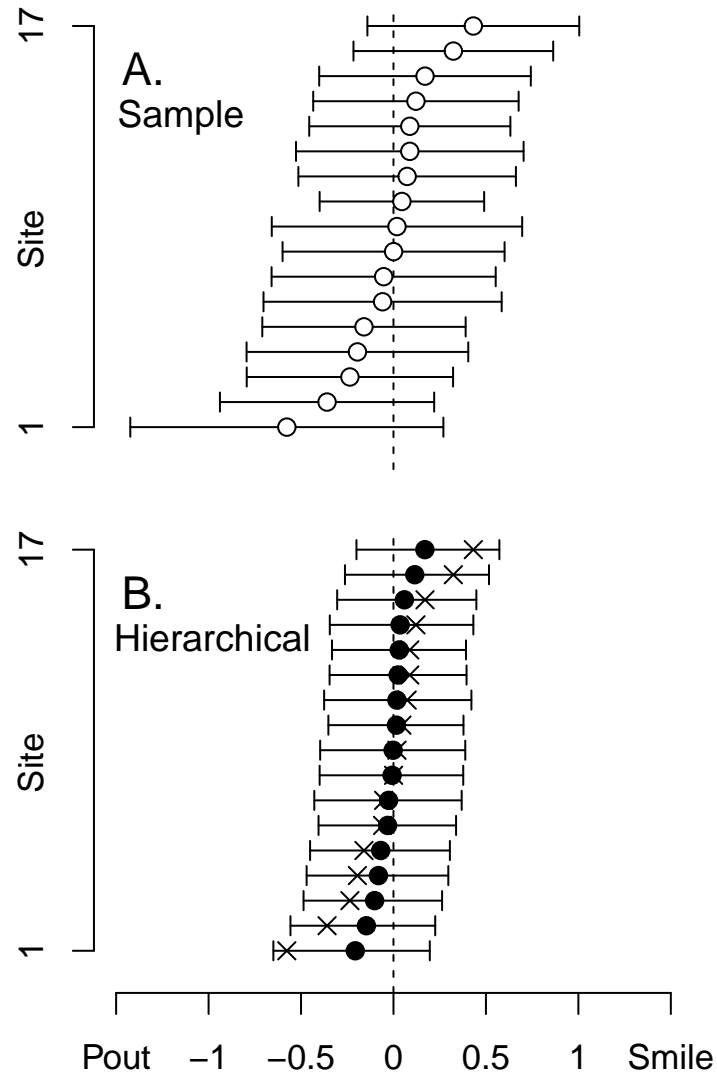


Figure 3. Reanalysis of Wagenmakers et al. (2016) registered replication report. **A.** Sample means with 95% confidence intervals for the 17 sites. **B.** Hierarchical model estimates with 95% credible intervals. These estimates show that after sample noise is accounted, there is not much heterogeneity.

