Many Mixture Components, Oh My: Extending the Spike and Slab to Bayesian Hypothesis Testing with Multinoulli Indicators

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Abstract

Bayesian analysis has become increasingly popular in the social-behavioral sciences. Because hypothesis testing has an important place on the mantel of psychological inquiry, an active area of research has been developing Bayesian analogs for commonly used frequentist tests. However, a major hurdle to this endeavour is computing the necessary ingredients, that is the marginal likelihood, resulting in the use of inflexible analytic solutions or approaches that avoid its computation altogether. In a similar spirit, I extend the spike and slab model, widely considered the gold standard for variable selection, to allow for flexible hypothesis testing. This is accomplished by employing multinoulli indicator variables, as opposed to Bernoulli, which results in a general solution for testing any number of hypotheses that correspond to components of a mixture prior distribution. In a motivating example, I first describe the qualitative relation of the proposed methodology to a popular Bayesian t-test, including extensions for one-sided and interval hypothesis tests. With the foundation laid, I proceed to a more complex example wherein the multinoulli spike and slab is used to model a correlation matrix, with the goal of testing joint hypotheses. This example investigated the associations among experimental effects from three cognitive inhibition tasks ($N = 121$), where the theoretical expectation is that they will be positively correlated. To the contrary, the results revealed that the null model of no associations better predicted the observed data than the positive effects model. The important topics of model selection and Bayesian model averaging are also discussed. I end with ideas to further extend the multinoulli spike and slab model. In addition, detailed `R` code is provided that can serve as the building block for developing custom Bayesian models.

Keywords: Bayes factor, hypothesis testing, spike and slab, model comparison

Many Mixture Components, Oh My: Extending the Spike and Slab to Bayesian Hypothesis Testing with Multinoulli Indicators

Bayesian analysis has become increasingly popular in the psychological literature (Heck et al., 2020; Mulder & Wagenmakers, 2016; Vandekerckhove, Rouder, & Kruschke, 2018). In part, this rise can be attributed to the mounting weight of criticisms against null hypothesis significance testing, that is frequentist statistics, which in practice is an amalgam of ideas stemming from the theories of Fisher and Neyman-Pearson (Hager, 2013; Schneider, 2015). It has been noted that the p-value is often misinterpreted (Greenland et al., 2016), for example, as providing the probability that the null hypothesis is true, when it only "indicates a misfit of the null hypothesis to the data" (Pernet, 2015). A well-established advantage of Bayesian methods is that evidence for the null hypothesis can be quantified (Dienes, 2014). On the other hand, the increase in popularity has run parallel to advances in computing power (Martin, Frazier, & Robert, 2020; Robert & Casella, 2011) and probabilistic software (e.g., Stan, Carpenter et al., 2017). This opened the flood gates to fitting custom models that are a bridge too far for customary approaches such as maximum likelihood estimation (Lee, Bock, Cushman, & Shankle, 2020; Rouder & Lu, 2005). With this computing power in hand, researchers are able to build richer models of psychological processes.

Because hypothesis testing has an important place on the mantel of psychological science, a particularly active area of research is exploring Bayesian analogs for commonly used frequentist tests. This spans from the seminal work of Jeffreys (1961), as synthesized in Ly, Verhagen, and Wagenmakers (2016), to the more recent literature. Mathematical psychology in particular has become a hotbed for developing these tests and software for their implementation, including for correlations (Mulder, 2016; Wetzels & Wagenmakers, 2012), partial correlations (Williams & Mulder, 2020), comparing means (e.g., t-test, Rouder, Speckman, Sun, Morey, & Iverson, 2009), analysis of variance (Rouder, Morey, Speckman, & Province, 2012), variances (Dablander, Bergh, Ly, & Wagenmakers, 2020),

and intraclass correlation coefficients (Mulder & Fox, 2019), to name but a few.

In contrast to significance testing, that adheres to the *free lunch property*, wherein "researchers need not make detailed assumptions about the alternative to test the null hypothesis" (p. 520, Rouder, Morey, Verhagen, Province, & Wagenmakers, 2016), Bayesian tests typically require specifying an explicit alternative in the form of a prior distribution that encapsulates a hypothesized effect size. Accordingly, the results can depend heavily on the prior distribution. Some have argued this is an inherent limitation, resulting in abandoning Bayes factors altogether (Gelman & Shalizi, 2013) and instead preferring Bayesian *estimation* (Kruschke, 2013). Alternatively, some approaches seek to mitigate the role of the prior distribution (e.g.. fractional and intrinsic Bayes factors, Berger & Pericchi, 1996; O'Hagan, 1995). Conversely, it has been argued that prior sensitivity is a desirable property, in that the results should depend on the alternative hypothesis (section 4.1 in Morey, Romeijn, & Rouder, 2016). My intention is not to promote either perspective, but rather to highlight the important role of the prior distribution in Bayesian hypothesis testing, including the need to develop innovative methodology.

Despite the prior distribution being sticking point, most approaches share a common theme still yet: they often employ analytic or computational strategies that aim to simplify Bayesian hypothesis testing. This is largely due to inherent challenges of computing the necessary ingredients, that is, the marginal likelihood (Carlin & Chib, 1995; Chib, 1995). It is the marginal likelihood that is considered *evidence*, with the Bayes factor corresponding to the ratio of two marginal likelihoods that provides "the degree to which the data are more likely under one model versus another" (p. 368, Ly et al., 2018). For example, variance explained and test statistics often have a direct correspondence to a Bayes factor with a particular prior distribution (Johnson, 2005; Liang, Paulo, Molina, Clyde, & Berger, 2008; Zellner, 1986). This computational attractiveness has led to their popularity in applied settings (Rouder & Morey, 2012; Rouder et al., 2009). Alternatively, there are approximations that side-step computing the marginal likelihood altogether; for example,

the encompassing prior approach of Klugkist, Kato, and Hoijtink (2005). This strategy is not restricted to particular prior distributions and thus it is extremely flexible, in that it can be used to seamlessly test precise, interval, and one-sided hypotheses (Faulkenberry, 2019; Wetzels, Grasman, & Wagenmakers, 2010)

The purpose of this work is to provide a general formulation that, in some sense, subsumes a variety prior formulations that have been proposed over the years. This is accomplished by extending the spike and slab approach, that is widely considered the gold standard for Bayesian variable selection, to accommodate flexible hypothesis testing, while also retaining computational feasibility. In the spike and slab, model comparison is typically formulated as a *two* component mixture for each coefficient: (1) a "spike" that is either narrowly concentrated around zero (George & McCulloch, 1993; George & Mcculloch, 1997) or a point mass at zero (Kuo & Mallick, 1998; Mitchell & Beauchamp, 1988) and (2) a diffuse "slab" component surrounding zero. A central aspect of this approaches is the addition of an Bernoulli indicator variable, which in essence allows for switching between the mixture components. This approach also circumvents directly computing the marginal likelihood. The proportion of Markov Monte Carlo samples spent in each component can then be used to compute the Bayes factor. Although typically used for exploratory variable selection, as described in Rouder, Haaf, and Vandekerckhove (2018) and Pang and Gill (2009), it can also be used for hypothesis testing.

My innovation to the spike and slab formulation is to introduce multinoulli indicators, as opposed to Bernoulli, which effectively allows for defining an arbitrary number of mixture components for a given parameter. Consider that hypothesis testing with the encompassing approach compares models that are obtained by truncating the encompassing prior distribution (Klugkist et al., 2005). In the proposed method, the same (more or less) constraints can also correspond to a truncated prior distribution, but with each mapping onto multinoulli indicator variable. Hence, this merges ideas stemming from two disparate approaches for hypothesis testing—the flexibility of the encompassing

approach with the long standing tradition of spike and slab variable selection. In this way, the proposed method fulfills the promise of Etz, Haaf, Rouder, and Vandekerckhove (2018), that is, "Bayesian inference and testing any hypothesis you can specify."

Overview

In what follows, I first introduce the basic idea of Bayesian hypothesis testing. Then the multinoulli indicator approach is described for a paired t-test. Here the inherent flexibility is highlighted by demonstrating that a prior of *many* mixture components can be employed, each of which corresponds to a hypothesis of interest. This serves as a motivation example, where special attention is given to the qualitative relation between the proposed prior distribution and various others that are commonly used for Bayesian testing. In the next section, the strategy is extended to modeling a correlation matrix.

