

Hypothesis Testing Using Bayes Factor in Behavioral Sciences

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Abstract

Recent times have seen a surge of Bayesian inference across the behavioral sciences. However, the process of testing hypotheses is often conceptually challenging or computationally costly. This tutorial provides an accessible, non-technical introduction that covers the most common scenarios in experimental sciences: Testing the evidence for an alternative hypothesis using Bayes Factor through the Savage Dickey approximation. This method is conceptually easy to understand and computationally cheap.

Keywords: statistics, Bayes, Bayes Factor, Savage Dickey, hypothesis testing, ROPE

1 Introduction

One of the most common scenarios in experimental research is to measure one or several (dependent) variable in an experiment which with one or more predictors (independent variables). Usually, we then want to test statistically whether the predictors affect the measured dependent variables. Traditionally, these statistical tests have been done within the *null hypothesis significance testing* (NHST) framework. The logic of NHST is to reason as follows: we assume—for the sake of argument—that a null hypothesis is correct, i.e., that there is no effect of the relevant predictors; then we ask our selves how likely different observations would be based on that assumption, and use this so-called *sampling distribution* to quantify how surprising the observed data is under the assumed null hypothesis. If this the observed data is very unlikely, i.e., very surprising, we *reject* the null hypothesis and conclude that there is an effect of the predictors on the dependent variable. While extensions of the NHST framework exist, in its basic form, NHST only allows to reject the null hypothesis, but not to provide evidence in favor of it.

Over the last decade or so, however, there has been rising interest in statistical approaches within an alternative inferential framework using *Bayesian inference*. One of the main reasons for this rising interest is that Bayesian inference allows to quantify evidence against an assumed null hypothesis, but also to yield quantitative evidence in favor the null hypothesis. Unfortunately, there are several approaches to hypothesis testing within the Bayesian framework, and many of them are either conceptually challenging, computationally too costly, or both. For example, there are good conceptual arguments that support Bayesian hypothesis testing through *model comparison* using Bayes factors (Kass & Raftery, 1995; Morey et al., 2016; Vandekerckhove et al., 2015), but the computation of Bayes factors can be quite costly, especially for complex models.

Yet, for some of the most common use cases, there are some simple and computationally cheap approaches to Bayesian hypothesis testing with Bayes factors that are easy to understand and implement. One such method is the *Savage-Dickey density ratio* (Dickey & Lientz, 1970; Wagenmakers et al., 2010). While prior work has prominently documented how to use this method for the case of point-valued null-hypotheses (Wagenmakers et al., 2010), this method can be hard to estimate reliably with posterior sampling, the most prevalent method for approximate Bayesian computation at the moment. This tutorial therefore focuses on the use of the Savage-Dickey density ratio for testing hypotheses that are grounded in *regions of practical equivalence* (ROPEs) (Kruschke, 2018) using the so-called *encompassing priors* approach (Klugkist et al., 2005; Klugkist & Hoijtink, 2007; Oh, 2014; Wetzels et al., 2010), which is both conceptually more meaningful and computationally more robust than point-valued hypothesis testing. In sum, this tutorial provides an accessible, non-technical introduction to Bayesian hypothesis testing that is easy to understand, computationally cheap and widely applicable (though not universally).

2 Motivation and intended audience

This tutorial provides a very basic introduction to hypothesis testing with Bayes factors using R (R Core Team, 2025). We wrote this tutorial with a particular reader in mind. If you have used R before and if you have a basic understanding of linear regression, and Bayesian inference, this tutorial is for you. We will remain mostly conceptual to provide you with an accessible tool to approach hypothesis testing within Bayesian inference. The form of hypothesis testing that we would like to introduce to you is, however, different from the traditional null hypothesis significance testing in that it requires more thinking about the quantitative nature of your data. This is not a bug but, at least for us, a feature that will allow you to understand both your data and what you can learn from them better.

If you don't have any experience with regression modeling, you will probably still be able to follow, but you might also want to consider doing a crash course. To bring you up to speed, we recommend the excellent tutorial by Bodo Winter (2013) on mixed effects regression in a non-Bayesian —a.k.a. frequentist— paradigm. To then make the transition to Bayesian versions of these regression models, we shamelessly suggest our own tutorial on “Bayesian Regression for Factorial Designs” as a natural follow-up using the same data that Winter used (Franke & Roettger, 2019). In a sense, the present tutorial on hypothesis testing could be considered the long-awaited sequel of the series started by Winter. For continuity, we will continue to use the original data set.

To actively follow this tutorial, you should have R installed on your computer (<https://www.r-project.org>). Unless you already have a favorite editor for tinkering with R scripts, we recommend to try out RStudio (<https://www.rstudio.com>). You will also need some packages, which you can import with the following code:

```
# package for convenience functions (e.g. plotting)
library(tidyverse)
library(ggdist)

# package for Bayesian regression modeling
library(brms)

# package for posterior wrangling and plotting
library(tidybayes)

# package for BF calculation and plotting
library(bayestestR)
```

```
options(brms.backend = "cmdstanr")
options(mc.cores = parallel::detectCores())
```

3 Data, research questions & hypotheses

In this section, we introduce the data set that we will use throughout this tutorial, the research question that we want to address, and how to formulate hypotheses in a way that allows us to test them with Bayes factors using ROPEs.

