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Portfolio Exam

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Methods 3: Multilayer Statistical Modeling and Machine Learning

Professor Riccardo Fusaroli

December 15, 2022

https://github.com/mthomasen/methods_3_exam.git

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Portfolio Exam - Part 1 | Methods 3 F2022, CogSci @ AU

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12/10/2022

Knitted script for assignment 1 at page 17 to 64

Q1

- *Briefly describe your simulation process, its goals, and what you have learned from the simulation.*

- *Add at least a plot showcasing the results of the simulation. Make a special note on sample size considerations: how much data do you think you will need?*

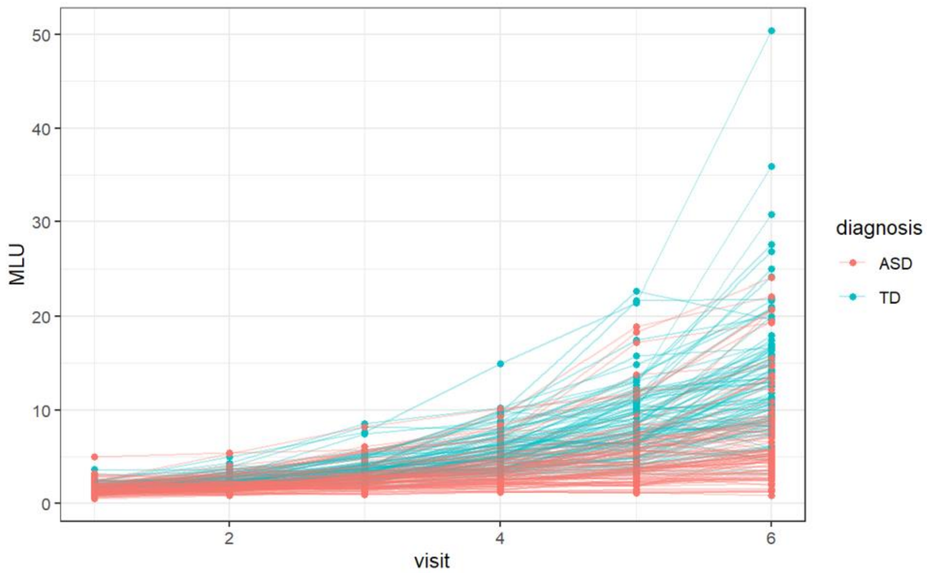
- *What else could you do to increase the precision of your estimates?*

(BR, MST) Our simulations were designed to provide an informed understanding of the model we need to build for practical purposes, such as predicting the number of participants necessary to run a significant study and to suggest factors with significance in the linguistic development of autistic children.

(BR)Considering that our cleaned experimental data was sourced from the performance of 29 ASD and 32 TD participants, the intention of raising the simulated population sample to 200 was to test the diagnostic precision of the prior data for our estimations and modeling strategy going forward.

(MST, BR) We ran a simulation of 200 participants, 100 classified as typically developed children (TD) and 100 diagnosed with Autistic Spectrum Disorder (ASD), with six independent visits each. The intercept and slope for each participant was sampled from a normal distribution based on the prior data from the literature described in the assignment; these variables were then used to simulate the Mean Length of Utterance (MLU). Plot 1 shows the results of the simulation, where we can see the MLU increases across visits and, as anticipated, it looks like there is a bigger increase in MLU for the TD participants.

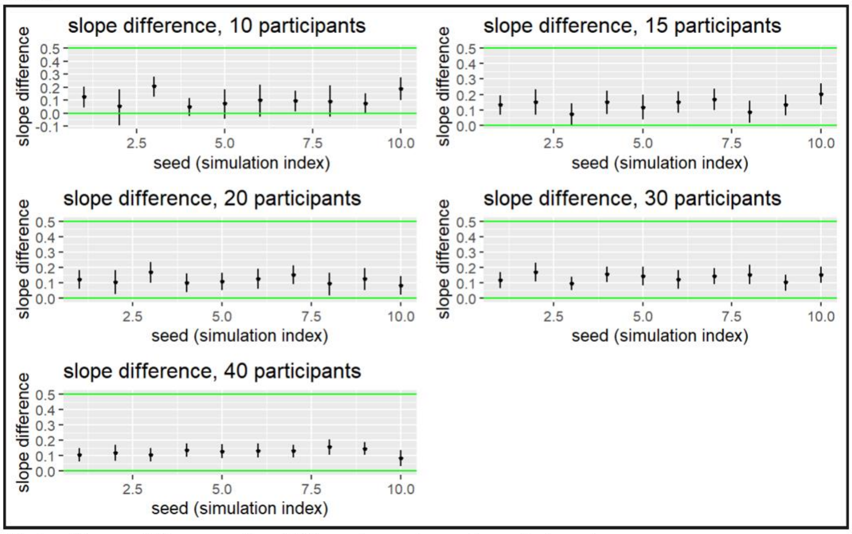
Plot 1



Note: plot 1 shows the development in mean length of utterance across visits, grouped by ASD and TD

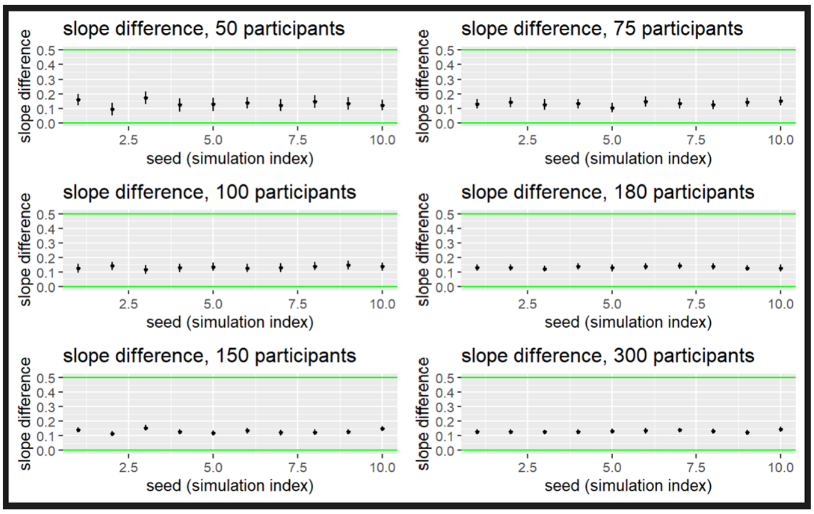
(MST) The simulated data was used to test our model and observe how it operates on data. We found that the model learns from the defined priors. To determine an appropriate sample size, a power analysis was run with the objective of finding a sample size that would give us an effect size of 0.8 or above. The result of the power analysis is visualized in plot 2 and 3. As seen in tibble 1 we achieve an effect size of 0.9 at 15 participants.

Plot 2



Note: Slope difference for different number of participants

Plot 3



Note: slope differences with different number of participants

Tibble 1

A tibble: 11 × 2

power <dbl>	number_of_participants <dbl>
0.4	10
0.9	15
1.0	20
1.0	30
1.0	40
1.0	50
1.0	75
1.0	100
1.0	180
1.0	250
1.0	300

Note: outcome of power analysis

(MST) The standard error is an indication of the precision of the estimates, so the lower the standard error, the higher the precision. A small standard error means that there is a small variation in the sample statistics across many repeats of the experiment. The standard error depends on the variability in the data and the sample size and is calculated by:

$$standard\ error = \frac{standard\ deviation}{\sqrt{sample\ size}}$$

(MST) We have already looked at how an increase in sample size affects the effect size, and the bigger the sample size, the bigger the precision and effect size. Standard deviation describes the variability in the data, which is due to the variation between the participants, but can also be caused by the methodology or some lurking variable, something that affects the results that has not been considered. Therefore, it is important to investigate what can cause the variability in the data and consider how to avoid it.

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Q2

- *Briefly describe the empirical data and how they compare to what you learned from the simulation (what can you learn from them?).*

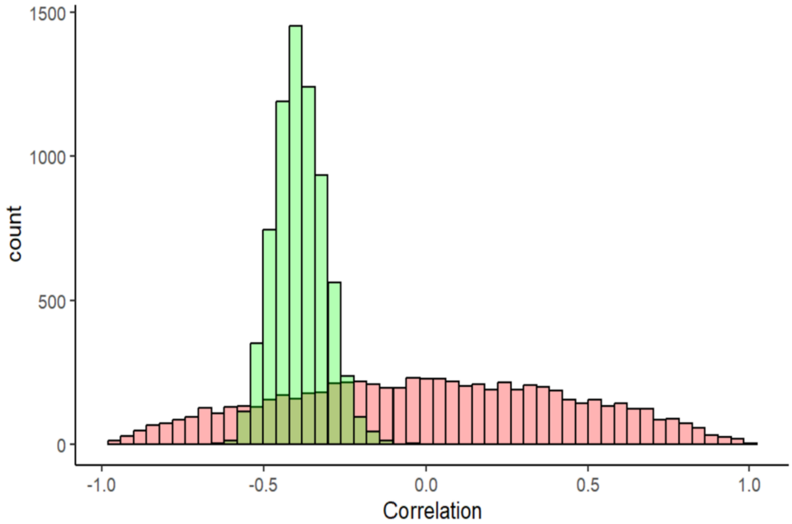
(SS) During the data cleaning process, certain data points were removed, so not all participants provided an equal number of data points. This is in accordance with the realistic expectation of children not being equally communicative at all times or having too much noise in the data, etc. (For example, the child with ID 1 only produced one data point that could be included in the final dataset). The data was recorded over the span of 6 visits, where parent-child interactions were recorded and later analyzed.

(SS) As a result of the cleaning, we obtained an R tibble containing 352 observations of 20 variables. Participants were anonymized via numeric IDs. 29 of the children were diagnosed with Autism Spectrum Disorder (ASD) and 32 were typically developed (TD). The variables describe the demographics of each participant, their diagnosis, measures of both verbal and non-verbal IQ, and their and their respective mothers' MLU throughout the 6 visits.

What did we learn from the simulated data?

(MST, SS) In contrast to the empirical data that contained incomplete data sets for some child participants, the simulated data contains the full 6 data points per participant. The simulated data showed us that MLU increases across visits and that the increase is bigger for TD children. Furthermore we saw that our model became more confident when running on the data and not just priors. Plot 4 is one of the plots made as part of the prior-posterior update check on the model. Here we see that the model becomes more confident as the standard deviation decreases for the posterior intercepts. Lastly the simulated data helped us determine a preferable sample size of 15 to get the wanted effect size of 0.8 or above.

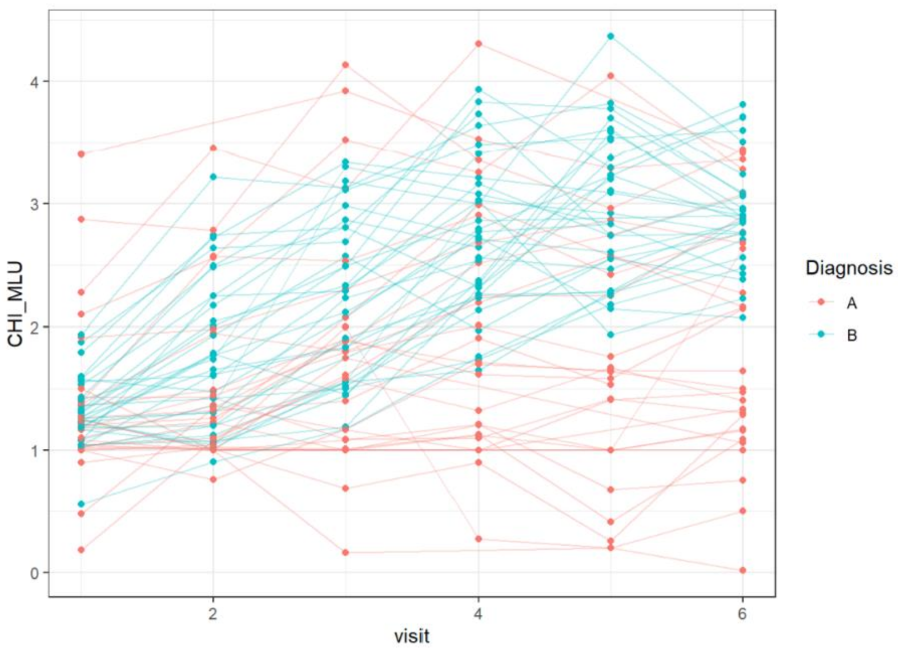
Plot 4



Note: prior-posterior update check on correlation between varying intercepts. Red is the prior and green is the posterior variable.

(MST, SS) Plot 5 is made on the empirical data and shows the MLU across visits, just like plot 1. With the empirical data we do not see as clear a difference between the ASD and TD group as we did with the simulated data. Plot 5 shows that some children still have an increase in MLU across visits but it is not all children and there is generally more variance in the empirical data.

Plot 5



Note:development in MLU across visits, grouped by diagnosis (A is children with autistic spectrum disorder and B is neurotypical children)

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-*Briefly describe your model(s) and model quality. Report the findings: how does development differ between autistic and neurotypical children*

(SS) model was defined as the following:

$$CHI\_MLU \sim 0 + Diagnosis + Diagnosis{:}visit + (1 + visit|id))$$

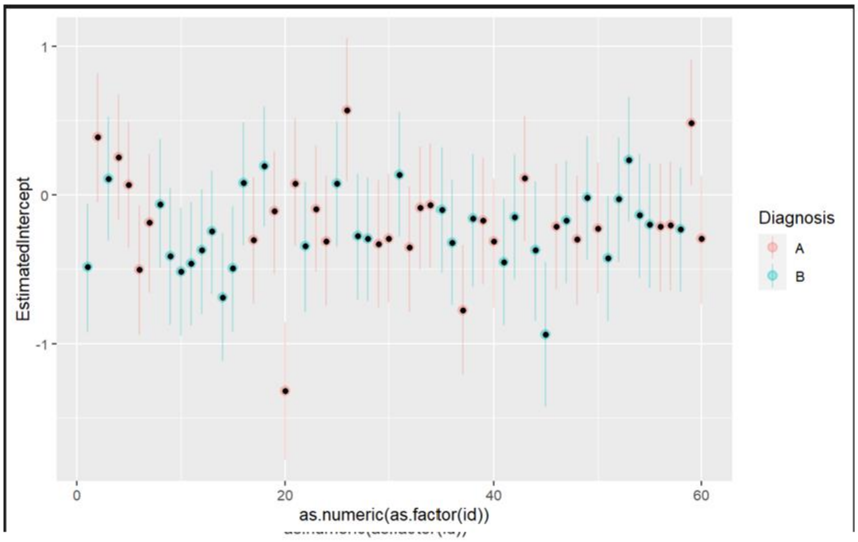
(SS) Our population-level effects gave an intercept estimate of 0.44 for autistic children with an error of 0.04 and of 0.49. with an error of 0.02 for neurotypical children. The estimate for the difference between visits was -0.01 (error: 0.02) for autistic children and 0.07(error:0.02) for neurotypical children, meaning that the model estimated autistic children to get lower MLU across visits.
The group-level effect estimated a standard deviation of the intercept between participants to be 0.42 (error: 0.05) and of the slope 0.15 (error: 0.02) which tells us that there is a lot of individual variation, which was also what we could see in plot 5.

- *which additional factors should be included in the model?*

(DK, BR) Using the population level estimates for slopes and intercept for the two groups, we want to visualize the individual variability within the data. In plot 6 (intercept) and 7 (slope) we have visualized the individual estimates. A refers to Autistic children and B refers neurotypical children. We see that there is a lot of variability between participants, especially in terms of their intercepts. With plot 6. In plot 7, we can visually confirm what the model is also telling us, neurotypical children, tend to have a higher slope. We can also see that some autistic children have a high slope, telling us that within the autistic group there are outliers.

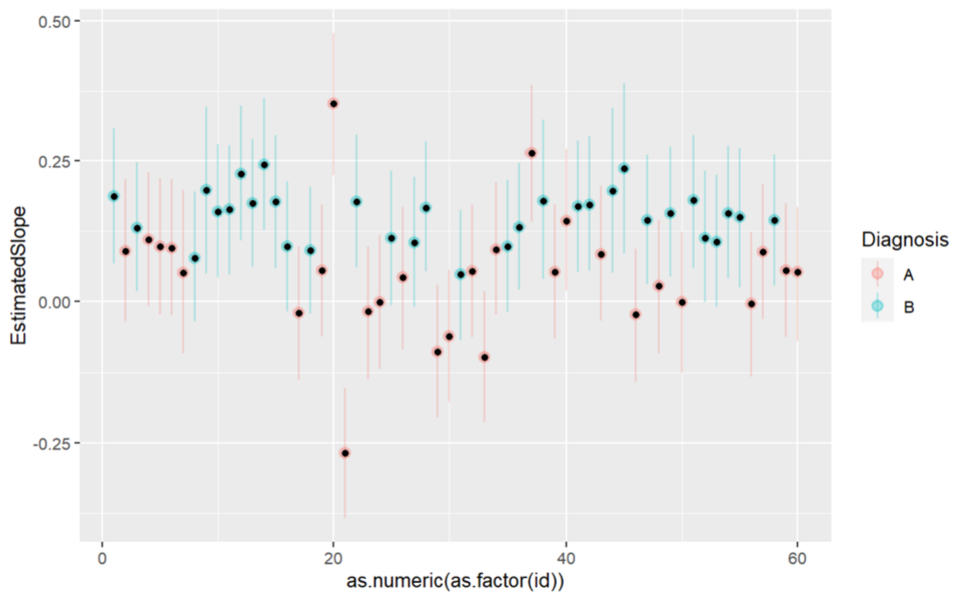
We fitted a model with random intercepts and slopes. By allowing for these random effects, we hoped to capture the individual variability between participants.

Plot 6



Note: visualization of estimates of intercepts

Plot 7



Note: visualization of estimates of slopes

Portfolio Exam - Part 2 | Methods 3 F2022, CogSci @ AU

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4/11/2022

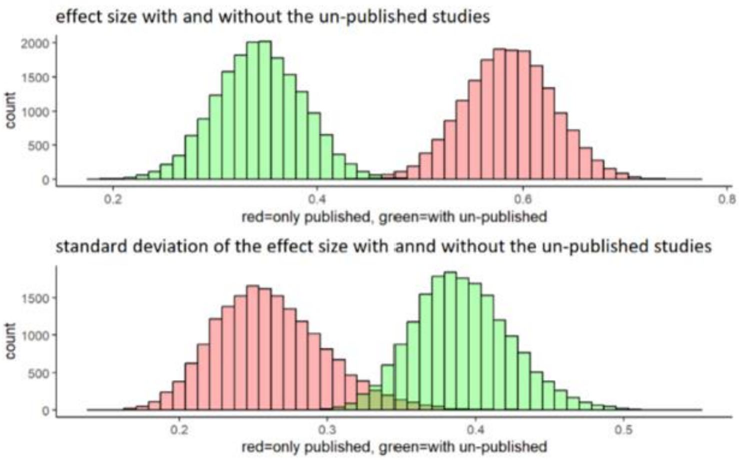
Knitted script for assignment 2 at page 65 to 97

Q1

```
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.34      0.04     0.26     0.43 1.00     4104     7005
```

(DK) In our simulation of the publication bias, we find the estimates of the intercept on *population level* to be 0.34 when unpublished studies are included and 0.59 mẃhen they are excluded. The 95% confidence interval for estimation of the intercept for the dataset containing both published and unpublished studies is (0.26 : 0.43), whereas the confidence interval for the same estimate for the data set containing only the published studies is (0.50 : 0.67).
Furthermore, the sd (standard deviation) of the intercept for data including unpublished studies is 0.43, and 0.39 for data only including published.