Before proceeding, note that a key aspect of this work is the far reaching generality, in that the approach can be applied to many models (e.g., mixed-effects, generalized linear, etc.). This stands in contrast to popular approaches for Bayesian testing that are often restricted to certain models (but see Gronau, Sarafoglou, et al., 2017). To keep the exposition manageable, however, I first focus on a relatively simple model and then proceed to a more complex example. The accompanying code in the Appendix can be used as a building block for developing custom Bayesian models.

Bayesian Hypothesis Testing

Bayesian hypothesis testing is synonymous with model comparison. In contrast to classical testing (i.e., using p-values), the Bayesian approach provides a measure of *relative* evidence for which model, or hypothesis, the data is more likely under. Thus, there must be at least two models under consideration, say, $\mathcal{M}_a$ and $\mathcal{M}_b$. The posterior odds is given by

$$\underbrace{\frac{p(\mathcal{M}_a|y)}{p(\mathcal{M}_b|y)}}_{\text{posterior odds}} = \underbrace{\frac{p(y|\mathcal{M}_a)}{p(y|\mathcal{M}_b)}}_{\text{Bayes factor}} \times \underbrace{\frac{p(\mathcal{M}_a)}{p(\mathcal{M}_b)}}_{\text{prior odds}}, \tag{1}$$

where $(\mathcal{M}_a|y)$ and $(y|\mathcal{M}_a)$ are the posterior probability and marginal likelihood for model a, respectively, and $p(\mathcal{M}_a)$ is the prior probability. In practice, it is common to set the prior odds to one, thereby remaining agnostic to either model. In this case, the posterior odds is equal to the Bayes factor. It is worth noting that the Bayes factor can be interpreted in a couple of ways: (1) as a measure of relative predictive accuracy for the observed data (Kass & Raftery, 1995) and (2) as an *updating factor* (Rouder et al., 2018), given that it is multiplied by the researchers prior beliefs.

Although this intuitive framework appears to provide a simple approach for comparing models, it turns out that computing the Bayes factor can be quite challenging. It requires computing the marginal likelihood, for which numerous approaches have been proposed, including, for example, Laplace's approximation (Ruli, Sartori, & Ventrua, 2016), bridge sampling (Gronau, Sarafoglou, et al., 2017), and various MCMC approximations (e.g., Siddhartha, 1995). Alternative strategies aim to side-step computing the marginal likelihood altogether. The spike and slab, described below, is one such example, in that latent variables are introduced to estimate the posterior model probabilities. Of course, given the posterior odds, it is possible to derive the Bayes factor from Equation (1), which is the approach adopted in this work.

One-Sample T-test

The comparison of means is one of the most commonly encountered problems in psychology. Accordingly, there is a long standing tradition of using the frequenist t-test. With the rise of Bayesian methods, the t-test has garnered quite a bit of attention (Gönen, 2010; Gronau, Ly, & Wagenmakers, 2019; Gu, Hoijtink, & Mulder, 2016; M. Wang & Liu, 2016). In pychology, perhaps the most popular Bayesian analog is the Jeffrey-Zellner-Siow

(JZS) t-test of Rouder et al. (2009), that provides an analytic solution, requiring only the sample size and a t-statistic. The following focuses on a paired t-test, but note that the model is easily extended to a two sample t-test.

The JZS t-test is parameterized in terms of an effect size, $\delta = \mu/\sigma$, that is assigned a Cauchy prior distribution, $\delta \sim \text{Cauchy}(0, r)$, where r is the scale parameter. In practice, r can be selected to reflect a hypothesized effect size. The two-sided hypothesis test is then

$$\begin{aligned} \mathcal{H}_0 &: \delta = 0 \\ \mathcal{H}_1 &: \delta \sim \text{Cauchy}(0, r). \end{aligned} \tag{2}$$

In reference to Equation (1), the Bayes factor in favor of the null hypothesis is given by $BF_{01} = p(y|\mathcal{H}_0)/p(y|\mathcal{H}_1)$. This can be computed with Equation (1) in Rouder et al. (2009).

Although analytic solutions are elegant, a downside is that they are by nature inflexible. Accordingly, the JZS t-test has been extended in two interesting ways, both of which rely on MCMC sampling. First, Wetzels, Raaijmakers, Jakab, and Wagenmakers (2009) provided a flexible alternative that permitted order-restrictions (i.e., one-sided hypothesis testing). More recently, Faulkenberry (2019) provided an approach that merged the JZS t-test with the encompassing prior approach of Klugkist et al. (2005). The idea was to accommodate interval hypotheses, say, the so-called region of practical equivalence (Kruschke & Liddell, 2017), in addition to testing the null hypothesis. This work provide a further extension to the JZS t-test that unites Rouder, Tuerlinckx, Speckman, Lu, and Gomez (2008), Wetzels et al. (2009), and Faulkenberry (2019) under the multinoulli spike and slab model.

JZS Spike and Slab Model

Given the aim of this work, it is informative to first translate the JZS t-test into a customary spike and slab model. The likelihood is given by

$$y_i|\mu, \sigma^2 \sim \mathcal{N}(\mu, \sigma^2) \tag{3}$$

where μ and σ^2 are the mean and variance of a normal distribution, respectively. Note that $\mu = \delta/\sigma$, where δ is the standardized effect size. By placing the prior on δ, as opposed to μ, this ensure that the Bayes factor does not depend on the unit of measurement, a desirable property known as *scale invariance*. For variance, Jeffrey's prior, $p(\sigma^2) \propto 1/\sigma^2$, is approximated with an inverse gamma distribution. The next consideration is the spike and slab for δ, that is,

$$\begin{aligned} \delta|\gamma, r &\sim \begin{cases} 0 & \text{if } \gamma = 0 \\ \text{Cauchy}(0, r) & \text{if } \gamma = 1 \end{cases} \\ \gamma|\pi &\sim \text{Bernoulli}(\pi). \end{aligned} \tag{4}$$

Here γ is an indicator variable, that follows a Bernoulli distribution, where π and $1 - \pi$ is the probability of drawing a one and zero. In other words, π governs the prior model probabilities, given that γ corresponds to the hypotheses in Equation (2). A common choice is $\pi = 0.50$, resulting in a prior odds of one for the hypotheses. Note that it would be possible to estimate r and π from the data, but this would require specifying two additional prior distributions. This is not pursued here, as, in my view, the alternative hypothesis and prior model probabilities should not be determined from the data, although this would be reasonable in exploratory variable selection.

In Wetzels et al. (2009) and Faulkenberry (2019), the Savage-Dickey ratio was used to approximate the Bayes factor,

$$BF_{01} = \frac{p(\delta = 0|y, \mathcal{H}_1)}{p(\delta = 0|\mathcal{H}_1)} \tag{5}$$

which is the unconstrained posterior density evaluated at zero divided by the prior density also evaluated at zero. Although this method is not the most accurate, it requires only samples from the prior and posterior distribution to compute, which provides a very flexible (and often acceptable) strategy for computing Bayes factors.

In the proposed method, it is readily apparent in Equation (4) that γ is the indicator for the spike and slab. When sampling from the posterior distribution, for $s = 1, 2, \ldots, S$, this results in a vector, $\boldsymbol{\gamma}$. The posterior model probabilities are computed with

$$p(\mathcal{H}_1|y) = \frac{1}{S}\sum_{s=1}^{S}\gamma_s, \tag{6}$$

which is the proportion of MCMC samples that were drawn from $\mathcal{H}_1$. Notice this is a key component of Equation (1), with $p(\mathcal{H}_0|y) = 1 - p(\mathcal{H}_1|y)$. When setting $\pi = 0.50$, the posterior odds in favor of $\mathcal{H}_0$, $p(\mathcal{H}_0|y)/p(\mathcal{H}_1|y)$, is equivalent to the Bayes factor in favor $\mathcal{H}_0$. For simplicity, I always assume equal prior model probabilities for the mixture components, although it is also possible to compute the Bayes factor from the posterior odds, given unequal prior probabilities.

Many Mixture Components

The above formulation is the customary spike and slab, in that there is a point mass at zero (i.e., Dirac spike) and an unconstrained slab, spanning both sides of zero, which is effectively a two-sided hypothesis test. With the foundation laid, I now extend the spike and slab to ones-sided and interval hypothesis testing. In the following, the likelihood in Equation (3) remains in tact and the only modification is replacing Equation (4) with the multinoulli spike and slab.