3.1 The data set: voice pitch in Korean across social contexts

This tutorial looks at a data set relevant for investigating whether voice pitch differs across social contexts in Korean. Korean is a language in which the social distance between speakers plays a central role. The way Korean speakers speak depends for example on whether they are in a formal context (e.g. during a job interview) or an informal context (e.g. chatting with a friend about the holidays) ([Winter & Grawunder, 2012](#)). To load and inspect the data into your R environment, run the following code:

```
# TO DO: STORE ONLINE
# TO DO: SIMPLIFY STORED DATA
polite = read_csv("../data/polite.csv") |>
  # remove men
  filter(gender == "F") |>
  # transform context to factor
  mutate(context = as.factor(context))

polite
```

```
# A tibble: 126 x 4
  subject gender context  pitch
  <chr>    <chr>  <fct>    <dbl>
1 F1      F      formal    215.
2 F1      F      informal  211.
3 F1      F      formal    285.
4 F1      F      informal  266.
5 F1      F      formal    211.
6 F1      F      informal  286.
7 F1      F      formal    252.
8 F1      F      informal  282.
9 F1      F      formal    230.
10 F1     F      informal  250.
# i 116 more rows
```

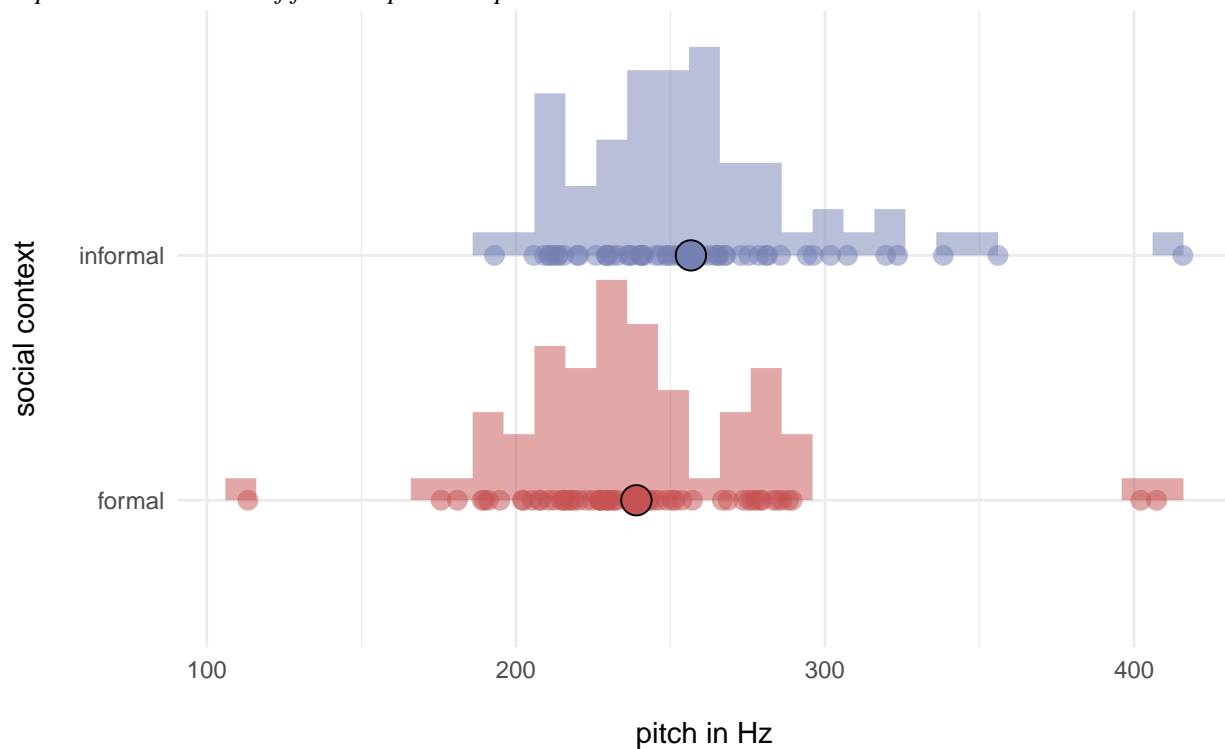
This data set contains anonymous identifiers for individual speakers stored in the variable `subject`. In this tutorial we will only be looking at the data from female speakers. Subjects produced different sentences, and the experiment manipulated whether the sentences were produced in a formal or an informal social context, indicated by the variable `context`. Crucially, each row contains a measurement of pitch in Hz stored in the variable `pitch`.

For most analyses of behavioral experiments, researchers are interested in whether an outcome variable is meaningfully affected by at least one manipulated variable and if so how the outcome variable is affected by it. In this case, Winter and Grawunder (2012) wanted to test whether pitch is meaningfully affected by the social context of the utterance.

As a first step, we can explore this question visually. Figure 1 displays the pitch values for all utterances in the dataset across contexts (semi-transparent points). The solid points indicate the average pitch values across all sentences and speakers. Looking at the plot, we can see that voice pitch from utterances in formal contexts are on average slightly lower than those in informal contexts. The red distribution is slightly shifted to the left of the blue distribution by around 1.3 semitones. In other words, speakers tend to slightly lower their voice pitch when speaking in a formal context. But there is also a lot of overlap between the two contexts. Now as Bayesians, we would like to translate the data into an expression of evidence: does the data provide evidence for our research hypotheses?

Figure 1

Empirical distribution of female speakers' pitch values across contexts



3.2 A Bayesian regression model to address our research question

Let us build a Bayesian linear model to approach an answer to this question. Using the package `brms` (Bürkner, 2018), our first step is to specify the model formula and check which priors need to be specified:

```
# contrast code predictor
contrasts(polite$context) <- c(-0.5,0.5)

# define linear model formula
```

```
# predict pitch by context and allow for that relationship
# to vary between subjects
formula <- bf(pitch ~ context + (1 + context | subject))

# get priors for this model
get_prior(formula, polite)[c(2,5,10,8,9,4),1:4]
```

	prior	class	coef	group	source
	(flat)	b	context1		(unknown)
student_t(3, 241.5, 35.6)		Intercept			(unknown)
student_t(3, 0, 35.6)		sigma			(unknown)
	(flat)	sd	context1	subject	(unknown)
	(flat)	sd	Intercept	subject	(unknown)
	(flat)	cor		subject	(unknown)

```
# NOTE: make the above prettier? (how to suppress the `source` column?)
```

The default priors that brms picks for the Intercept and the variance parameters are mostly reasonable as they are derived from the data, weakly informative and symmetrical. However the prior for our critical parameter context1 should also be weakly informative ([Gelman et al., 2017](#)), i.e. the prior assumption about the difference between informal and formal contexts should be that we don't know, but our best guess is that it is close to zero and equally likely to be more or less than zero. So we specify a normal distribution centered on zero for this parameter. (NB: We use default priors for the other parameters for convenience here, but you should always critically reflect on all of your priors.)

```
# pick a weakly informative prior for the critical parameter
priors <- prior(normal(0, 20),
               class = b,
               coef = "context1")
```

