A tutorial on analyzing ecological momentary assessment data in psychological research with Bayesian (generalized) mixed-effects models

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1/31/2024

This paper has been accepted for publication at *Advances in Methods and Practices in Psychological Science*

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Abstract

This tutorial introduces the reader to analyzing ecological momentary assessment (EMA) data as applied in psychological sciences with the use of Bayesian (generalized) linear mixed-effects models. We discuss practical advantages of the Bayesian approach over frequentist methods as well as conceptual differences. We demonstrate how Bayesian statistics can help EMA researchers to (1) incorporate prior knowledge and beliefs in analyses, (2) fit models with a large variety of outcome distributions that reflect likely data-generating processes, (3) quantify the uncertainty of effect size estimates, and (4) quantify the evidence for or against an informative hypothesis. We present a workflow for Bayesian analyses and provide illustrative examples based on EMA data, which we analyze using (generalized) linear mixed-effects models to test whether daily self-control demands predict three different alcohol outcomes. All examples are reproducible, with data and code made available at https://osf.io/rh2sw/. Having worked through this tutorial, readers should be able to adopt a Bayesian workflow to their own analysis of EMA data.

Keywords: *Bayesian statistics, mixed-effects modeling, ecological momentary assessment, brms, tutorial*

Introduction

Ecological momentary assessment (EMA; also variously called experience sampling or ambulatory assessment) refers to study designs that repeatedly collect data from participants in real time in their natural environment. For example, participants might respond to five short surveys throughout the day for 30 consecutive days. In recent years, EMA designs have become popular in various areas of psychology (e.g., cognitive psychology: Crawford et al., 2022; social psychology: Depow et al., 2021; work psychology: Dora et al., 2021; clinical psychology: Fried et al., 2022). One key advantage of EMA is its ability to capture complex and fine-grained temporal associations between psychological phenomena (e.g., thoughts, feelings, and behaviors), which allows researchers to harmonize theoretical and statistical models (Kaurin et al., 2023). Another advantage is EMA's potential for improved causal inference (Hamaker et al., 2020). EMA also maximizes ecological validity and minimizes recall bias (Hektner et al., 2007; Moskowitz & Young, 2006; Piasecki, 2019; Shiffman, 2009; Shiffman et al., 2008). Since the smartphone has become ubiquitous, the prevalence of EMA research is increasing rapidly compared to other research designs and the method is becoming a common tool for psychological research. For instance, Figure 1 illustrates that the number of published studies using EMA methodology has grown exponentially in recent decades, unlike other methods such as clinical and randomized controlled trials[1]. Although publications on trials increased slowly over the past 30 years, EMA studies have increased much more rapidly since 2010, demonstrating an increase of over 2000% in the past decade.

[1]We performed this search with the help of the bibliobanana library in Python (Dalmaijer et al., 2021).

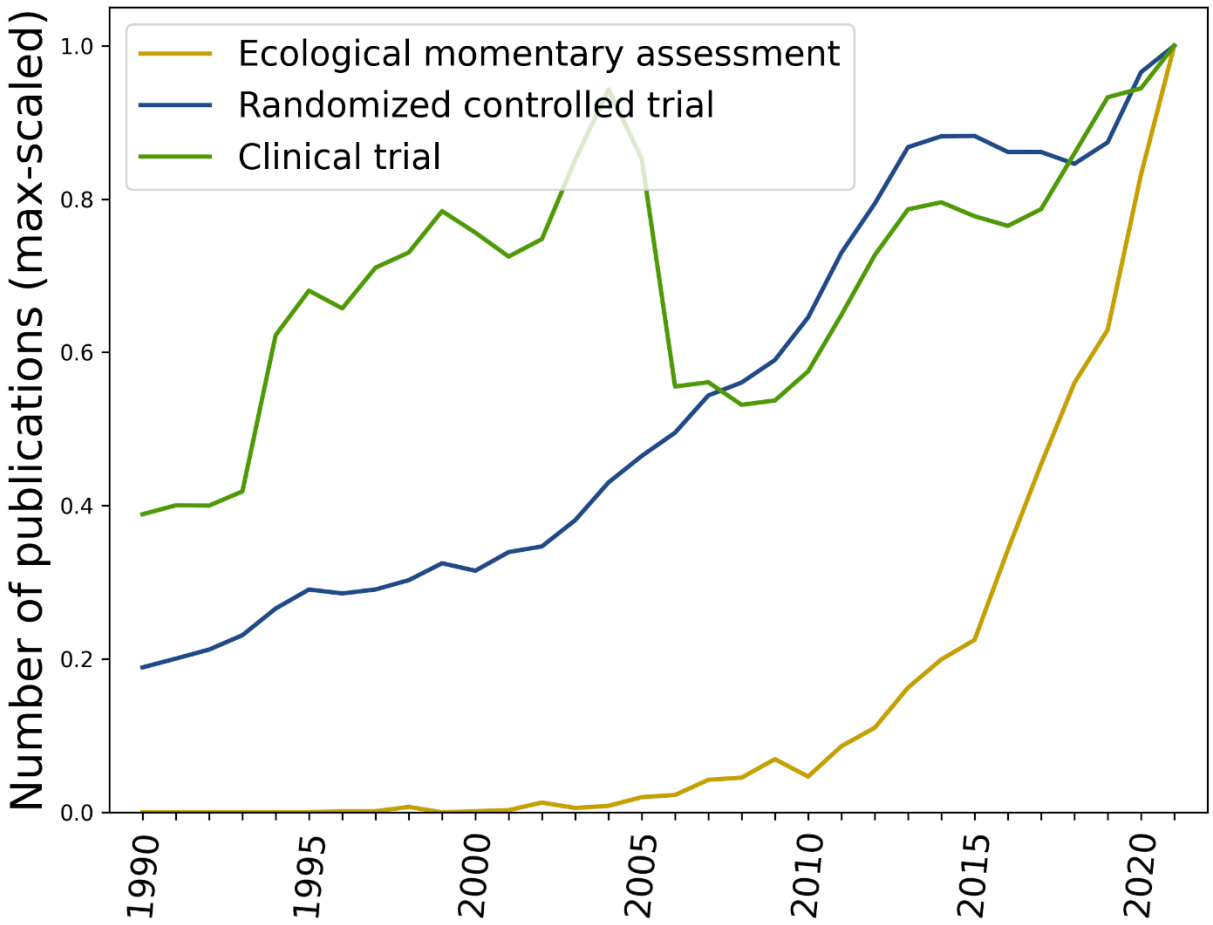

Figure 1. The ratio of yearly number of papers indexed in PubMed that reference 'Ecological momentary assessment' compared against 'Clinical trial' and 'Randomized controlled trial' between 1990 and 2021 (each scaled to their own maximum).

Analyzing data from EMA studies involves specific challenges. One key challenge is that the assumption of independence of observations is violated when each participant contributes many (sometimes hundreds of) data points. Thus, the repeated observations (e.g., responses to a question asking the participant how bored they feel at each assessment) are nested in participants, as responses to this question from the same participant tend to be more alike than responses from other participants, which is why we cannot treat these responses as independent of one another. Some EMA designs result in even more complex data structures, with additional levels of nesting (e.g., observations-within-days-within-people or observations-within-people-within-groups; Stevens et al., 2022). To account for this nested data structure, psychologists often analyze such data with (generalized) linear *mixed-effects models* (Dora, Smith, et al., 2022;

Feil et al., 2020; Hepp et al., 2017; Howard et al., 2015; Patrick et al., 2021; Spronken et al., 2016; van Hooff et al., 2011), which are a type of multilevel model (Pinheiro & Bates, 2000). A mixed-effects model is essentially an extension of a regular regression or ANOVA model and contains both *fixed* and *random effects*. Fixed effects are factors that are assumed to be constant across participants (or other clusters in which data are nested), while random effects are factors that are assumed to vary randomly from one cluster to another. In other words, fixed effects are assumed to have a systematic influence on the outcome (comparable to the parameters in a regular regression or ANOVA model), and the model estimates this average effect of the fixed factor on the outcome variable. Random effects, on the other hand, indicate processes on which participants (or other clusters) differ from each other in meaningful ways, and that cannot be easily modeled with the group-level average. In mixed-effects models, random effects can also estimate *variability* in the fixed effects, which estimate how the fixed effects vary from one cluster to another. For example, a random intercept can reflect that some participants might score higher or lower on the outcome variable on average, and a random slope can reflect that for some participants the association between predictor and outcome might be stronger or weaker.

Why a tutorial on Bayesian analysis of EMA data?

To date, the vast majority of EMA research has relied on frequentist methods, which use maximum likelihood to estimate model parameters, and commonly use *p*-values for inference. In *Psychological Science*, for example, more than 95% of EMA studies published between 2011 and 2021 used such approaches[2]. Setting aside differences in inferences (which we will return to in a bit), the frequentist approach has a few practical limitations that might make it suboptimal for many EMA data analysis projects. First, a major practical disadvantage of frequentist mixed-effects models is that they often fail to converge when there is too little variability in one part of the model (e.g., almost no variability in an EMA item over time; McCoach et al., 2018). As a result, we often have to adjust our statistical model post-hoc and cannot include all random effects that we would like to include in our mixed-effects models. Often times method sections of EMA papers state that the authors wished to include a random slope to account for variability

[2]We searched Web of Science for papers published in *Psychological Science* with the search terms ‘Ecological momentary assessment OR Experience sampling OR Ambulatory assessment OR Daily diary’ and counted how many papers drew inferences from frequentist models.

between participants in the strength of the association between predictor and outcome, but that they had to remove this parameter to get the model to converge. This is especially relevant when analyzing EMA data since the testing of cross-level interactions (i.e., interaction effects between levels of nesting, which are common in EMA studies) necessitates modeling of a random slope of the lower-level variable (e.g., observations within individuals; Heisig & Schaeffer, 2019). Cross-level interactions are often of theoretical interest in EMA research as they model how processes that unfold *within* people (e.g., the association between feeling bored and drinking alcohol later that day) are affected by features that differ *between* people (e.g., people's personality or environment). Having to adjust a model after seeing the data is undesirable from an Open Science perspective where we would prefer not to diverge from our preregistration if possible (Nosek et al., 2018).

A second practical disadvantage is that available frequentist software packages cannot accommodate the full range of models we commonly need for our EMA research. For example, the R package *nlme* (Pinheiro, 2010) can only fit linear models, but it can model different structures in the residuals such as auto-correlation and heteroskedasticity. The R package *lme4* (Bates, Maechler, et al., 2015) cannot model residual structures but can handle some non-normal outcomes via the *glmer or glmer.nb* command. However, even *lme4* cannot model zero-inflated or hurdle count outcomes, or other nonlinear options. Additional frequentist options are available (such as *glmmTMB;* Magnusson et al., 2017), but the cost of changing packages (and their associated estimators, syntax, and troubleshooting methods) makes it more difficult to effectively estimate a wide range of models we may want to fit on our data.

On the other hand, Bayesian approaches to EMA data analysis handle these practical challenges well. Because Bayesian models incorporate prior information, which guides the estimator towards plausible values (or at least restricts it to possible values), Bayesian models are much less likely to encounter convergence problems when fitting mixed-effects models (Aguilar & Bürkner, 2022; Barr et al., 2013), which may be especially helpful in the estimation of random effects parameters (Bates et al., 2015). Second, a Bayesian software package exists (the R package *brms*, which we will use in this tutorial) that can accommodate a much wider range of models without having to switch software or packages. Thus, using a Bayesian rather than

frequentist approach gives us more flexibility and much higher confidence that the model we have in our mind will converge and be interpretable.

There are also conceptual differences between frequentist and Bayesian approaches, though it is important to highlight that nearly all of these differences can be addressed in some way in the frequentist framework. Thus, our argument is not that Bayesian analyses are conceptually superior to frequentist ones, but rather that more emphasis has been placed on statistical reasoning and inferences in the Bayesian literature that we consider to be informative in the context of EMA studies and mixed-effects models. A big difference is that a Bayesian analysis typically does not contain any *p*-values. Computing *p*-values (and by extension, frequentist confidence intervals) from mixed-effects models is not straightforward (Bates, 2006) and in many cases obtaining "correct" *p*-values and confidence intervals requires researchers to implement extra steps, such as using an additional overlay package (such as lmerTest) to obtain *p*-values using approximations of the correct degrees of freedom, using Markov Chain Monte Carlo sampling, or bootstrapping (Bates, Maechler, et al., 2015). In other words, obtaining accurate *p*-values and confidence intervals in traditional frequentist analyses is difficult and adds many extra steps that are challenging and may lead to invalid inferences.

Encouraging *p*-values is especially problematic for EMA studies, because collecting EMA data is expensive, time-intensive, and effortful, resulting in many EMA studies employing rather small sample sizes. For example, in an individual participant data meta-analysis of 69 EMA studies, 41% included fewer than 100 participants (Dora, Piccirillo, et al., 2022). Small samples tend to have low power to detect true effects, and are at elevated risk of overfitting noise in the data. Consequently, statistically significant findings in low-powered studies tend to overestimate the population effect size and replicate poorly (Vasishth et al., 2018). Indeed, the prevalence of underpowered studies has likely contributed to the "replication crisis": the finding that many statistically significant findings do not replicate (Hagger et al., 2016; Open Science Collaboration, 2015; Wagenmakers et al., 2016).