One-Sided Hypothesis Test. In Wetzels et al. (2009), extended the JZS t-test to accommodate a one-sided hypothesis test.[1] This is critically important, given that researchers often have expectations regarding the direction of their hypothesized effect. To this end, I employ the categorical (i.e., mulitnoulli) distribution, which generalizes the Bernoulli distribution, to the case of several categories

$$\gamma|\boldsymbol{\pi} \sim \text{Cat}(\boldsymbol{\pi}),\ \gamma \in \{1, 2, K\}, \tag{7}$$

where K is the number of categories, or mixture components that corresponds to the hypotheses, and $\boldsymbol{\pi}$ is a $1 \times K$ vector of prior probabilities for each, such that $\sum_{k=1}^{K} \pi_k = 1$. I assume equal prior probabilities $1/K$. However, it should be noted that if there is an expectation for a given component this is easily accommodated. Also, if desired, a Dirichlet prior can be employed for $\boldsymbol{\pi}$.

In this example, the mixture prior distribution is defined as

$$\delta|\gamma, r \sim \begin{cases} \text{Cauchy}(0, r \cdot c^{-1}) & \text{if } \gamma = 1,\ c \gg 1 \\ \text{Cauchy}(0, r)^{+} & \text{if } \gamma = 2 \\ \text{Cauchy}(0, r)^{-} & \text{if } \gamma = 3. \end{cases} \tag{8}$$

where there are three components (i.e., $K = 3$). In Equation (8), Cauchy$(\cdot)^{+}$ and Cauchy$(\cdot)^{-}$ are half-Cauchy distributions restricted to positive and negative values. I have simplified this formulation by assuming that each component has the same scale, r, although this is not necessary. Furthermore, c^{-1} is a constant, that when multiplied by r, creates the "spike" component that is narrowly peaked at zero. This is different than the point mass at zero, as in Equation (4), and it is referred to as stochastic search variable selection (SSVS, George & McCulloch, 1993). The basic idea is to have a mixture of

[1] Note unequal variances were also permitted in Wetzels et al. (2009). In the two sample t-test, this is also possible with the presented methodology.

(typically) two continuous distributions, but in this case there are three. Compared to the Dirac spike, SSVS lends itself to more efficient posterior sampling (e.g., Table 6 in Malsiner-Walli & Wagner, 2011). This formulation effectively allows for sampling from a null model ($\gamma = 1$), a model with a positive constraint ($\gamma = 2$), and a model with a negative constraint ($\gamma = 3$). Both r and c are determined by the researcher. The former can be chosen to reflect a hypothesized effect size, whereas the latter is used to create an approximate spike at zero.

The proposed one-sided hypothesis test can then be thought of in reference to k (Equation 8), that is,

$$\begin{aligned} \mathcal{H}_0 &: \delta \sim \text{Cauchy}(0, r \cdot c^{-1}) \\ \mathcal{H}_1 &: \delta \sim \text{Cauchy}(0, r)^{+} \\ \mathcal{H}_2 &: \delta \sim \text{Cauchy}(0, r)^{-} \end{aligned} \tag{9}$$

where $\mathcal{H}_0$, $\mathcal{H}_1$, and $\mathcal{H}_2$, correspond to $\gamma = 1$, $\gamma = 2$, and $\gamma = 3$, respectively. What remains is computing the necessary ingredients for the Bayes factor (Equation 1). The hypothesis probabilities, say, $p(\mathcal{H}_0|y)$ and $p(\mathcal{H}_1|y)$, are again computed as the proportion of MCMC samples that were drawn from $\gamma = 1$ and $\gamma = 2$, respectively. Accordingly, the Bayes factor for a one-sided test (in this case a positive effect) is

$$\begin{aligned} BF_{10} &= \frac{p(\mathcal{H}_1|y)}{p(\mathcal{H}_0|y)} \\ &= \frac{p(\gamma = 2|y)}{p(\gamma = 1|y)}, \end{aligned} \tag{10}$$

assuming equal prior model probabilities. When employing unequal prior probabilities, the Bayes factor is then

$$BF_{10} = \frac{p(\gamma = 2|y)}{p(\gamma = 1|y)} \cdot \frac{p(\gamma = 1)}{p(\gamma = 2)}. \tag{11}$$

Furthermore, given that there are three mixture components, it might be desirable to test the complement, $\mathcal{H}_c$: "not $\mathcal{H}_1$," that corresponds to both $\gamma = 2$ and $\gamma = 3$. This is a case

were unequal prior probabilities arise naturally, in that, even when using equal priors for each mixture component, $p(\mathcal{H}_c) = p(\gamma = 2) + p(\gamma = 3)$, thereby resulting in a prior odds that must be accounted for when computing the Bayes factor.

Interval Hypotheses. In Faulkenberry (2019), the JZS t-test was extended to consider a null interval. This was accomplished by using the encompassing prior approach and taking advantage of the transitivity property of the Bayes factor. When wanting test $\mathcal{H}_1$ and $\mathcal{H}_2$, for example, both can be compared to the same, unconstrained hypothesis, $\mathcal{H}_u$, resulting in BF_{1u} and BF_{2u}. The hypotheses can then be compared to arrive at $BF_{12} = BF_{1u}/BF_{2u}$. This same logic applies to the multinoulli spike and slab, but the indicator variable can be used in such a way that it maps onto interval hypotheses. The advantage being that the respective hypotheses (or models) are visited during MCMC sampling, as opposed to the encompassing approach that entails computing everything from the unconstrained prior and the posterior distribution. Although a full discussion is beyond the scope of this paper, I refer to section 4 in Faulkenberry (2019) for an introduction to the encompassing approach.

Assuming the same mulitnoulli distribution (i.e., three mixture components), it is possible to test the following interval hypotheses,

$$\begin{aligned} \mathcal{H}_0 &: -\varepsilon < \delta < \varepsilon \\ \mathcal{H}_1 &: \delta > \varepsilon \\ \mathcal{H}_2 &: \delta < \varepsilon, \end{aligned} \tag{12}$$

where $\mathcal{H}_0$ is the null region spanning from $\pm\,\varepsilon$. Further, $\mathcal{H}_1$ and $\mathcal{H}_2$ are testing for the presence of a meaningful effect in either direction. With the hypotheses in hand, the next step is mapping them to mixture components, that is,

$$\delta|\gamma, r \sim \begin{cases} \text{Cauchy}(0, r \cdot c^{-1}, -\varepsilon, \varepsilon) & \text{if } \gamma = 1 \; c \gg 1 \\ \text{Cauchy}(0, r, \varepsilon, \text{Inf}) & \text{if } \gamma = 2 \\ \text{Cauchy}(0, r, -\text{Inf}, -\varepsilon) & \text{if } \gamma = 3, \end{cases} \tag{13}$$

The additional two values are the lower and upper truncation points, and hence the assumed prior is now a truncated Cauchy distribution. For example, $\text{Cauchy}(0, r, \varepsilon, \text{Inf})$ corresponds to a Cauchy distribution truncated to approximately ε (lower) and Infinity (upper). There it is constrained to positive values that exceed ε. A caveat worth noting is that the prior distributions must overlap, just a touch, or else the model is difficult to sample from. To overcome this issue, for $\gamma = 2$ and $\gamma = 3$, it suffices to set $\varepsilon_2 - 0.001$ and $\varepsilon_3 + 0.001$, resulting in an approximate, non-overlapping, interval hypotheses. The Bayes factors are again computed from the posterior model probabilities (e.g., Equation 10)

Bayes Factor Consistency

The Bayes factors computed with the multinoulli spike and slab model should have a property known as *consistency*: with increasing data, the Bayes factor should tend toward infinity in favor of the true hypothesis (Chib & Kuffner, 2016). There could be a problem, however, because the proposed one-sided hypothesis test is overlapping. This arises because the approximate spike shares some of the same support with the alternative hypothesis. As demonstrated in Morey and Rouder (2011), overlapping hypotheses can compromise Bayes factor consistency, wherein the shared support translates into an upper (lower) bound. An important question is whether the proposed, *slightly* overlapping, hypotheses compromise Bayes factor consistency.