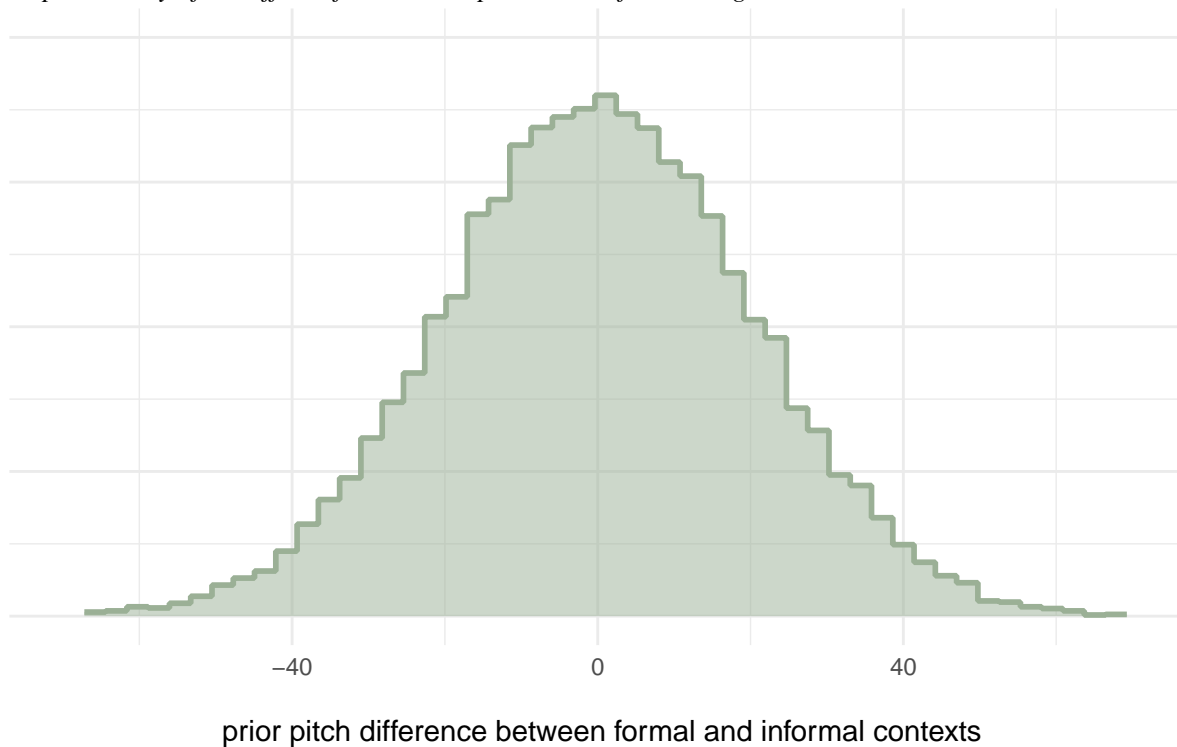
Now we do a so-called prior predictive check, in other words we want to know what the posterior distribution looks like before having seen the data, based on the priors only. This is a useful exercise to make sure that the priors results in reasonable quantitative assumptions. We usually do it for all parameters, but here we will focus only on the critical parameter context1, i.e. the difference between formal and informal contexts. Let us also have a look at the predictions for the prior-only model.

```
# NOTE: CAN WE STORE THE SAMPLING PARAMETERS (seed, iter, chains, cores, backend, data)
# NOTE: Done for 'cores' and 'backend', but for the rest we'd have to define a custom
#       brms-function but that's likely less reader friendly.
```

```
# run the model
fit_prior <- brm(formula, prior = priors, data = polite,
                 # sample prior only
                 sample_prior = "only",
                 # store / load model output
                 file = "../models/fit_prior",
                 # common sampling specifications)
```

Figure 2

Prior probability of the effect of context on pitch, i.e. before seeing the data



```
seed = 1234, iter = 8000
)
```

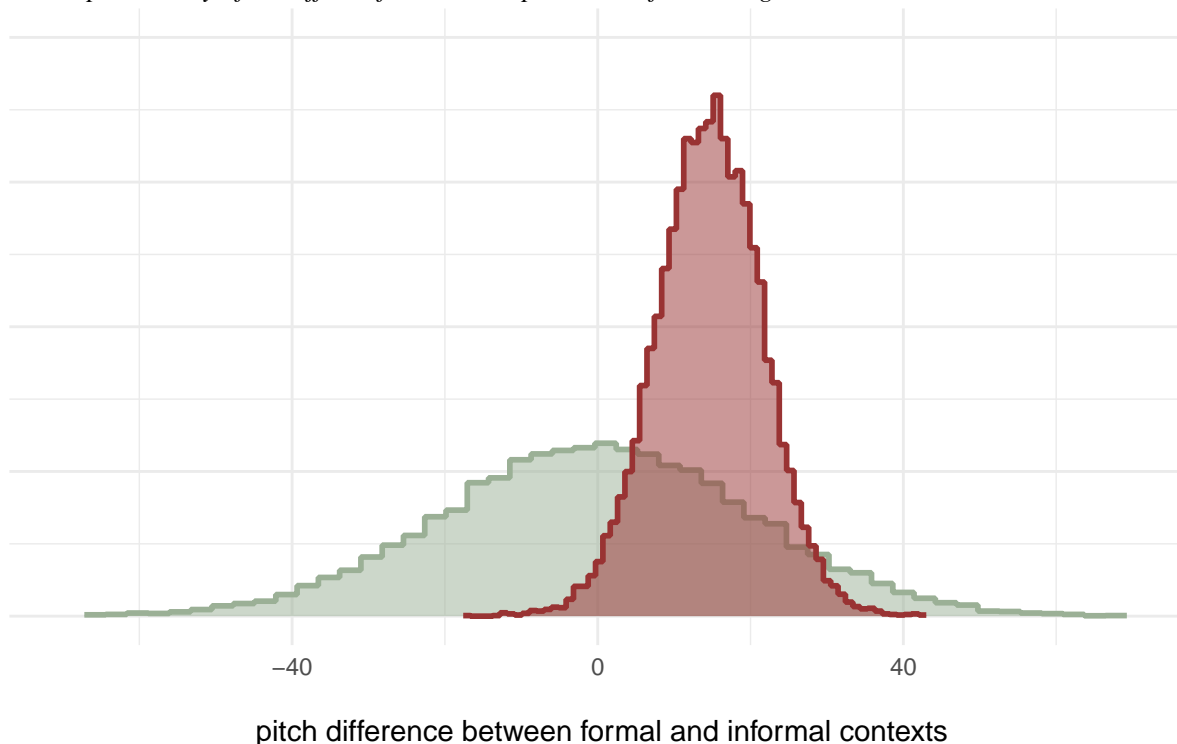
Looking at the distribution in Figure 2, the priors for the effect of context on pitch seems sensible. The most plausible value is zero. Values that are smaller or larger than zero become less plausible the further they are away from zero and values being smaller or larger than zero are equally likely. Good. Before we have seen the data, our model is somewhat pessimistic about the effect of context on on pitch. Now we can run the full model that integrates the likelihood (our data) with the priors and visualize the posteriors for the critical parameter.

```
# run the model
fit <- brm(formula, prior = priors, data = polite,
  # store / load model output
  file = "../models/fit",
  # common sampling specifications
  seed = 1234, iter = 8000
)
```