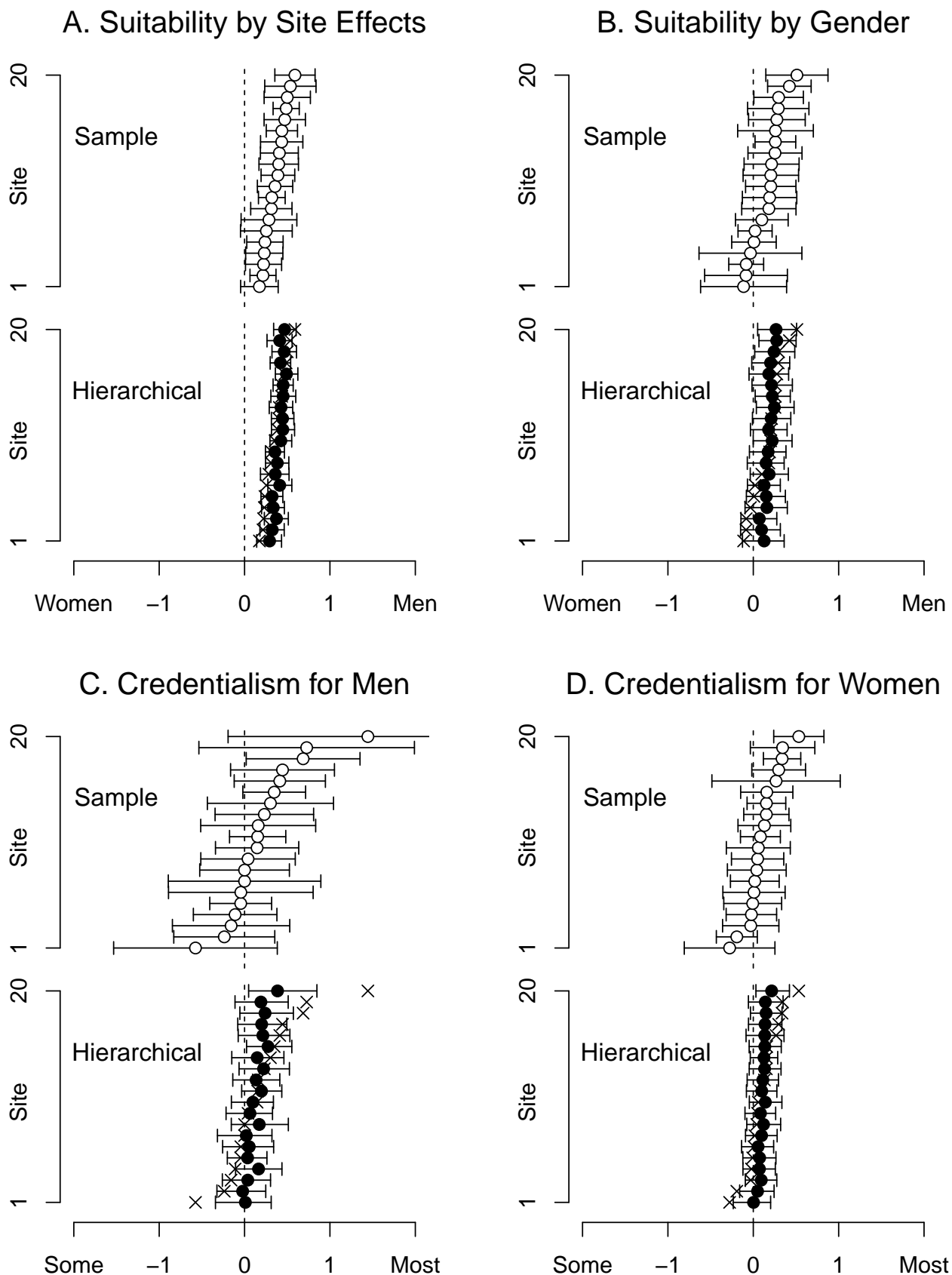


Figure 4. Reanalysis of Ebersole et al.'s (2016) replication of the moral-credentialism effect. **A.** Sample means with 95% confidence intervals for the 20 sites. **B.** Hierarchical model estimates with 95% credible intervals. There is little evidence for heterogeneity across labs.

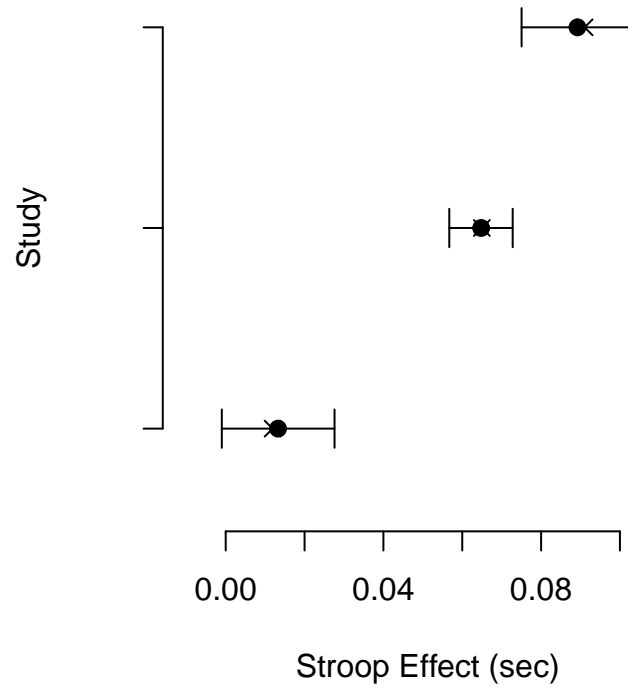


Figure 5. Meta-analytic hierarchical-model estimates for Haaf and Rouder's (2017) collection of Stroop experiments. The effect varies from study to study, but the sign is consistently positive.