To this end, I answered this question numerically by following the example in Morey and Rouder (2011, Figure 4 therein). The true effect size was set to $\delta = 0.5$. Three models were included: (1) as a reference point, the exact hypothesis test of Morey and Rouder (2011), but with a two component approximate "spike" and slab. The scale was set to

$r_0 = 0.1$ and $r_1 = 1$ for the null and alternative hypotheses; (2) given that $r_0 = 0.1$ can hardly be consider a spike, an additional model was included with $r_0 = 0.001$; and (3) the interval formulation (Equation 13; $\varepsilon = 0.10$, $r = 1$, $c = 1$). For each sample size, $n \in \{10, 20, \ldots, 50\}$, BF_{10} was averaged across 100 simulation trials. For aesthetic reasons, the posterior probability for $\mathcal{H}_1$ is reported.[2]

For the proposed method, the results revealed that the Bayes factor approaches infinity with more data, given that $p(\mathcal{H}_1|y) \to 1$, whereas this was not the case for the two component mixture with $r_0 = 0.1$ and $r_1 = 1$. A point worth emphasizing is that setting $r_0 = 0.1$ does not reflect a nil-null hypothesis, or spike, as this translates into a 50% prior probability the effect is greater than ± 0.10. On the other hand, when setting $r_0 = 0.001$, which places almost no prior mass greater than ± 0.10, the Bayes factor had the expected behavior. The approximate interval hypotheses also performed well. Interestingly, the advantage of one-sided testing was also apparent for the interval hypothesis, as indicated by the larger Bayes factors than the two-sided test provided by the customary "spike" and slab. This is similar in spirit to a frequentist t-test, where the p-value will be smaller for a one-sided test, assuming the effect is in the hypothesized direction.

Before proceeding, this does not provide rigorous evaluation of the Bayes factor consistency property and overlapping hypotheses. The basic idea was to highlight that specifying an approximate spike or interval is reasonable, especially when the shared support is minimal. Of course, if the *true* effect is (very) very small but nonzero, it will likely escape detection when using an approximate spike. This is a known issue of using a mixture of two continuous distributions (p. 344, George & Mcculloch, 1997), which is quite popular in the literature, with the rationale the effect might as well be null anyhow if it is that small. Similarly, for the interval hypotheses, unless the true effect happens to fall exactly within the very small overlapping region (e.g., $\delta \in \varepsilon + 0.001$), the test should work well.

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[2] $p(\mathcal{H}_1|y) = BF_{10}/(1 + BF_{10})$

Illustrative Example

In this section, the above models are applied to test for a mean difference in a cognitive inhibition task. The data originally come from von Bastian, Souza, and Gade (2016), which includes Flanker, Simon, and Stroop tasks. In the name of transparency, I purposely selected the Flanker task. My intention is not to cook the books, but rather because there is a non-significant effect. This allows for highlighting important aspects of the proposed method. There are 121 subjects that each completed roughly 90 trials for congruent and incongruent conditions. For each subject and condition, I first computed the means and then subtracted them, resulting in a difference score.

Estimation and Software. All aspects of this work were implemented in `R` (version 4.0.2, R Core Team, 2017). The models were fitted with the popular Bayesian software JAGS (Plummer, 2013), whereas the figures were made with **ggplot** (Wickham, 2016). r was set to $1\sqrt{2}$. For the interval hypothesis, the interval was set according to $\varepsilon = 0.2$. Each fitted model included four chains of 25,000 iterations after discarding a burn-in of 5,000 iterations. This resulted in a total of 100,000 samples from the posterior distribution. This number of samples provided a good quality of the parameter estimates in which the models converged with potential scale reduction factors $\hat{R}$ smaller than 1.1 (Brooks & Gelman, 1998).

Results. Figure 2 (panel B) includes the model averaged posterior distributions. Bayesian model averaging is discussed further in the next example. The color scheme corresponds to the posterior samples from each model (i.e., the mixture components). As indicated by samples being drawn from either side of zero, the customary spike and slab is agnostic to the direction of the effect (a two-sided hypothesis test). Further, notice the point mass spike at zero. The posterior distribution for the one-sided test, on the other hand, consists of samples drawn from three models. The restriction at zero (both negative and positive) is readily apparent, as is the approximate spike model. The interval test is particularly interesting, in that the posterior is truncated at ε and it is mostly contained

within the negligible region. Due to the interval width, the posterior does not have a "spike" at zero, which stands apart from the other two approaches.

The posterior probabilities are computed directly from the posterior distribution of the indicator variable. In relation to panel B, the proportion of samples drawn from a given model corresponds to the model probabilities. In the customary spike and slab, the Bayes factor was $BF_{01} = 7.61$, indicating the data were 7 times as likely under $\mathcal{H}_0$. The one-sided and interval formulations are quite flexible, in that a variety of Bayes factors can be computed. For example, in the one-sided model, $BF_{01} = 4.60$ and $BF_{02} = 13.66$, provides the relative evidence for $\mathcal{H}_0$ verses the positive and negative effect models, respectively. Using the transitivity property, the Bayes factor for comparing the positive versus negative effect model is $BF_{12} = 2.96 = BF_{02}/BF_{01}$. Finally, for the interval formulation, the Bayes factors for the negligible region versus the (non-negligible) positive and negative effect models are $BF_{01} = 30.47$ and $BF_{02} \approx 3,000$. This can be seen from panel B, where hardly any samples were drawn from $\mathcal{H}_2$. Together, this demonstrates that the multinoulli spike and slab can be used to test a variety of hypotheses.

Figure 2 (panel C) includes the trace plots for each model. It is clear that each shows adequate mixing. This is comforting to see, given that the idea of many mixtures components and the software implementation are novel contributions. Of note is the interval model. The trace plot reflects that the majority of samples were obtained from the interval surround zero. Hence, although the trace plot looks a bit different than the others, this is expected when most samples are drawn from an interval. Intuitively, this is because the trace plots capture the journey of visiting different models, each corresponding to component of the mixture prior distribution.

Correlations Coefficients

The Pearson correlation coefficient, herein denoted r, provides a measure of linear association between two variables, where values of 1, -1, and 0 imply a perfectly positive,

perfectly negative, and no relationship. Much attention has been given to Bayesian alternatives to frequentist hypothesis tests. For example, Wetzels and Wagenmakers (2012) provided a JZS Bayes factor computed as "a comparison between two linear regression models" (p. 1061). Although this provides an analytic solution, a downside is that it only applies to the case of two variables (one correlation). In general, however, it may be of interest to consider joint hypotheses, say, that all relations within the same correlation matrix are positive, compared to a null model (all are equal to zero), or to apply Bayesian variable selection to a correlation matrix. In the spike and slab context, this can be thought of as *covariance* selection.

In the following, I build upon approaches described in H. Wang (2015) and Frühwirth-Schnatter and Tüchler (2008), each of which employed a two component mixture of continuous distributions for covariance selection. The former was in the context of graphical models, whereas the latter was for random effects covariance matrices. They used a binary indicator, whereas my innovation is to use multinoulli indicator variables. Further, a Dirac spike and slab is employed, as well as two different prior distributions for the slab component. This further highlights the flexibility of the proposed method.

Multinoulli Covariance Selection

The first hurdle for testing several correlations is choosing an adequate prior distribution for the covariance matrix . Historically, the inverse-Wishart (IW) distribution has been a popular choice, because it is the conjugate prior for the covariance matrix, $\boldsymbol{\Sigma}$, of a multivariate normal distribution, $\boldsymbol{y}|\boldsymbol{\Sigma} \sim \mathcal{N}(\mathbf{0}, \boldsymbol{\Sigma})$ (Gutiérrez-Peña et al., 1997). There are at least three downsides to the IW prior for hypothesis testing in particular. First, it has been criticized for being overly restrictive, as one parameter governs *all* elements (i.e., the variances and covariance Hsu, Sinay, & Hsu, 2012; Leonard & Hsu, 1992). Second, it is a joint prior for the implied correlations. This means that it is not technically possible to restrict a given correlation to zero (the null model). Third, due to being the prior for $\boldsymbol{\Sigma}$, it

is not possible to place a prior directly on the correlations. Because r is an effect size, however, it is the natural target for covariance selection and Bayesian hypothesis testing. Together, the ideal approach would directly target each correlation, with the possibility of using a variety of prior distributions.

With these goals in mind, I use the separation strategy to decompose of $\mathbf{\Sigma}$ (see Equation 1 in Barnard, McCulloch, & Meng, 2000). To ease describing the formulation, I focus on the case of three variables. The separation strategy is given by

$$\mathbf{\Sigma}|\boldsymbol{\tau}, \mathbf{\Omega} = \text{diag}(\boldsymbol{\tau})\, \mathbf{\Omega}\, \text{diag}(\boldsymbol{\tau}), \tag{14}$$

where $\boldsymbol{\tau}$ is a 3×1 vector that contains the standard deviations (SD) for each variable, $\text{diag}(\boldsymbol{\tau}) = \text{diag}(\tau_1, \tau_2, \tau_3)$ is a diagonal matrix, and $\mathbf{\Omega}$ is a 3×3 correlation matrix, that is,

$$\mathbf{\Omega} = \begin{bmatrix} 1 & r_{12} & r_{13} \\ r_{12} & 1 & r_{23} \\ r_{13} & r_{23} & 1 \end{bmatrix}, \tag{15}$$

where r_{12} denotes the correlation between the first and second variables.