Figure 3 shows the prior (green distribution) and posterior (red distribution) probability of the effect of context on pitch. The distribution of posterior samples (red) suggests that the majority of plausible values after seeing the data are positive, or in other words, informal contexts elicit larger pitch values. Negative values are not very plausible posterior values, but also not completely implausible. Compared to our prior probability (green distribution) for which roughly 50% of posteriors are negative, this decrease in plausibility of negative values is quite noteworthy already.

Figure 3

Posterior probability of the effect of context on pitch, i.e. after seeing the data



What we have done here should be quite familiar. We compare our model predictions to a reference point. It is a single point value: zero. But do we really care that much for such point hypotheses? Is zero really that special? We might think so because years of using null hypothesis significance testing has conditioned us to think that way. But this tutorial would like to break this cycle and move forward. Bear with us and let's approach hypothesis testing a bit differently today.

3.3 Grounding hypotheses in regions of practical equivalences

Above we claimed that we wanted to test “whether pitch is **meaningfully affected** by the social context of the utterance”. We snuck the word **meaningfully** in there for a reason. But what does “meaningful” mean? This is an interesting yet deep questions and (un)fortunately requires quite a bit of thinking. As we argue here, what a meaningful difference is, depends on the context of the data. So let's have a closer look at our data.

This tutorial deals with speech data. Speech is, in spoken languages at least, *the* vehicle to transmit linguistic information in order to communicate with each other. Speech is also very complex and very noisy: Not everything that can be measured in the acoustic signal matters for the listener. For example, if something cannot be perceived reliably, it is at least conceivable that it might play little to no role in communication. While the speech sciences have a rich research tradition to estimate what can and what cannot be reliably heard, exact estimation depends on a lot of moving parts. Such thresholds are referred to as *Just Noticeable Differences* (JNDs) and can be used to define what constitutes meaningful differences when we look at speech data.

For example, Liu (2013) report on JNDs ranging from 3 to 14 Hz. Jongman et al. (2017) report on JNDs between 6 and 9 Hz. Turner et al. (2019) reported on JNDs between 17 and 25 Hz for non-speech

stimuli and between 35 and 40 Hz for speech stimuli. While these studies are hard to compare, they give us at least an idea about the rough order of magnitude for JND values to work with when it comes to speech data like the data set at hand.

Based on these considerations, we could interpret the original hypothesis the following way: If a pitch difference is below the JND, it is not meaningful. So, instead of testing against a point-valued hypothesis, we can test against a range of parameter values that are equivalent to the null value for practical purposes. In our case, let us begin with the lowest reported JND of the above studies on pitch perception in speech (3 Hz), but be extra conservative and double the reported JND to 6 Hz. We then assume that pitch values between -6 and 6 are meaningless. Such ranges are sometimes called *regions of practical equivalence* (ROPEs), range of equivalence, equivalence margin, smallest effect size of interest, or good-enough belt (see [Kruschke, 2018](#)).

```
rope <- c(-6,6)
```

With a ROPE being defined, we can now test our hypothesis “whether pitch is **meaningfully affected** by the social context of the utterance” using Bayes Factors.

4 Testing hypotheses using Bayes Factor

4.1 What is Bayes Factor?

Suppose we have two hypotheses H_0 and H_1 and want to know which of these is correct. We do so by looking at some observed data D . As Bayesians, the first most obvious thing to look at is how likely each hypothesis is after seeing the data, i.e., something like $P(H_0 | D)$ and $P(H_1 | D)$. Now, it turns out that these *posterior probabilities of hypotheses* are problematic, because they depend on the prior probabilities of the hypotheses $P(H_0)$ and $P(H_1)$, which are often hard to justify. To see this, imagine that the hypotheses on the table are deep issues like a contrast between Darwinian evolutionary theory and intelligent design. Proponents of either view would have a hard time agreeing on priors for these hypotheses, but may find it much easier to agree on whether a given observation D is more likely under the assumption that one of the two hypotheses is correct, rather than the other. Therefore, Bayes factors are defined as the *likelihood ratio* of the data given each hypothesis:

$$\text{Bayes factor in favor of hypothesis 1 over hypothesis 2} : = \frac{P(D | H_1)}{P(D | H_0)}$$

To see how this is an objective and actually quite intuitive measure of observational evidence in scientific reasoning, consider the case of Darwinian evolution (H_1) versus intelligent design H_0 again. Let's take the historical case where the observed data D is that the beak sizes of finches on the Galápagos islands changed over time as a functional adaptation to environmental changes. What is a better explanation of that observation? To begin with, let's notice that this observation is *not* ruled out by either hypothesis. But the probability of observing D (adaptively changing beak sizes) is much higher under Darwinian evolution (H_1) than under intelligent design (H_0). This is because the latter is compatible with many more counterfactual observations, such as beak sizes staying the same over time, or even beak sizes changing in a way that is not adaptive. So, the probability of the observed data is much higher under Darwinian evolution than under intelligent design, so that $P(D | H_1) > P(D | H_0)$, irrespective of what we initially believed is the correct hypothesis. This is what corroborates the intuition that the observation D is an argument in favor of H_1 over H_0 , and this is exactly what the Bayes factor quantifies.