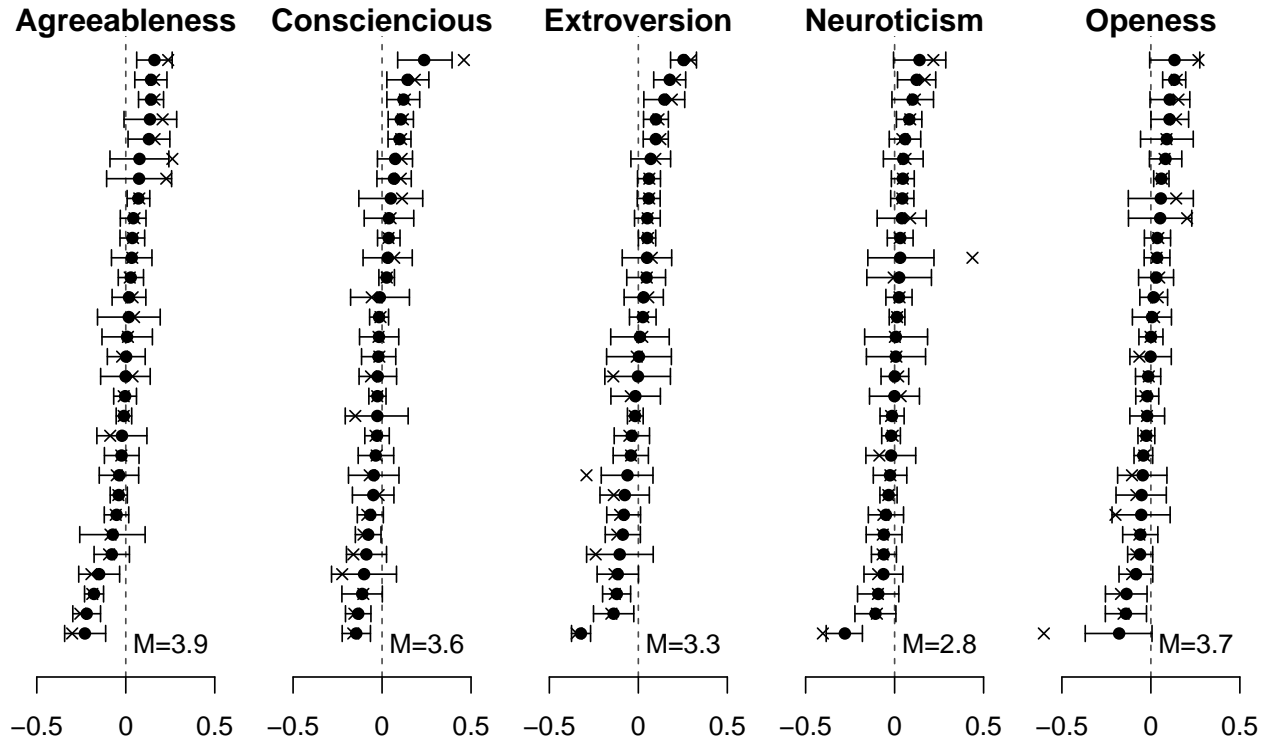


Figure 6. Meta-analytic hierarchical-model (regularized) estimates for Big Five personality characteristics across the 30 sites in Corker et al. (2017). It is apparent that there is substantial variation across the labs.

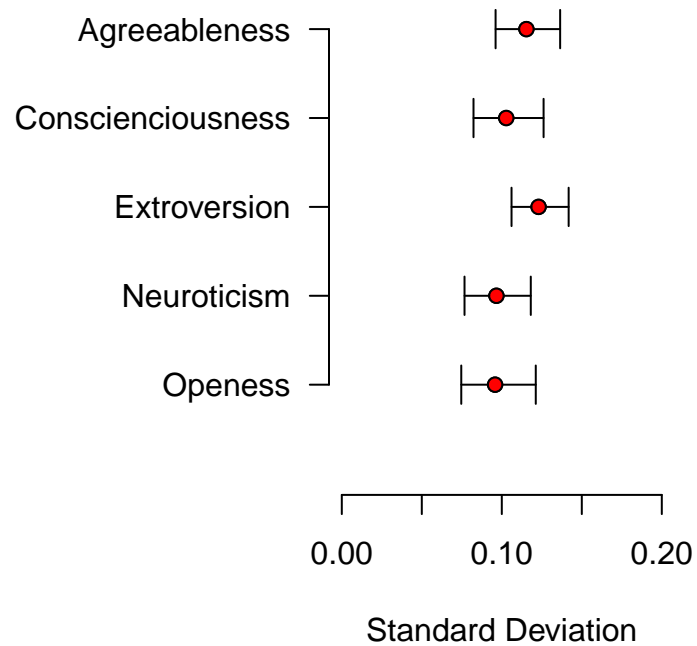


Figure 7. Estimates of variability of personality characteristics. Posterior distribution of standard deviations were computed and plotted are the means and 95% credible intervals of these distributions.