Plot 8



(DK) Our simulation of the true underlying effect is centered around 0.4. This means that the publication bias results in a tendency to overestimate the underlying signal. We simulate the standard deviation of the effect size to be 0.4, and a measurement error of 0.8. Therefore we can show that the publication bias also results in an underestimation of variance/deviation.

(DK) We can see this effect in plot 8, the red (only published) has a higher estimate for the intercept (effect size) and lower standard deviation, whereas the green (all studies) has a lower estimated intercept and higher standard deviation.

(DK) This conclusion is based on our findings from the simulation. However, the simulation has its flaws. It would be better to run the simulation many times, record how much the publication bias influences the estimates, and then estimate the publication bias' effect from that. Furthermore, our process of determining the chance of publication is very simple; one could imagine that many other factors, than the effect size and standard error, plays a role. Such as reputation of the author(s), experimental design, and factors which are not as easily quantifiable. With all this in mind, we should not draw strong conclusions from our simulation, but rather keep it in mind as we evaluate the results of the meta analysis.

Q2

What is the current evidence for distinctive vocal patterns in schizophrenia?

(DK, SS) After filtering NAs, the following demographic values - grouped by patients with schizophrenia and healthy controls – the dataset contained 48 studies with the demographics described in tibble 2.

Tibble 2

	M sample size	M nr. Of males	M nr. Of females	Mean age	mean_sd_age
Schizophrenia	40.5	27.3	14.3	35.9	8.39
Healthy control	31.2	17.7	14.7	34.9	8.92

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(SS) In this analysis we are using the function escalc(). The function calculates *Hedges' g,* the standardized mean difference between two groups. The value represents the effect size, and is similar to *Cohen's d*.

The formula for g is = (x1 – x2) / √((n1-1)*s12 + (n2-1)*s22) / (n1+n2-2)

$$g = (x_1 - x_2) : \sqrt{\frac{(n_1-1)*{s_1}^2+(n_2-1)*{s_2}^2}{n_1+n_2-2}}$$

and

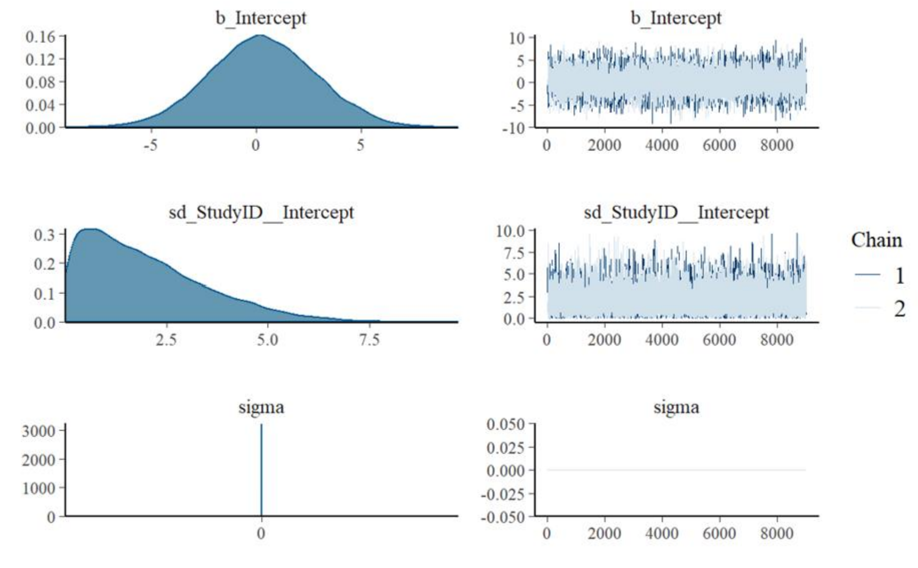
the formula for d is = (x1 – x2) / √(s12 + s22) / 2

$$d = (x_1 - x_2) : \sqrt{\frac{s_1^2+s_2^2}{2}}$$

(SS) Hedges' g takes the sample size of each group into account, and g = d when the two sample sizes are equal. Therefore we have chosen to use *Hedges' g* to calculate the effect size of the different studies.

(BR) Our model gives us an estimated intercept (effect size) of 0.3 with an estimated standard deviation of 2, which is due to the effect sizes of the studies varying a lot.

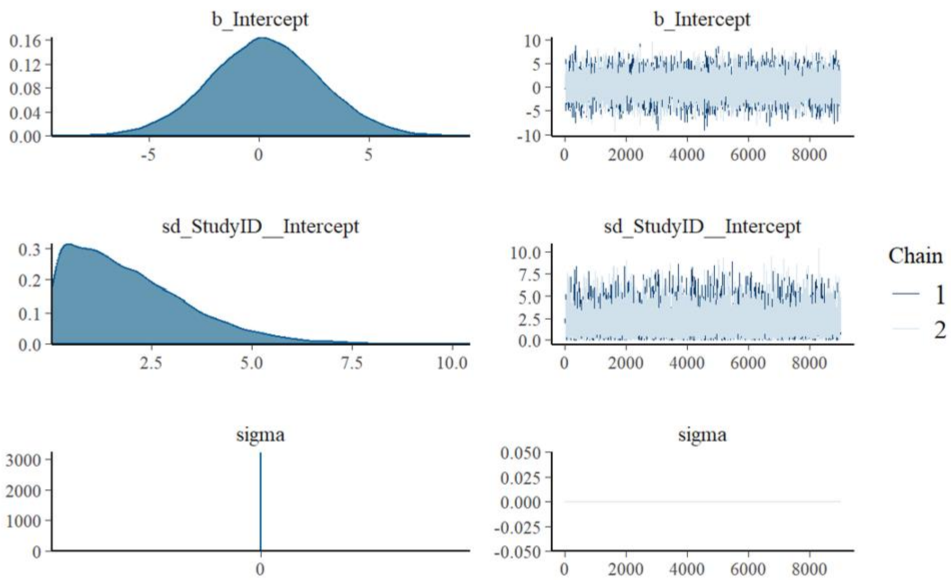
Plot 9



Note: model with priors and empirical data

(BR) As for influential studies, for example, the study by Cohen et al. (2014), with an effect size of -3.30 (sd=0.90, se=0.11, n=76) was taken into consideration, therefore we have run our model fit again. Here we have excluded the study by Cohen, to see how influential it is on the estimates.

Plot 10



Note: After removing Cohen et al. (2014)

(BR) When we compare the population-level estimate of the effect size, “Intercept” in the summary, between the estimates including the Cohen et al. study and the estimates excluding the study, we see, quite surprisingly, that there is very little difference. The estimated error remains the same, at 2.5, and the estimated effect size differs by 0.04 points from 0.29 to 0.33.

(BR, PM, MST) Publication bias is the tendency in scientific literature for studies with positive results to be published more often than those with negative results. For research investigating correlations between vocal patterns and schizophrenia diagnoses, publication bias may manifest, as a greater number of conclusions finding significance between these variables compared to studies finding potentially significant reasons to be critical of the hypothesis. This bias can lead to a skewed representation of the research data, resulting in an overestimation of the role of vocal patterns in the diagnosis of schizophrenia, and consequently, inaccurate or ineffective treatment of patients and utilization of healthcare resources.

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Portfolio Exam - Part 3 | Methods 3 F2022, CogSci @ AU

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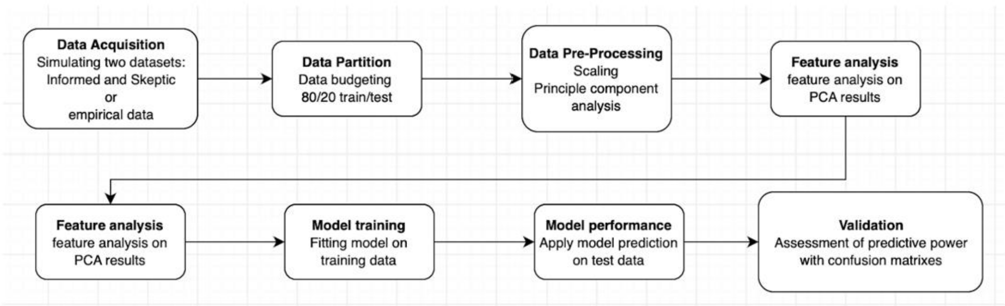
30/11/2022

Knitted script for assignment 3 at page 98 to 152

Diagram 1



Note: Diagram of machine learning pipeline (PM, MST)

(PM, MST) Diagram 1 shows the steps in the machine learning pipeline that is described further in the following section.

Data budgeting: Based on the standard practice and information presented in the lectures, we decided to split the data in 80/20 ratio.

Data preprocessing: We removed demographic data, except gender, from the data set. The data was split using initial_split() from rsample version 1.1.0. We specify we want a balanced ratio of men and women, using the argument strata = Gender. We scale the variables using the juice() and bake() functions from recipes version 1.0.3. By using the juice() and bake() functions we can define our recipe for scaling and make sure there is no leakage between the two datasets. After we split the data we run a principle component analysis using recipes version 1.0.3. We specify in the code that we want 5 principle components, from the results of the principal components analysis. A feature analysis is run to determine which variables to use when building our model.

(BR) Model choice and training: Our model is built based on the results of the feature analysis. We expect to include a random intercept in the model to account for individual differences. The model is then trained on only the training data set and made predictions of diagnosis on each trial.

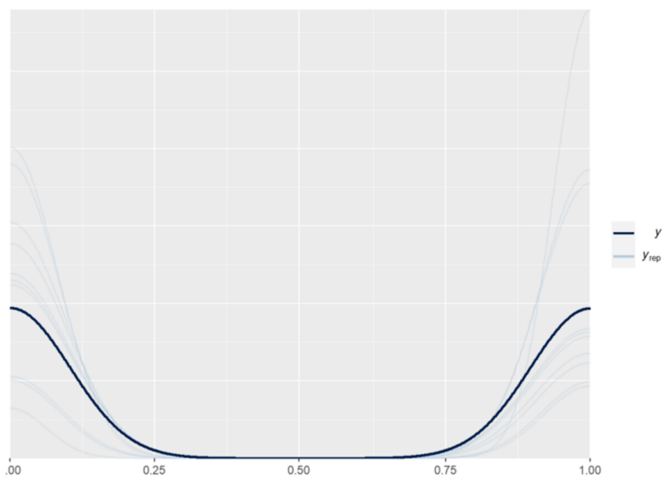
(BR) Assessment of performance: To assess the performance we ran the model on the test data and did a confusion matrix to determine how precise the model was in its predictions.

Briefly justify and describe your use of simulated data, and results from the pipeline on them.

(DK, PM) The data simulation was set to create a population of 100 pairs of schizophrenia and control and simulates 10 repeated measures with the informed and skeptical effect mean and standard deviation.

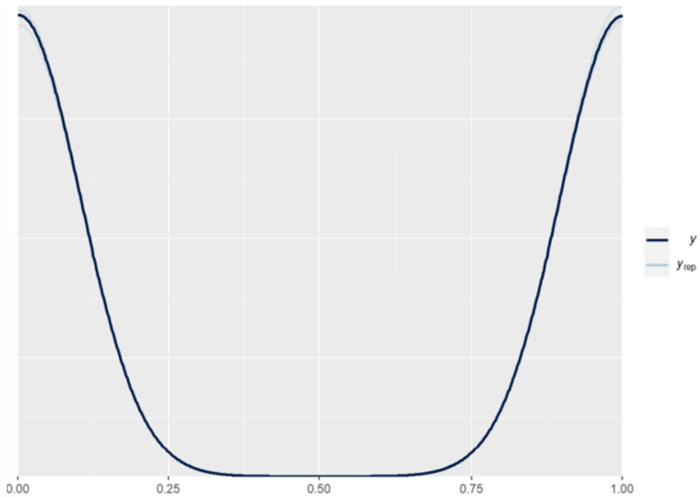
(DK, PM) The informed effect mean is set based on the literature, to a vector of 10 values. In 6 of them the values are ranging from -0.5 to 1.89, and in 4 of them, the values are set to 0 to account for random noise in measurement. While the Skeptic effect mean is set to 0 for all 10 trials. The individual variability from the population is also defined with Informed Standard Deviation set to 1 and Skeptical Standard Deviation is set to 0.5, while measurement error is set to 0.2.

Plot 11



Note: pp-check on model run on only priors

Plot 12



Note: pp-check on model fit on the informed simulated data

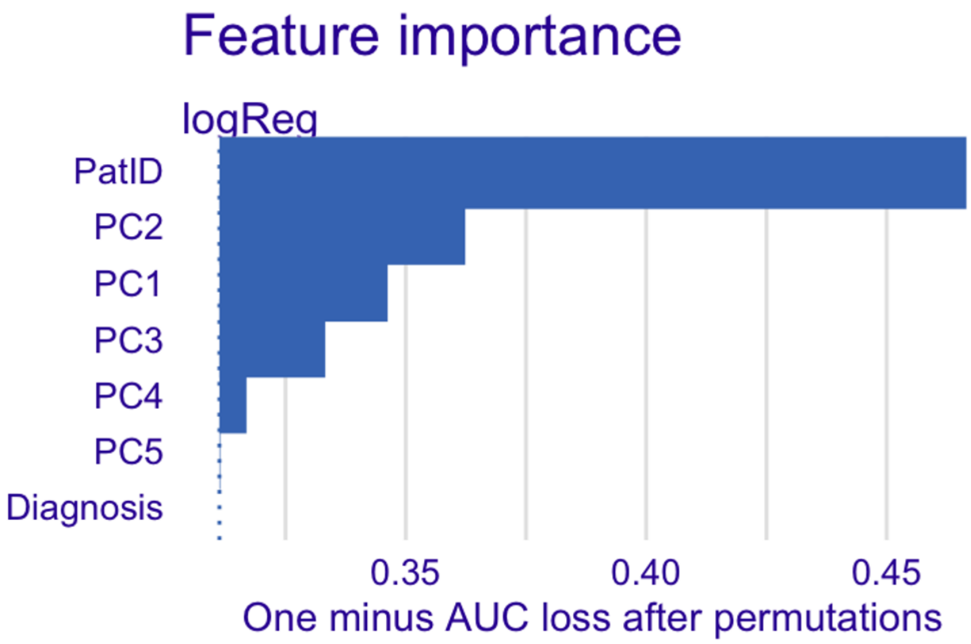
(MST, PM) Based on the plots 11 and 12, we can see that the model learnt when not only based on priors, but the simulated data.

(DK, PM) The results from the confusion matrices on both training and test sets for both conditions showed that the models on simulated data are performing well in predicting the condition. The models have a high accuracy and wide confidence intervals, above 95%. The models also have a high sensitivity and Positive Predictive Value, above 0.95. This is consistent with the information from the data simulation. The results indicate that the models are accurately predicting the condition and have low error.

Describe results from applying the ML pipeline to the empirical data and what we can learn from them.

(DK, PM, MST) The data budgeting resulted in a training dataset of 1510 observations and a test data set of 379 observations. As part of the data preprocessing we ran the feature analysis on the results of principal component analysis. The results shown in plot 13 tell us that PC2, PC1, PC3 and PC4 are the most important features found in the principle component analysis. PatID is the most important feature.

Plot 13



(DK, PM, MST) Based on the feature analysis we defined a model with the following formula:

$$Diagnosis \sim 1 + PC2 + PC1 + PC3 + PC4 + (1|PatID)$$

We allowed for random intercepts to account for individual variability.

(PM) The performance of the model is decent. The Group-level estimate values are within the expected range, considering the informed Standard Deviation and Skeptical Standard Deviation values of 1 and 0.5. The Estimate values for the Population-Level Effects are also close to the informed and skeptical effect mean values reported in the data simulation. In addition, the Rhat values for each parameter are close to 1, indicating that the model has converged. The Bulk_ESS and Tail_ESS are also high, indicating that the model is performing well.

(DK) To the right we see the results from our ML algorithm's predictions on the test data, and the results on the training data to the right. We see the model predicts roughly at chance level, meaning the model either does not pick up on the signal in the data, or there simply is no signal in the data. In our simulated data set the model picked up on the signal given almost the same model-fit, fixed effects plus random slope. The only difference is the fact that we ran a principal component analysis. The PCA makes new variables, composed of the original data, this might be the cause of the poor performance of the model. If we wanted to test this, we could run a feature analysis on the "raw" data, and build our model from that, and see if the model then picks up on a signal. If it does not, we might be inclined to conclude that there is no signal for the model to pick up on.

```
Confusion Matrix and Statistics

          Reference
Prediction  CT SCZ
       CT  115  78
       SCZ 104  82

               Accuracy : 0.5198
```

```
Confusion Matrix and Statistics

          Reference
Prediction  CT SCZ
       CT  545 251
       SCZ 444 270

               Accuracy : 0.5397
```

Assignment 1 - Language development in autistic and neurotypical children

Assignment 1 - Language development in autistic and neurotypical children

Quick recap

Autism Spectrum Disorder is often related to language impairment. However, this phenomenon has rarely been empirically traced in detail: i) relying on actual naturalistic language production, ii) over extended periods of time.

We therefore videotaped circa 30 kids with ASD and circa 30 comparison kids (matched by linguistic performance at visit 1) for ca. 30 minutes of naturalistic interactions with a parent. We repeated the data collection 6 times per kid, with 4 months between each visit. We transcribed the data and counted: i) the amount of words that each kid uses in each video. Same for the parent. ii) the amount of unique words that each kid uses in each video. Same for the parent. iii) the amount of morphemes per utterance (Mean Length of Utterance) displayed by each child in each video. Same for the parent.

This data is in the file you prepared in the previous class, but you can also find it here:https://www.dropbox.com/s/d6eerv6cl6eksf3/data_clean.csv?dl=0

The structure of the assignment

We will be spending a few weeks with this assignment. In particular, we will:

Part 1) simulate data in order to better understand the model we need to build, and to better understand how much data we would have to collect to run a meaningful study (precision analysis)

Part 2) analyze our empirical data and interpret the inferential results

Part 3) use your model to predict the linguistic trajectory of new children and assess the performance of the model based on that.

As you work through these parts, you will have to produce a written document (separated from the code) answering the following questions:

Q1 - Briefly describe your simulation process, its goals, and what you have learned from the simulation. Add at least a plot showcasing the results of the simulation. Make a special note on sample size considerations: how much data do you think you will need? what else could you do to increase the precision of your estimates?

Q2 - Briefly describe the empirical data and how they compare to what you learned from the simulation (what can you learn from them?). Briefly describe your model(s) and model quality. Report the findings: how does development differ between autistic and neurotypical children (N.B. remember to report both population and individual level findings)? which additional factors should be included in the model? Add at least one plot showcasing your findings.

Q3 - Given the model(s) from Q2, how well do they predict the data? Discuss both in terms of absolute error in training vs testing; and in terms of characterizing the new kids' language development as typical or in need of support.

Below you can find more detailed instructions for each part of the assignment.

Part 1 - Simulating data

Before we even think of analyzing the data, we should make sure we understand the problem, and we plan the analysis. To do so, we need to simulate data and analyze the simulated data (where we know the ground truth).

In particular, let's imagine we have n autistic and n neurotypical children. We are simulating their average utterance length (Mean Length of Utterance or MLU) in terms of words, starting at Visit 1 and all the way to Visit 6. In other words, we need to define a few parameters: - average MLU for ASD (population mean) at Visit 1 and average individual deviation from that (population standard deviation) - average MLU for TD (population mean) at Visit 1 and average individual deviation from that (population standard deviation) - average change in MLU by visit for ASD (population mean) and average individual deviation from that (population standard deviation) - average change in MLU by visit for TD (population mean) and average individual deviation from that (population standard deviation) - an error term. Errors could be due to measurement, sampling, all sorts of noise.