Concretely, a Bayes factor of 1 corresponds to the case of $P(D | H_1) = P(D | H_0)$, i.e., the data is equally likely under both hypotheses, so the data does not provide any evidence for or against either hypothesis. Any Bayes factor larger than 1 indicates that the data is more likely under H_1 than under H_0 , and the larger the Bayes factor, the stronger the evidence in favor of H_1 . Conversely, any Bayes factor smaller than

1 indicates that the data is more likely under H_0 than under H_1 . Notice that the Bayes factor is symmetric in the sense that a Bayes factor of 3 in favor of H_1 over H_0 corresponds to a Bayes factor of 1/3 in favor of H_0 over H_1 . There are various conventions for interpreting the strength of evidence of Bayes factors, such as to consider as “*mild evidence*” Bayes factors bigger than 3, “*strong evidence*” Bayes factors bigger than 10, and “*decisive evidence*” Bayes factors bigger than 30.

One way to interpret Bayes factors in absolute terms is this. A Bayes factor of n in favor of H_1 over H_0 means that after seeing the data, a rational researcher who thought both hypotheses were equally likely would consider H_1 to be n times more likely than H_0 after observing D . In other words, if you are maximally uncertain before, and if you then observe D and that makes you weight H_1 n times more than H_0 , then the Bayes factor is n .

4.2 Bayes factors for statistical models

After motivating Bayes factors in general, let’s have a look at the definition of Bayes factors in the context of statistical models in this section. What follows in this section is a bit more technical but can be skipped without substantial loss.

In the context of statistical models, we can use Bayes factors to compare two statistical models M_0 and M_1 that instantiate two competing hypotheses (or assumptions) H_0 and H_1 . A Bayesian statistical model M consists of:

1. a *likelihood function* $P(D | \theta, M)$ that specifies how likely the observed data D is given the model M and the model’s parameters θ , and
2. a *prior distribution* $P(\theta | M)$ that specifies how likely different parameter values are before seeing the data.

The probability of some observed data $P(D | M)$ under a model M is then obtained by integrating over all possible parameter values θ :

$$P(D | M) = \int P(D | \theta, M) P(\theta | M) d\theta$$

This is called the *marginal likelihood* of the data under the model M . We can think of this quantity as obtained from sampling repeatedly parameter values from the prior and then sampling, for of these, a potential data observation. (Notice that this is the *prior predictive data distribution* of the model.)

Putting things together, the resulting definition for Bayes factors in statistical models is:

$$\text{Bayes factor in favor of model 1 over model 2} := \frac{P(D | M_1)}{P(D | M_0)} = \frac{\int P(D | \theta, M_1) P(\theta | M_1) d\theta}{\int P(D | \theta, M_0) P(\theta | M_0) d\theta}$$

4.3 Approximating Bayes Factor with the Savage-Dickey method (for point-valued hypotheses)

While Bayes factors are a very intuitive and useful measure of evidence, they are often hard to compute. There are various approximation methods, such as bridge sampling (Gronau et al., 2017), which can be used for any arbitrary pair of models, but these can still be computationally costly and sometimes hard to implement. However, for the special case of *nested models*, there is a simple and computationally cheap approximation method called the *Savage-Dickey density ratio* (Dickey & Lientz, 1970; Wagenmakers et al., 2010).

Intuitively speaking, model M_0 is nested in model M_1 if M_0 can be obtained from M_1 by fixing one or more parameters to a specific value. For example, we may consider a model M_1 that has a normal distribution on the context coefficient as a prior, and a nested model M_0 that has a degenerate prior on the

context coefficient that puts all its mass on zero. That model M_0 would then correspond to the (standard, point-valued) null hypothesis that there is no effect of context on pitch.

So, suppose that M_0 is nested in M_1 by fixing a critical parameter θ^* to a specific value x . Then, the Savage-Dickey density ratio states that the Bayes factor in favor of M_1 over M_0 can be computed as the ratio of the prior and posterior density of the critical parameter at the point value that defines the null hypothesis:

$$\text{Bayes factor in favor of model 1 over model 2} = \frac{P(\theta^* = x \mid D, M_1)}{P(\theta^* = x \mid M_1)}$$

Let's unpack this. First of all, this seemingly magical result is actually not that magical, but follows directly from the definition of Bayes factors and Bayes' theorem, but we skip the derivation here. What this means is that in practice we do not have to calculate or approximate any integrals at all, but we can simply look at one model and run posterior inference, like we routinely do with brms, for example. Look at the formula above: we would only need to run one model, M_1 , and then look at the prior and posterior density of the critical parameter θ^* at the point value x . The prior, we should usually be able to get easily because it is in our hands to specify it. The posterior probably, we could get by estimating it from the samples that are returned by software like brms ...

... well, at least in principle. One problem here is that estimating $P(\theta^* = x \mid D, M_1)$ from posterior samples is fickle. We can do it with some mathematical methods, but we may need a lot of samples and do some post-processing (e.g., using splines). The main point is that posterior samples are not reliable for estimating densities at specific points, but they are reliable for estimating probabilities over ranges of values. Ah, if only there was a generalization of the Savage-Dickey density ratio that works for ranges of values!

Wait: there is!

4.4 Calculating Bayes Factor for a specified Region of Practical Equivalence (ROPE)

The Bayes Factor in favor of model M_0 over alternative model M_1 is:

$$BF_{01} = \frac{P(\theta \in I_0 \mid D, M_e)}{P(\theta \in I_1 \mid D, M_e)} \frac{P(\theta \in I_1 \mid M_e)}{P(\theta \in I_0 \mid M_e)}$$

Figure 4 shows ...