Prior Specification. What remains is specifying a prior for the SDs and correlation coefficients. For the latter, I assume that

$$\tau_i \sim \text{Student-t}(\mu = 0, \sigma = 1, \nu = 10)^+,\ i = 1, 2, 3, \tag{16}$$

where each is assigned a half Student-t distribution, with a scale of 1 and degrees of freedom 10 (which governs the tail heaviness, with $\nu \to \infty$ approaching a normal distribution). This family of priors was proposed in Gelman (2006) and then Huang and Wand (2013) extended the idea to multivariate settings. Because I standardize the data, this prior is not overly restrictive, given that the SDs are equal to one by construction. Further, this also results in not having to estimate the mean of each variable.

Beta Prior Distribution. For the correlations, I employ two different mixture prior distributions, each consisting of three components. This is meant to showcase the flexibility of the proposed method. The first extends the "Jeffreys test" that was eloquently described in Ly et al. (2016), including an extension to a one-side test. This approach was explicitly for bivariate normal and hence the derivations would not apply to covariance selection models (to my knowledge). In Ly et al. (2016), r was assigned a so-called stretched beta prior distribution. I follow this approach, but within the multinoulli spike and slab model, that is,

$$r_{ij}|\kappa, \gamma_{ij} \sim \begin{cases} 0 & \text{if } \gamma = 1 \\ \mathcal{B}(\frac{\kappa}{1}, \frac{\kappa}{1})^{+} & \text{if } \gamma = 2 \\ \mathcal{B}(\frac{\kappa}{1}, \frac{\kappa}{1})^{-} & \text{if } \gamma = 3 \end{cases} \tag{17}$$
$$\gamma_{ij} \sim \text{Cat}(\boldsymbol{\pi}),\ \gamma \in \{1, 2, 3\}$$

for $i = 1, 2$ and $j = 2, 3$ ($i \neq j$, $i < j$). Notice this prior is a truncated beta distribution, and as such, $k = 2$ and $k = 3$ are restricted to positive and negative values, respectively. κ governs the scale, with $k = 1$ resulting in a uniform distribution, and $\kappa \to \infty$ approaching a normal distribution with increasing prior mass concentrated around zero. In this case, $\gamma = 1$ corresponds to a precise null hypothesis, or a Dirac spike, as opposed the approximate spike in Equation 8. Furthermore, $\boldsymbol{\pi}$ is a 1×3 vector of prior probabilities for each category, such that $\sum_{k=1}^{K} \pi_k = 1$, and γ_{ij} is the indicator for each correlation. I again assume equal prior probabilities 1/3. This prior is visualized in Figure 3.

Normal Prior Distribution. A key advantage of the spike and slab model is flexibility for choosing the alternative hypothesis (or prior distribution). In my opinion, just how κ in Equation (17) governs the beta distribution is not very intuitive. Employing a normal distribution, on the other hand, would offer an air of familiarity. Of course, a normal prior cannot be used directly on r, given that correlations are bounded between ± 1.

This can accomplished by placing the prior on the (inverse) Fisher$-z$ transformed correlation, effectively putting the prior on a $z-$score. This can be written as

$$
\begin{aligned}
r_{ij} &\sim F^{-1}(z_{ij}) \\
z_{ij}|\sigma &\sim \begin{cases} 0 & \text{if } \gamma = 1 \\ \mathcal{N}(0,\sigma)^{+} & \text{if } \gamma = 2 \\ \mathcal{N}(0,\sigma)^{-} & \text{if } \gamma = 3 \end{cases} \\
\gamma_{ij}|\boldsymbol{\pi} &\sim \text{Cat}(\boldsymbol{\pi}),\ \gamma \in \{1,2,3\}
\end{aligned}
\tag{18}
$$

for $i = 1, 2$ and $j = 2, 3$ ($i \neq j$, $i < j$). $\mathcal{N}(\cdot)^{+}$ is a half-normal distribution restricted to positive values and $\mathcal{N}(\cdot)^{-}$ is a half-normal distribution restricted to negative values. Consequently, σ is the scale (standard deviation) of a half-normal distribution ($k = 2$ and 3). I again employ the Dirac spike approach of (Kuo & Mallick, 1998), resulting in a point mass at zero. After taking the inverse of the Fisher z transformation, $F^{-1}(z_{ij})$, this results in the prior for the correlation. Assuming a prior on z was described in Daniels and Kass (section 2.3.2, 1999), which was motivated by approaches for covariance matrix estimation (pp. 5 - 6 in Lin & Perlman, 1985).

A Note on Model Selection. When several parameters are being modeled, this raises the question of how "best" to select a model. One approach is to focus on the posterior inclusion probabilities (PIP), that is $p(\gamma = k|y), k = 1, 2, 3$, and select relations for which the PIP exceeds 0.50 (indicating a component was included in half of the models visited). This results in the median probable model, that is known provide optimal predictions in regression, assuming an orthogonal design matrix (Barbieri & Berger, 2004). Alternatively, it is possible to select the highest posterior model (HPM) from the indicator variables.

There is an important distinction between selecting relations with the PIP or choosing the HPM and hypothesis testing. Bayesian variable selection is typically used in

exploratory contexts. This was echoed in O'Hara and Sillanpää (2009):

> Whilst the use of variable selection can be criticised as being hypothesis testing in a fake beard and glasses, there are still occasions when it can be useful, in particular when the purpose of the analysis is exploratory (p. 113).

When the spike and slab is used for hypothesis testing, it is explicitly a means to compute the Bayes factor of interest. In other words, the hypotheses should not be suggested by the data, but rather a priori predictions.

Bayesian Model Averaging. An additional advantage of the proposed methodology is *automatic* Bayesian model averaging (BMA), which can be particularly beneficial for prediction. In the presence of model selection uncertainty (no clear winner), Bayesian model averaging (BMA) can be used (see for example Gronau, Van Erp, et al., 2017). This avoids the well-known pitfalls of selecting one model from a candidate set (Hinne, Gronau, Bergh, & Wagenmakers, 2019; Leeb & Pötscher, 2005). I do not explicitly pursue this here, because the posterior distributions, for example those in Figure 3, were composed of all visited models, and thus effectively weighted (i.e., the proportion of samples) by the model probabilities. I refer interested readers to Raftery, Madigan, and Hoeting (1997) and Hoeting, Madigan, Raftery, and Volinsky (1999) for a full discussion of BMA.

Illustrative Example

In this example, data from all three tasks, including the Flanker, Simon, and Stroop, are considered von Bastian et al. (2016). The question of interest is the correlation among the difference scores, with the idea being that they should be highly correlated with one another, assuming they are measuring the same thing. This is similar to Hedge, Powell, and Sumner (2018), where a frequenitst approach was used to test a similar hypothesis. As shown below, the proposed method opens the door for testing richer models. There are 121 subjects that each completed roughly 90 trials for congruent and incongruent conditions.

For each subject, condition, and task, I first computed the means and then the difference scores. This resulted in three inhibition effects per person (variable 1 = Flanker, variable 2 = Simon, variable 3 = Stroop).

Estimation and Software. The model fitting information is provided above (i.e., Section One-Sample T-test). For the beta prior, a uniform distribution was employed by setting $\kappa = 1$, whereas, for the normal prior, the scale was set to $\sigma = 0.50$. Both priors are visualized in Figure 3.

Results. Figure 3 includes the posterior distributions for both models. The colors again correspond to the respective mixture components. From visual inspection, it is clear that each correlation has some probability of being zero ($\gamma = 1$), positive ($\gamma = 2$), or negative ($\gamma = 3$). Although descriptive, this is quite surprising because we would expect the inhibition effects to be positively correlated.

Hypothesis Testing. In light of this expectation, a variety of (a priori) hypotheses can be tested. Recall that Hedge et al. (2018) conducted a frequentist test, that, by its nature, is a limited source of information. Indeed, the majority of tests were non-significant (see Table 3 in Hedge et al., 2018). But with Bayesian hypothesis testing, models of theoretical relevance can be directly compared, say,

$$\begin{aligned} \mathcal{H}_0 &: (\rho_{12}, \rho_{13}, \rho_{23}) = 0 \\ \mathcal{H}_1 &: (\rho_{12}, \rho_{13}, \rho_{23}) > 0, \end{aligned} \tag{19}$$

where $\mathcal{H}_0$ is null model that *all* of the relations are zero and $\mathcal{H}_1$ captures the expectation that all relations should be positively correlated. The Bayes factor, BF_{01}, then provides the relative evidence in favor of $\mathcal{H}_0$. If supported, this would suggest a null model better predicted the observed data. After computing the respective model probabilities, it was revealed that there was strong evidence in favor of $\mathcal{H}_0$ ($BF_{01}^{\mathcal{B}} \approx 300$ and $BF_{01}^{\mathcal{N}} = 64$). Of

note, the Bayes factor was larger for the beta prior, although both models reached the same conclusion. This is due to being more diffuse, given that it was a uniform between ± 1 (Figure 3). This is revisited in the discussion.