Note that this makes a few assumptions: population means are exact values; change by visit is linear (the same between visit 1 and 2 as between visit 5 and 6). This is fine for the exercise. In real life research, you might want to vary the parameter values much more, relax those assumptions and assess how these things impact your inference.

We go through the literature and we settle for some values for these parameters: - average MLU for ASD and TD: 1.5 (remember the populations are matched for linguistic ability at first visit) - average individual variability in initial MLU for ASD 0.5; for TD 0.3 (remember ASD tends to be more heterogeneous) - average change in MLU for ASD: 0.4; for TD 0.6 (ASD is supposed to develop less) - average individual variability in change for ASD 0.4; for TD 0.2 (remember ASD tends to be more heterogeneous) - error is identified as 0.2

This would mean that on average the difference between ASD and TD participants is 0 at visit 1, 0.2 at visit 2, 0.4 at visit 3, 0.6 at visit 4, 0.8 at visit 5 and 1 at visit 6.

With these values in mind, simulate data, plot the data (to check everything is alright); and set up an analysis pipeline.

Remember the usual bayesian workflow: - define the formula - define the prior - prior predictive checks - fit the model - model quality checks: traceplots, divergences, rhat, effective samples - model quality checks: posterior predictive checks, prior-posterior update checks - model comparison

Once the pipeline is in place, loop through different sample sizes to assess how much data you would need to collect. N.B. for inspiration on how to set this up, check the tutorials by Kurz that are linked in the syllabus.

BONUS questions for Part 1: what if the difference between ASD and TD was 0? how big of a sample size would you need? What about different effect sizes, and different error terms?

Bryan ### Simulating data To make beta values between each visit we would need the standard diviation between visits

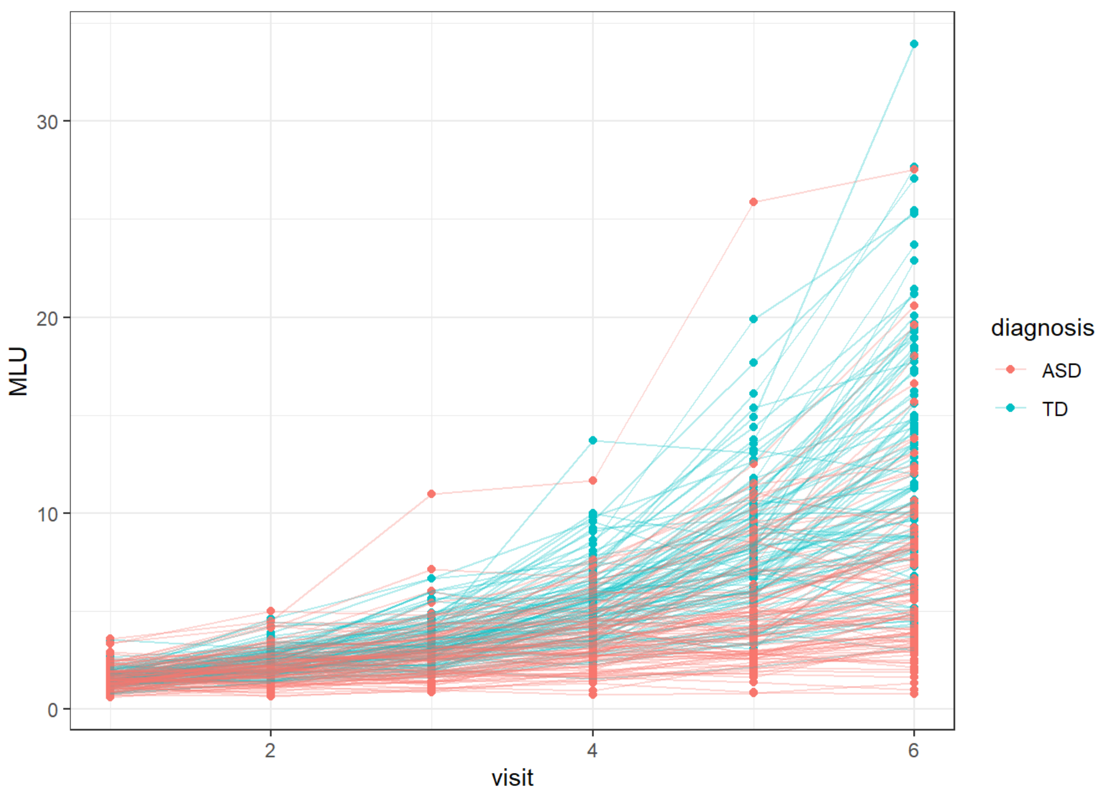
```
average_mlu <- log(1.5)
 sd_mlu_asd <- log(1.5+0.5)-log(1.5)
 sd_mlu_td <- log(1.5+0.3)-log(1.5)

 change_mlu_asd <- 0.4/1.5
 change_mlu_td <- 0.6/1.5
 change_sd_mlu_asd <- 0.4*(0.4/1.5)
 change_sd_mlu_td <- 0.2*(0.6/1.5)
 e <- 0.2

n <- 100
int_asd <- rnorm(n, mean=average_mlu, sd=sd_mlu_asd)
int_td <- rnorm(n, mean=average_mlu, sd=sd_mlu_td)

slope_asd <- rnorm(n, mean=change_mlu_asd,
sd=change_sd_mlu_asd)
slope_td <- rnorm(n, mean = change_mlu_td,
sd=change_sd_mlu_td)
 sim_data <-
   tibble(diagnosis=rep(c('TD', 'ASD'), each=n)) %>%
   mutate(intercept=ifelse(diagnosis=='TD', int_td,
int_asd)) %>%
   mutate(slope=ifelse(diagnosis=='TD', slope_td,
slope_asd)) %>%
   mutate(error=ifelse(diagnosis=='TD', e, e)) %>%
   dplyr::mutate(ID=row_number()) %>%
   slice(rep(1:n(), each=6)) %>%
   add_column(visit=rep(c(1,2,3,4,5,6), times=n+n))

 for(i in seq(nrow(sim_data))){
```

```
   sim_data$MLU[i] <- exp(rnorm(1,
sim_data$intercept[i]+
(sim_data$slope[i]*(sim_data$visit[i]-1)),
sim_data$error[i]))
 }
```

```
## Warning: Unknown or uninitialised column: `MLU`.
```

plot simulated data

```
ggplot(sim_data, aes(visit,MLU, color=diagnosis,
group=ID))+
  theme_bw()+
  geom_point()+
  geom_line(alpha=0.3)
```



##Analysing simulated data

###define formula

```
MLU_f1 <- bf(MLU ~ 0 + diagnosis + diagnosis:visit + (1
+ visit|ID))
```

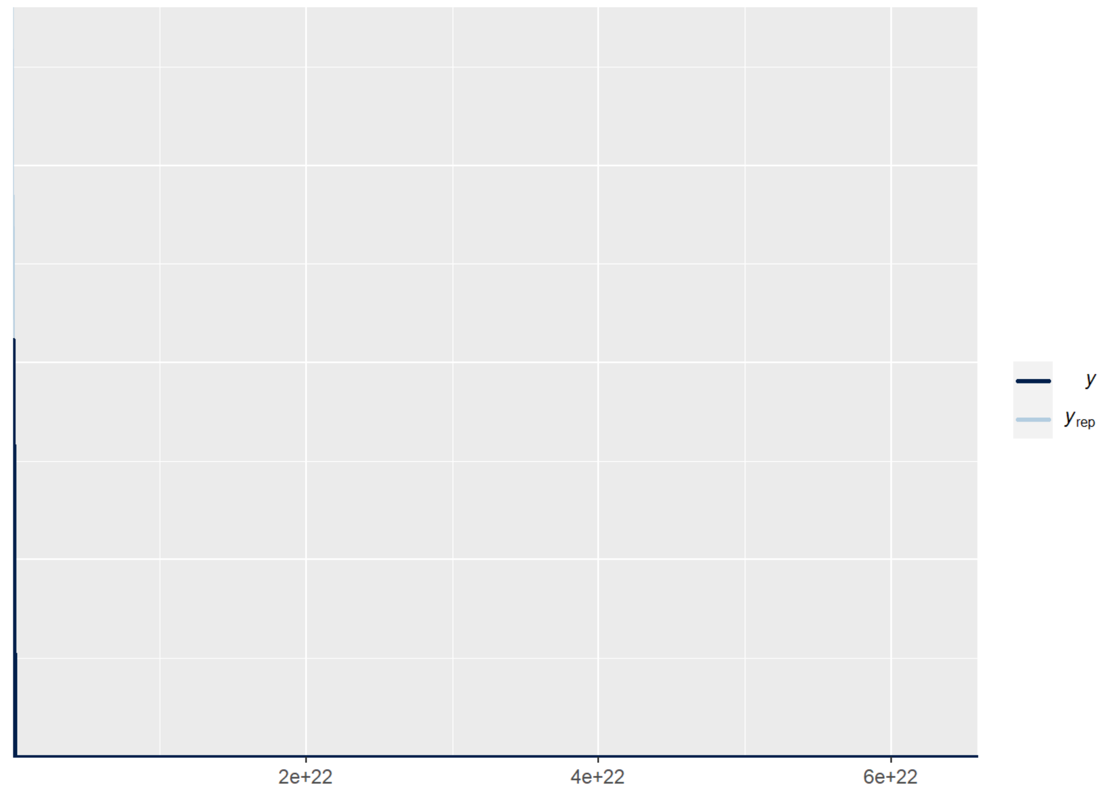
```
lognorm_fam <- brmsfamily('lognormal', bhaz =
list(Boundary.knots=c(-1,31)))
```
###Investigate and set priors

```
get_prior(data = sim_data, family = lognorm_fam,
MLU_f1)
```

```
priors <- c(
prior(normal(1.5,0.5),class=b,coef="diagnosisASD"),
prior(normal(1.5,0.3),class=b,coef="diagnosisTD"),
prior(normal(0,0.5),class=b),
prior(normal(0,0.5),class=sd),
prior(lkj(2),class=cor))
```
###Model using priors

```
MLU_prior_m1 <- brm(
  MLU_f1,
  data = sim_data,
  prior = priors,
  family = lognorm_fam,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```
###prior predictive checks

```
pp_check(MLU_prior_m1, ndraws=100)
```



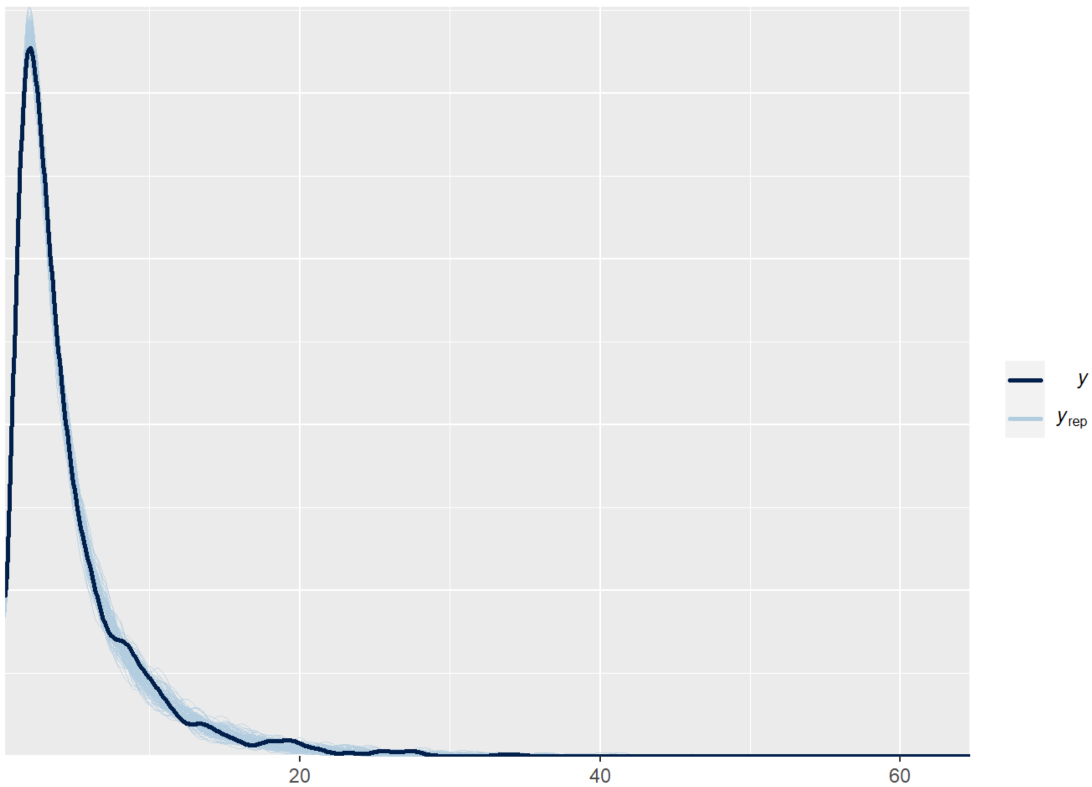
###fit the model

```
MLU_prior_m1_fit <- brm(
  MLU_f1,
  data = sim_data,
  prior = priors,
  family = lognorm_fam,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
```

```
)
)
```

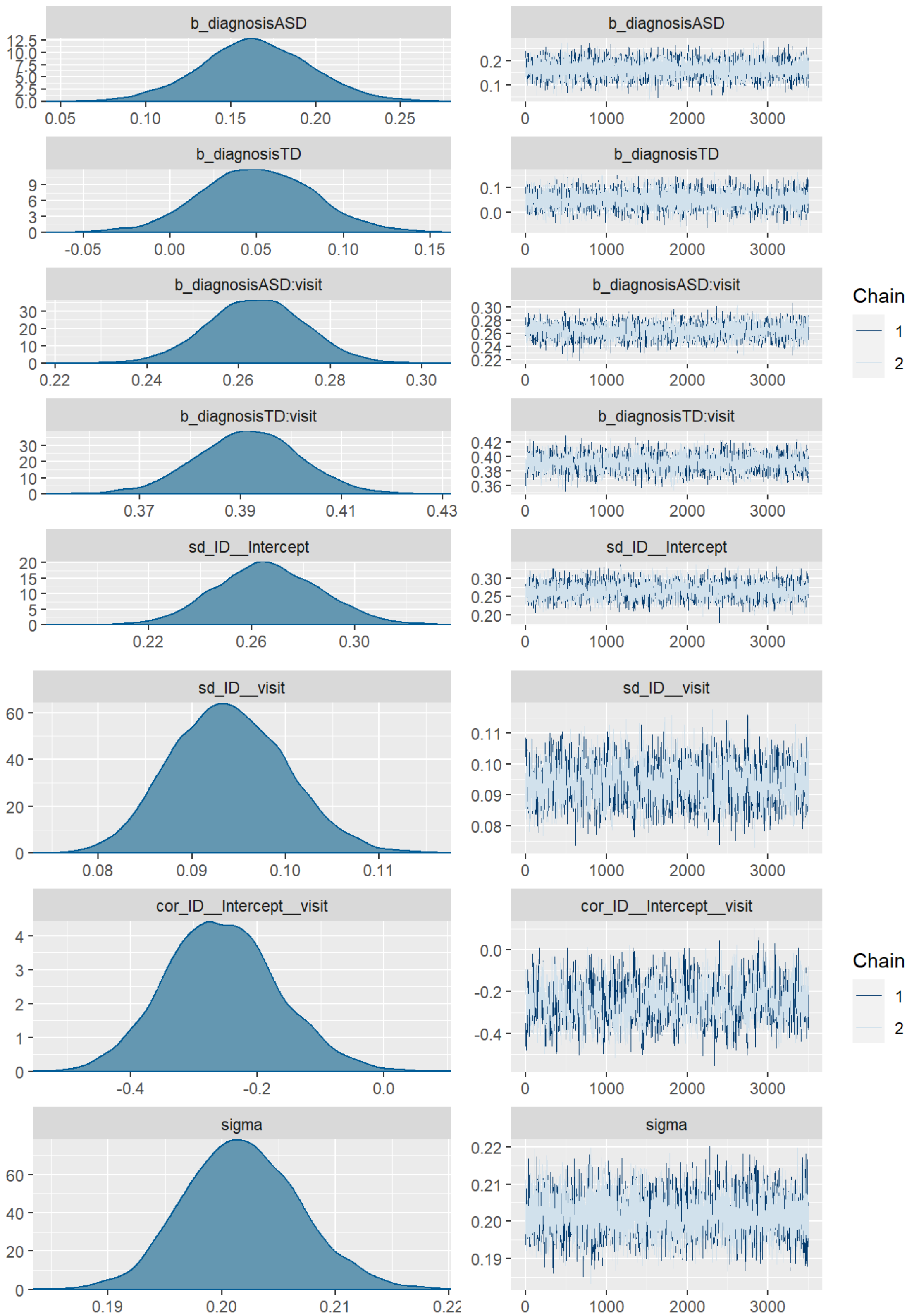
###posterior predictive check

```
pp_check(MLU_prior_m1_fit, ndraws = 100)
```



###traceplot for fitted model

```
plot(MLU_prior_m1_fit)
```



Ditlev ### parameter recovery from fitted model