Instead of doing it by hand, we can calculate the Savage Dickey ratio with the `bayesfactor_parameters()` function from the `bayesfactorR` package. What happens behind the scenes is that the function will sample posteriors from your specified model based on priors only (so before seeing any data) and calculates the posterior probability of the specified null hypothesis (here the range specified by our ROPE).

```
#|warning: FALSE
#|message: FALSE

BF_1 <- bayesfactor_parameters(posterior = fit,
                              null = rope,
                              parameter = "b_context1")
```

Before interpreting the number we get, let us visually explore what our BF corresponds to.

```
posterior_plot +
  geom_vline(xintercept = c(rope[1], rope[2]),
            lty = "dashed")
```

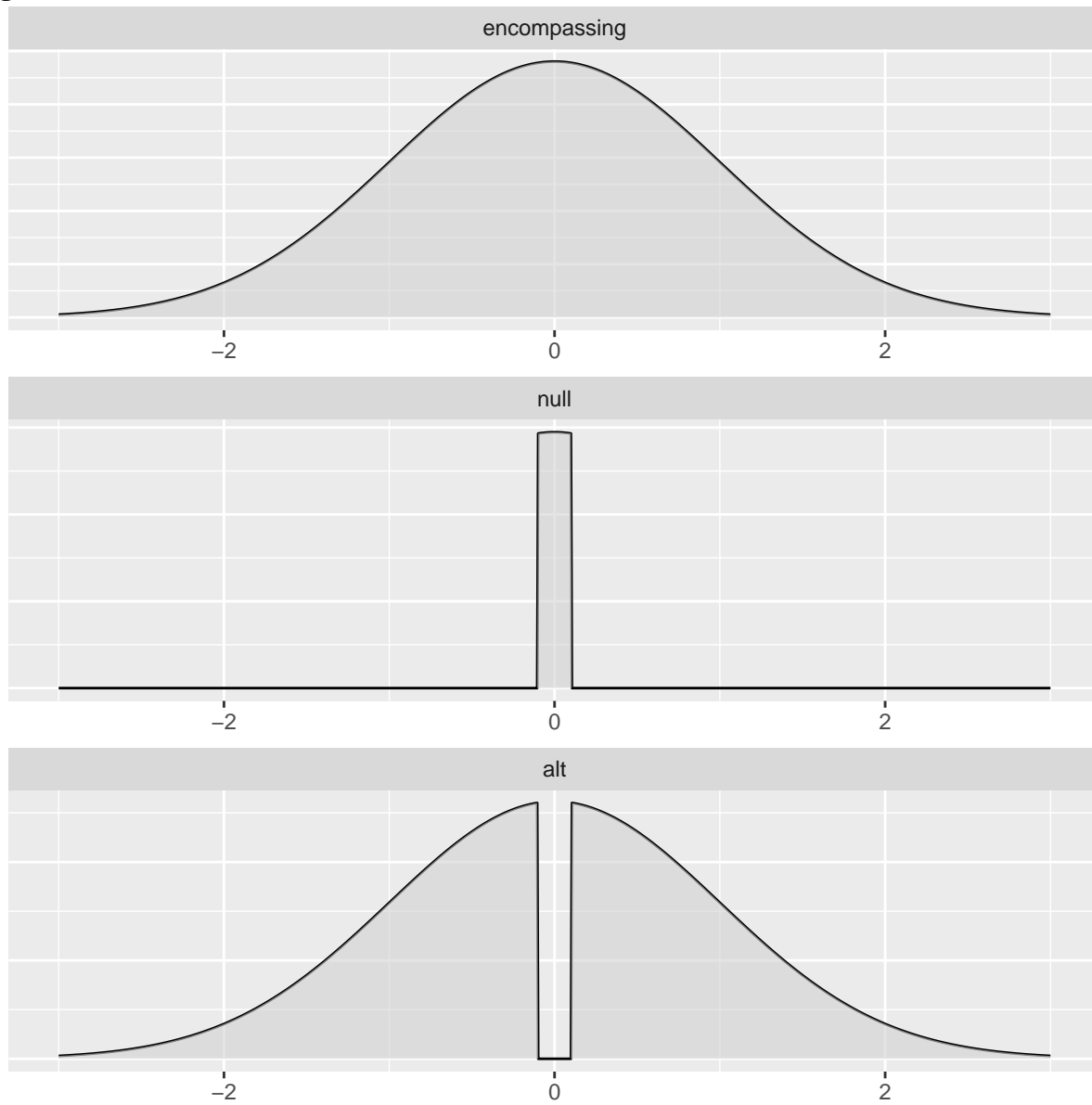
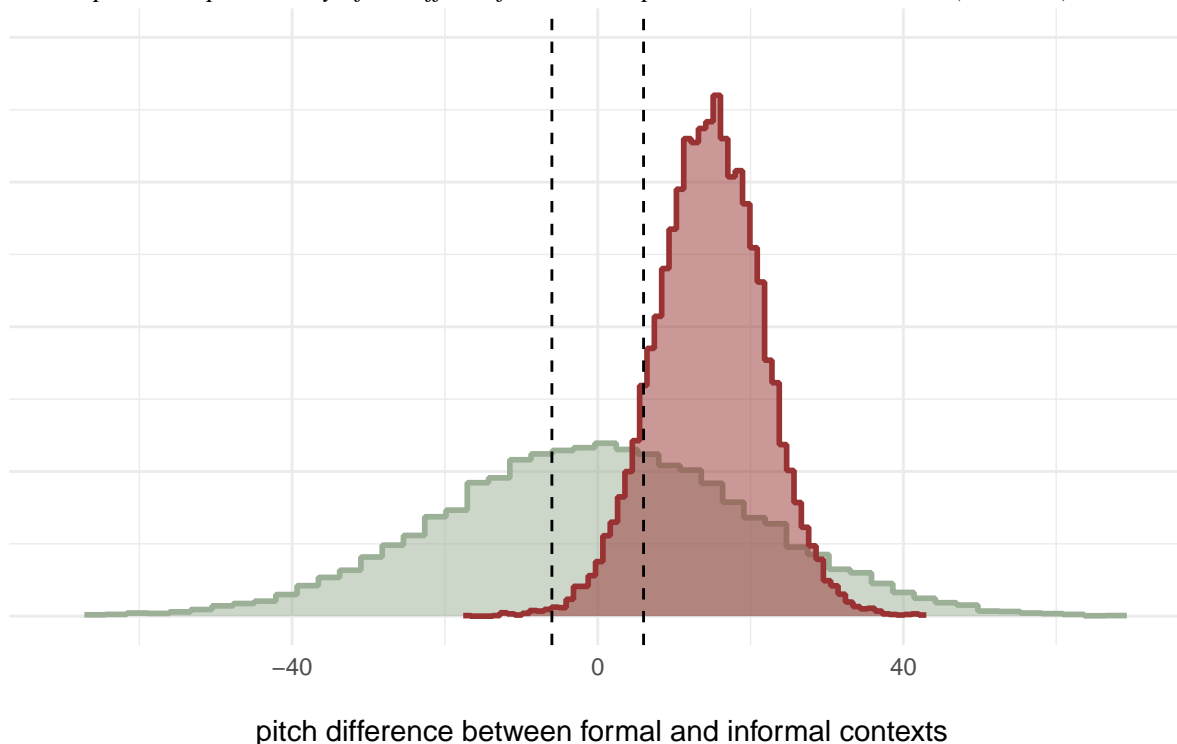
Figure 4