Conceptually, Bayesian models encourage users to focus on effect sizes and uncertainty. In a Bayesian analysis, results focus on the updating of our beliefs following the analysis of our data rather than statistical significance. Did our analysis reduce our uncertainty regarding the size of an effect? What is the probability that the effect we study is zero or too-small-to-care-for,

what is the probability that it is a medium or large effect? Answers to these questions can be derived from Bayesian analyses and often are more informative than the difference between statistically significant and not significant. Quantifying uncertainty about effect sizes allows us to determine whether our study provides sufficient evidence to assess our hypotheses. This information can be used to decide whether we need to design another high-effort EMA study to test our research question, or whether it is time to move on and allocate our resources elsewhere. Thinking about an entire literature of EMA research, studies would not be summarized by counting significant and non-significant findings but to the extent that their estimates of uncertainty converge (or not), thereby contributing to a more thorough evaluation of a research question. Moreover, these inferences are valid even if models are adjusted after seeing the data, because Bayesian analyses depend only on our prior and the data but not on the number of tests that we run on the data (though also when using Bayesian statistics; we need to make sure not to cherry-pick results that fit a narrative; Dienes, 2011). Proper use of prior distributions also helps us to deal with limitations of small sample size or highly parametrized models; such models incur a risk of overfitting (i.e., capturing idiosyncratic noise in the sample rather than generalizable effects), which results in increased Type-I errors (i.e., an increased risk of obtaining a non-replicable significant *p*-value; Gelman et al., 2008). Overfitting can be curtailed by specifying priors that assign greater probability mass to values near zero, a process called regularization.

A short review of Bayesian reasoning

The primary distinction between frequentist and Bayesian statistics is a different definition of probability. In frequentist statistics, probability refers to the frequency of an event's occurrence if the study was, hypothetically, to be repeated many times. This so-called long-run probability considers each possible outcome equally likely *a priori* and thus the parameters are contingent only on the *likelihood of the present sample*. The Bayesian definition of probability, by contrast, reflects the degree of belief or confidence in a particular event. This probability is contingent on both the *likelihood of the present sample and the prior probability assigned to different parameter values*. The two perspectives can be bridged by viewing frequentist statistics as a special case of the Bayesian approach where one assumes a complete absence of prior

knowledge. If one assumes that all parameter values are exactly equally likely before seeing the data, the results from the Bayesian approach will mirror those from the frequentist approach.

Under frequentist logic, we can learn about the *probability of observing the collected data (or more extreme data) under the assumption that the null hypothesis is true* (i.e., p[data | hypothesis]). For example, let us say we are interested in learning whether people are more likely to report a hangover the more alcoholic drinks they consumed the night before. After conducting a study, we find that on average people are 10% more likely to report a hangover with each additional alcoholic drink consumed the night before. We can then estimate how (im)probable that observed effect is when we assume that the true effect in the population is 0. To do this, we need to clearly define our sampling strategy and analysis plan ahead of time (i.e., make every data-analytic decision so that we have one path through the forking garden), because the risk of making a Type-I error is inflated if we run our test more than once. In contrast, under Bayesian logic, we can learn about the probability of our *hypothesis being true, given the data we observed* (i.e., p[hypothesis | data]). Thus, we can estimate how (im)probable it is that people are more likely to report a hangover when they had more to drink from the data we collected, irrespective of our sampling and analysis plan. The Bayesian approach to data analysis allows for this inference by assigning prior probabilities to competing hypotheses. Thus, the interpretation of a Bayesian analysis only depends on these priors and the data at hand. Every Bayesian analysis is built on Bayes' rule, which 'updates' the prior belief with the data to arrive at a posterior belief and can be written as:

$$P(hypothesis \mid data) = \frac{P(data \mid hypothesis)P(hypothesis)}{P(data)}$$

Consider the (made-up) example above: say you want to know the probability that an individual reports a hangover after having six alcoholic drinks the night before. Based on your clinical experience, you believe that roughly one in four times people feel hungover after having six drinks (prior). You then conduct an EMA study and find that two out of three times when people report a hangover, they also had six drinks (likelihood), and that they had six drinks in one out of three drinking episodes. Using these numbers, you can then use Bayes' rule to determine that the probability that a person reports a hangover after having six drinks is 51%:

$$P(hangover \mid six\ drinks) = \frac{0.67\ x\ 0.25}{0.33} = 0.51$$

All probabilities in this example are "point probabilities"; the probability of a specific event occurring or not. EMA models rarely deal with point probabilities, however; instead, we often work with *probability distributions*, which describe the probability of a range of possible parameter values. The mathematical underpinnings are the same, however. We can apply Bayes' rule to compute a *posterior probability distribution* based on a *prior probability distribution* and the *likelihood of the data*. We will elaborate on this below.

For whom is this tutorial?

This tutorial is aimed at psychological researchers who use or are interested in using EMA study designs in their work. We will use the *brms* package (version 2.17.0; Bürkner, 2017) in R (version 4.2.0; R Core Team, 2021), which is built on the probabilistic programming language Stan (Stan Development Team, 2022) . This package gives us by far the most flexibility in our Bayesian EMA analyses while being reasonably accessible, especially for people familiar with R. For interested readers, we have put together a step-by-step tutorial for installing *brms* here: https://osf.io/rh2sw/wiki/home/. The principles of Bayesian mixed-effects modeling we illustrate here generalize to many other proprietary software packages as well. In general, working through this tutorial should enable readers to apply a Bayesian workflow to their EMA data analyses in their preferred software of choice.

This tutorial is organized as follows: first, we outline the key steps in a Bayesian analysis. Second, we will go through three applied examples of analyzing EMA data with a Bayesian workflow. This tutorial is written as a practical first step into Bayesian data analysis for EMA researchers. We will not cover all aspects of Bayesian modeling in detail but will provide a short list of resources for further reading in our concluding remarks.

Key steps in a Bayesian analysis

A Bayesian data analysis consists of the following steps:

1. Define your model.

2. Specify your priors.
3. Fit the model to your data.
4. Check your model for convergence.
5. Assess your model fit.
6. Draw your inferences.

Defining the model. There is nothing unique about this step in a Bayesian analysis. As explained before, EMA models typically contain a mix of fixed and random effects. In the majority of EMA research, the fixed effects, which represent the estimated average intercepts and slopes across participants, are the parameters of theoretical interest which are evaluated to test the hypothesis or answer the research question. However, especially in a Bayesian framework, in which random effects (representing intercepts and slopes varying across participants) are estimated parameters, random effects can convey important information and should be paid attention to. For example, random effects allow us to make predictions for individual participants and can be summarized to illustrate for how many participants in the sample a meaningful effect is estimated, see the applied examples below. Aside from specifying the fixed and random effects, we also specify a distribution for the unexplained variance in our outcome. In traditional linear regression, this is typically a Gaussian (normal) distribution, but we can specify other distributions, like the binomial or Poisson, depending on the type of data.

Defining priors. Next, we need to explicitly define priors for all parameters in the model. Defining priors is the biggest practical difference between a frequentist and a Bayesian analysis. The priors represent our expectations about the *a priori* plausibility of different values of our model parameters. In other words, the priors can be thought of as reflecting your knowledge (or lack thereof) regarding the phenomenon that you study. For parameters that can take continuous values, priors come in the form of *distributions* (prior probability distribution). Let us consider the simple example in which you want to estimate the difference in average alcoholic drinks consumed during a drinking episode between people who say they have and do not have a drinking problem.

In theory, you can use any distribution for your prior. Priors fall along a range from uninformative to strongly informative. For regression coefficients, a *flat or uniform prior* is the most uninformative distribution possible. It assigns equal prior probability to all possible

outcomes. If all other priors are also uninformative, the posterior probability distribution will be entirely dependent on your data, just like in frequentist analysis. In our specific example, this would mean that you consider it just as likely that people who say they do not have a drinking problem on average consume three drinks more as that both groups will not differ in their alcohol consumption. The other extreme is an *informative* prior, which expresses a strong belief about what the effect should be by assigning a high probability density to a specific value. In our example, specifying a normally distributed prior with a mean of 2 and a standard deviation of 0.1 would imply that you believe (before seeing any data) that on average people who say they have a drinking problem will consume between 1.8 and 2.2 more drinks with 95% probability, and that values below 1.5 and above 2.5 are virtually impossible. This strongly biases the results of your study towards your prior expectation. While this kind of prior has a place in some psychological research (e.g., for cumulative knowledge acquisition in replication studies), it may be less relevant for most EMA studies.

In between uninformative and informative priors are so-called weakly-informative or regularizing priors (Gelman et al., 2017), which assign lower prior probability to extreme parameter values. Such priors often make sense, because we know that most effect sizes in psychology tend to be small (Richard et al., 2003; Schäfer & Schwarz, 2019). In that way, weakly-informative priors have minimal influence on our inferences while simultaneously providing a conservative safeguard against improbably large effect sizes (especially when data are sparse) and help our models converge by providing a better starting point to locate parameter estimates (Bates, Maechler, et al., 2015; Eager & Roy, 2017; Gelman, 2009). In our example, a reasonable weakly-informative prior might be a normally distributed prior with a mean of 0 and a standard deviation of 1.5, implying a 95% probability that either group will consume up to three drinks more but that values closer to 0 are more likely. What constitutes a reasonable prior is entirely dependent on the context and the scale of your variables. Priors should reflect our knowledge of the phenomena we study. Whenever we are not sure what outcome to expect from our study, weakly-informative priors should perform well for the reasons outlined above. One important consideration is to avoid to formulate priors based on the collected data. This practice is termed ‘double-dipping’, because we are using the data twice, once to formulate a prior belief, and then to update this belief with the data. This will likely result in overconfident and biased

estimates and credible intervals (comparable to inflating the Type-I error rate in frequentist statistics.

Fitting the model. There are a few differences in this step compared to when fitting a frequentist model. The reason is that unlike in our hangover example above, the posterior distribution (which was obtained by updating the prior distribution with the data) is rarely analytically defined for complex models, like mixed-effects models. However, it can be approximated reasonably well by sampling from the posterior using Hamiltonian Monte Carlo simulation. To understand the concept behind this method, consider the following example: imagine we want to estimate the joint posterior distribution for two parameters, b1 and b2. We can think of this posterior as a three-dimensional landscape, with b1 on the x-axis and b2 on the y-axis. The elevation of the landscape, or z-axis, is the posterior probability of these two parameters. The most likely combination of parameter values is a deep valley in the landscape. Now think of Hamiltonian Monte Carlo as a game of marbles, where you drop marbles onto this landscape at random points, and record where they stop rolling. Many marbles will land in the deep valley of the most likely combination of parameter values, but other marbles may get stuck on a ledge or somewhere out on the sides of the landscape. After dropping many marbles, their final coordinates combined give us a good approximation of the shape of the landscape. In technical terms, this process is called *sampling from the posterior*, and every marble represents a single sample. We will explain the process of approximating the posterior distribution in our running example below. What you should take away from this section is that for most EMA research it is not feasible to exactly compute the posterior distribution; instead, we try to approximate this distribution, and we need to make sure that we approximated it well (see below).

Checking model for convergence. Before we can interpret the results, we need to check whether our Bayesian model failed to converge. The most important thing we need to check is if we were able to approximate the posterior distribution well. Given the complexity of this problem, it happens reasonably often that our model initially does not explore the full distribution. Consider the marble analogy: We must ascertain that marbles rolled around the entire landscape. Bayesian statisticians have developed multiple approaches to check this as well

as solutions should we have reason to believe that it failed (Carpenter et al., 2017), which we describe in detail in our running example below.

Assessing model fit. As a final step before we can interpret our model, we need to check whether our model adequately fits our data. To assess this, we can make use of posterior predictive checks. To perform a posterior predictive check, we simulate new values for our outcome from the joint posterior distribution and then compare these values to the observed data. If our model fits the data well, the distribution of simulated outcome values should closely resemble the distribution of observed outcomes in our dataset. If this is not the case, we have strong reason not to trust the predictions of our model. This approach might sound familiar if you ever plotted predicted against observed values for your regression models. However, a posterior predictive check is Bayesian in the sense that the simulation comes from the posterior distribution and thus incorporates the uncertainty around parameter estimates rather than relying on maximum likelihood. We will give a concrete example of this below. It is important to point out that when we perform a posterior predictive check, we are also using our data twice, something we generally want to avoid as explained above. The difference between using the data to specify priors and using it to assess model fit is that here we are using the posterior predictive check solely as a tool to check for a severe problem of our model (that we cannot simulate data from it that mirror the observed data) and not as a tool to compare models or to draw inferences. As a consequence, it is important to use posterior predictive checks only as a diagnostic tool and not to make decisions about which of several models to report or base our conclusions on.