```
print(MLU_prior_m1_fit)
##  Family: lognormal
##   Links: mu = identity; sigma = identity
## Formula: MLU ~ 0 + diagnosis + diagnosis:visit + (1
+ visit | ID)
##    Data: sim_data (Number of observations: 1200)
##   Draws: 2 chains, each with iter = 6000; warmup =
2500; thin = 1;
##          total post-warmup draws = 7000
##
## Group-Level Effects:
## ~ID (Number of levels: 200)
##                       Estimate Est.Error l-95% CI
u-95% CI Rhat Bulk_ESS
## sd(Intercept)             0.27      0.02     0.23
0.31 1.00     3180
## sd(visit)                 0.09      0.01     0.08
0.11 1.00     1420
## cor(Intercept,visit)     -0.26      0.09    -0.42
-0.08 1.00      818
##                       Tail_ESS
## sd(Intercept)             4997
## sd(visit)                 2859
## cor(Intercept,visit)      1449
##
## Population-Level Effects:
##                     Estimate Est.Error l-95% CI u-95%
CI Rhat Bulk_ESS Tail_ESS
## diagnosisASD            0.16      0.03     0.10
0.23 1.00     7144     5530
## diagnosisTD             0.05      0.03    -0.01
0.11 1.00     7420     5327
## diagnosisASD:visit      0.26      0.01     0.24
0.28 1.00     3753     3858
## diagnosisTD:visit       0.39      0.01     0.37
```

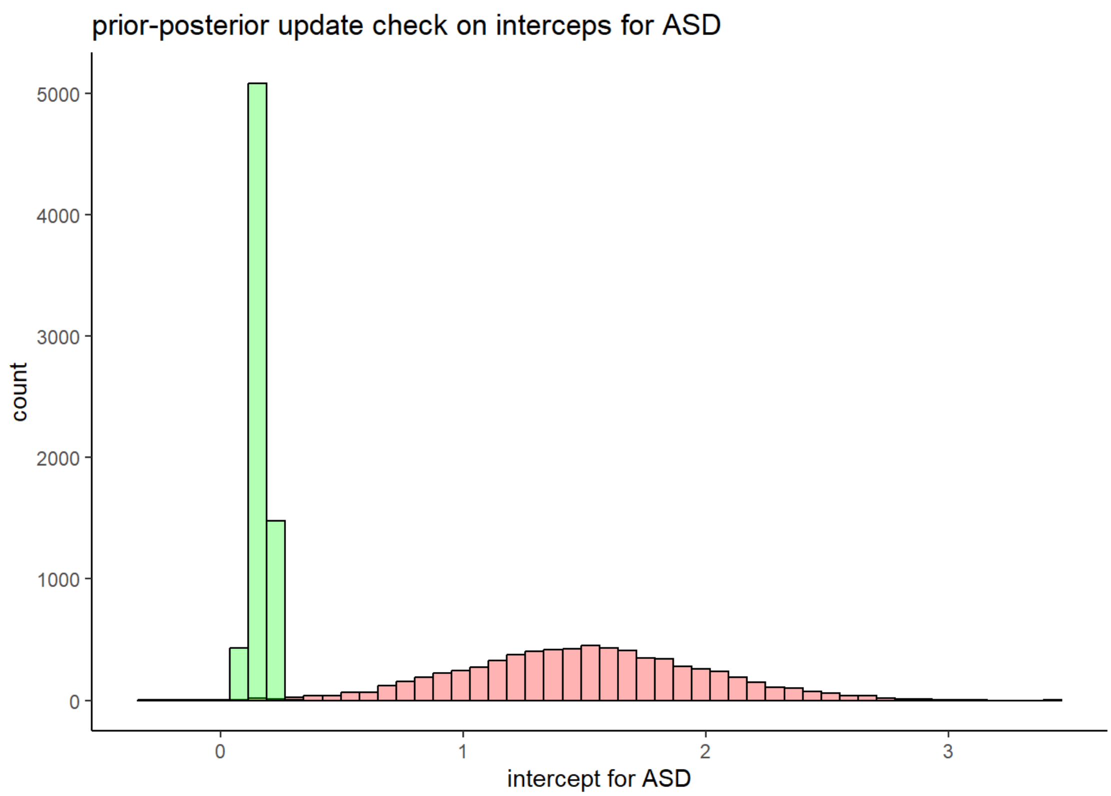
```
0.41 1.00     4086     4820
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat
Bulk_ESS Tail_ESS
## sigma     0.20      0.01     0.19     0.21 1.00
4407     4653
##
## Draws were sampled using sample(hmc). For each
parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and
Rhat is the potential
## scale reduction factor on split chains (at
convergence, Rhat = 1).
```

prior posterior update check

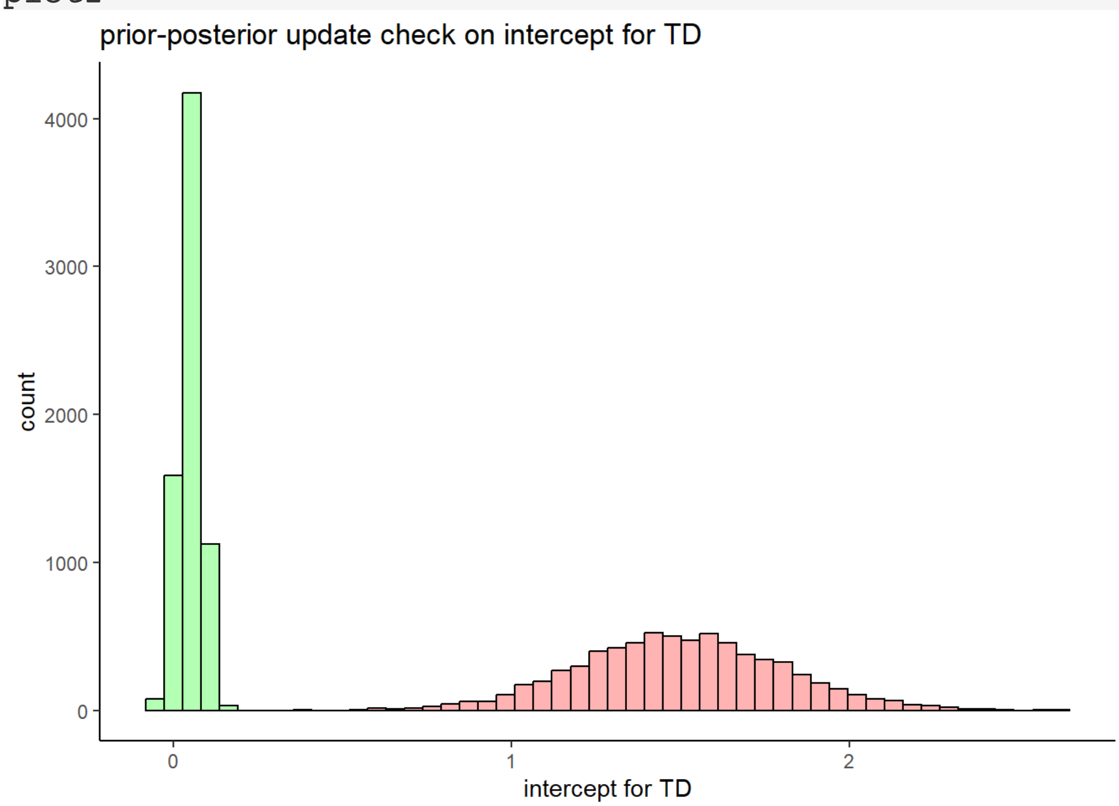
```
posterior <- as_draws_df(MLU_prior_m1_fit)

plot1 <- ggplot(posterior)+
  geom_histogram(aes(prior_b_diagnosisASD), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(b_diagnosisASD), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on interceps
for ASD')+
  xlab('intercept for ASD')

plot2 <- ggplot(posterior)+
  geom_histogram(aes(prior_b_diagnosisTD), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(b_diagnosisTD), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on intercept
```

```
for TD')+
  xlab('intercept for TD')

plot3 <- ggplot(posterior)+
  geom_histogram(aes(`prior_b_diagnosisASD:visit`),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(`b_diagnosisASD:visit`),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on slope for
ASD')+
  xlab("Slope for ASD")

plot4 <- ggplot(posterior)+
  geom_histogram(aes(`prior_b_diagnosisTD:visit`),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(`b_diagnosisTD:visit`),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on slope for
TD')+
  xlab("slope for TD")


plot5 <- ggplot(posterior)+
  geom_histogram(aes(prior_cor_ID), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(cor_ID__Intercept__visit),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on correlation
between varying intercepts and slopes')+
  xlab("Correlation")

plot6 <- ggplot(posterior)+
```

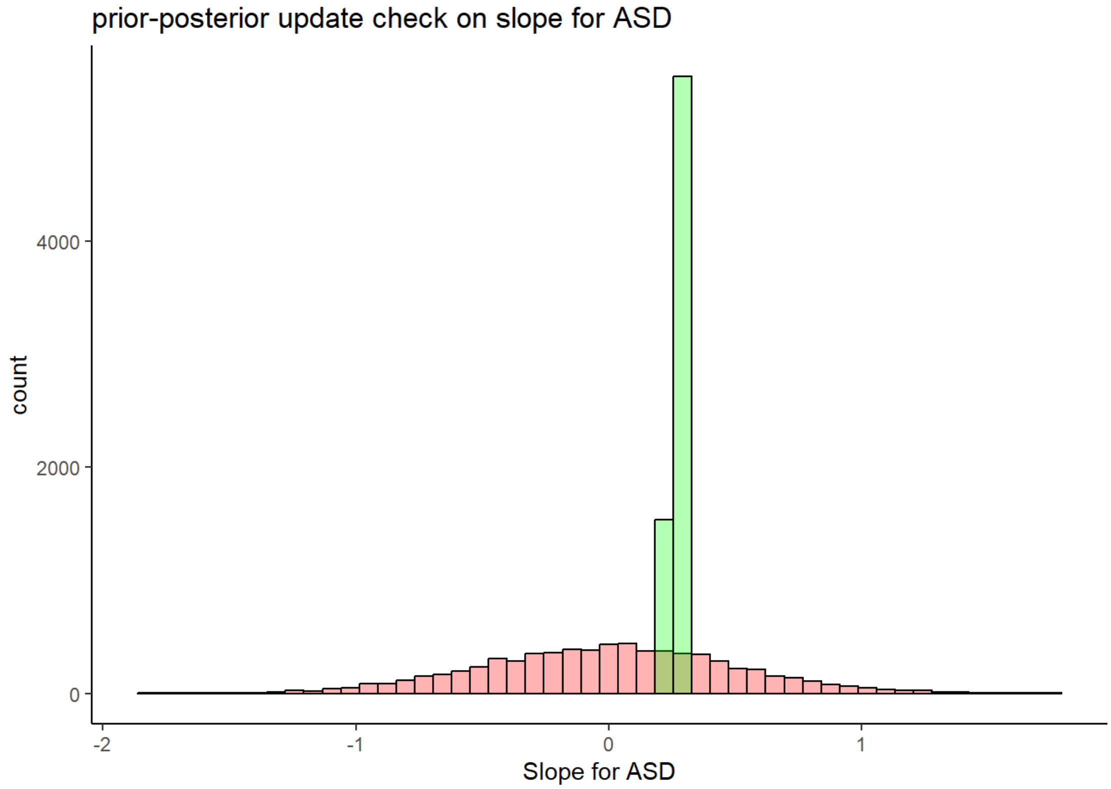
```
  geom_histogram(aes(prior_sd_ID), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(sd_ID__Intercept), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('Prior-posterior update check, the
variability of the intercept')+
  xlab("Intercept")

plot7 <- ggplot(posterior)+
  geom_histogram(aes(prior_sd_ID), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(sd_ID__visit), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('Prior-posterior update check, the
variability of the slopes')+
  xlab("Intercept")



plot1
```


prior-posterior update check on interceps for ASD
count
5000
4000
3000
2000
1000
0
0
1
2
3
intercept for ASD

```
plot2
```

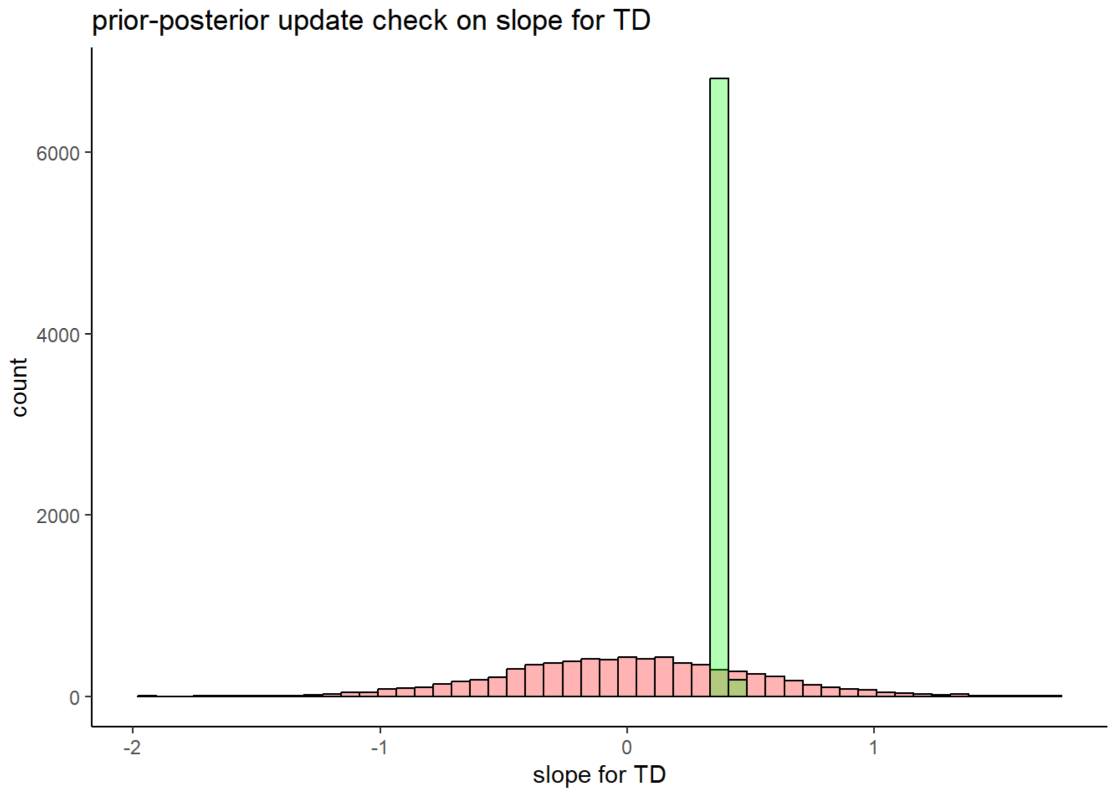

prior-posterior update check on intercept for TD
count
4000
3000
2000
1000
0
0
1
2
intercept for TD

```
plot3
```

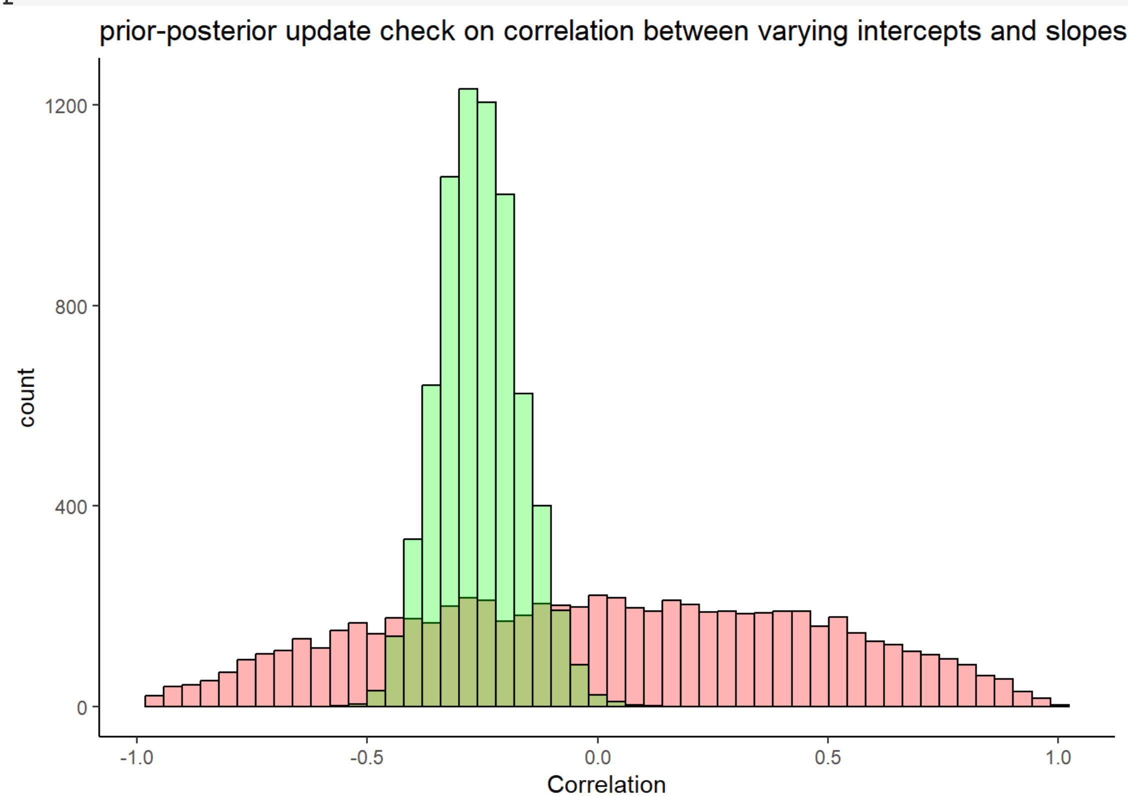


prior-posterior update check on slope for ASD
count
4000
2000
0
-2
-1
0
1
Slope for ASD

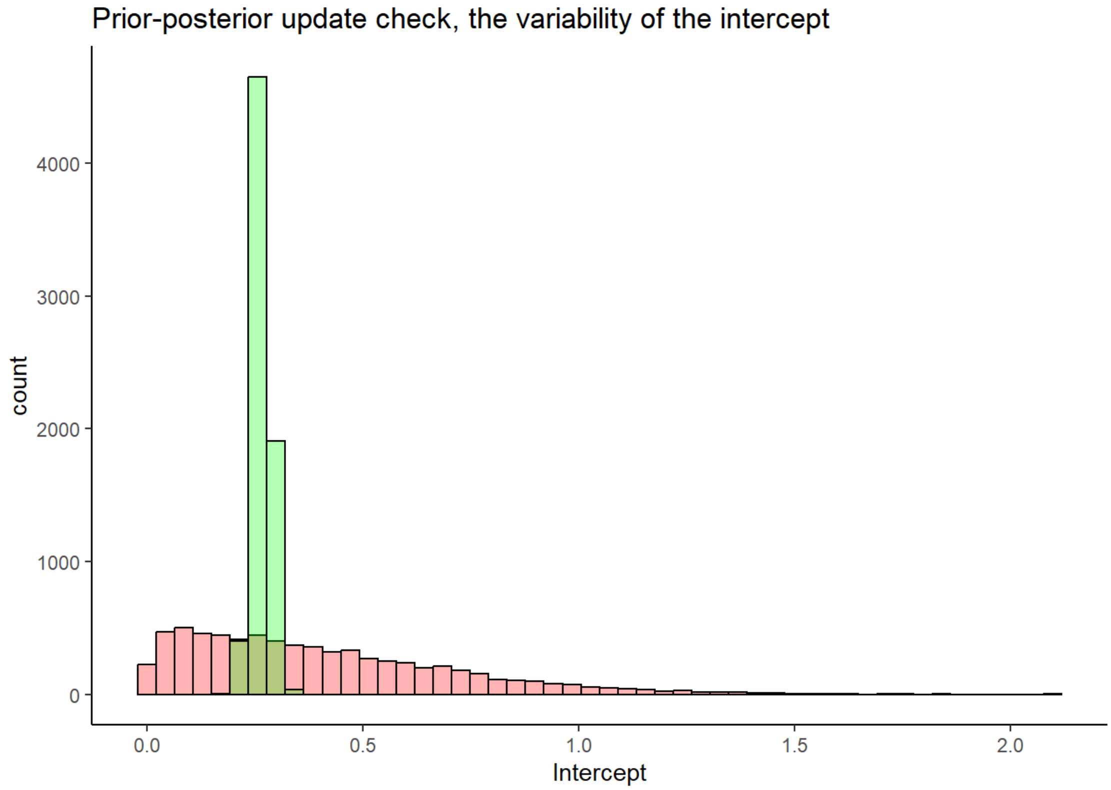