Figure 5

Prior and posterior probability of the effect of context on pitch relative to the ROPE (-0.1, 0.1)



What the BF does is relating two numbers: (a) The prior probability of parameter values outside the rope, i.e. the proportion of the green distribution that falls outside the dashed lines, and (b) the posterior probability of parameter values outside the rope, i.e. the proportion of the red distribution that falls outside the dashed lines. Eye-balling the plot, we can maybe already see that more of the red distribution is outside the ROPE than of the green distribution.

BF_1

Bayes Factor (Null-Interval)

Parameter	BF
context1	2.88

* Evidence Against The Null: [-6.000, 6.000]

To be exact, 2.7 times for of the red distribution is outside of the ROPE than of the green distribution.

That means the model that has seen the data provide 2.7 times more evidence for pitch being outside of the ROPE, or in other words, it is 2.7 times more likely (after having seen the data), that context affects pitch meaningfully. According to Lee and Wagenmakers (2014) criteria for interpreting BFs, this value corresponds to only anecdotal evidence for the alternative hypothesis.

4.5 Sensitivity analysis for different priors and ROPEs

Now as you probably have guessed already, all these probabilities are very much dependent on the priors of the model, so it is important to evaluate the robustness of our Bayes Factor-based interpretation across a range of sensible priors. And as long as we are not a 100% sure about what a meaningful difference is, we might as well explore the robustness of the Bayes Factor across different ROPEs. We won't bore you with the code for that process, but you can follow it along in our scripts. Let us explore the following ROPE intervals as informed by the three studies cited above on pitch perception: we test a range of ROPE intervals from 6 Hz to 40 Hz. We also assume the following five prior values for the width of the standard deviation of the critical parameter (centered on zero): 10, 15, 20, 25, 30. These are all sensible prior widths assuming that medium to strong effects in either direction are plausible.

The combination of Bayes Factors is visualized in Figure X. Orange cells indicate evidence for the alternative. Green cells indicate evidence for the null. It becomes clear that the conclusions we can draw from our data are rather dependent on the choices we made along the way.

By comparing the Bayes Factors along the y-axis, we can see that they are heavily dependent on the chosen ROPE. We here chose (theoretically speaking) a quite large range of ROPEs, all of which are informed by psychoacoustic studies of what pitch differences can be reliably heard and thus likely are meaningful for communication. In light of this range of possible definitions what constitutes meaningful differences, our data seem not very robust, as illustrated by the shift from orange to green. Even the smallest ROPE intervals provide only anecdotal to moderate evidence for the alternative. And the most conservative ROPEs, following Turner et al. (2019), leads to moderate to very strong evidence against the alternative hypothesis.

Additionally, when comparing the Bayes Factors along the x-axis, we can see that they are comparatively consistent for different standard deviations of the critical prior. However, we can also see that the Bayes Factors decrease with the width of the priors (from left to right). This is not surprising and a known phenomenon, often discussed under the Jeffreys-Lindley paradox (Lindley, 1957): The more diffuse the priors are (i.e. wider priors), the larger is the probability that a specific parameter values is not compatible with the data.

Combined, we can see that the larger the ROPE and the wider the priors, the more likely becomes the null hypothesis. In an ideal world, the evidence provided by the data should be robust across these choices. However, this exploration of our inference is a fantastic opportunity to assess the boundaries of our conclusions. In this case, the original conclusions by Winter and Grawunder (2012) was based on the null hypothesis significance testing and traditionally tested the compatibility of the data with a point-null hypothesis. They concluded "that in formal speech, Korean [...] female speakers lowered their average fundamental frequency [...]" This statement is still true according to their inferential criteria, but thinking more deeply about the theoretical consequences of differences in pitch, it might be less clear that these differences are truly meaningful.