Drawing inferences. The Bayesian definition of probability allows us to perform inference directly on the posterior distribution. This probability distribution represents the probability assigned to specific population values for the parameter in question, conditional on the prior and the data. To interpret the posterior distribution, firstly, we can consider its shape, location, and scale. For example, a sharply peaked distribution centered around a particular location indicates a narrow range of plausible population values (low uncertainty). A flatter distribution with lower probabilities for most values indicates a large amount of uncertainty about the population parameter. In general, the posterior distribution can be plotted and interpreted as the full range of possible values that may represent the true effect size that differ in plausibility (values closer to the peak are more likely, values closer to the tails are less likely but

not impossible). The posterior distribution can be paired with one of two Bayesian probability intervals. In Bayesian analyses, intervals can be interpreted as a "window of uncertainty" within which the population value falls with 95% certainty, given the prior and data. Two commonly used intervals are the credibility interval, which simply consists of the 2.5^{th} and 97.5^{th} quantiles of the posterior distribution, and the highest posterior density interval (HDPI), which is the narrowest possible interval that contains 95% probability. Theoretically, we could use this interval to reject the null hypothesis if it were desired. Generally, we believe it is more informative to focus on effect sizes and use the posterior distribution and 95% credible interval as measures of uncertainty around the estimate. This encourages readers to think more deeply about our theories and models and in that way build a more robust body of empirical evidence (Halvorson et al., 2022; King & Dora, 2022; McCabe et al., 2022; Tackett et al., 2019).

Due to the different definition of probability, Bayesian analyses do not provide the "traditional" p-value. However, probabilities about population parameters can be directly calculated from the posterior. For instance, it is possible to calculate the probability that the population effect is of opposite sign from the posterior mode, which can be interpreted as the probability of incorrectly concluding that an effect is positive if the posterior mode is positive. It is also possible to calculate the probability contained between plus and minus some small value representing a minimum effect size of interest (Anvari & Lakens, 2021); this can be interpreted as the probability that the effect is too small to be of practical relevance.

Bayesian analyses also allow quantifying evidence in favor over, versus against, an informative hypothesis (Van Lissa et al., 2021; Wagenmakers et al., 2012). This can be achieved by computing a Bayes factor, which is a ratio of evidence in favor of one hypothesis over the evidence in favor of another hypothesis. As such, a Bayes factor of 1 indicates that the data support both hypotheses equally well, whereas Bayes factors of 3, 10, and 30 respectively indicate that one hypothesis is 3, 10, and 30 times more likely than the other, given the data and the prior. Unlike a frequentist *p*-value, a Bayes factor provides a continuous measure of evidence, either for or against our hypothesis.

It is important to point out that all inferences in a Bayesian analysis, but especially Bayes factors, are contingent on the priors (Schad et al., 2022; Wagenmakers et al., 2010). With this in mind, it is best practice to conduct sensitivity analyses to demonstrate that inferences are robust

to different choices of priors. If one wishes to entirely eliminate researcher degrees of freedom introduced by the choice of prior and evidence threshold, these quantities can be preregistered ahead of time to eliminate researcher degrees of freedom that are introduced by a free choice of priors (Munafo et al., 2017; Nosek et al., 2018). In fact, as Bayesian models can be run based on just the priors, it is possible to preregister an entire reproducible analysis, along with placeholder results, prior to the collection or analysis of real data. For more on this approach, see the work on "Preregistrations-As-Code" (Peikert et al., 2021; Van Lissa et al., 2021).

Running example

Now that we introduced the key steps in a Bayesian analysis, we will use a running example based on real EMA data collected in regularly drinking college students (Smith et al., 2022; Witkiewitz et al., 2012) to illustrate these steps. A total of 213 undergraduate students aged 18 to 27 (54.0% female) completed 9,366 momentary surveys and responded to at least one survey on 2,801 days. We will examine the association between perceived self-control demands and three alcohol use outcomes. Two earlier studies suggest that an association between self-control demands and alcohol outcomes exists in EMA data (DeHart et al., 2014; Muraven et al., 2005), whereas a recent study failed to replicate such a within-person association (Walters et al., 2018). All data and R code are available at https://osf.io/rh2sw/. We suggest following along in R while reading the remainder of this paper.

Measurements

Perceived self-control demands. At each EMA assessment, participants reported perceived self-control demands in the past ten minutes via four items taken from a prior study (Muraven et al., 2005). They indicated to what extent they needed to 1) control or fix their mood, 2) control or fix their thoughts, 3) deal with anything stressful, and 4) felt overwhelmed on a scale from 0 ("not at all") to 100 ("very much"). Scale scores were computed by taking the mean of these items, which showed high reliability across items and time (RkF = .98; Shrout & Lane, 2012).

Alcohol intoxication. At each morning EMA assessment, participants reported (if they drank alcohol the previous night) how drunk or intoxicated they got with a single item on a scale from 0 ("not at all") to 6 ("very much").

Alcohol use. At each morning EMA assessment, participants reported how many alcoholic drinks they consumed the previous day on a slider from 0 to 30 or more.

Alcohol consequences. At each morning EMA assessment, participants reported (if they drank alcohol the previous night) whether they experienced any of the following four consequences of their drinking: having a hangover, failing to remember events within the drinking episode, experiencing nausea from drinking, and experiencing an intoxication-related injury.

Running example 1: A fully Bayesian analysis

For our first example, we hypothesized that, on drinking days, perceived self-control demands would predict increased subsequent alcohol intoxication. Before we can get started with our analysis, we need to process our dataset. While the necessary steps differ from dataset to dataset and analysis to analysis, we illustrate here one example of such processing. This is necessarily idiosyncratic, and you might have made different decisions when faced with the same data and hypothesis. We start with our data in long format, so that each row represents the momentary data from one participant (e.g., if a participant responded to thirty surveys across eight days, we have thirty rows of data for this individual). For this analysis, we remove data from days on which participants reported no alcohol use. We then average self-control demands *prior to the onset of alcohol use* (to get a daily estimate of self-control demands prior to the drinking episode), format our data so that each row of our dataset reflects the daily data from one participant (e.g., a participant reported any amount of alcohol use on four days, we now have four rows of data for this individual), and finally standardize self-control demands within-participant so that they have a mean of 0 and a standard deviation of 1 to help with the intuitive interpretation of prior and posterior probabilities. For example, with the help of the *dplyr* package (Wickham et al., 2019), we could accomplish the data processing like this:

```
data.intox <- data %>%
 filter(alc.drinks > 0) %>% # removing days on which no alcohol was consumed
 mutate(control.fixmood = ifelse(hour >= alc.onset, NA, control.fixmood),
      control.fixthought = ifelse(hour >= alc.onset, NA, control.fixmood),
      dealt.stress = ifelse(hour >= alc.onset, NA, control.fixmood),
      felt.overwhelm = ifelse(hour >= alc.onset, NA, control.fixmood),
      # previous 4 lines remove demands reports that occurred after drinking onset
      demands = rowMeans(across(all_of(demands.items)), na.rm=T)) %>% # mean EMA signal
 group_by(PID, study.day) %>%
 mutate(demands = mean(demands, na.rm=T)) %>% # daily mean
 slice(1) %>% # retain 1 row per participant and day
 ungroup() %>%
 group_by(PID) %>%
 mutate(demands = scale(demands, center = T, scale = T)) %>% # standardize on pid-level
 ungroup()
```

Defining the model. We will want to fit a model predicting alcohol intoxication of participant *i* on day *t* from self-control demands of participant *i* on day *t* (prior to the onset of drinking). Because each participant contributes observations on multiple days, we want to fit both fixed and random intercepts and slopes to account for variation between participants in alcohol intoxication and the effect of self-control demands on alcohol intoxication. Both fixed and random effects are assumed to be normally distributed. For educational purposes, we are first going to fit a linear model to these data as is common in psychology, although we do not expect this model to fit the data well; we will fit a more appropriate model afterwards.

Defining priors. We can use the *brms* command get_prior() to figure out which priors can be specified for our model. In most models, we want to consider separate priors for our (1) fixed intercept, (2) fixed slope(s), (3) all standard deviations for all random effects, (4) the standard deviation of the residual error term, and (5) the correlation between random effects. For our example, let us define the following priors:

```
priors.intox = c(set_prior('normal(3, 1)', class = 'Intercept'), # prior on fixed intercept
          set_prior('normal(0, 1)', class = 'b', coef = 'demands'), # prior on fixed slope
          set_prior('normal(0, 0.5)', class = 'sd'), # prior on sds and sigma
          set_prior('lkj(2)', class = 'cor')) # prior on random correlations
```

First, we specify that our prior for the fixed intercept is normally distributed with a mean of 3 and a standard deviation of 1. Alternatively, we could use another symmetrical distribution such as the Cauchy or Student t's distribution, which might make sense if we have reason to believe that our data exhibit kurtosis or we are working with a small sample size. This implies that we believe that the intercept, which represents the average level of alcohol intoxication at average levels of self-control demands across all participants and drinking episodes, will lie between 1 and 5 (remember alcohol intoxication is answered on a scale from 0 to 6) with 95% probability, with more probability mass assigned to values that are closer to 3. Whether this is reasonable depends on the context of your research; for example, if we had collected a sample of people who say they never have more than one alcoholic drink, we would have distributed more prior probability mass towards the lower end of the scale. If we had sampled from the same population previously, we would have chosen a more informative prior with a smaller standard deviation.

Next, we specified a normally distributed prior for the fixed effect of self-control demands on alcohol intoxication with a mean of 0 and a standard deviation of 1, which implies that we assign 95% of the prior probability mass to effect sizes between an increase or decrease of 2 points as demands increase by one standard deviation. In the majority of projects, we want to center our prior for our parameters of theoretical interest on 0, as this does not introduce bias in favor of our hypothesis (Gelman, 2009). In other words, by centering the prior on 0, we retain the advantages of prespecifying that large values are unlikely, but we do not bias the model towards negative or positive parameter values. This is advantageous when estimating a parameter for the first time. On the other hand, if we attempt to replicate an earlier finding, it might be advantageous to use the results from that earlier study as priors in our new study to observe how much the probability distribution shifts with novel data.

For the standard deviations and the sigma parameter we specify the prior $Normal_{+}(0, 0.5)$. As standard deviations cannot take on negative values, *brms* automatically truncates these priors at 0 if one specifies them to be normal. Without any additional information, in our experience it works reasonably well to take the prior on the fixed slope and cut the standard deviation in half for the standard deviation and sigma prior. Finally, it is recommended to specify

the LKJ(2) prior for the correlation parameter[3], as this prior seems to be weakly informative across many different random correlation matrices (Lewandowski et al., 2009; McElreath, 2020). We visualized our four prior probability distributions in Figure 2.

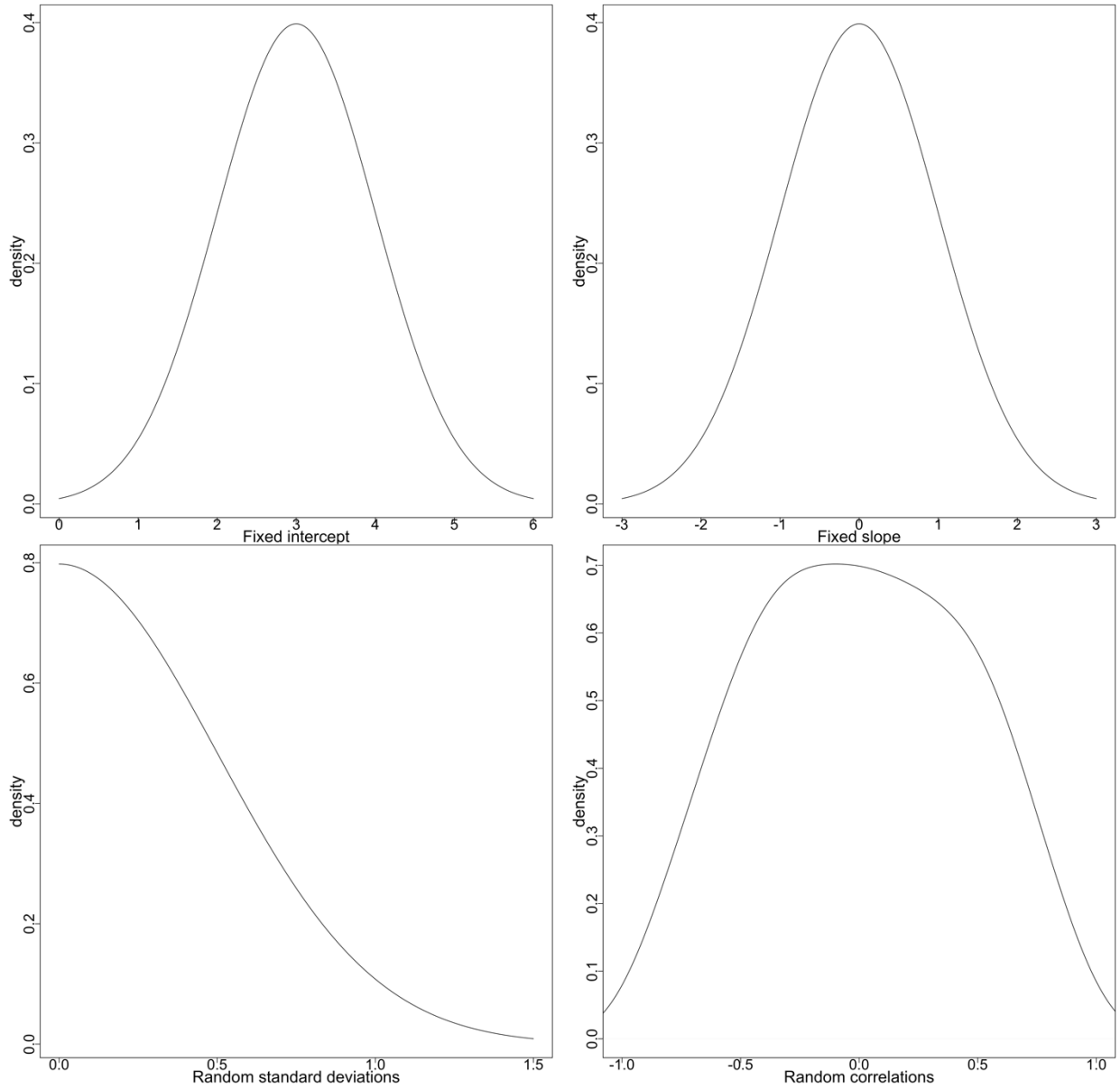

Figure 2. Prior probability distributions for the parameters in our model.