```
plot4
```


prior-posterior update check on slope for TD
count
6000
4000
2000
0
-2
-1
0
1
slope for TD

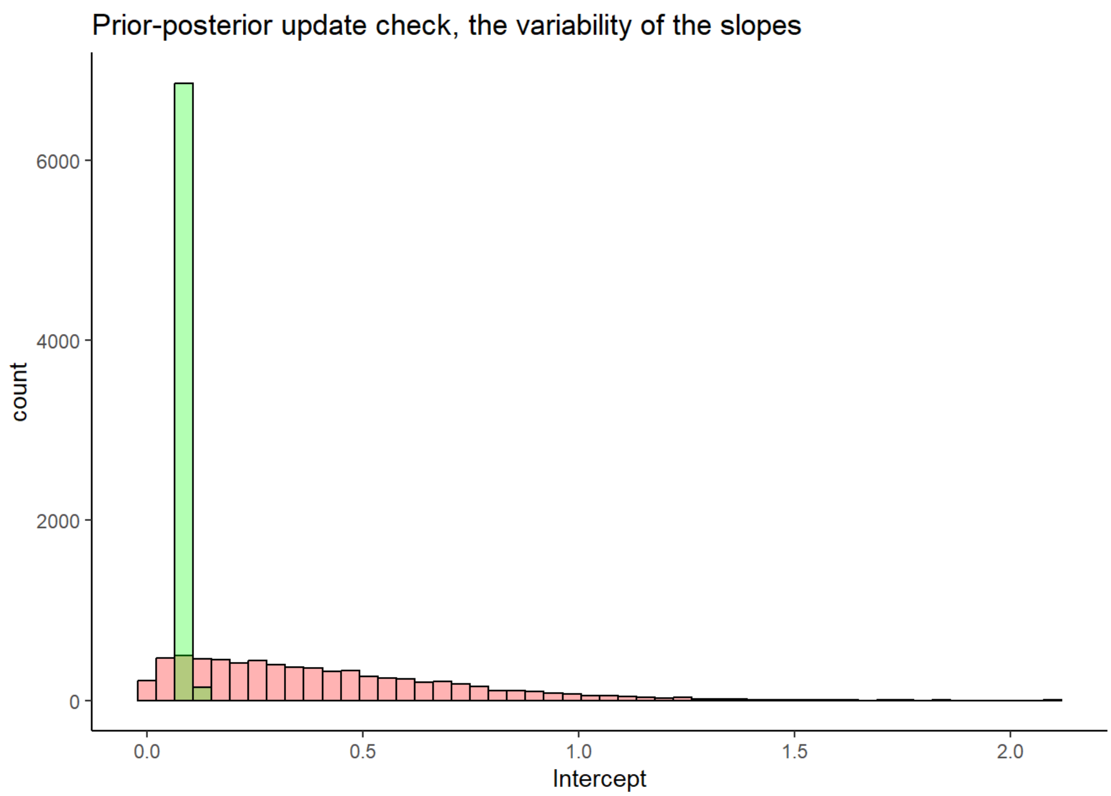
```
plot5
```


prior-posterior update check on correlation between varying intercepts and slopes
count
1200
800
400
0
-1.0
-0.5
0.0
0.5
1.0
Correlation

```
plot6
```


Prior-posterior update check, the variability of the intercept
count
4000
3000
2000
1000
0
0.0
0.5
1.0
1.5
2.0
Intercept

```
plot7
```



Estimating effectsize, baysian power analysis

Function simulates data and return CI of slope difference

```
fun_sim_data <- function(seed,n){
  set.seed(seed)

  average_mlu <- log(1.5)
sd_mlu_asd <- log(1.5+0.5)-log(1.5)
sd_mlu_td <- log(1.5+0.3)-log(1.5)

change_mlu_asd <- 0.4/1.5
change_mlu_td <- 0.6/1.5
change_sd_mlu_asd <- 0.4*(0.4/1.5)
change_sd_mlu_td <- 0.2*(0.6/1.5)
```

```
 e <- 0.2

 int_asd <- rnorm(n, mean=average_mlu, sd=sd_mlu_asd)
int_td <- rnorm(n, mean=average_mlu, sd=sd_mlu_td)

slope_asd <- rnorm(n, mean=change_mlu_asd,
sd=change_sd_mlu_asd)
slope_td <- rnorm(n, mean = change_mlu_td,
sd=change_sd_mlu_td)



   data <-
     tibble(diagnosis=rep(c('TD', 'ASD'), each=n)) %>%
     mutate(intercept=ifelse(diagnosis=='TD', int_td,
int_asd)) %>%

     mutate(slope=ifelse(diagnosis=='TD', slope_td,
slope_asd)) %>%
     mutate(error=ifelse(diagnosis=='TD', e, e)) %>%
     dplyr::mutate(ID=row_number()) %>%
     slice(rep(1:n(), each=6)) %>%
     add_column(visit=rep(c(1,2,3,4,5,6), times=n+n))

 for(i in seq(nrow(data))){
   data$MLU[i] <- exp(rnorm(1,data$intercept[i]+
(data$slope[i]*(data$visit[i]-1)), data$error[i]))
 }
   data <- data[,c(1,5,6,2,3,4,7)]
   post <- update(MLU_prior_m1_fit,
                  newdata = data,
                  seed=seed) %>%
     as_draws_df() %>%
     mutate(slope_diff=(`b_diagnosisTD:visit`-
`b_diagnosisASD:visit`))
```

```
   CI <- as.data.frame(t(quantile(post$slope_diff,
probs=c(0.025, 0.975)))) %>%
     add_column(mean=mean(post$slope_diff))
   return(CI)}
```

Manuela #### running the functiong with different amount of participants

```
# n_sim <- 10
#
# s10 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=10)) %>%
#   unnest(b1)
#
# s15 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=15)) %>%
#   unnest(b1)
#
# s20 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=20)) %>%
#   unnest(b1)
#
# s30 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=30)) %>%
#   unnest(b1)
#
# s40 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=40)) %>%
#   unnest(b1)
#
# s50 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=50)) %>%
#   unnest(b1)
#
# s75 <- tibble(seed=1:n_sim) %>%
```

```
#   mutate(b1=purrr::map(seed, fun_sim_data, n=75)) %>%
#   unnest(b1)
#
# s100 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=100))
%>%
#   unnest(b1)
#
# s180 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=180))
%>%
#   unnest(b1)
#
# s250 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=250))
%>%
#   unnest(b1)
#
# s300 <- tibble(seed=1:n_sim) %>%
#   mutate(b1=purrr::map(seed, fun_sim_data, n=300))
%>%
#   unnest(b1)
```

Effectsize of slope difference (plots)

```
# plot_s10 <- s10 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 10 participants")
#
# plot_s15 <- s15 %>%
```

```
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 15 participants")
#
# plot_s20 <- s20 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 20 participants")
#
# plot_s30 <- s30 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 30 participants")
#
# plot_s40 <- s40 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
```

```
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 40 participants")
#
# plot_s50 <- s50 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 50 participants")
#
# plot_s75 <- s75 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 75 participants")
#
# plot_s100 <- s100 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 100 participants")
#
# plot_s180 <- s180 %>%
```

```
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 180 participants")
#
# plot_s250 <- s250 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 150 participants")
#
# plot_s300 <- s300 %>%
#   ggplot(aes(x=seed, y=mean, ymin = `2.5%`, ymax=
`97.5%` ))+
#   geom_pointrange(fatten = 1/2)+
#   geom_hline(yintercept = c(0, 0.5), colour= 'green')
+
#   labs(x="seed (simulation index)", y= "slope
difference")+
#   ggtitle("slope difference, 300 participants")
#
# grid.arrange(
#   plot_s10,
#   plot_s15,
#   plot_s20,
#   plot_s30,
#   plot_s40)
```

```
# grid.arrange(
#   plot_s50,
#   plot_s75,
#   plot_s100,
#   plot_s180,
#   plot_s250,
#   plot_s300)
```

Patrik #### Power analysis

```
# power_analysis_fun <- function(sim_nr, n){
#   sim_nr %>%
#     mutate(two_half=ifelse(`2.5%`>0,1,0 )) %>%
#     summarise(power=mean(two_half)) %>%
#     add_column(number_of_participants=n)
# }
#
# power_analysis_sum <- bind_rows(
#   power_analysis_fun(s10, 10),
#   power_analysis_fun(s15, 15),
#   power_analysis_fun(s20, 20),
#   power_analysis_fun(s30, 30),
#   power_analysis_fun(s40, 40),
#   power_analysis_fun(s50, 50),
#   power_analysis_fun(s75, 75),
#   power_analysis_fun(s100, 100),
#   power_analysis_fun(s180, 180),
#   power_analysis_fun(s250, 250),
#   power_analysis_fun(s300, 300))
#
# power_analysis_sum
```

Part 2 - Strong in the Bayesian ken, you are now

ready to analyse the actual data

- Describe your sample (n, age, gender, clinical and cognitive features of the two groups) and critically assess whether the groups (ASD and TD) are balanced. Briefly discuss whether the data is enough given the simulations in part 1.

- Describe linguistic development (in terms of MLU over time) in TD and ASD children (as a function of group). Discuss the difference (if any) between the two groups.

- Describe individual differences in linguistic development: do all kids follow the same path? Are all kids reflected by the general trend for their group?

- Include additional predictors in your model of language development (N.B. not other indexes of child language: types and tokens, that'd be cheating). Identify the best model, by conceptual reasoning, model comparison or a mix. Report the model you choose (and name its competitors, if any) and discuss why it's the best model.

```
real_data <- read_csv('assignment_data_clean.csv')
## Rows: 352 Columns: 20
## ── Column specification
────────────────────────────────────────────────────────────
─
## Delimiter: ","
```

```
## chr  (3): Diagnosis, Ethnicity, Gender
## dbl (17): id, ADOS1, non_verbalIQ1, verbalIQ1,
Socialization1, visit, Age, A...
##
## ℹ Use `spec()` to retrieve the full column
specification for this data.
## ℹ Specify the column types or set `show_col_types =
FALSE` to quiet this message.
```

```
unique(real_data$id)
```

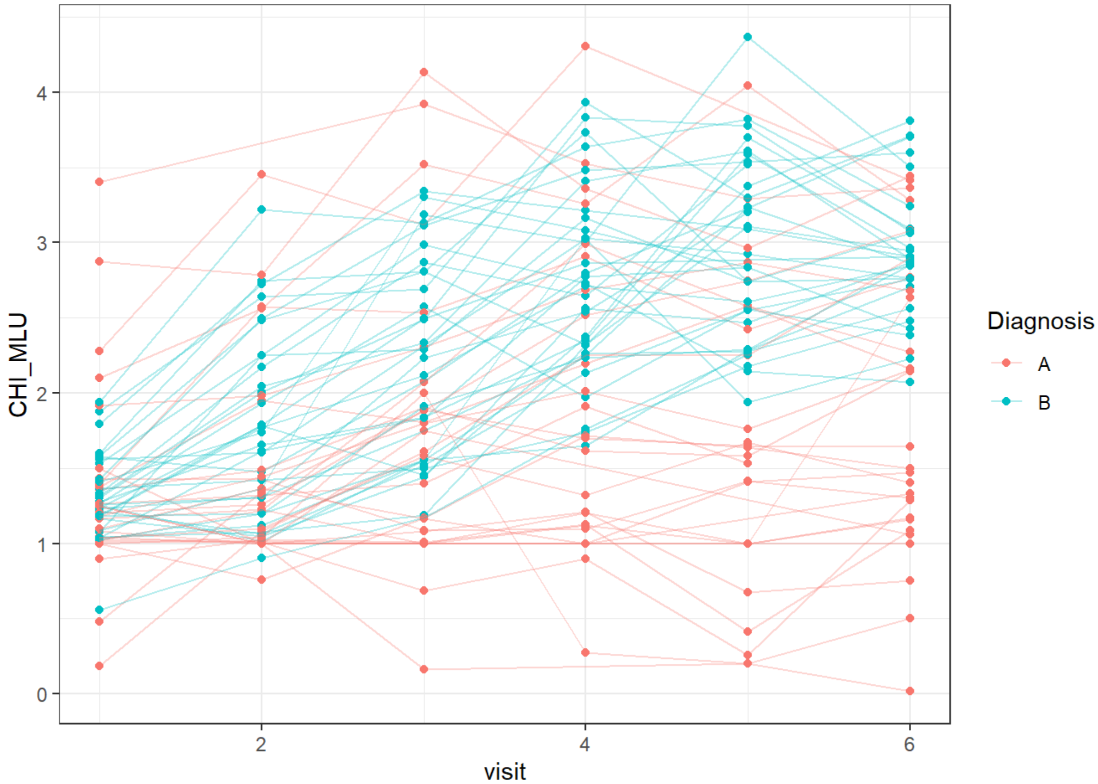
```
##  [1]  1 10 11 12 13 14 15 16 17 18 19  2 20 21 22 23
24 25 26 27 28 29  3 30 31
## [26] 32 33 34 35 36 37 38 39  4 40 41 42 43 44 45 46
47 48 49  5 50 51 52 53 54
## [51] 55 56 57 58 59  6 60 61  7  8  9
```

```
real_data <- real_data %>%
  mutate(Diagnosis=as.factor(Diagnosis))

real_data %>%
  group_by(Gender) %>%
  filter(visit==1) %>%
  count()
```

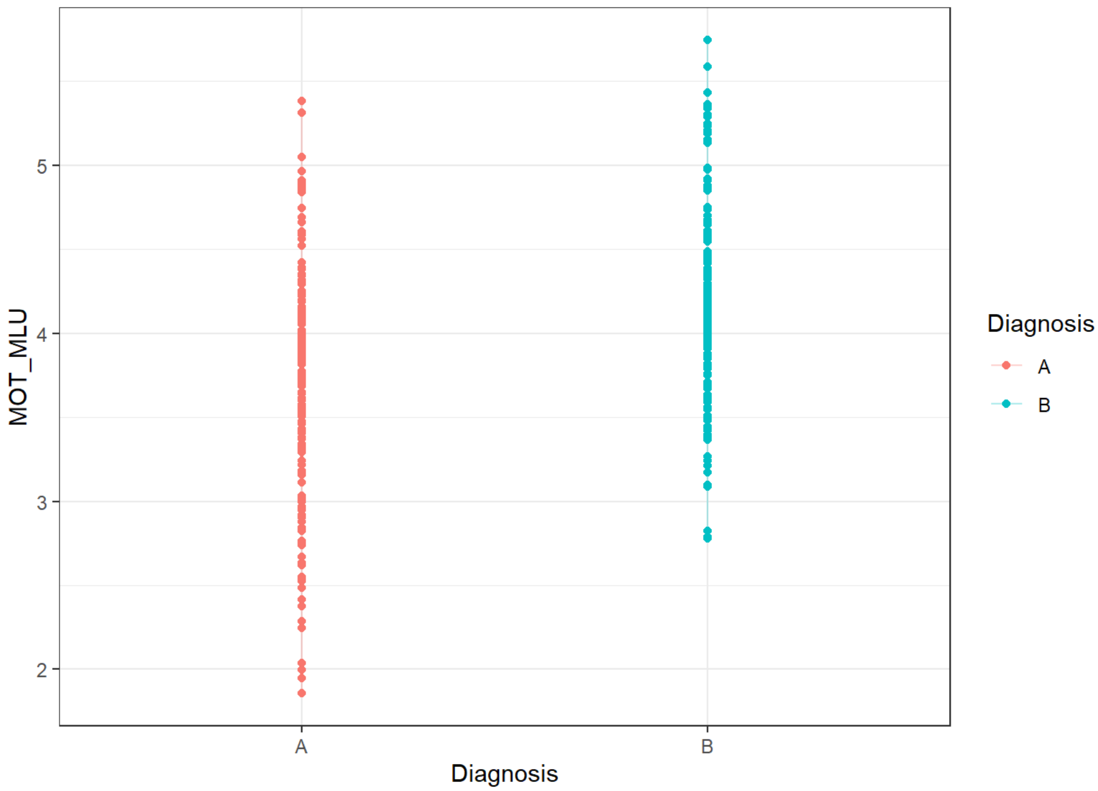
```
#Counting participants
real_data %>%
  group_by(Diagnosis) %>%
  filter(visit==1) %>%
  count()
```

```
##o use lognormal distribution we cannot have negative
MLU, so we filter it
real_data <- real_data %>%
  filter(!CHI_MLU<=0)
ggplot(real_data, aes(visit,CHI_MLU, color=Diagnosis,
group=id))+
  theme_bw()+
```

```
  geom_point()+
  geom_line(alpha=0.3)
```




```
ggplot(real_data, aes(Diagnosis, MOT_MLU,
color=Diagnosis))+
  theme_bw()+
  geom_point()+
  geom_line(alpha=0.3)
```




```
MLU_fit<- bf(CHI_MLU ~ 0 + Diagnosis + Diagnosis:visit
+ (1 + visit|id))

get_prior(data = real_data, family = lognorm_fam,
MLU_fit)
```

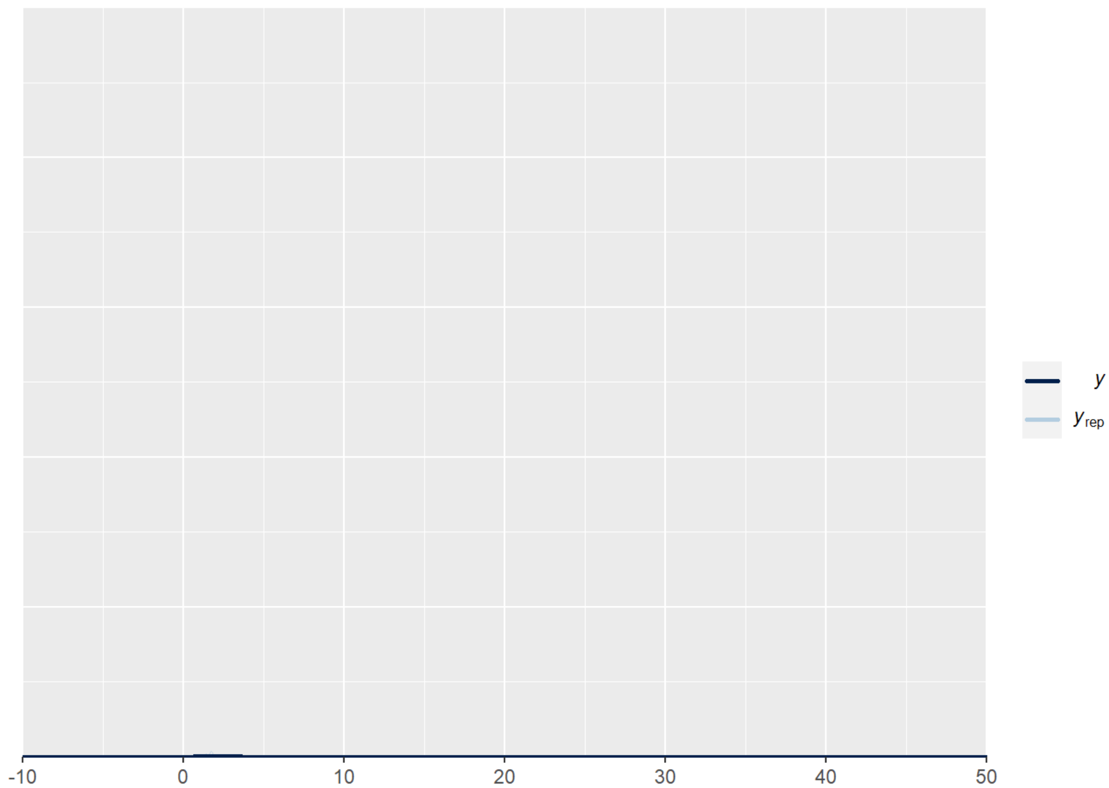
```
#Simulating priors
priors_sim<-c(
prior(normal(0,0.2),class=b),
prior(normal(0.5,0.05),class=b,coef="DiagnosisA"),
prior(normal(0.5,0.02),class=b,coef="DiagnosisB"),
prior(normal(0,0.06),class=b,coef="DiagnosisA:visit"),
prior(normal(0,0.03),class=b,coef="DiagnosisB:visit"),
prior(normal(0,0.2),class=sd,coef=Intercept,group=id),
prior(normal(0,0.1),class=sd,coef=visit,group=id),
prior(normal(0,0.2),class=sigma),
prior(lkj(2),class="cor"))
MLU_prior <- brm(
```

```
  MLU_fit,
  data = real_data,
  prior = priors_sim,
  family = lognorm_fam,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

###prior predictive checks

```
pp_check(MLU_prior, ndraws = 100)+
  xlim(-10,50)+
  ylim(0,500)
```

```
## Warning: Removed 9 rows containing non-finite values
(`stat_density()`).
```