Model Probabilities. Although this work is specifically geared towards hypothesis testing, the HPM is readily available, if desired. Being mindful that these hypotheses were determined from the data, I compared the HPM to the top five ranking models. Here it was revealed that the evidence in favor of the HPM was not strong. For the beta prior, the HPM was that *all* associations were null, receiving a posterior probability of 0.30. However, the Bayes factor was "not worth more than a bare mention" compared to the second most probable model (p. 777 Kass & Raftery, 1995). The same picture emerged for the normal prior. This is a defining feature of Bayesian variable selection, in that it provides insights into model selection uncertainty. Further, rather ignore the inherent uncertainty and select a model, the approach provides Bayesian model averaged posteriors (i.e., Figure 3).

Model Averaged Estimates. Table C1 includes the summarized BMA and maximum likelihood (ML) estimates. Recall that the BMA posteriors are effectively weighted by the respective model probabilities, which corresponds to the proportion of the total samples drawn from each particular model. Accordingly, when the null hypothesis has non-negligible probability, there will be regularization (or shrinkage) towards zero. This can be seen for all relations, in that the posterior means are all smaller than the ML based estimates. It should be noted that there is some debate about the utility of making inference from model averaged parameters (see for example, Banner & Higgs, 2017; Cade, 2015), whereas model averaging for prediction is a widely accepted practice (Kaplan & Lee, 2018; Raftery, Gneiting, Balabdaoui, & Polakowski, 2005).

Discussion

In this work, I extended to spike and slab model to allow for prior distributions comprised of many mixture components. The illustrative examples demonstrated that the

proposed methodology provides a flexible approach for Bayesian hypothesis testing. Although the spike and slab model is not novel to psychological science, its utility was thought to be limited to exploratory variable selection and "big data applications" (p. 111, Rouder et al., 2018). To the contrary, as shown in the illustrative examples, many popular Bayes factors tests can be recast into a multinoulli spike and slab— the advantage being a general formulation. This novel contribution extends beyond psychology and to the broader scientific literature.

The illustrative examples were intentionally simple models. This decision was made to focus on the underlying idea and the connection to popular Bayesian hypothesis tests. Accordingly, this work barely scratched the surface of possibilities. The spike and slab can be fit with the popular Bayesian software, JAGS, so the presented ideas can be seamlessly applied to more complex models. This opens the door to Bayesian hypothesis testing without being hamstrung to particular models and overly restrictive assumptions. As but one example, in the spike and slab has been used test random intercepts for the within-person variance in a mixed-effects location-scale model (Williams, Martin, & Rast, 2019). My hope is that this work provides a foundation from which Bayes factor testing is no longer considered a bridge too far for certain models.

Sensitivity Analyses

This work omitted a very important aspect of Bayesian analysis in practical application, that is, sensitivity analyses to investigate the extent to which the prior affects the inference. In part, this decision was made because the foremost contribution is a novel approach for Bayesian hypothesis testing. In practice, the posterior inclusion probabilities and/or Bayes factors can be plotted against the scale of the slab component (see for example Figure 8 in Malsiner-Walli & Wagner, 2011)

Additionally, much is already known about prior sensitivity that applies directly to the spike and slab model (see discussion on p. 110 of Rouder et al., 2018). When testing a

precise hypothesis with certain equality constraints on the parameters of interest, it is well-known that the prior for the free parameters under the alternative should be carefully chosen based on the anticipated effect size (Bartlett, 1957; Jeffreys, 1961; Lindley, 1957). If the prior is unrealistically vague, it places too much probability mass at unrealistic values of the parameters, resulting in an overestimation of the evidence for the null when observing moderately sized effects. On the other hand, if the prior is too informative by placing too much probability mass near the origin, it becomes difficult to distinguish between the null and the alternative hypothesis when quantifying the relative evidence in the data between the hypotheses. This general idea can be seen in Table 1, where the Beta prior (set to uniform) indicated that null model had the largest posterior probability. This was not so for the normal, more informative prior, where the null model was not in the top five. It was also the case, however, that both priors arrived at *mostly* the same models and there was not strong evidence for any of them. Hence, the conclusion reached was largely the same.

Extensions

The multinoulli spike and slab can be applied to basically all models and parameters of interest. The limiting factor is programming ability in JAGS (or BUGS), which is the go to software for fitting spike and slab models. (see code in Ntzoufras, 2002; O'Hara & Sillanpää, 2009; Perrakis & Ntzoufras, 2018). Although I focused on three, there is no limit to the number of mixture components. In the correlation example, several interval hypotheses could have been compared, say, to determine whether the data is more likely under a model that predicts a null, small, medium, or large in effect size. The slab component can also have different mode than the spike, analogously to the non-local alternative priors of Johnson and Rossell (2010, p. 164 therein), that "can increase the evidence that is reported in favour of both true null and true alternative hypotheses." This may have resulted in more decisive evidence reported in the illustrative examples (e.g., Table 1). Extending the multinoulli spike and slab model to non-local alternatives or even

informative prior distributions more generally is an interesting future direction.

Moreover, as a bonus, the idea of defining a prior that is a mixture of several distribution leads to a novel approach for exploratory variable selection in regression models. Whereas the customary spike and slab is essentially a two-sided test (see Figure 2), utilizing multinoulli indicators permits one-sided and/or interval variable selection. This is similar in spirit to the recent approach of Gu, Hoijtink, and Mulder (2020), where the encompassing approach with the g-prior for one-sided variable selection was employed for linear regression. The multinoulli spike and slab is more flexible in that a variety of prior distributions can be used and it can be applied to a variety of models (e.g., logistic regression). This points towards my future work.

Limitations

Despite the spike and slab having great potential for hypothesis testing, there is an important caveat to consider. As a result of moving away from the elegance of analytic solutions, that is, brute force must be relied upon. By this I am referring to MCMC sampling, of which many samples are needed to adequately compute the model probabilities. This can quickly become cumbersome in larger models, with patience providing the only solution. Further, with many parameters subject to selection, there is no guarantee that all models will be explored. Consider the correlation example. With three components each, the number of possible models is 3^3. This model space is not prohibitive. Indeed, all 27 models were visited. But, in general, it might not be possible to compute the Bayes factor of interest when increasing the number of components and/or parameters. If the model of interest was not visited, this would imply that it is not all that probable, although not providing the Bayes factor. In my experience, however, hypotheses are typically focused on one or perhaps a few parameters at most, even in relatively complex models (e.g., Williams, Rouder, & Rast, 2019). These situations are ideal for the proposed testing strategy.

Alternative Spike and Slab Formulations

The point mass at zero (Dirac) spike approach is omnipresent in the psychological literature (Rouder et al., 2018). Yet, there are a variety of ways to parameterize a spike and slab model, over and above what was described in this work. Most of these approaches focus on how the posterior is affected when visiting different models (O'Hara & Sillanpää, 2009). To my knowledge, there are two exceptions. The first was introduced in Ishwaran and Rao (2005), where "a normal mixtures of inverse gamma distributions" was used for regression coefficients. The resulting marginal prior for the spike and slab then has a Student $t-$distribution (p. 224, Malsiner-Walli & Wagner, 2011), with selection carried out on the hyperparameter variance of the prior distribution. Further, there also exists a "random effects" model, described in O'Hara and Sillanpää (2009), that treats the slab component variance as a parameter to be estimated from the data. This approach "considers the regression coefficients to be exchangeable and be drawn from a common distribution" (p. 89, O'Hara & Sillanpää, 2009) and is meant to facilitate self-tuning. Although a full discussion is beyond the scope of this work, it is clear that there is a largely unexplored literature. I refer interested readers to extensive reviews in O'Hara and Sillanpää (2009) and Malsiner-Walli and Wagner (2011).

Conclusion

The purpose of this paper was to present the multinoulli spike and slab as a flexible approach for hypothesis testing in psychological applications. The proposed model is suited for t-test and correlations, as presented in this work, but it can also be used more generally. By framing hypotheses as many mixture components, this approach opens up possibilities for testing a variety of hypotheses within the spike and slab framework.