[3] We only learned about this prior while preparing this manuscript and will have to start following this advice in our own research.

Fitting the model in brms. In estimating our Bayesian model, we will regress alcohol intoxication on self-control demands (reported prior to onset of alcohol use) and will include both a random intercept and a random slope for demands to allow intercepts and slopes to vary across individuals in the sample. We can specify the model formula with the *brm* command:

```
model.intox <- brm(formula = alc.intox ~ 1 + demands + (1 + demands | PID), # model formula
        data = data.intox, family = gaussian(),  prior = priors.intox,
        chains = 4, iter = 2000, sample_prior = TRUE)
```

The *brm* command can be used for models with a variety of outcome distributions, which we specify with the *family* term. In this case, as we foreshadowed, we use a Gaussian distribution. If we do not specify our priors with the *prior* term, default priors will be used. These were strategically chosen by the developers to be appropriate in as many scenarios as possible. However, whether these defaults are in fact appropriate depends on the data and research question at hand. We recommend to always specify at least the most relevant priors, as outlined above. As explained before via the marbles analogy, the model is estimated using Hamiltonian Markov Chain Monte Carlo (MCMC) sampling. The *chains* argument specifies how many independent iterations of the MCMC sampler to run; typically, this should not be higher than the number of processor cores, so that calculations can be parallelized. By default, *brms* uses four independent chains, which often is sufficient to approximate the posterior distribution well (Bürkner, 2017). In the marbles analogy, each chain is a separate game of marbles in the same landscape. The *iter* argument specifies how many samples from the posterior distribution should be drawn; in the marbles analogy, each sample is a marble. In each iteration, the chain 'shoots' a marble from one point in the distribution to another, accepting or rejecting the point where the marble settles down based on a probabilistic acceptance criterion. By default, *brms* uses 2,000 iterations per chain, and runs diagnostics to determine whether the samples adequately represent the posterior distribution. If there are any indications that this is not the case, *brms* models will produce warnings that the posterior distribution might not have been properly explored, in which case the recommendation often is to increase the number of iterations.

Assessing model convergence. We need to ensure that our Bayesian model converged and fits the data well before we can interpret the results. The *brms* package gives us several ways to check this. First, we can visually inspect whether the four chains mixed. The plot() function

produces a trace plot (see Figure 3 for two trace plots, one indicating that the chains mixed well, one indicating that the chains did not mix as you can observe the traces for the four individual chains). If the chains mix well, this suggests that multiple chains arrived at similar values for the posterior distributions, which indicates that the posterior distribution has been explored well. By contrast, if the chains do not mix, this suggests a problem with the model – perhaps it has not converged yet, or the model may be mis-specified. A second indication that the chains are mixing well is that the variability within each of the four chains is approximately the same as the variability between the four chains. This ratio is represented by the *Rhat* statistic, which should be close to 1.00 for all parameters in the model. Third, for each parameter, there should be sufficient independent samples to get a good representation of the posterior. Although we asked for 2,000 samples from four chains, sometimes the algorithm "gets stuck" in the same region of the posterior, and samples there repeatedly. We can say that these samples are not independent, because they do not provide unique information about different regions of the posterior. The *effective sample size* is an estimate of the number our independent samples. This number should be sufficiently high; one could set an absolute threshold, like 1,000, or use the rule of thumb that the effective sample size should be larger than 10% of the number of samples across the four chains (McElreath, 2020). In our example, we have 4,000 samples (4 x 1,000, as half of the samples are discarded as warmup/burn-in), and thus effective sample size should be larger than 400 for each parameter. Both *Rhat* and effective sample size can be retrieved from the model output. Again, if any of these metrics suggest convergence problems, *brms* will print a warning paired with a helpful suggestion, such as increasing iterations, adding a *control* term to the command (such as increasing adapt_delta or max_treedepth), or considering a different prior. A more detailed discussion of convergence issues, warnings, and potential fixes can be found at https://mc-stan.org/misc/warnings.html.

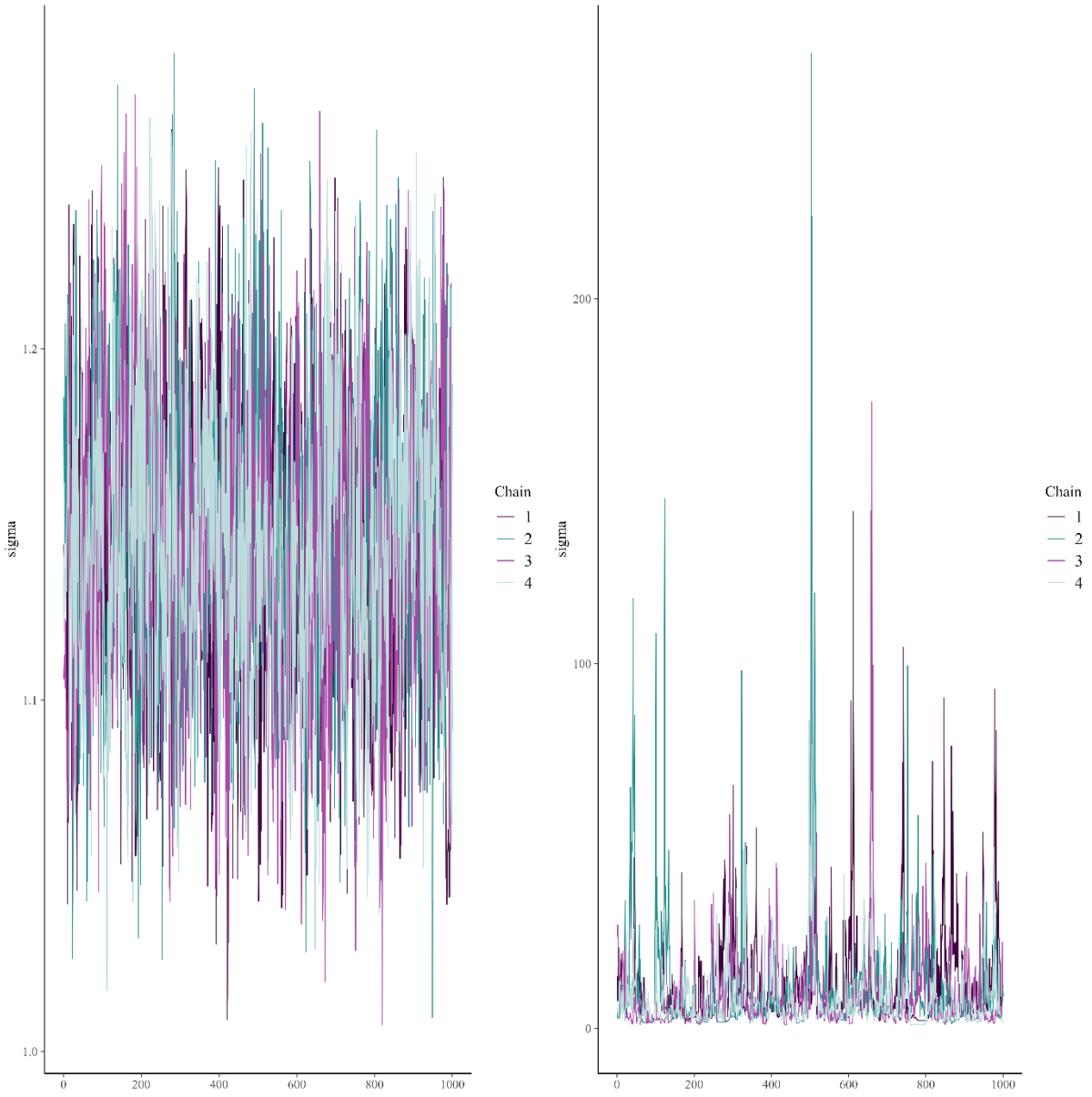

Figure 3. Trace plot indicating that the chains mixed (left) and a poorly mixed trace plot showing clear signs of separation across chains (right).

Assessing model fit. To assess whether our model fits the data well, we perform a posterior predictive check by simulating new values from the joint posterior distribution for our outcome, then compare these to the observed data. If our model fits the data well, the distribution of simulated outcome values should closely resemble the distribution of observed outcomes in our dataset. Such a simulation can be easily carried out and plotted via the *pp_check()* command, which in our case produces the plot in Figure 4:

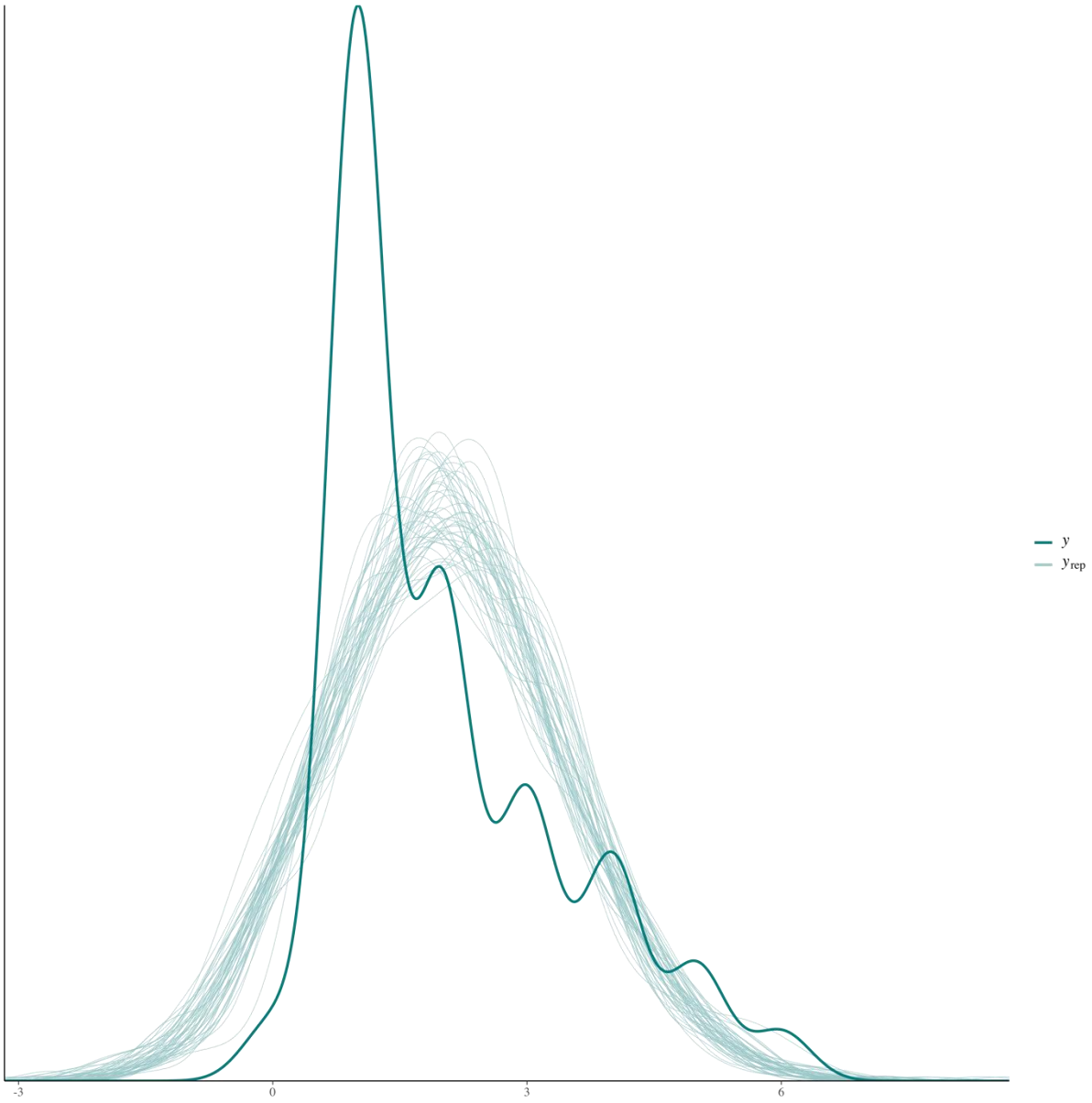

Figure 4. Posterior predictive check of the model predicting alcohol intoxication with a Gaussian distribution. The line corresponding to *y* represents the observed data, and the lines corresponding to y_{rep} represent the distributions generated by simulating from the model.