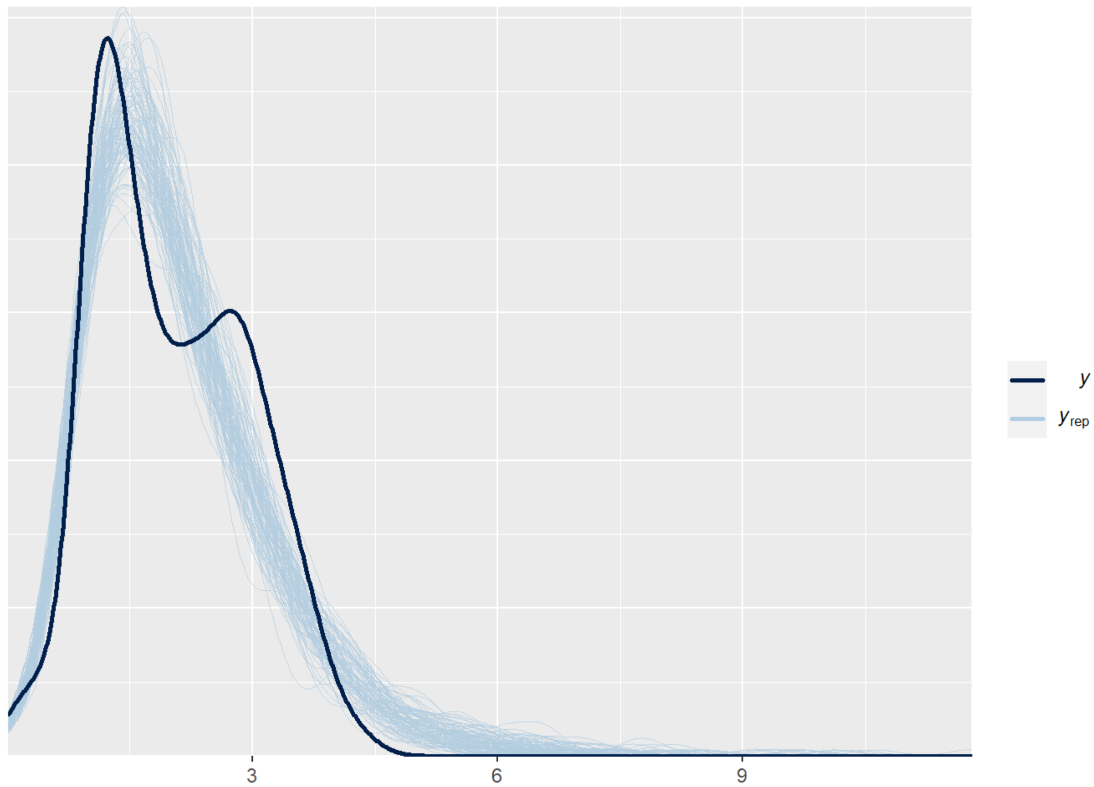
###fit the model

```
MLU_prior_fit <- brm(
  MLU_fit,
  data = real_data,
  prior = priors_sim,
  family = lognorm_fam,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
```

```
)
)
```

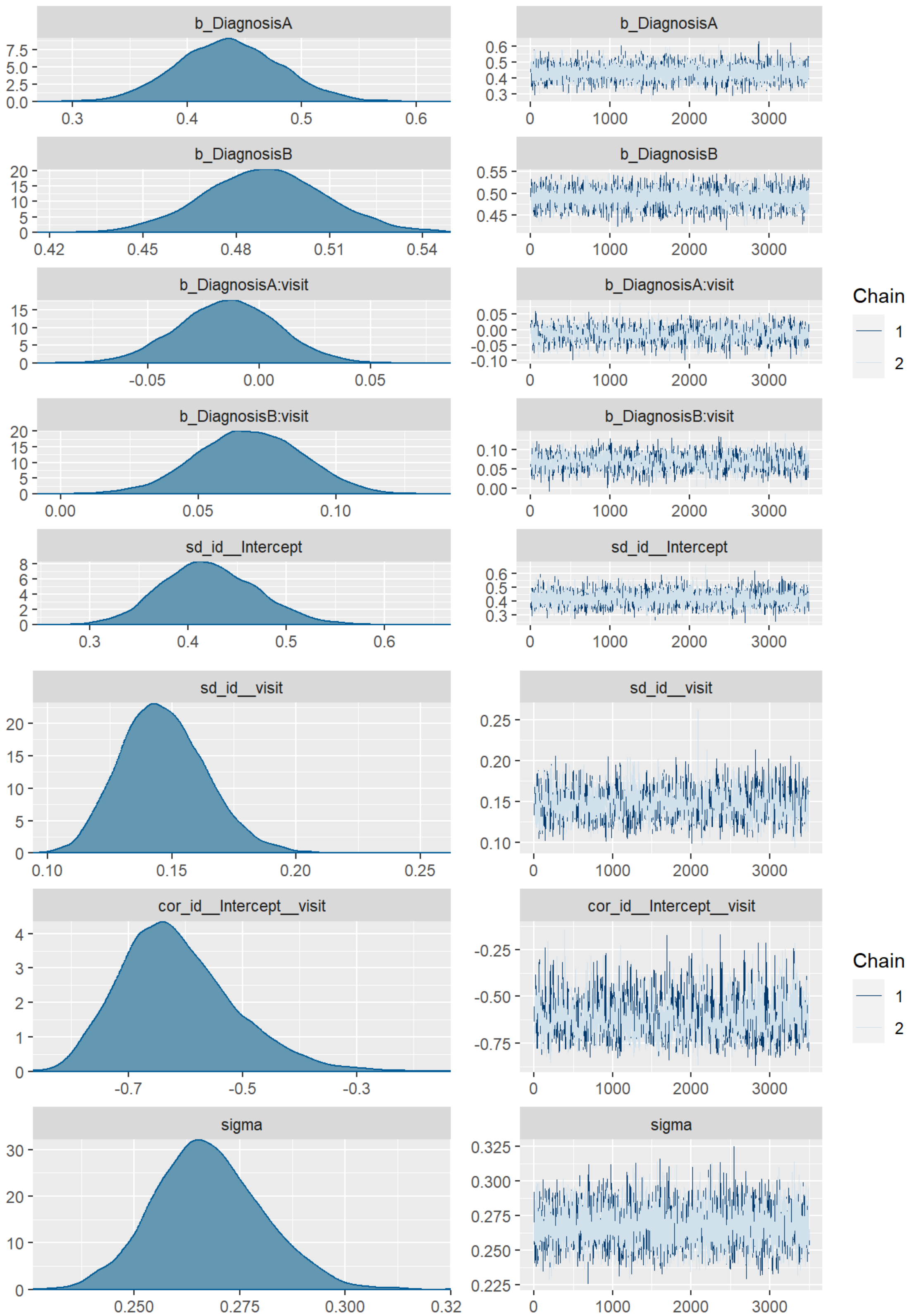
Sara ###posterior predictive check

```
pp_check(MLU_prior_fit, ndraws = 100)
```



###traceplot for fitted model

```
plot(MLU_prior_fit, ndraws = 100)
```


b_DiagnosisA
b_DiagnosisB
b_DiagnosisA:visit
b_DiagnosisB:visit
sd_id__Intercept
sd_id__visit
cor_id__Intercept__visit
sigma
Chain
1
2

parameter recovery from fitted model

```
print(MLU_prior_fit)
```

```
##  Family: lognormal
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ 0 + Diagnosis + Diagnosis:visit +
(1 + visit | id)
##    Data: real_data (Number of observations: 349)
##   Draws: 2 chains, each with iter = 6000; warmup =
2500; thin = 1;
##          total post-warmup draws = 7000
##
## Group-Level Effects:
## ~id (Number of levels: 61)
##                      Estimate Est.Error l-95% CI
u-95% CI Rhat Bulk_ESS
## sd(Intercept)            0.42      0.05     0.33
0.52 1.00     2532
## sd(visit)                0.15      0.02     0.12
0.18 1.00      891
## cor(Intercept,visit)    -0.61      0.10    -0.78
-0.39 1.00      770
##                      Tail_ESS
## sd(Intercept)            4522
## sd(visit)                2270
## cor(Intercept,visit)     1836
##
## Population-Level Effects:
##                  Estimate Est.Error l-95% CI u-95%
CI Rhat Bulk_ESS Tail_ESS
## DiagnosisA           0.44      0.04     0.35
0.53 1.00     6348     5528
## DiagnosisB           0.49      0.02     0.45
0.53 1.00    10730     5376
## DiagnosisA:visit    -0.01      0.02    -0.06
```

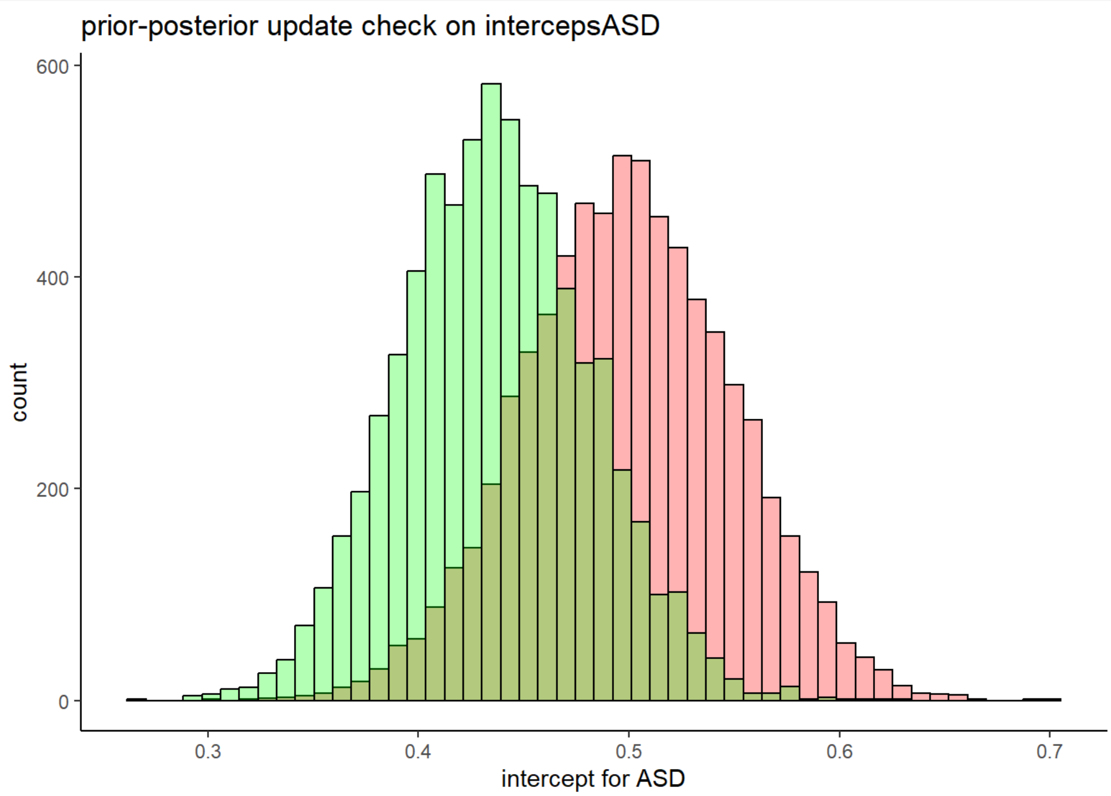
```
0.03 1.00     1301     2684
## DiagnosisB:visit     0.07      0.02     0.03
0.11 1.00     1158     2346
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat
Bulk_ESS Tail_ESS
## sigma     0.27      0.01     0.24     0.29 1.00
4392     4575
##
## Draws were sampled using sample(hmc). For each
parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and
Rhat is the potential
## scale reduction factor on split chains (at
convergence, Rhat = 1).
```

```
posterior <- as_draws_df(MLU_prior_fit)

plot1 <- ggplot(posterior)+
  geom_histogram(aes(prior_b_DiagnosisA), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(b_DiagnosisA), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on
intercepsASD')+
  xlab('intercept for ASD')

plot2 <- ggplot(posterior)+
  geom_histogram(aes(prior_b_DiagnosisB), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(b_DiagnosisB), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on intercept
```

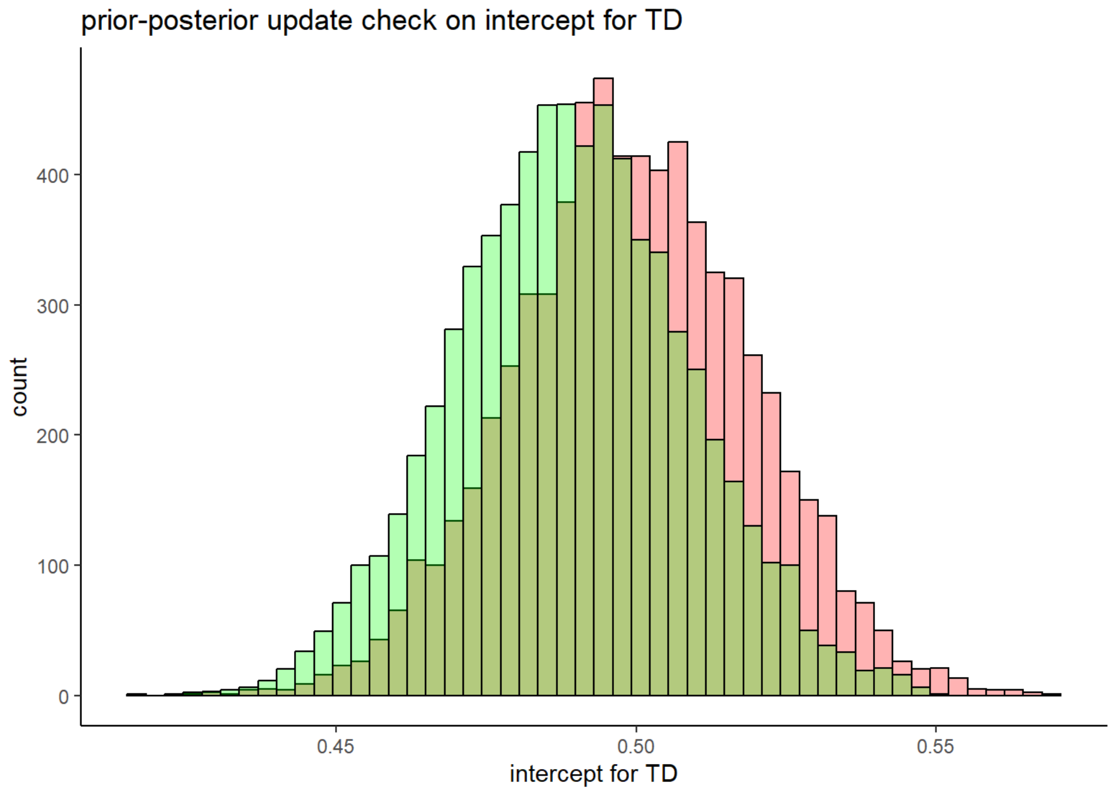
```
for TD')+
  xlab('intercept for TD')

plot3 <- ggplot(posterior)+
  geom_histogram(aes(`prior_b_DiagnosisA:visit`),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(`b_DiagnosisA:visit`),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on slope for
ASD')+
  xlab("Slope for ASD")

plot4 <- ggplot(posterior)+
  geom_histogram(aes(`prior_b_DiagnosisB:visit`),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(`b_DiagnosisB:visit`),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on slope for
TD')+
  xlab("slope for TD")


plot5 <- ggplot(posterior)+
  geom_histogram(aes(prior_cor_id), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(cor_id__Intercept__visit),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on correlation
between varying intercepts and slopes')+
  xlab("Correlation")

plot6 <- ggplot(posterior)+
```

```
  geom_histogram(aes(prior_sd_id__Intercept),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(sd_id__Intercept), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('Prior-posterior update check, the
variability of the intercept')+
  xlab("Intercept")

plot7 <- ggplot(posterior)+
  geom_histogram(aes(prior_sd_id__visit), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(sd_id__visit), fill='green',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('Prior-posterior update check, the
variability of the slopes')+
  xlab("Intercept")

plot8 <- ggplot(posterior)+
  geom_histogram(aes(`prior_b_DiagnosisA:visit`),
fill='red', color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(`b_DiagnosisA:visit`),
fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  geom_histogram(aes(`b_DiagnosisB:visit`),
fill='yellow', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on slope')+
  xlab("Slope")

plot9 <- ggplot(posterior)+
  geom_histogram(aes(prior_b_DiagnosisA), fill='red',
color='black', alpha=0.3, bins=50)+
  geom_histogram(aes(b_DiagnosisA), fill='green',
```

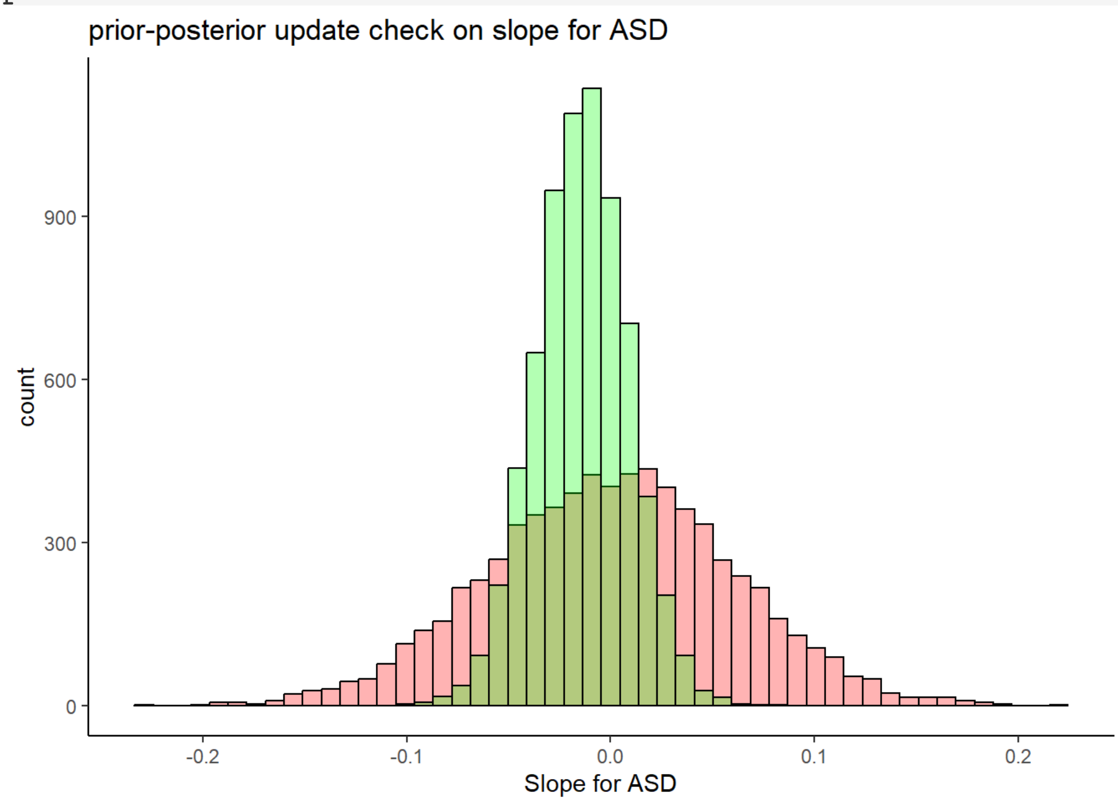
```
color='black', alpha=0.3, bins=50)+
  theme_classic()+
   geom_histogram(aes(b_DiagnosisB), fill='yellow',
color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on interceps')+
  xlab('intercept')


plot1
```