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Table 1

Top five most probable models

	Beta Prior ($\kappa = 1$)					Normal Prior ($\sigma = 0.5$)			
Model	BF_{1i}	r_{12}	r_{13}	r_{23}	Model	BF_{1i}	r_{12}	r_{13}	r_{23}
$\mathcal{M}_1^{\text{HPM}}$	-	$\gamma = 1$	$\gamma = 1$	$\gamma = 1$	$\mathcal{M}_1^{\text{HPM}}$	-	$\gamma = 1$	$\gamma = 3$	$\gamma = 1$
$\mathcal{M}_2$	1.27	$\gamma = 1$	$\gamma = 3$	$\gamma = 1$	$\mathcal{M}_2$	1.19	$\gamma = 2$	$\gamma = 3$	$\gamma = 1$
$\mathcal{M}_3$	3.24	$\gamma = 2$	$\gamma = 1$	$\gamma = 1$	$\mathcal{M}_3$	1.80	$\gamma = 2$	$\gamma = 3$	$\gamma = 1$
$\mathcal{M}_4$	3.54	$\gamma = 2$	$\gamma = 3$	$\gamma = 1$	$\mathcal{M}_4$	2.45	$\gamma = 2$	$\gamma = 1$	$\gamma = 1$
$\mathcal{M}_5$	5.31	$\gamma = 1$	$\gamma = 1$	$\gamma = 2$	$\mathcal{M}_5$	3.00	$\gamma = 1$	$\gamma = 3$	$\gamma = 2$

Note. $\mathcal{M}_1^{\text{HPM}}$ is the highest probability model. The posterior odds, for $\mathcal{M}_i$, $i = 2, 3, 4, 5$, was computed as the ratio of model probabilities $p(\mathcal{M}_1|y)/p(\mathcal{M}_i|y)$. This corresponds to the Bayes factor BF_{1i}, because each model had equal prior probabilities. $k = 1, 2, 3$ correspond to the null, positive, and negative mixture components. r_{12}: correlation between Flanker and Simon effects. r_{13}: correlation between Flanker and Stroop effects. r_{23}: correlation between Simon and Stroop effects.

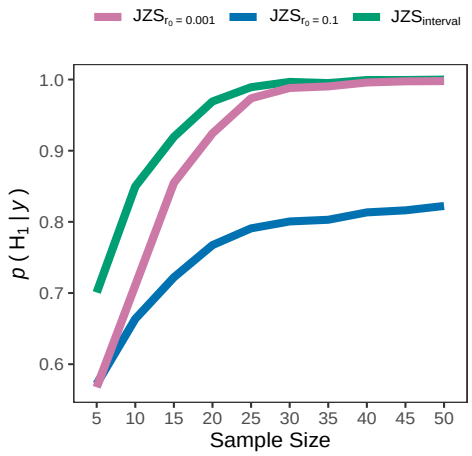

Figure 1. Bayes factor consistency for (slightly) overlapping hypotheses, where $p(\mathcal{H}_1|y)$ should approach 1, given that the true effect size was set to $\delta = 1$. r_0 corresponds to the scale of the null hypothesis. Note that $r_0 = 0.1$ was used in Morey and Rouder (2011) to demonstrate overlapping hypotheses can compromise the Bayes factor. On the other hand, the Bayes factor computed with the approximate spike ($r_0 = 0.001$) and interval formulation had the expected behavior.

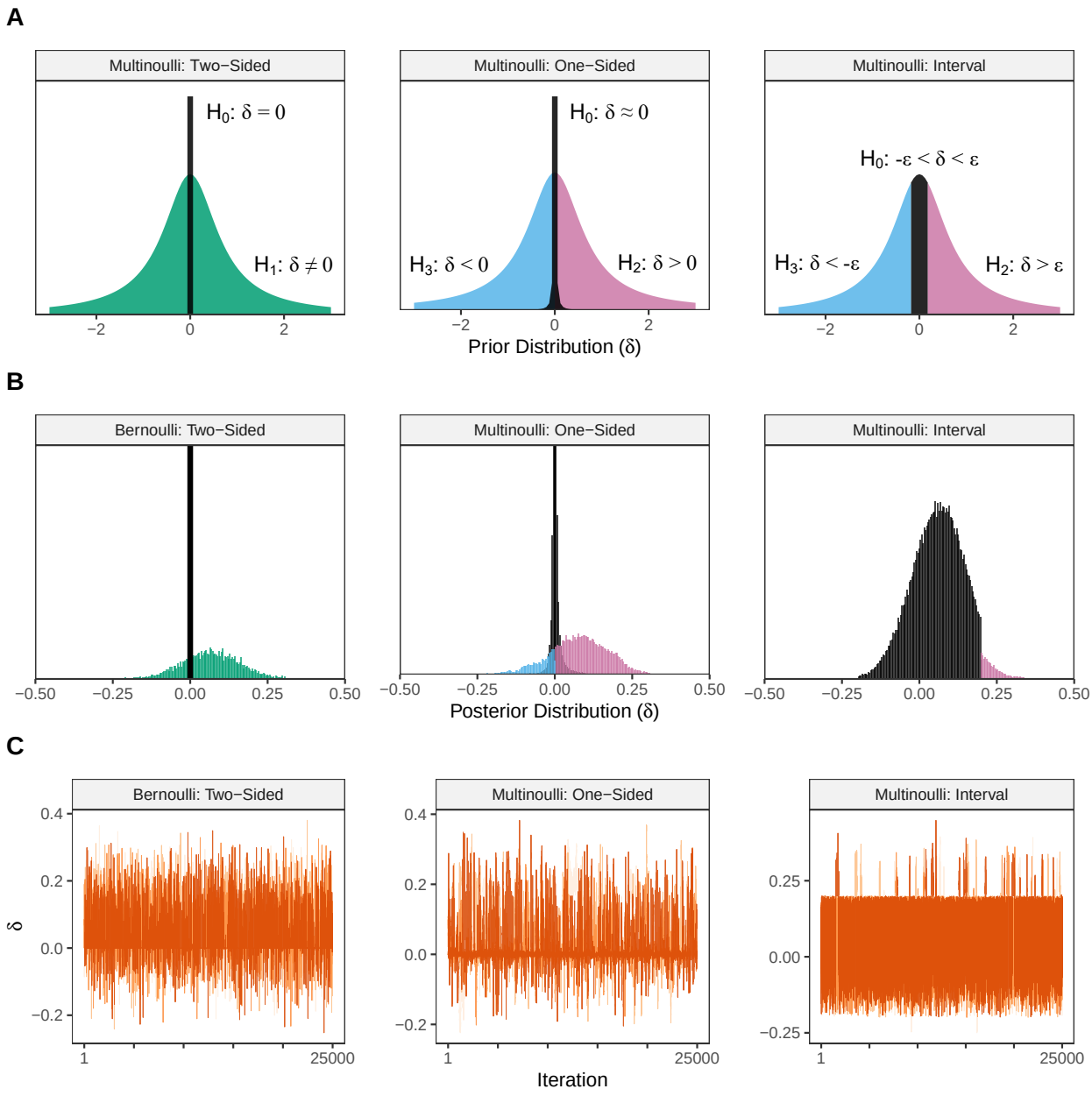

Figure 2. A) The mixture prior distribution for the customary spike and slab that uses Bernoulli indicator variable and the proposed method that uses a multinoulli indicator variable. This is reflected in the color scheme that corresponds to a component of the mixture prior distribution (i.e., the competing hypotheses or models). B) Bayesian model averaged posterior distributions. The colors correspond to the posterior samples that were drawn from each model. C) Trace plots demonstrating adequate mixing of the MCMC chains for each model.