We can see that our model does not fit the data at all, because the model-predicted data all follow a normal distribution, whereas the observed data follow a right-skewed distribution, and the central tendency of both distributions differs. This should be hardly surprising to us. First, statisticians have warned against the use of analyzing Likert-scale items with linear regression for decades and have recommended to use ordinal models instead (Coombs, 1960).

Second, we need to consider the data-generating process of alcohol intoxication reports. It is reasonable to assume that by-and-large subjective alcohol intoxication increases as people consume additional alcoholic drinks. This suggests a sequential process, wherein higher levels of alcohol intoxication are only reached after lower levels were reached earlier in the drinking episode. In responding to the ordinal alcohol intoxication item, participants are attempting to quantify their level of alcohol intoxication (which may well be linear) by choosing among rank-ordered categories. Choosing between, for example, "very" and "very much" reflects a nonlinear threshold, where the probability of choosing the greater option increases slowly at first, and then very quickly after some threshold, and the declines as the probability of choosing the next response option increases. Luckily, such a sequential ordinal model (Tutz, 1991) can be easily implemented in *brms* (Bürkner & Vuorre, 2019) by specifying *family = sratio*. Let us fit our updated model with a sequential ordinal outcome distribution and perform another posterior predictive check (Figure 5):

```
model.intox.seq <- brm(formula = alc.intox.ordinal ~ 1 + demands + (1 + demands | PID),
                       data = data.intox, family = sratio(), prior = priors.intox, # updated family
                       iter = 10000, warmup = 2000, chains = 4, sample_prior = TRUE, # increased iter
                       save_pars = save_pars(all = TRUE), control = list(adapt_delta = .95))
```

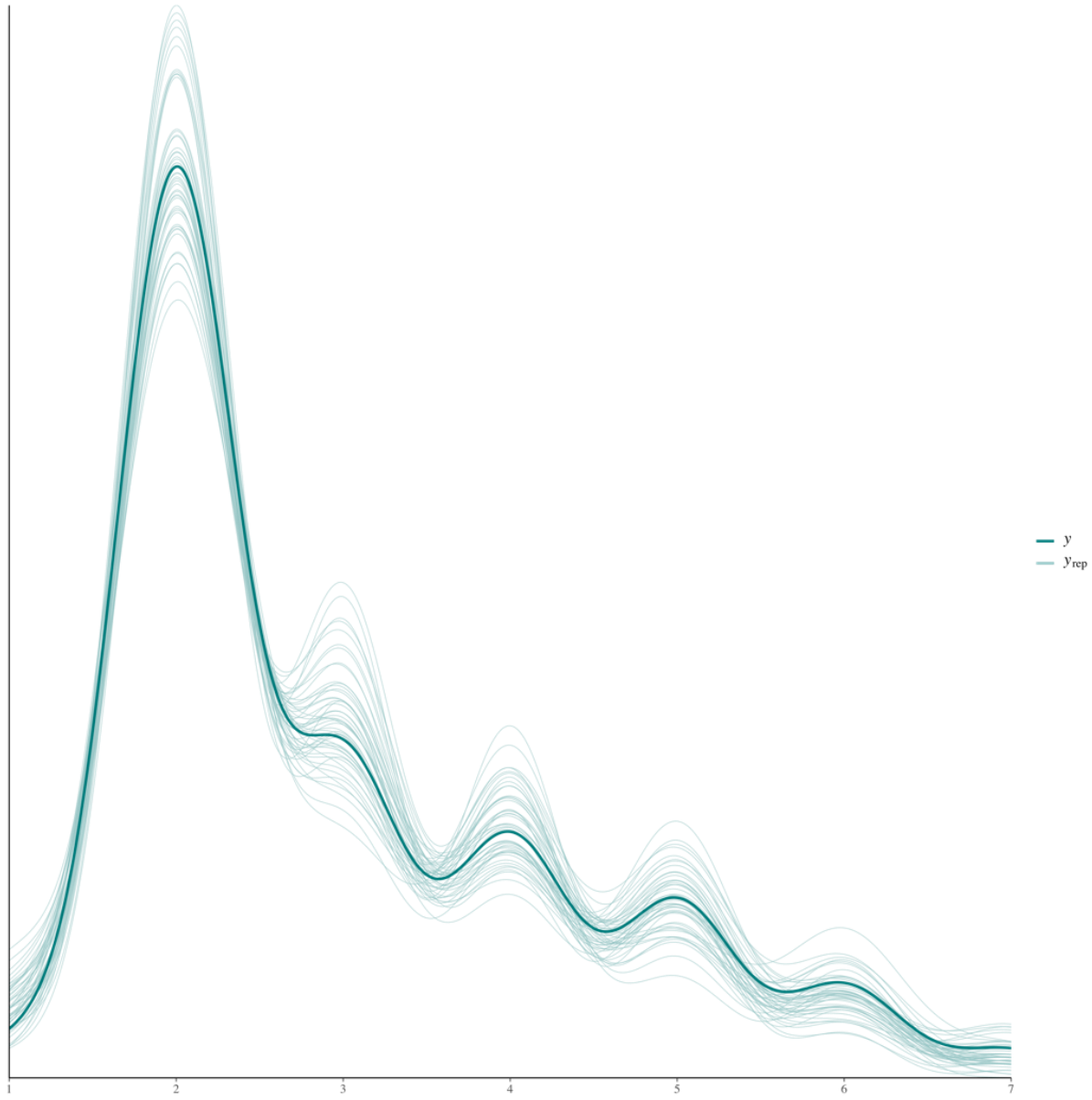

Figure 5. Posterior predictive check of the model predicting alcohol intoxication with a sequential ordinal distribution. The line corresponding to *y* represents the observed data, and the lines corresponding to y_{rep} represent the distributions generated by simulating from the model.

We can see that this model fits our data much better, which is unsurprising given that it more accurately represents a plausible data-generating process. As the *Rhat* values and effective sample sizes look good too, we will proceed with interpreting the results of our model.

Bayesian inference. Remember that the posterior distribution is the product of our pre-specified prior distribution and the likelihood (i.e., data). We can plot the posterior distribution with the *mcmc_plot()* command (Figure 6).

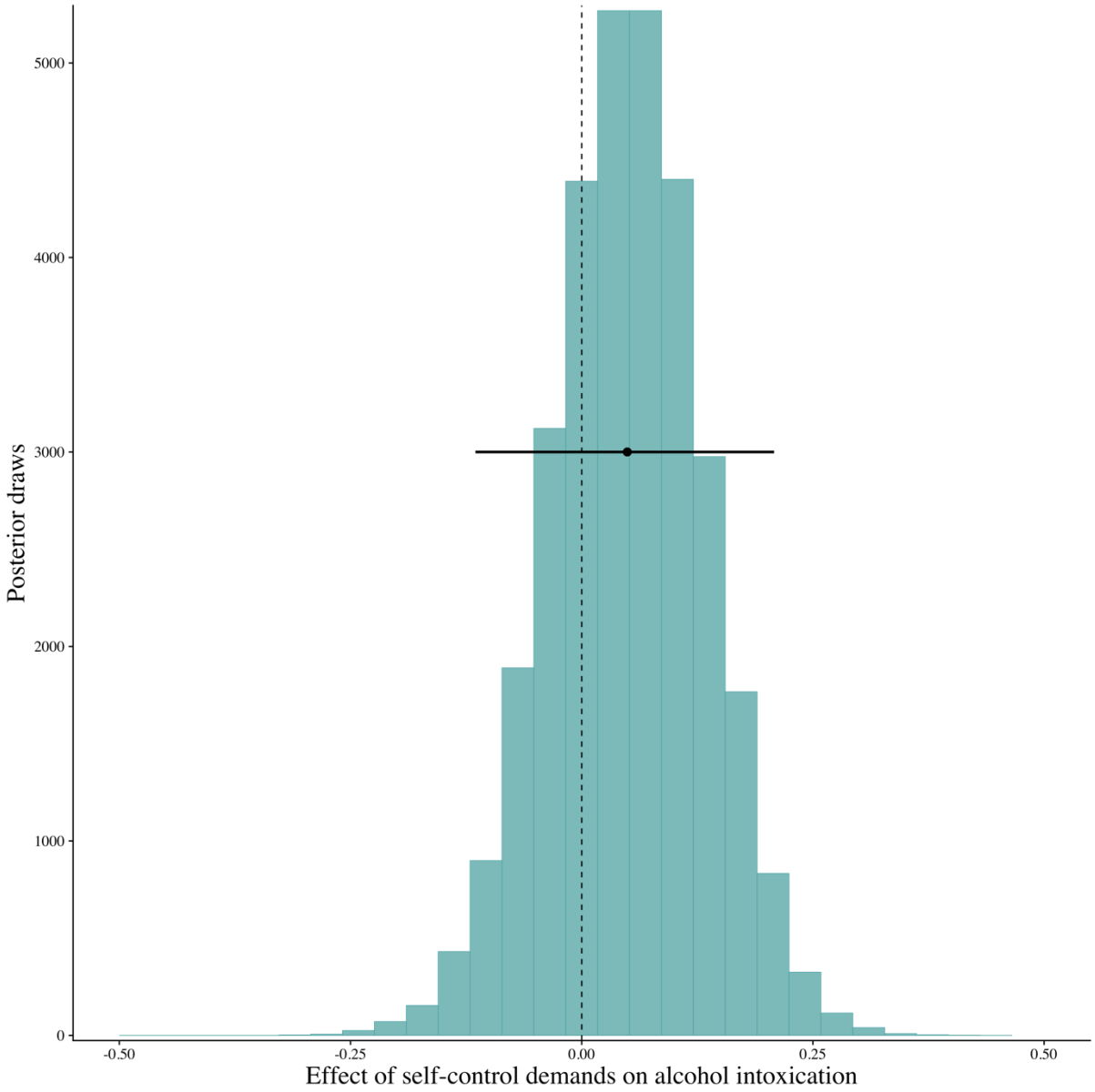

Figure 6. Posterior distribution of the fixed main effect of self-control demands on alcohol intoxication. Plotted on top of the distribution is the 95% Bayesian credible interval.

Here, we learn that self-control demands on drinking days does not appear to be associated with alcohol intoxication (b = 0.05, 95% CI = [-0.11, 0.21]). As this is an ordinal model, we need to exponentiate these values to learn by how many points alcohol intoxication

increases as demands increase by one standard deviation (OR = 1.05, 95% CI = [0.90, 1.23]). Whereas this would be the end of many frequentist analyses ("not significant"), the posterior distribution reveals more than might be immediately obvious. Recall that we specified a priori that we believe with 95% certainty that the effect size lies somewhere between an increase or decrease of 2 points. You can see that once we updated our beliefs by adding the data to the model, this uncertainty has decreased considerably, and we can now be 95% certain that the effect lies somewhere between a decrease of ~ 0.1 points and in increase of ~ 0.2 points. Thus, we can conclude that most likely the effect is trivially small, but a miniscule plausibility of a small-but-meaningful effect in the expected direction remains.

If we wanted to calculate a Bayes factor for the hypothesis that the effect of self-control demands on alcohol intoxication is unequal to 0, we would compare a model including demands as a fixed effect (alc.intox~ 1 + demands + (1 + demands | PID)) to a null model without it (alc.intox ~ 1 + (1 + demands | PID)). We can then feed both models into the *bayes_factor()* command to quantify the evidence for our hypothesis (Schad et al., 2022). We learn that the Bayes factor in favor of our hypothesis (BF_{10}) is 0.10, or one in ten, which means that the data provide ten times more support for the null hypothesis than for our informative hypothesis. However, when using default *brms* priors, the Bayes factor in favor of H_0 is only 4.12, illustrating the importance of preregistering one's priors.