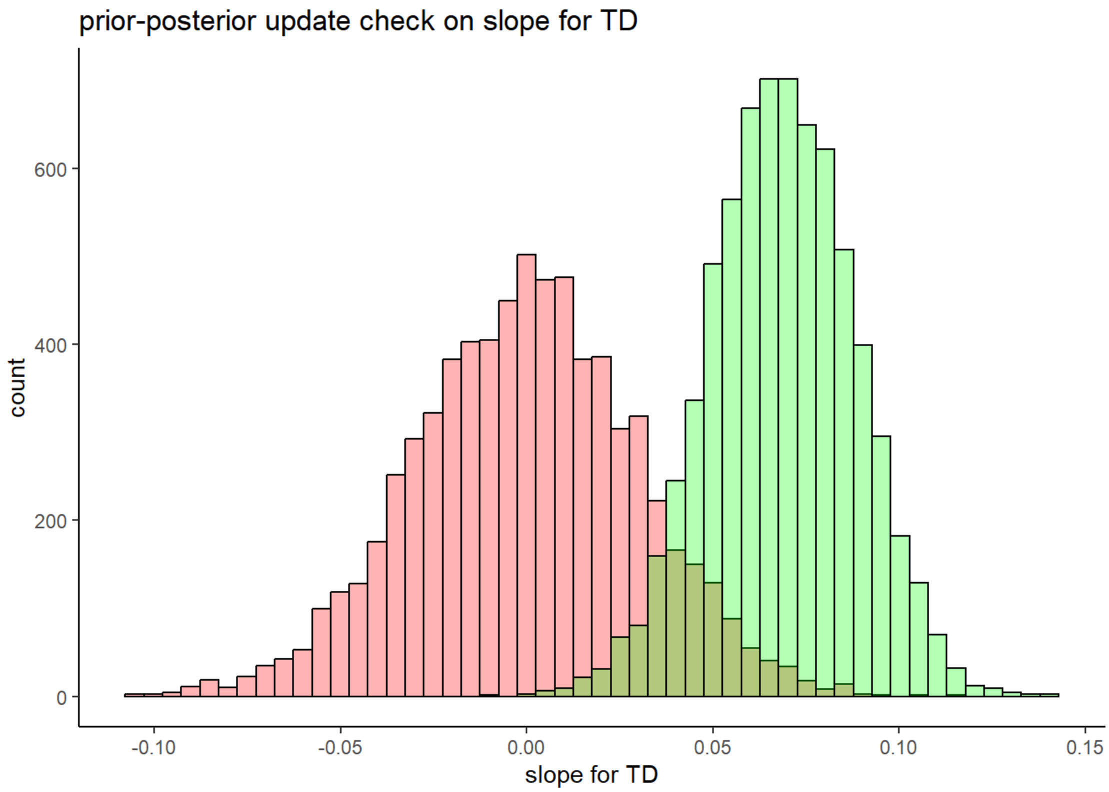

```
plot2
```


prior-posterior update check on intercept for TD
count
400
300
200
100
0
0.45
0.50
0.55
intercept for TD

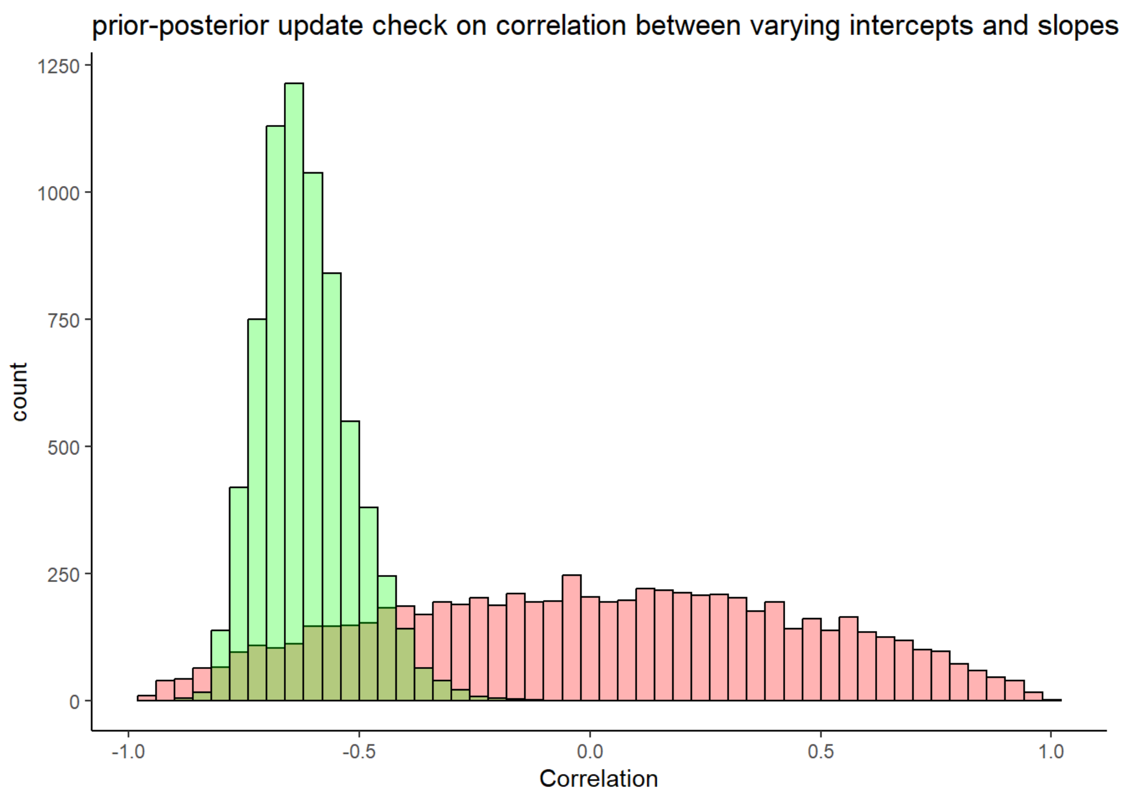
```
plot3
```


prior-posterior update check on slope for ASD
count
900
600
300
0
-0.2
-0.1
0.0
0.1
0.2
Slope for ASD

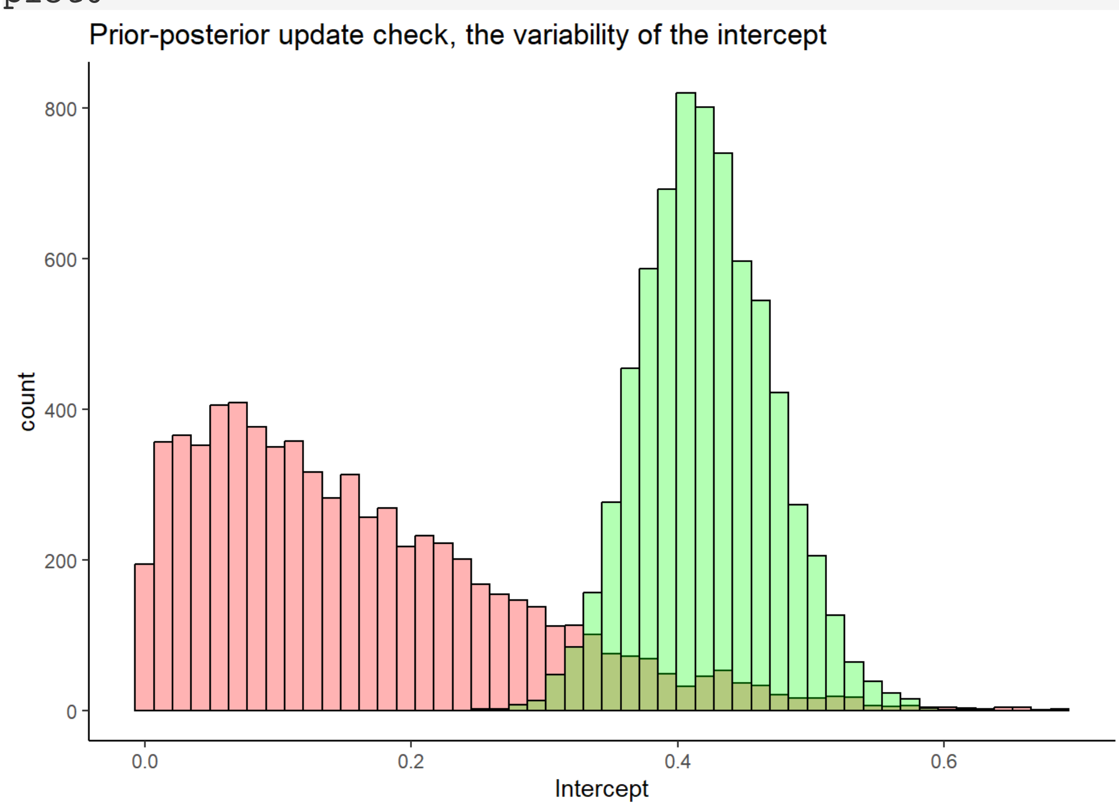
```
plot4
```


prior-posterior update check on slope for TD
count
600
400
200
0
-0.10
-0.05
0.00
0.05
0.10
0.15
slope for TD

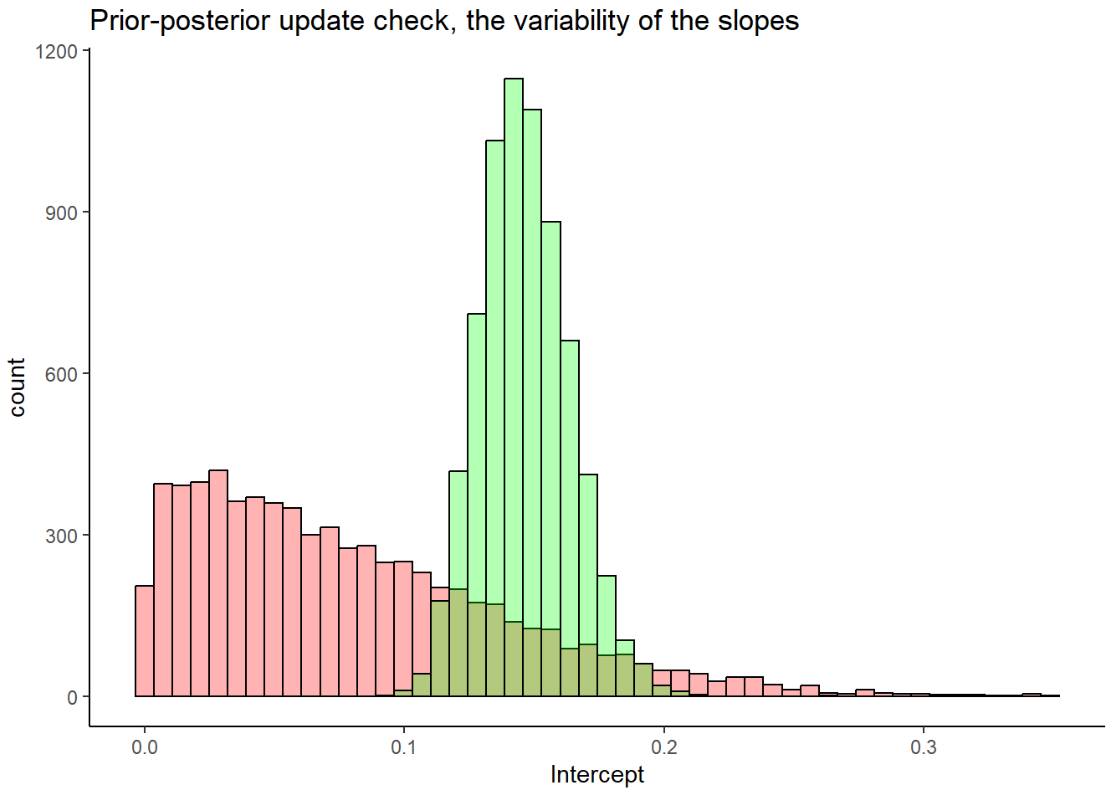
```
plot5
```


prior-posterior update check on correlation between varying intercepts and slopes
count
1250
1000
750
500
250
0
-1.0
-0.5
0.0
0.5
1.0
Correlation

```
plot6
```


Prior-posterior update check, the variability of the intercept
count
800
600
400
200
0
0.0
0.2
0.4
0.6
Intercept

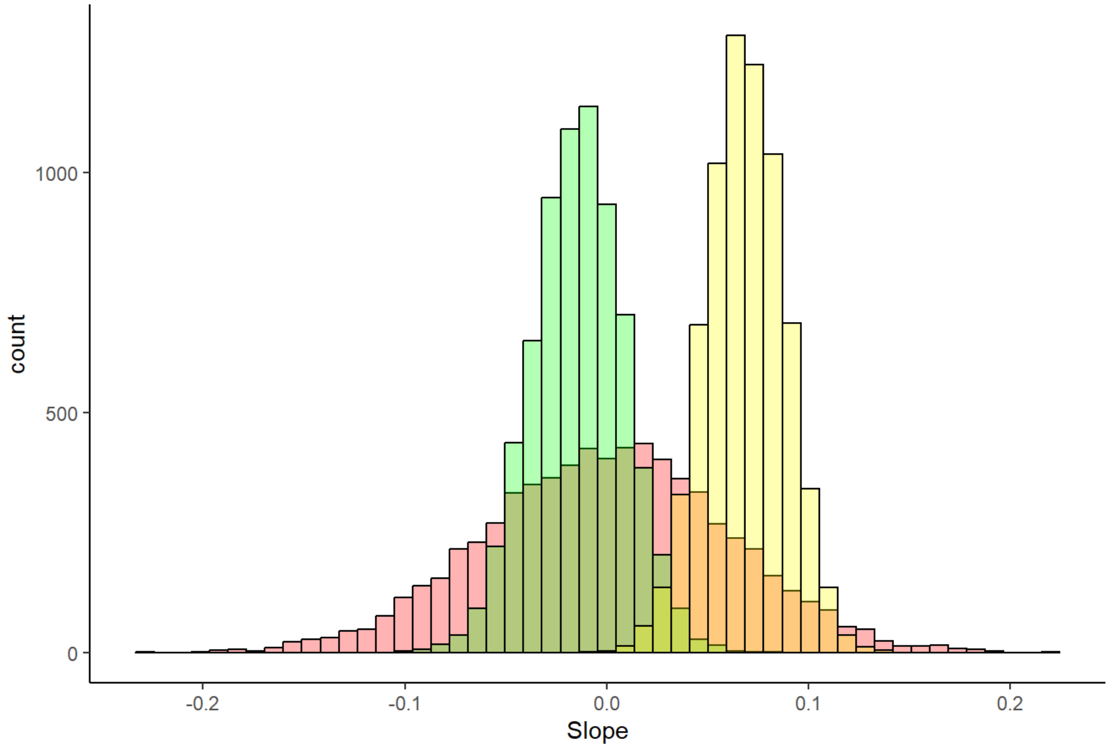
```
plot7
```



Prior-posterior update check, the variability of the slopes
1200
900
600
300
0
count
0.0
0.1
0.2
0.3
Intercept

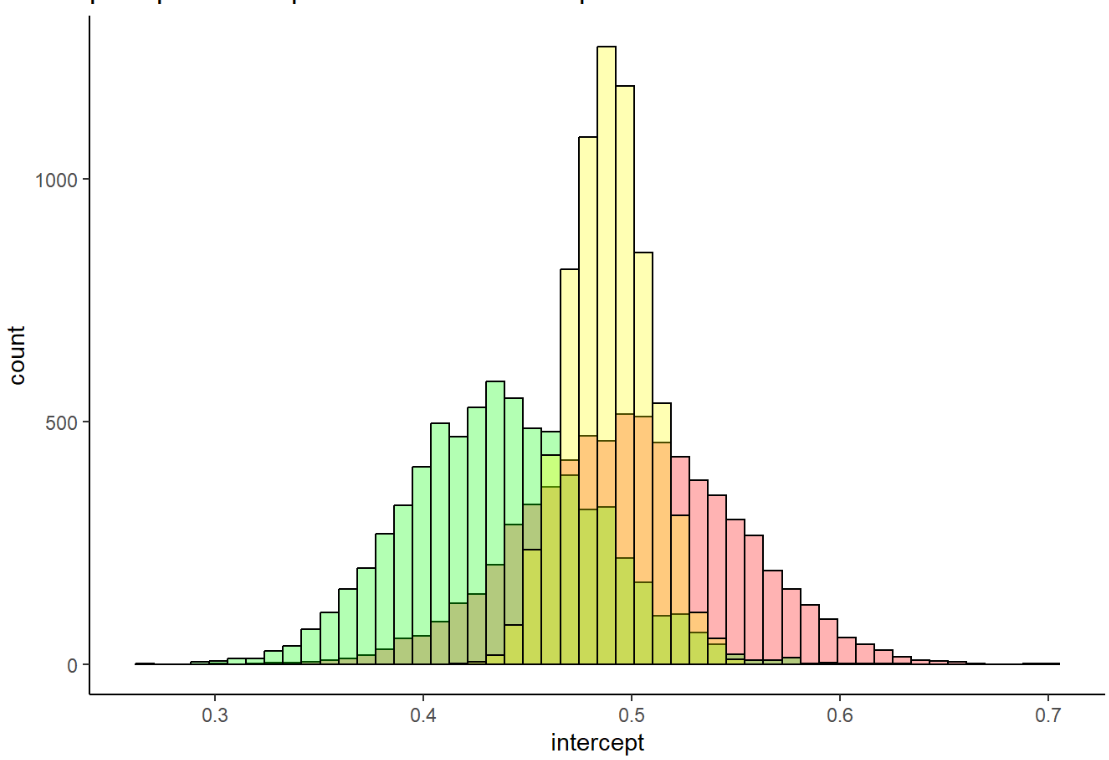

```
plot8
```

prior-posterior update check on slope




```
plot9
```

prior-posterior update check on interceps



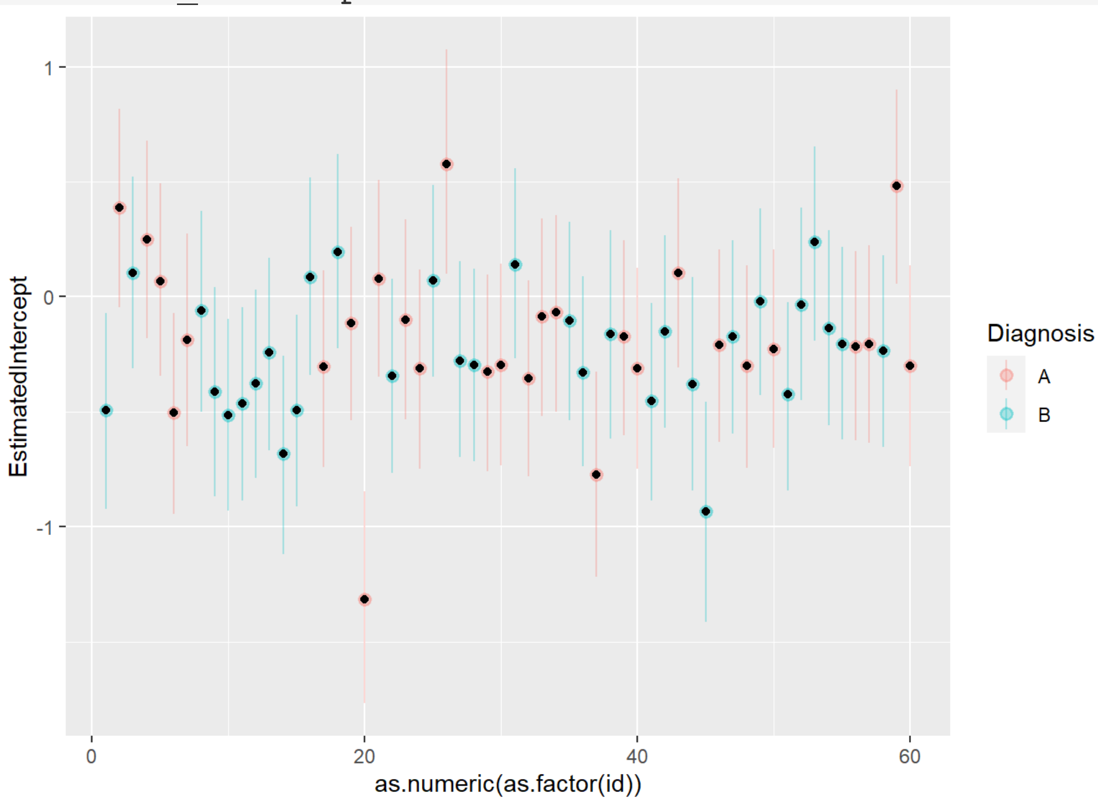
```
temp_re <- ranef(MLU_prior_fit)$id
for (i in unique(real_data$id)) {
  temp <- as.character(i)
  real_data$EstimatedIntercept[real_data$id == i] <-
temp_re[,,'Intercept'][temp,1]
  real_data$EstimatedIntercept_low[real_data$id == i]
<- temp_re[,,'Intercept'][temp,3]
  real_data$EstimatedIntercept_high[real_data$id == i]
<- temp_re[,,'Intercept'][temp,4]
  real_data$EstimatedSlope[real_data$id == i] <-
temp_re[,,'visit'][temp,1]
  real_data$EstimatedSlope_low[real_data$id == i] <-
temp_re[,,'visit'][temp,3]
  real_data$EstimatedSlope_high[real_data$id == i] <-
temp_re[,,'visit'][temp,4]
}
```

```
## Warning: Unknown or uninitialised column:
`EstimatedIntercept`.
## Warning: Unknown or uninitialised column:
`EstimatedIntercept_low`.
## Warning: Unknown or uninitialised column:
`EstimatedIntercept_high`.
## Warning: Unknown or uninitialised column:
`EstimatedSlope`.
## Warning: Unknown or uninitialised column:
`EstimatedSlope_low`.
## Warning: Unknown or uninitialised column:
`EstimatedSlope_high`.
```