4.6 BF for point hypothesis

don't lol

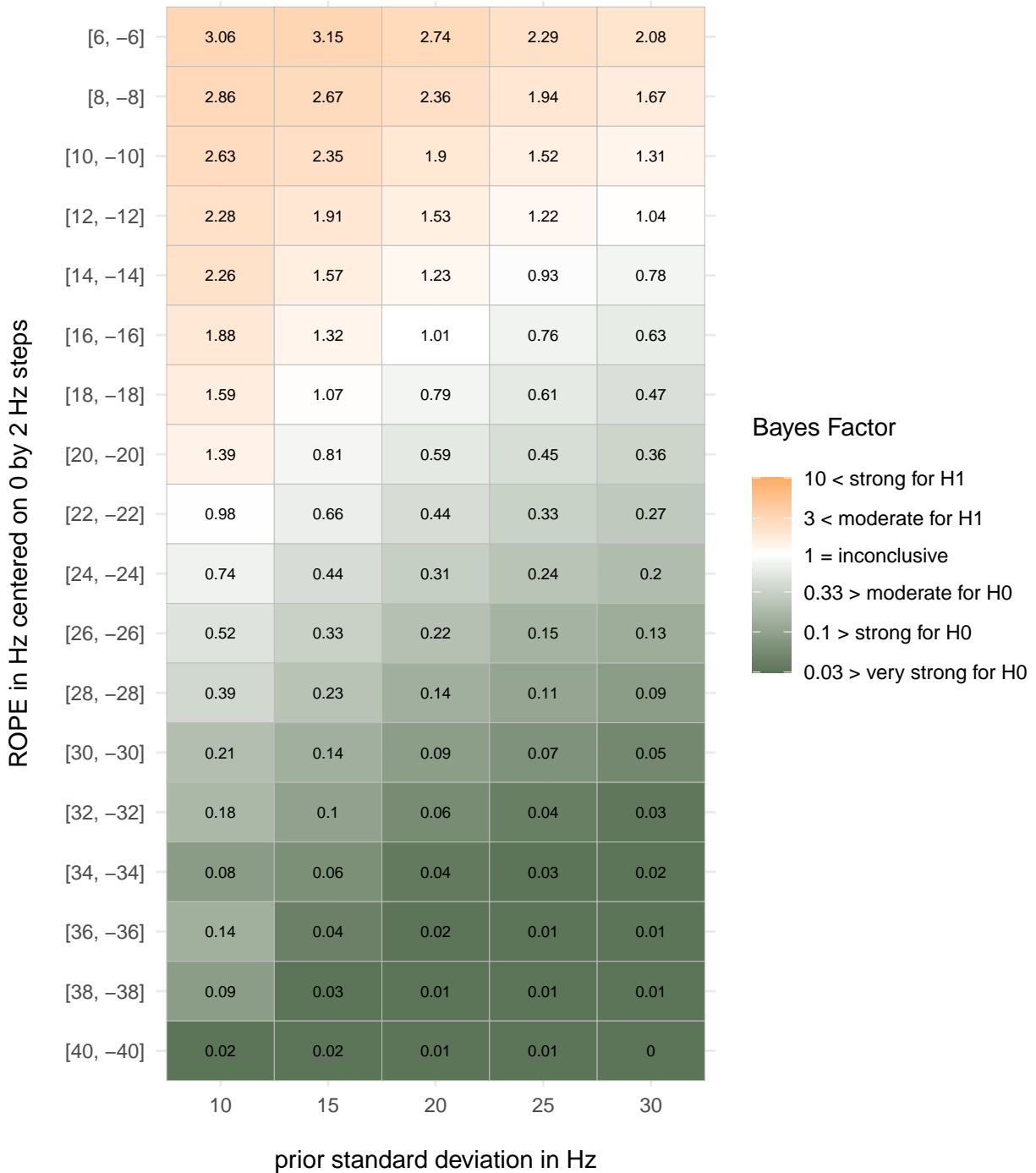
5 How to write things up

6 Some words of encouragement

Bayesian inference in general and this form of hypothesis testing in particular require much more thinking than we might be used to. We think this is a good thing. Many voices have criticized the lack of engagement that we behavioral scientists invest into thinking how our theoretical ideas connect to concrete predictions in the quantitative systems under investigation (Coretta et al., 2023; e.g. Scheel, 2022; Woensdregt et al., 2024). The presented form of hypothesis testing is easy to understand, but does require to think

Figure 6*Bayes Factors for a range of priors and a range of ROPEs*

(A) Bayes factor in favour of alternative
from moderate evidence against the null
to very strong evidence for the null



deeply about prior quantitative assumptions as well as what it means for observations to be meaningfully different. That is neither trivial nor easy. But we would like to encourage you to engage in exactly this thinking to better understand our data and how they might link with our understanding of cognition and behavior.

7 Other Resources

There are many fantastic resources out there to help you learn about the wonderful world of statistics. Here are a few recommendations. - A very accessible introduction to linear models in R is Winter (2019). - ...

8 References

R version 4.5.1 (2025-06-13)

Platform: aarch64-apple-darwin20

Running under: macOS Sequoia 15.6

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib; LAPACK

locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Amsterdam

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] bayestestR_0.16.1	tidybayes_3.0.7	brms_2.22.0	Rcpp_1.1.0
[5] ggdist_3.3.3	lubridate_1.9.4	forcats_1.0.0	stringr_1.5.1
[9] dplyr_1.1.4	purrr_1.1.0	readr_2.1.5	tidyr_1.3.1
[13] tibble_3.3.0	ggplot2_3.5.2	tidyverse_2.0.0	

loaded via a namespace (and not attached):

[1] gtable_0.3.6	tensorA_0.36.2.1	xfun_0.53
[4] insight_1.4.0	processx_3.8.6	lattice_0.22-7
[7] tzdb_0.5.0	vctrs_0.6.5	tools_4.5.1
[10] ps_1.9.1	generics_0.1.4	parallel_4.5.1
[13] cmdstanr_0.9.0	pkgconfig_2.0.3	Matrix_1.7-3
[16] checkmate_2.3.3	RColorBrewer_1.1-3	distributional_0.5.0
[19] RcppParallel_5.1.10	lifecycle_1.0.4	compiler_4.5.1
[22] farver_2.1.2	Brodingnag_1.2-9	tinytex_0.57
[25] codetools_0.2-20	htmltools_0.5.8.1	bayesplot_1.13.0
[28] yaml_2.3.10	crayon_1.5.3	pillar_1.11.0
[31] arrayhelpers_1.1-0	bridgesampling_1.1-2	abind_1.4-8
[34] nlme_3.1-168	posterior_1.6.1	tidyselect_1.2.1
[37] digest_0.6.37	svUnit_1.0.6	mvtnorm_1.3-3

```
[40] stringi_1.8.7      fastmap_1.2.0      grid_4.5.1
[43] cli_3.6.5          magrittr_2.0.3     loo_2.8.0
[46] withr_3.0.2        scales_1.4.0       backports_1.5.0
[49] bit64_4.6.0-1      timechange_0.3.0   rmarkdown_2.29
[52] matrixStats_1.5.0  bit_4.6.0          hms_1.1.3
[55] coda_0.19-4.1      evaluate_1.0.4     knitr_1.50
[58] rstantools_2.4.0   rlang_1.1.6        glue_1.8.0
[61] vroom_1.6.5        rstudioapi_0.17.1  jsonlite_2.0.0
[64] R6_2.6.1
```

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