Running example 2: Fitting models with complex outcome distributions

For our second example, we will explore whether people are more likely to drink and consume more drinks on days they reported higher self-control demands. Number of alcoholic drinks consumed is a count variable, as it can only take on non-negative integer values. Count variables are often modeled using the Poisson or negative binomial distribution. However, number of drinks consumed in EMA data tends to be zero-inflated, as even regular drinkers tend to abstain on 50-80% of days (Dora et al., 2022), which implies a higher number of zeroes than expected by the Poisson or negative binomial distribution. Such data can be accounted for by using mixture models. For example, a zero-inflated model represents the outcome as a count distribution, but with additional expected zeroes. A hurdle model first predicts the probability of not drinking, and then separately predicts the number of drinks consumed on drinking days. Based on our experience predicting alcohol use in EMA data, a hurdle model with a negative

binomial distribution for the non-zero values is often best-matched with the data-generating process for daily alcohol use[4]. However, an important first step in analysis is to choose and compare various outcome distributions. In our own work predicting the number of drinks in EMA data, we often sequentially compare zero-inflated and hurdle Poisson or negative binomial models, choosing the simplest distribution that best fits the data. We first specify some weakly-informative priors, which are based on earlier preregistered analyses of alcohol use predicted by affect (Dora et al., 2022; Dora et al., 2022). Because this model uses a logit link, we need to specify the log of our priors. For example, if we believe that participants on average consume ~4.5 drinks ± 2.7 drinks per drinking episode with 95% probability (fixed intercept), we need to specify a normal(1.5, 0.3) prior. If we believe that the effect of demands on the number of drinks per drinking episode (fixed slope) should be somewhere between ± 3 drinks, we need to specify a normal(0, 0.5) prior:

```
priors.drinks = c(set_prior('normal(1.5, 0.3)', class = 'b', coef = 'Intercept'),
            set_prior('normal(0.75, 0.75', class = 'b', coef = 'Intercept', dpar = 'hu'),
            set_prior('normal(0, 0.5)', class = 'b', coef = 'demands'),
            set_prior('normal(0, 0.5)', class = 'b', coef = 'demands', dpar = 'hu'),
            set_prior('normal(0, 0.25)', class = 'sd'), set_prior('lkj(2)', class = 'cor'))
```

Next, we fit our *brms* model. We use the *bf()* command to easily specify two separate parts of our model, one predicting the zero values (i.e., whether or not drinking occurs; "hu"), and one predicting the non-zero values (i.e., how many drinks are consumed on drinking days; "alc.drinks"):

```
model.drinks <- brm(bf(alc.drinks ~ 0 + Intercept + demands + (0 + Intercept + demands | PID),
              hu ~ 0 + Intercept + demands + (0 + Intercept + demands | PID)),
            data = data.drinks, family = hurdle_negbinomial(),  prior = priors.drinks,
            iter = 10000, warmup = 2000, chains = 4, sample_prior = TRUE, init = 0,
            save_pars = save_pars(all = TRUE), control = list(adapt_delta = .95))
```

[4] However, the distinction between the two is often theoretical, as the hurdle model assumes one distinct process producing zeros and non-zero values, while the zero-inflated model assumes two processes producing zeros.

We check the trace plots to make sure that the chains mixed, ensure that *Rhat* values are close to 1 and effective sample sizes are adequate, and perform a visual posterior predictive check (Figure 7), which shows that the model fits the data well.

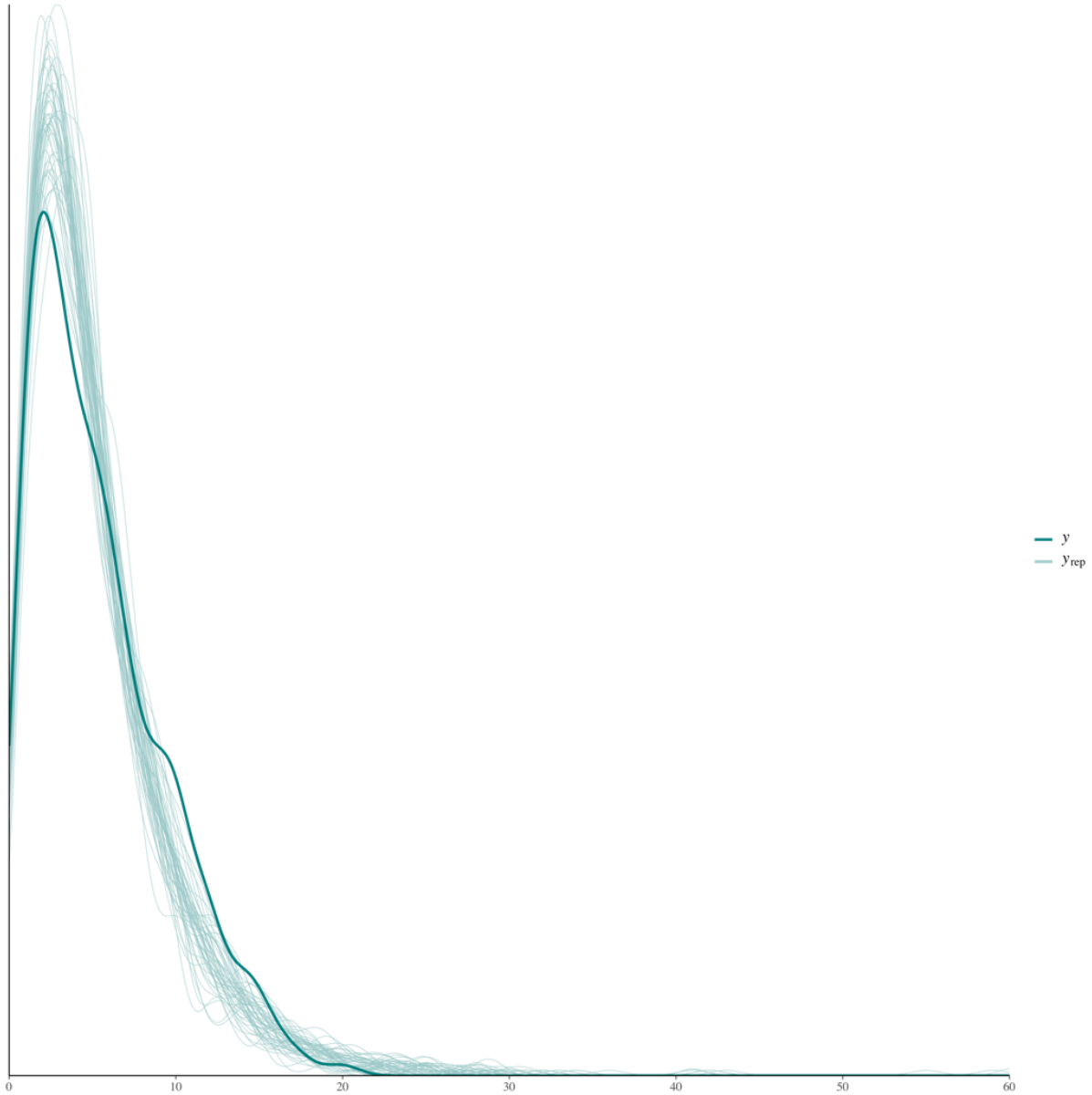

Figure 7. Posterior predictive check of the hurdle model predicting number of alcoholic drinks with a negative binomial distribution for the non-zero counts. The line corresponding to y represent the observed data, and the lines corresponding to y_{rep} represent the distributions generated by simulating from the model.

We learn that demands are not associated with the odds of drinking on any given day (OR = 0.85, 95% CI = [0.47, 1.48]), nor are they associated with the number of drinks on drinking days (RR = 0.99, 95% CI = [0.91, 1.07]). Nonetheless, we can see that the uncertainty around the effect on the count (i.e., non-zero) portion of the model is much smaller than the effect on the logit (i.e., zero) portion. Thus, we learn that we can be much more confident that higher self-control demands are not associated with drinking quantity (conclusive) than that they are not associated with the likelihood to drink (inconclusive), as meaningful effect sizes in both directions retain posterior probability. We can visualize this conclusion by plotting prior and posterior distributions on top of one another (Figure 8), which shows the improvement in posterior precision of the count portion of the model, relative to the very minor improvement in the hurdle portion.

One question you might ask yourself at this point is to what extent the priors we chose influence the results. This always depends on the chosen priors and the amount of data you have available. As a rule of thumb, less informative priors will influence the results less, and all priors will influence the results less when more data are available. For example, in the hurdle model we fitted above, let us replace our weakly informative priors on the fixed effects with uninformative flat priors that distribute equal prior probability to effects ± 3. This hardly affected the result for drinking quantity (RR = 0.99, 95% CI = [0.91, 1.07]), but the results for the likelihood to drink shifted somewhat (OR = 0.76, 95% CI = [0.36, 1.54]). Thus, in this example the prior did not matter much for the substantive interpretation of the results, but you can imagine how this might change the conclusion in other applied settings. Here, the null result for drinking likelihood is still conclusive and the uncertainty around the inconclusive result for drinking quantity is slightly bigger, meaning meaningful effect sizes larger and smaller than zero retain posterior probability. As we have argued above, we recommend using weakly informative priors and hence trust the results of that analysis more.

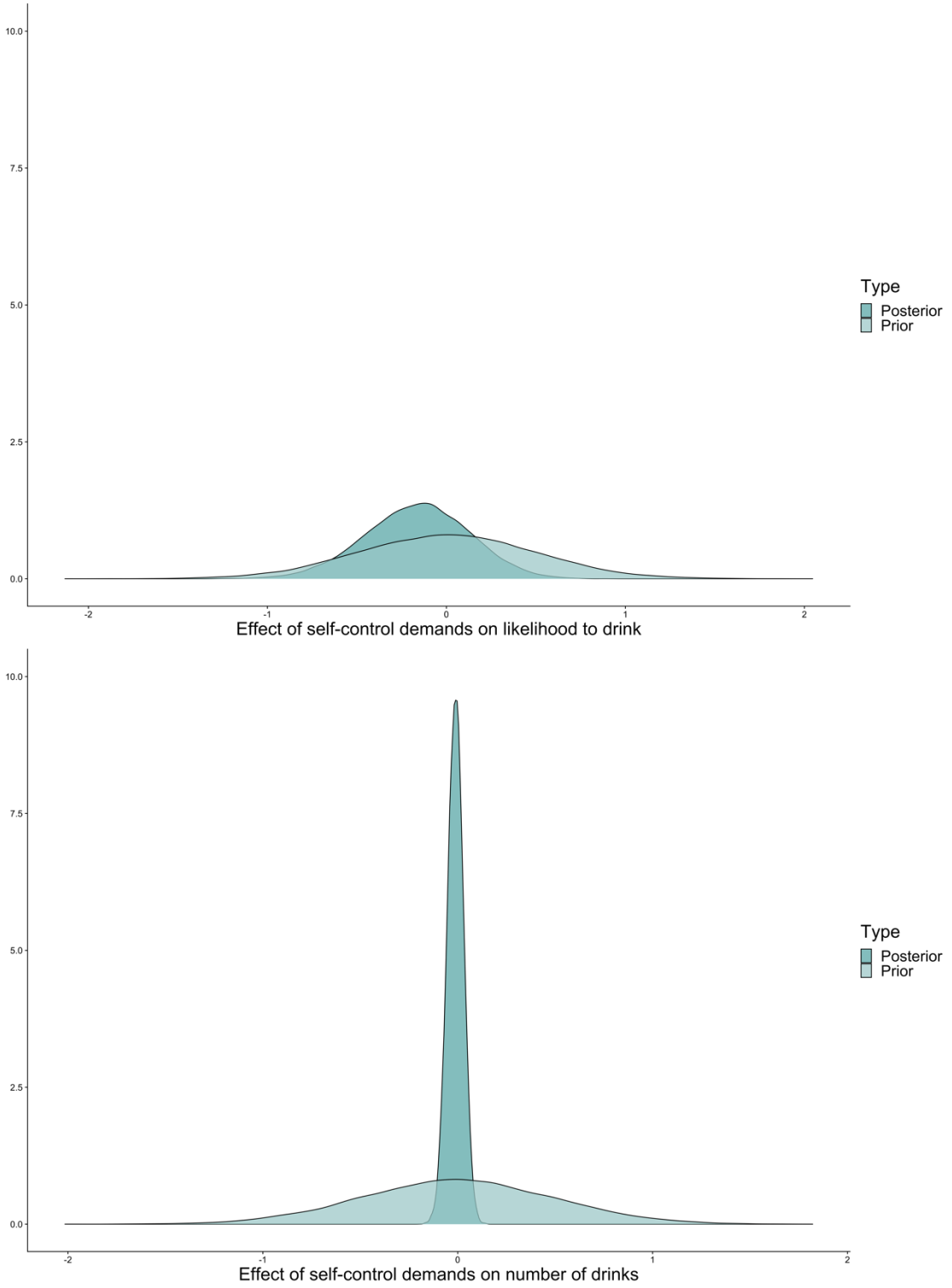

Figure 8. Prior and posterior distributions for the effect of demands on the daily likelihood to drink (left) and the number of drinks consumed on drinking days (right).

While we are mostly interested in the fixed effects of our mixed-effects models, to better understand the results of our models it is often useful to explore the random per-participant effects in our EMA data. For example, in case of null results this helps us to understand whether there is potentially a subsample of participants who display the hypothesized effect. This could imply that an important between-person moderator was missed that could explain for whom we should and should not expect the theoretical prediction to hold true. One way to do this is with the help of the *tidybayes* package (Kay, 2022). In this case, we have plotted the random per-participant effects of demands on the number of drinks consumed during drinking episodes for ten of our participants (it is hard to plot slopes for hundreds of participants in a visually clear way; Figure 9). We can see that the slopes differ somewhat and especially the intercepts differ substantially between participants. This type of plot can help us learn to understand what is going on in our data.