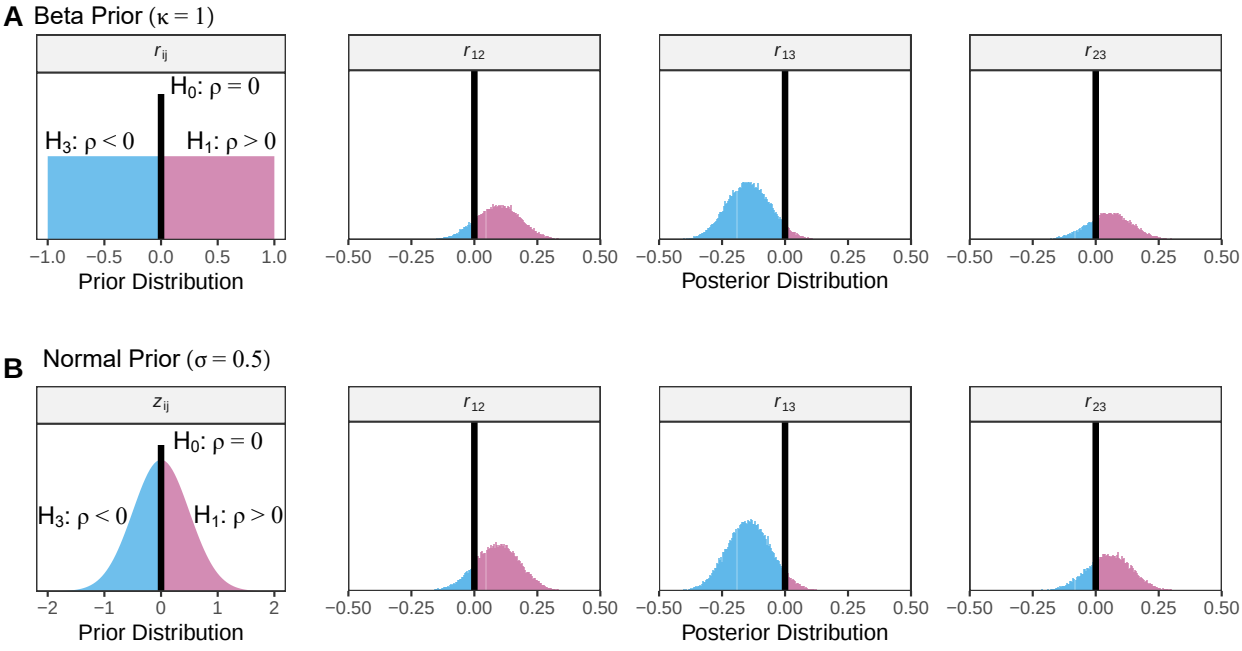

Figure 3. A) The covariance selection model with a beta prior distribution for the correlations (Equation 17). B) The covariance selection model with a normal prior distribution for the Fisher$-z$ transformed correlations (Equation 18). In each panel, the color scheme corresponds to a component of the mixture prior and posterior distributions. r_{12}: correlation between Flanker and Simon effects. r_{13}: correlation between Flanker and Stroop effects. r_{23}: correlation between Simon and Stroop effects.

Appendix A

One Sample T-test

JZS Spike and Slab

```
jzs_ss <- "model{

# likelihood
for(i in 1:n){
  y[i] ~ dnorm(mu, prec)
}

# precision (i.e., 1/sigma^2)
prec ~ dgamma(0.0001, 0.0001)

# indicator
# pi: prior model probs
gamma ~ dbern(pi)
pi <- 0.50

# effect size
# r: Cauchy scale
delta ~ dt(0, r, 1)
r <- pow(1/sqrt(2), -2)
delta_new <- delta * gamma

# mean
mu <- delta_new * 1/sqrt(prec)
}"
```

Multinoulli: One-Sided

```
multi_onesided <- "model{

# likelihood
for(i in 1:n){
y[i] ~ dnorm(mu, prec)
}

# precision (i.e., 1/sigma^2)
prec ~ dgamma(0.0001, 0.0001)

# indicator
# pi: prior model probs
gamma ~ dcat(pi[])
pi[1] <- 1
pi[2] <- 1
pi[3] <- 1

# effect size
# r_slab: 1 / sqrt(2); r_spike: 0.001
delta ~ dt(0, r[gamma], 1)T(lb[gamma], ub[gamma])
r[1] <- pow(.001, -2)
r[2] <- pow(1/sqrt(2), -2)
r[3] <- pow(1/sqrt(2), -2)

# mean
mu <- delta * 1/sqrt(prec)

# truncation points
lb[1] <- -1e10
ub[1] <- 1e10

# positive effects
lb[2] <- 0
ub[2] <- 1e10

# negative effects
lb[3] <- -1e10
ub[3] <- 0
}"
```

Multinoulli: Interval

```
multi_interval <- "model{

# likelihood
for(i in 1:n){
y[i] ~ dnorm(mu, prec)
}

# precision (i.e., 1/sigma^2)
prec ~ dgamma(0.0001, 0.0001)

# indicator
# pi: prior model probs
gamma ~ dcat(pi[])
pi[1] <- 1
pi[2] <- 1
pi[3] <- 1

# effect size
# r: 1 / sqrt(2)
delta ~ dt(0, r[gamma], 1)T(lb[gamma], ub[gamma])
r[1] <- pow(1/sqrt(2), -2)
r[2] <- pow(1/sqrt(2), -2)
r[3] <- pow(1/sqrt(2), -2)

# mean
mu <- delta * 1/sqrt(prec)

# truncation points
lb[1] <- -0.20
ub[1] <- 0.20

# positive effects
lb[2] <- 0.199
ub[2] <- 1e10

# negative effects
lb[3] <- -1e10
ub[3] <- -0.199
}"
```

Appendix B

Correlations

Multinoulli: Covariance Selection

```
cov_select <- "model{

# likelihoood
for(i in 1:n){
    y[i, 1:3] ~ dmnorm.vcov(mu[], Sigma[1:3,1:3])
}

# zero means
mu[1] <- 0
mu[2] <- 0
mu[3] <- 0

# covariance matrix
Sigma[1:3,1:3] <- Tau %*% Omega %*% Tau

# diag(tau)
Tau[1,1] ~ dt(0, pow(1,-2), 10)T(0,)
Tau[2,2] ~ dt(0, pow(1,-2), 10)T(0,)
Tau[3,3] ~ dt(0, pow(1,-2), 10)T(0,)

Tau[1,2] <- 0; Tau[2,1] <- 0; Tau[2,3] <- 0
Tau[3,2] <- 0; Tau[1,3] <- 0; Tau[3,1] <- 0

# correlation matrix
Omega[1,1] <- 1
Omega[2,2] <- 1
Omega[3,3] <- 1

Omega[1,2] <- rho[1]
Omega[2,1] <- Omega[1,2]

Omega[1,3] <- rho[2]
Omega[3,1] <- Omega[1,3]

Omega[2,3] <- rho[3]
Omega[3,2] <- Omega[2,3]
```

```
for(i in 1:3){
# indicator
lambda[i] ~ dcat(pi[])

# fisher-z scale
# sigma: 0.5
fz[i] ~ dnorm(0, pow(0.5, -2))T(lb[lambda[i]], ub[lambda[i]])

# transform to r
rho[i] <- ifelse(lambda[i] == 1, 0, tanh(fz[i]))
}

# pi: prior model probs
pi[1] <- 1
pi[2] <- 1
pi[3] <- 1

# truncation points
lb[1] <- -1e10
ub[1] <- 1e10

# positive effects
lb[2] <- 0
ub[2] <- 1e10

# negative effects
lb[3] <- -1e10
ub[3] <- 0
}"
```

Appendix C

Model Averaged Estimates

Table C1

Bayesian model averaged and maximum likelihood estimates

Model	Parameter	BF_{10}	M	SD	95% CI
BMA$^{\mathcal{B}}$	r_{12}	0.33	0.04	0.06	$[-0.03, 0.21]$
BMA$^{\mathcal{N}}$	r_{12}	0.52	0.03	0.07	$[-0.04, 0.23]$
MLE	r_{12}	–	0.09	0.11	$[-0.14, 0.31]$
BMA$^{\mathcal{B}}$	r_{13}	0.04	−0.07	0.09	$[-0.28, 0.00]$
BMA$^{\mathcal{N}}$	r_{13}	0.08	−0.08	0.10	$[-0.29, 0.01]$
MLE	r_{13}	–	−0.14	0.09	$[-0.31, 0.04]$
BMA$^{\mathcal{B}}$	r_{23}	0.20	0.01	0.05	$[-0.06, 0.16]$
BMA$^{\mathcal{N}}$	r_{23}	0.31	0.02	0.05	$[-0.07, 0.17]$
MLE	r_{23}	–	0.06	0.11	$[-0.18, 0.27]$

Note. $\mathcal{B}$ and $\mathcal{N}$ denote the beta and normal prior distributions. BF_{10}: marginal Bayes factor comparing the positive effects ($\mathcal{H}_1$) versus the null model ($\mathcal{H}_0$). r_{12}: correlation between Flanker and Simon effects. M: posterior and bootstrapped mean. SD: posterior and bootstrapped standard deviation, respectively. r_{13}: correlation between Flanker and Stroop effects. r_{23}: correlation between Simon and Stroop effects.