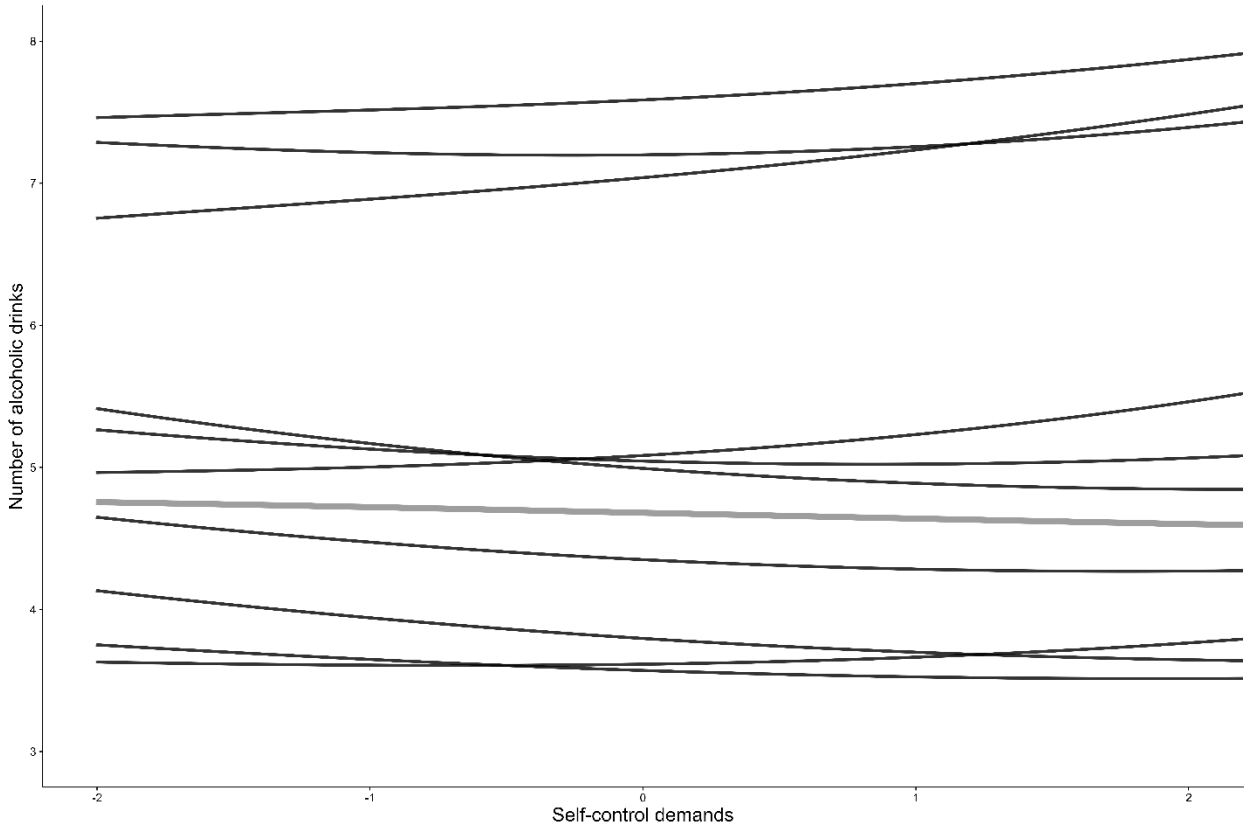

Figure 9. Per-participant random slopes (in black) surrounding the fixed effect (in grey) for the effect of perceived self-control demands on the number of drinks consumed during drinking episodes.

Running example 3: Accounting for missing data in our Bayesian models

For our third example, we will demonstrate how to account for missing data in Bayesian models using multiple imputation. We would like to predict whether people are more likely to experience negative alcohol-related consequences following drinking on drinking days they reported higher self-control demands. Commonly, EMA researchers assess multiple alcohol consequences and then sum them for each drinking episode, so that a higher score reflects more reported consequences (Wray et al., 2014). As these "variety scores" ignore the uniqueness of each consequence (e.g., experiencing a hangover vs injury), and reflect an assumption that all consequences are interchangeable in severity (as each experience equally increases the sum score by one), we prefer to predict each consequence by itself. Here, we will show the analysis predicting the likelihood of experiencing a hangover. Because we expect the likelihood of experiencing a hangover to be higher after more intense drinking, we will additionally predict consequences from the number of drinks consumed.

Accounting for missing data. One common struggle for EMA researchers we have not yet addressed is missing data. EMA studies almost always contain some amount of missing data, either by design or to minimize participant burden (Rhemtulla & Little, 2012) or due to participant non-response (a meta-analysis found an average response rate of 72 - 77% across 126 EMA studies; Jones et al., 2019). Multiple imputation, which describes the general approach to create multiple datasets in which we replace missing values with plausible values randomly drawn from distributions and then pool the results across these multiple datasets, is widely regarded as a state-of-the-art solution to address missing data (van Buuren & Groothuis-Oudshoorn, 2011). Although alternatives are available (e.g., full information maximum likelihood, in which we do not impute missing values but estimate the single most plausible value based on the observed data), multiple imputation has several advantages pertinent to the study of EMA data. First, MI has demonstrated greater efficiency in parameter estimation compared to maximum likelihood-based approaches (Enders, 2017). Second, modern multiple imputation methods have been designed to accommodate complex multilevel and nonlinear design (i.e., interactions and polynomial effects; Enders et al., 2020), both of which are central to the structure of EMA data and hypotheses of EMA design. Third, FIML only accounts for data

missing on Y but not X at the lowest level of clustering, meaning it uses listwise deletion for any observation that is missing a value on a predictor.

Although a full review of imputing missing data that is nested in clusters (e.g., nested in participants in the case of EMA) is beyond the scope of this tutorial, here we will show how we can easily fit a model on multiple imputed datasets with *brms* and how pooling inferences across these sub-models is straightforward in the Bayesian framework. For example, here we could perform a quick-and-dirty[5] multiple imputation with the *mice* package (van Buuren & Groothuis-Oudshoorn, 2011) using the following code:

```
ini <- mice(data.conseq, maxit = 0)
meth <- ini$meth
meth[c(8:11)] <- "pmm"
meth[c(13)] <- "2l.binary"
pred <- ini$pred
pred["control.fixmood",] <-     c(-2, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1)
pred["control.fixthought",] <-  c(-2, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1)
pred["dealt.stress",] <-        c(-2, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1)
pred["felt.overwhelm",] <-      c(-2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1)
pred["alc.hangover",] <-        c(-2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0)
data.conseq.imp <- mice(data.conseq, pred = pred, meth = meth, m = 10, maxit = 20)
```

We will use the data.conseq.imp object, which contains the 10 imputed datasets, in our model fitting below. Consequences were either endorsed or not endorsed for each drinking episode, meaning they are a binary outcome which we will model with the *bernoulli()* family. Once more, we need to remember that our priors are on the log-scale. Our priors specify that we believe that a hangover is experienced roughly every five drinking episodes at average levels of demands and drinks, and that experiencing a hangover would be no more or less likely than three times for any increase in one standard deviation in demands or one alcoholic drink:

[5] It really is quick-and-dirty, we would not be satisfied with this imputation model in our substantive research but it works here due to low amount of missingness and the purpose being illustrating the fitting of a Bayesian model on imputed datasets.

```
priors.hangover = c(set_prior('normal(-1.5, 0.5)', class = 'Intercept'),
            set_prior('normal(0, 0.5)', class = 'b'),
            set_prior('normal(0, 0.25', class = 'sd'),
            set_prior('lkj(2)', class = 'cor'))
```

We can use the brm_multiple() command to simply fit our model on multiple datasets:

```
model.hangover.imp <- brm_multiple(alc.hangover ~ 1 + demands + alc.drinks + (1 + demands +
            alc.drinks |  PID), data = data.conseq.imp, prior = priors.hangover, family =
            bernoulli(), iter = 4000, chains = 4, sample_prior = TRUE, save_pars = save_pars(all
            = TRUE), control = list(adapt_delta = .95))
```

After fitting this model, *brms* warns us that parts of the model may not have converged as indicated by *Rhat* values larger than 1.05. Fitting a model on multiple datasets often results in false positive convergence warnings, as the chains for each dataset may not overlap even when the model converged in each individual dataset. We can confirm that the model converged by inspecting the individual *Rhat* values via model.hangover.imp$rhats, which clarifies that the *Rhat* values in each of the datasets is exactly 1. We can also perform a posterior predictive check on our brm_multiple() object, however this will perform the check only in one of the imputed datasets (Figure 10). Whereas pooling results across multiple frequentist models is not straightforward and can lead to biased inferences (Zhou & Reiter, 2010), in a Bayesian analysis we can achieve a pooled inference by simply combining the posterior draws of the sub-models. Once again, this results in a single posterior distribution (Figure 11).

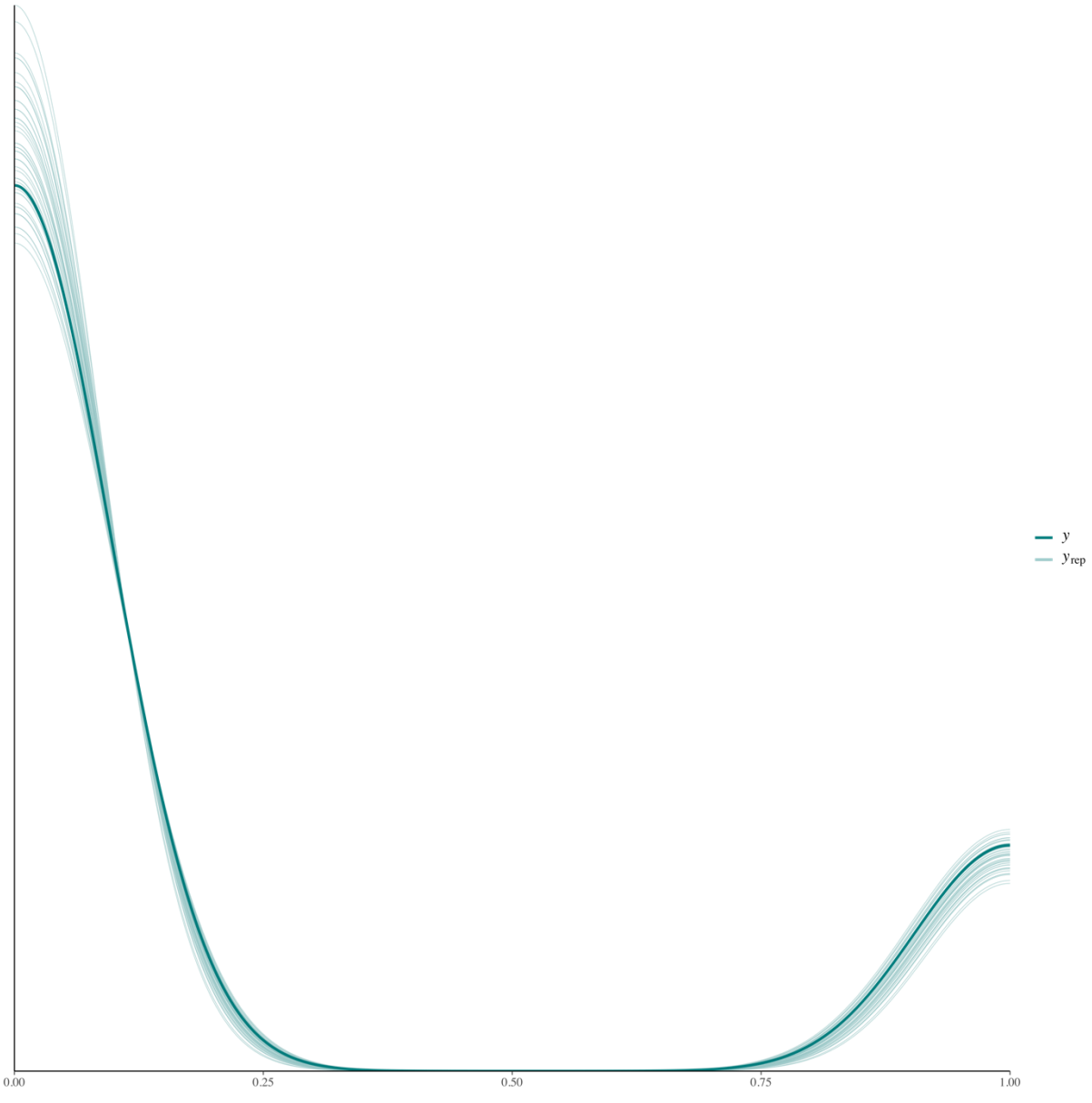

Figure 10. Posterior predictive check of the model predicting the likelihood of reporting a hangover. The line corresponding to *y* represents the observed data, and the line corresponding to y_{rep} represents the distribution generated by simulating from the model.

We can see that, according to a frequentist interpretation of the results, demands are not significantly associated with the likelihood of experiencing a hangover (OR = 0.79, 95% CI = [0.59, 1.07]). However, note that the Credible Interval is very wide here indicating high uncertainty regarding the population-level effect size. In a Bayesian analysis, there is nothing

magical about the value of 0 (or 1 in the case of odds ratios). Whether this result provides evidence in favor of or against demands being associated with a reduced likelihood to experience a hangover the same day depends on what effect sizes we consider meaningful. For example, with the following code we can realize that the posterior probability that a 1-standard-deviation increase in demands is associated with at least a 10% lowered likelihood to experience a hangover (assuming this is the smallest effect size we care about) is 80%:

```
model.hangover.imp %>%
 gather_draws(b_demands) %>%
 filter(.value <= -0.1) %>%
 nrow() /40000 * 100
```

The posterior probability that it is associated with at least a 20% lowered likelihood is only 56%. On the other hand, the posterior probability that the effect is positive is only 7%. Thus, controlling for the number of drinks participants consumed, the data overall provide some evidence that participants are slightly less likely to report a hangover on days they report higher self-control demands. The uncertainty in this conclusion is large, and thus more data are required in the future to improve our confidence in this conclusion.

Unsurprisingly, number of drinks consumed was a consistent predictor of consequences. For example, our model estimates that with every additional drink the likelihood of reporting a hangover increased by 21% (95% CI = [11%, 32%]. As this may be hard to interpret, we like to plot this effect with the *conditional_effects()* command (Figure 12). The plot shows that our model estimates that hangovers are rare even after five drinks, and it takes roughly fifteen drinks to reach 50% probability. But we can also see that the uncertainty interval widens with increasing numbers of drinks, as those are less often reported. Thus, our main conclusion from this result is that, contrary to previous findings indicating that hangover severity declines with age (Tolstrup et al., 2014; Verster et al., 2021), college students in our datasets seem to be much more immune to hangovers than the authors of this paper.

In summary, the results of our Bayesian analysis are more consistent with a recent EMA study (Walters et al., 2018) and do not corroborate two earlier studies that reported such

associations (DeHart et al., 2014; Muraven et al., 2005). The current study does not provide support for an association between perceived self-control demands and alcohol use among college students. In the case of subjective alcohol intoxication, a Bayes factor provided 10-fold evidence *against* such a prediction.

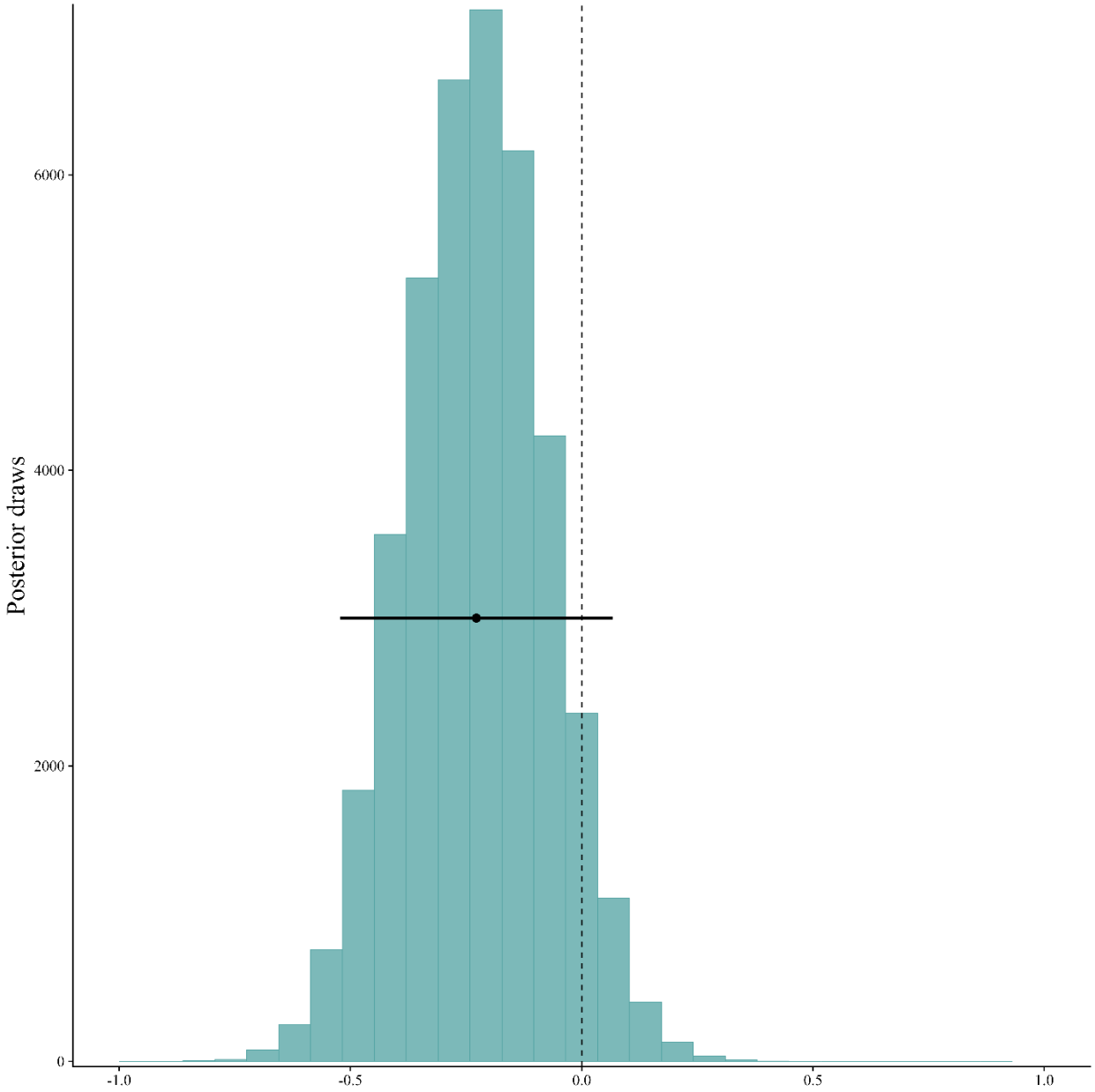

Figure 11. Posterior distributions of the fixed main effect of self-control demands on the likelihood to report a hangover. Plotted on top of the distribution is the 95% Bayesian credible interval.

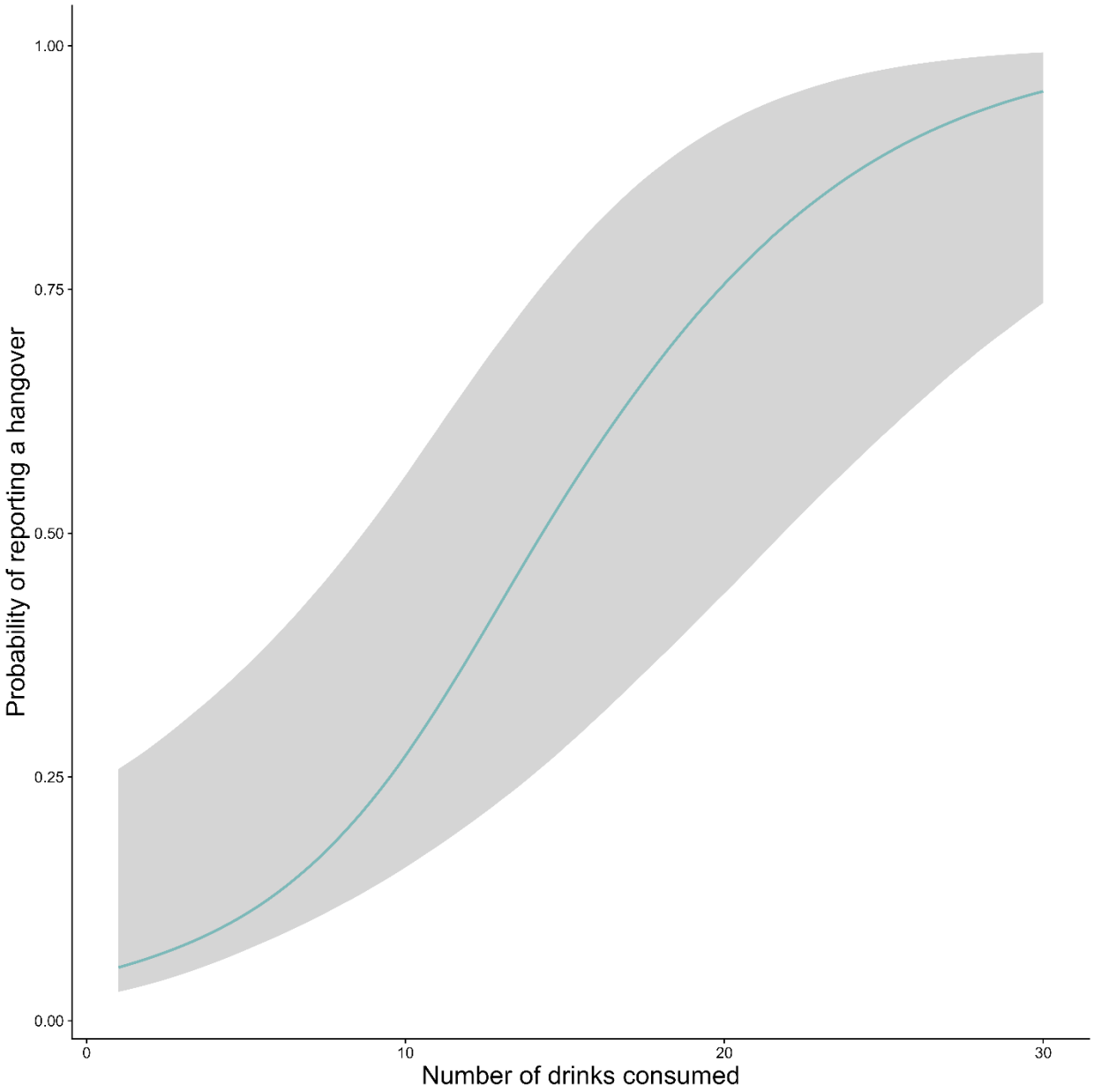

Figure 12. Effects plot displaying the estimated increased probability to report a hangover with additional alcoholic drinks consumed.

Discussion

In the present tutorial, we aimed to provide a gentle introduction to how EMA data can be analyzed using Bayesian (generalized) mixed-effects models. We presented several strengths of the Bayesian approach for EMA data analysis. These are 1) how weakly informative priors aid convergence for models with random effects, 2) how weakly informative priors reduce the risk of overestimating the true effect size, and 3) how imputation of missing data can be implemented in a Bayesian framework. However, we argue that the Bayesian approach has additional advantages that are especially suitable and important when analyzing EMA data, which are expensive and time consuming to collect. Specifically, Bayesian models de-emphasize mindless conclusions based on defaults and instead emphasize pre-specifying a prior belief for each model parameter and deciding which effect sizes we deem *plausible and meaningful* prior to conducting our analysis. This is especially compatible with an Open Science perspective (Munafo et al., 2017), where it is important to be transparent about what we expected from our data analysis *prior to conducting a study*. Moreover, by quantifying and presenting the uncertainty of our models after analysis, the Bayesian perspective encourages us to provide interpretations of our models that are more closely grounded in our data, rather than treating significance as a license to interpret our effects however we wish (Cohen, 1994; Cortina & Landis, 2011). This also provides us a better understanding of when our results provide strong evidence in favor of the *presence or absence* of an effect, as well as when our results turn out to be *inconclusive*.

There are many theoretical and methodological issues in EMA research that we have not addressed. First, it is critical to harmonize our statistical test with our theoretical prediction (Kaurin et al., 2023), especially when it comes to the time scale at which hypothesized associations play out. Bayesian EMA models allow tremendous flexibility in modeling multiple timescales from contemporary or lagged associations at multiple lags, to modeling trajectories within and across days. Alternatively, we may want to estimate an autoregressive correlation or an autoregressive moving average (Hamaker & Dolan, 2009) to model temporal dynamics in a variable. Location-scale models allow prediction of not only levels, but variation (Williams et al., 2019). You might want to apply growth curve modeling (Armey et al., 2011) or survival analysis (ten Broeke et al., 2020) to your EMA data. All of these modeling procedures and more are implemented in *brms* along the vast array of outcome distributions, enabling you to perform all possible EMA analyses in the context of one software package, which makes learning *brms* an extremely efficient and rewarding endeavor. An advantage of fitting such complex models in

a Bayesian framework is once more that priors help with parameter estimation and model convergence. One potential limitation of (generalized) linear mixed-effects models worth highlighting is that when studying lagged associations, these models do not account for the unequal time that passed between two consecutive EMA surveys. Recently, some work has been done to develop continuous-time models in which the lagged association decays over time (since it is reasonable to assume that any association that exists should get weaker as more time passes between two surveys). As of the time of writing this tutorial, it is hard to guess to what extent the discrete-time assumption biases our inferences, as simulation studies have come to different conclusions (De Haan-Rietdijk et al., 2017; Loossens et al., 2021). Continuous-time models such as the Ornstein-Uhlenbeck model, which has been used to analyze EMA data (Nowak et al., 2023), are currently not implemented in *brms* but can be specified in Stan, the infrastructure on which the package was built.

This tutorial provided a hands-on guide to Bayesian mixed-effects modeling of EMA data to EMA researchers new to Bayesian data analysis and highlights the immense flexibility the *brms* package gives us when analyzing a variety of outcomes. In reiteration, the steps we discussed are (1) defining our model, (2) defining outcome distributions and prior probability distributions for the parameters of interest, which involves consideration of the data-generating process as well as the expression of beliefs of the plausibility and meaningfulness of effect sizes, (3) fitting the model in *brms*, (4) assessing model convergence and model fit, and (5) drawing inferences via posterior distributions and Bayes factors. In this tutorial, we have not covered every aspect of Bayesian data analysis nor the analysis of EMA data. To those readers who would like to dive deeper into Bayesian data analysis, we recommend to start with the textbook by McElreath (2020) and an annotated reading list by Etz and colleagues (2018).

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