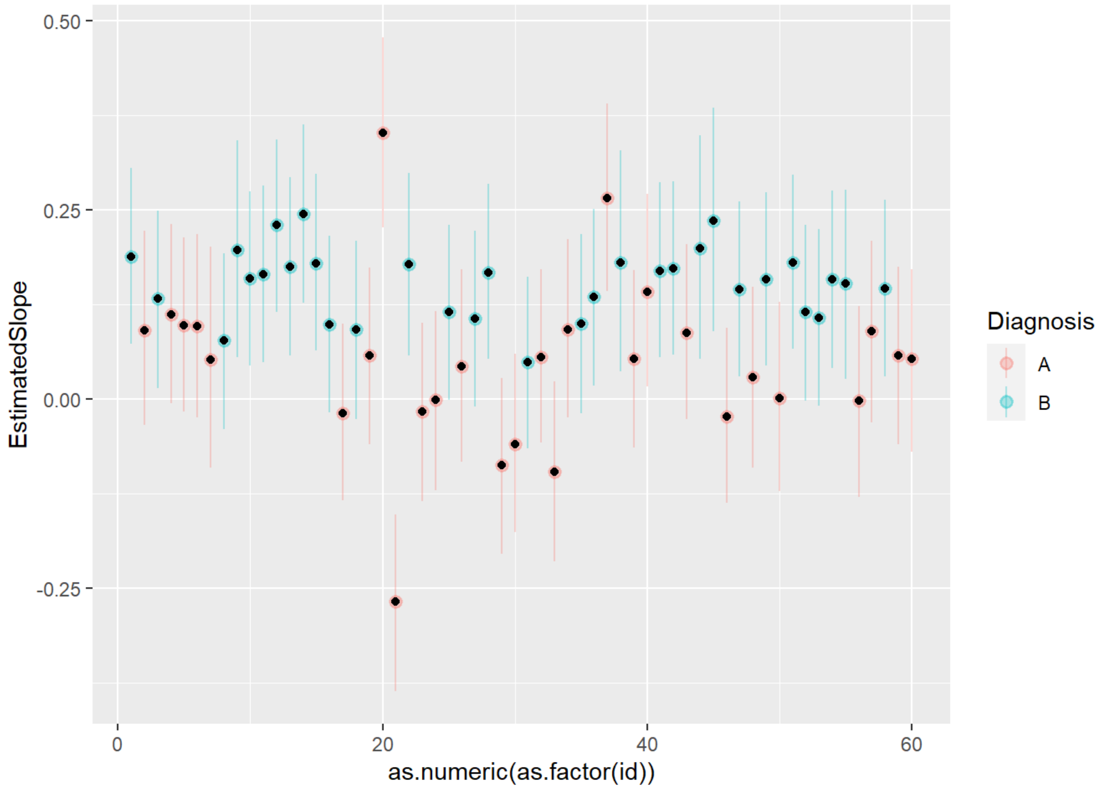
```
d <- real_data %>% subset(visit == 1) %>%
  mutate(
    EstimatedIntercept = ifelse(Diagnosis == 'A',
                                EstimatedIntercept
+ 0.44,
                                EstimatedIntercept
+ 0.49),
```

```
    EstimatedIntercept_low = ifelse(Diagnosis == 'A',

EstimatedIntercept_low + 0.44,

EstimatedIntercept_low + 0.49),
    EstimatedIntercept_high = ifelse(Diagnosis == 'A',

EstimatedIntercept_high + 0.44,

EstimatedIntercept_high + 0.49)
)


d <- real_data %>% subset(visit == 1) %>%
  mutate(
    EstimatedSlope = ifelse(Diagnosis == 'A',
                                    EstimatedSlope -
0.01,
                                    EstimatedSlope +
0.07),
    EstimatedSlope_low = ifelse(Diagnosis == 'A',
                                   EstimatedSlope_low -
0.01,
                                   EstimatedSlope_low +
0.07),
    EstimatedSlope_high = ifelse(Diagnosis == 'A',

EstimatedSlope_high - 0.01,

EstimatedSlope_high + 0.07)
)

estimates_intercept <- ggplot(d) +
  geom_pointrange(aes( x = as.numeric(as.factor(id)), y
= EstimatedIntercept,
```

```
                       ymin = EstimatedIntercept_low,
ymax = EstimatedIntercept_high,
                       color = Diagnosis), alpha = 0.3)
+
  geom_point(aes( x = as.numeric(as.factor(id)), y =
EstimatedIntercept))

estimates_slopes <- ggplot(d) +
  geom_pointrange(aes( x = as.numeric(as.factor(id)), y
= EstimatedSlope,
                       ymin = EstimatedSlope_low, ymax
= EstimatedSlope_high,
                       color = Diagnosis), alpha = 0.3)
+
  geom_point(aes( x = as.numeric(as.factor(id)), y =
EstimatedSlope))

estimates_intercept
```



```
estimates_slopes
```



A_2.final

Study group 3

2022-11-04

Loading required packages

```
pacman::p_load(glue,
       tidyr,
       data.table,
       moments,
       tidybayes,
       tibble,
       cowplot,
       viridis,
       brms,
       stringr,
       rstan,
       cmdstanr,
       magrittr,
       gridExtra,
       grid,
       lattice,
       ggplot2,
       ggridges,
       ellipse,
       Rmisc,
       dplyr,
       "rmarkdown",
       knitr)
pacman::p_load(tidyverse)
```

```
## Error in completeSubclasses(classDef2, class1, obj, where) :
##   trying to get slot "subclasses" from an object of a basic class ("NULL") with
no slots
##
## The downloaded binary packages are in
##  /var/folders/hf/2cjx77xd24b01rtsfd8v4mmh0000gn/T//RtmpGE2FYm/downloaded_packag
es
## Error in completeSubclasses(classDef2, class1, obj, where) :
##   trying to get slot "subclasses" from an object of a basic class ("NULL") with
no slots
```

```
pacman::p_load(purrr)
pacman::p_load(MCMCglmm)
pacman::p_load(readxl)
pacman::p_load(metafor)
```

Assignment 2: meta-analysis

Questions to be answered

1. Simulate data to setup the analysis and gain insight on the structure of the problem. Simulate one dataset of 100 studies (n of participants should follow a normal distribution with mean of 20, sd of 10, but no fewer than 10 participants), with a mean effect size of 0.4, average deviation by study of .4 and measurement error of .8. The data you get should have one row per study, with an effect size mean and standard error. Build a proper bayesian model to analyze the simulated data. Then simulate publication bias (only some of the studies you simulate are likely to be published, which?), the effect of publication bias on your estimates (re-run the model on published studies, assess the difference), and use at least one technique to assess publication bias. remember to use at least one plot to visualize your results. BONUS question: do a power/precision analysis.
2. What is the current evidence for distinctive vocal patterns in schizophrenia? Use the data from Parola et al (2020) - https://www.dropbox.com/s/0l9ur0gaabr80a8/Matrix_MetaAnalysis_Diagnosis_updated290719.xlsx?dl=0 (https://www.dropbox.com/s/0l9ur0gaabr80a8/Matrix_MetaAnalysis_Diagnosis_updated290719.xlsx?dl=0) - focusing on pitch variability (PITCH_F0SD). Describe the data available (studies, participants). Using the model from question 1 analyze the data, visualize and report the findings: population level effect size; how well studies reflect it; influential studies, publication bias. BONUS question: add the findings from https://www.medrxiv.org/content/10.1101/2022.04.03.22273354v2 (https://www.medrxiv.org/content/10.1101/2022.04.03.22273354v2). BONUS question: assess the effect of task on the estimates (model comparison with baseline model)

Sara

Question 1

Simulation

Outlining prior parameter provided by the assignment description

```
mean_effect <- 0.4
effect_sd <- 0.4
meas_error <- 0.8
par_mean <- 20
par_sd <- 10
n <- 100
```

A simulation of participant data of multiple visits using the provided data

```
set.seed(954)

sim_studies <-
  tibble(
    study_ID = seq(1:n),
    n_participants =
        round(rtnorm(n, mean=par_mean, sd=par_sd, lower=10))
    )


for (i in seq(nrow(sim_studies))){
    sim_studies$study_effect[i] <-
      rnorm(1,mean_effect,effect_sd)
    temp <-
      rnorm(sim_studies$n_participants[i],sim_studies$study_effect[i], meas_error)
    sim_studies$mean_effect_size[i] <-
      mean(temp)
    sim_studies$sd_effect[i] <-
      sd(temp)
    sim_studies$standard_error[i] <-
      sim_studies$sd_effect[i]/sqrt(sim_studies$n_participants[i])
  }
```

Bayesian model

A Bayesian model illustrating potential effect sizes on individual participants

```
model_study <- bf(mean_effect_size|se(standard_error) ~1 + (1|study_ID))
```

Priors

Generating prior data simulations to model, using parameters provided in class

```
get_prior(data = sim_studies, family = gaussian, model_study)
```

```
##                    prior     class      coef    group resp dpar nlpar lb ub
##  student_t(3, 0.3, 2.5) Intercept
##    student_t(3, 0, 2.5)        sd                                  0
##    student_t(3, 0, 2.5)        sd           study_ID               0
##    student_t(3, 0, 2.5)        sd Intercept study_ID               0
##        source
##       default
##       default
##  (vectorized)
##  (vectorized)
```

```
priors <- c(
  prior(normal(0, 0.3), class=Intercept),
  prior(normal(0, 0.3), class=sd))
```

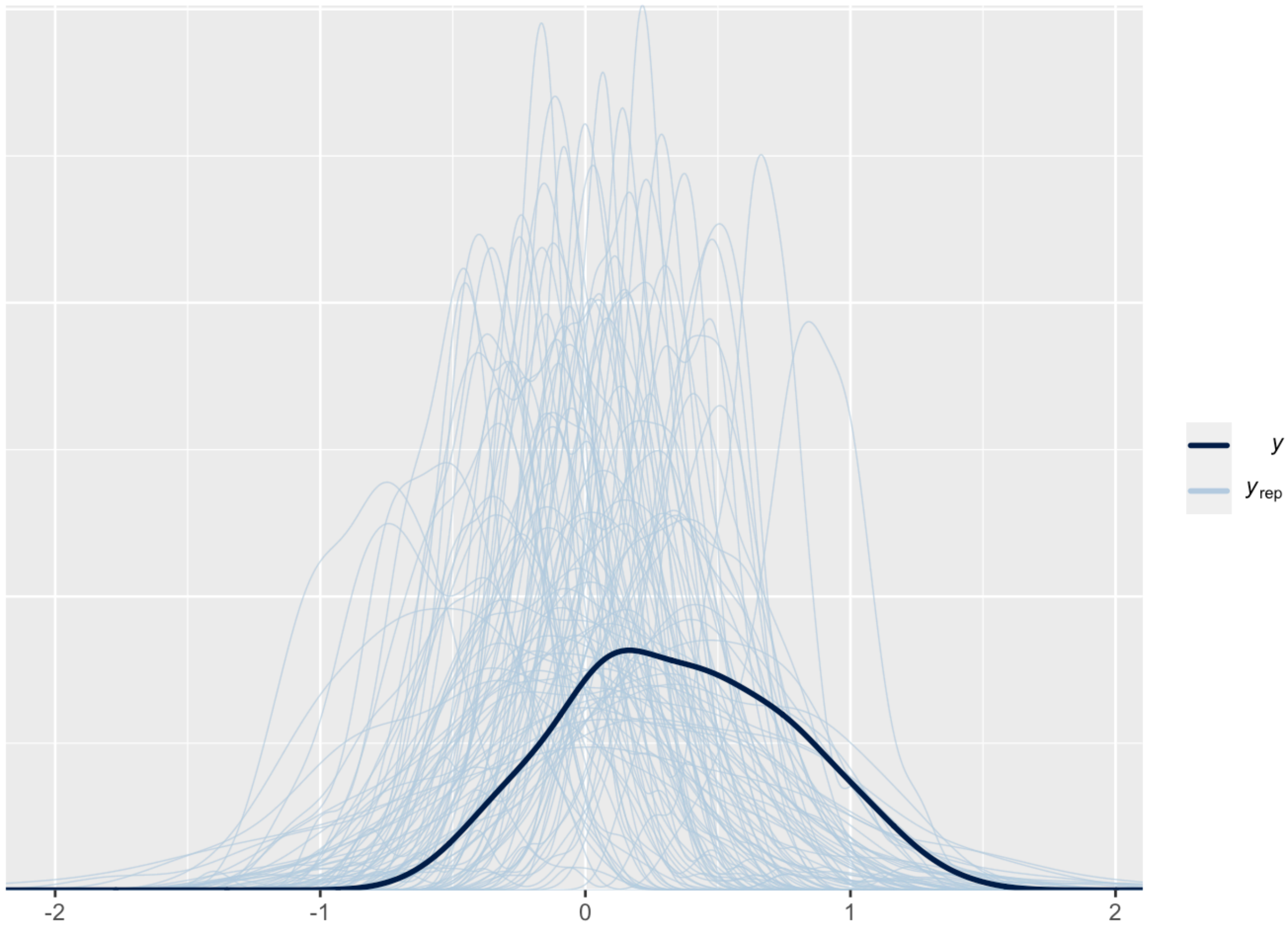
Model

Modeling using sample_prior = 'only'

```
model_prior <- brm(
  model_study,
  data = sim_studies,
  prior = priors,
  family = gaussian,
  refresh=0,
  sample_prior = 'only',
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 1 finished in 1.6 seconds.
## Chain 2 finished in 1.6 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 1.6 seconds.
## Total execution time: 1.6 seconds.
```

```
pp_check(model_prior, ndraws=100)
```



Manuela

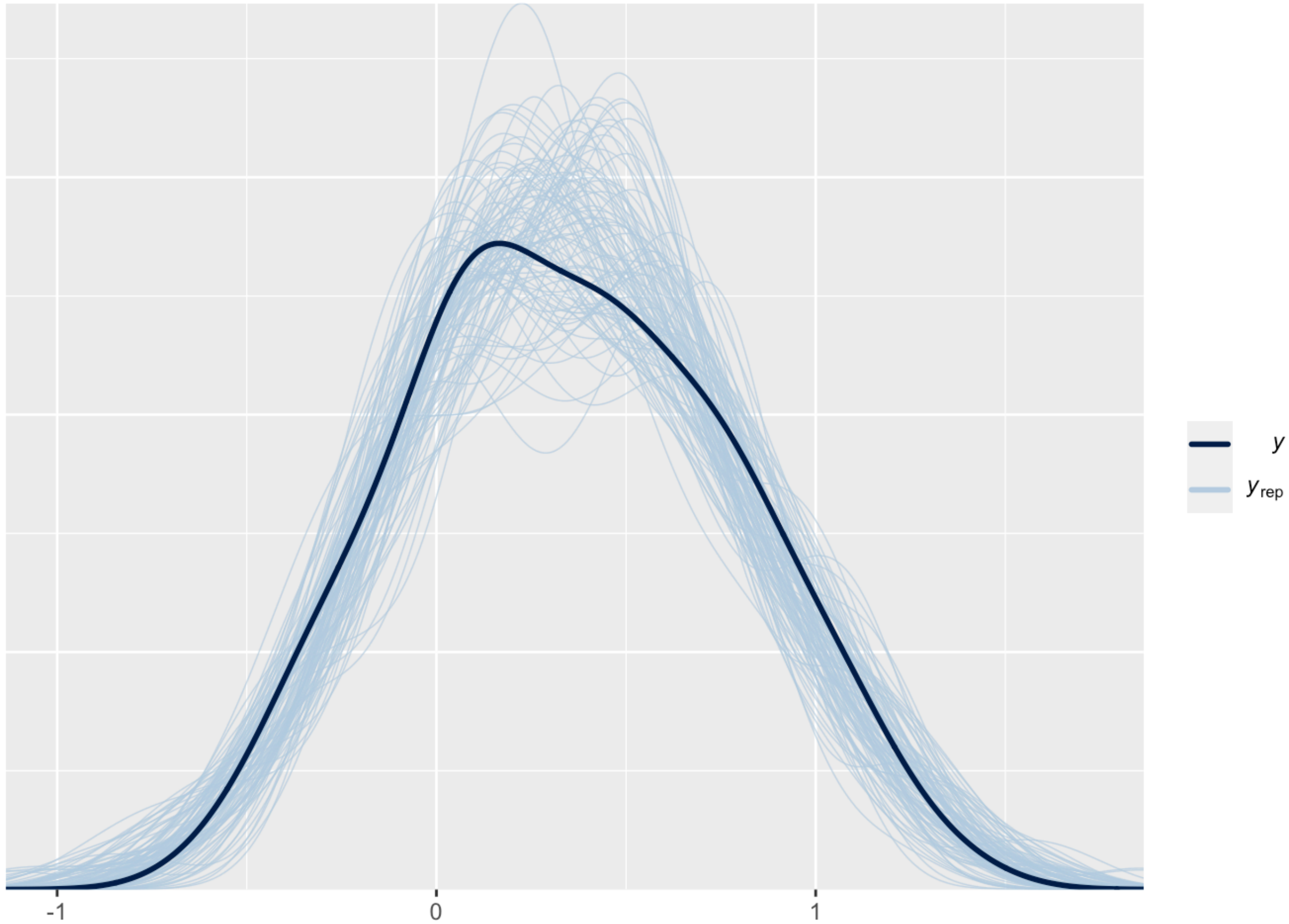
Fitting model

Modeling the sampled priors along with the simulation

```
model_prior_fit <- brm(
  model_study,
  data = sim_studies,
  prior = priors,
  family = gaussian,
  refresh=0,
  sample_prior = TRUE,
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

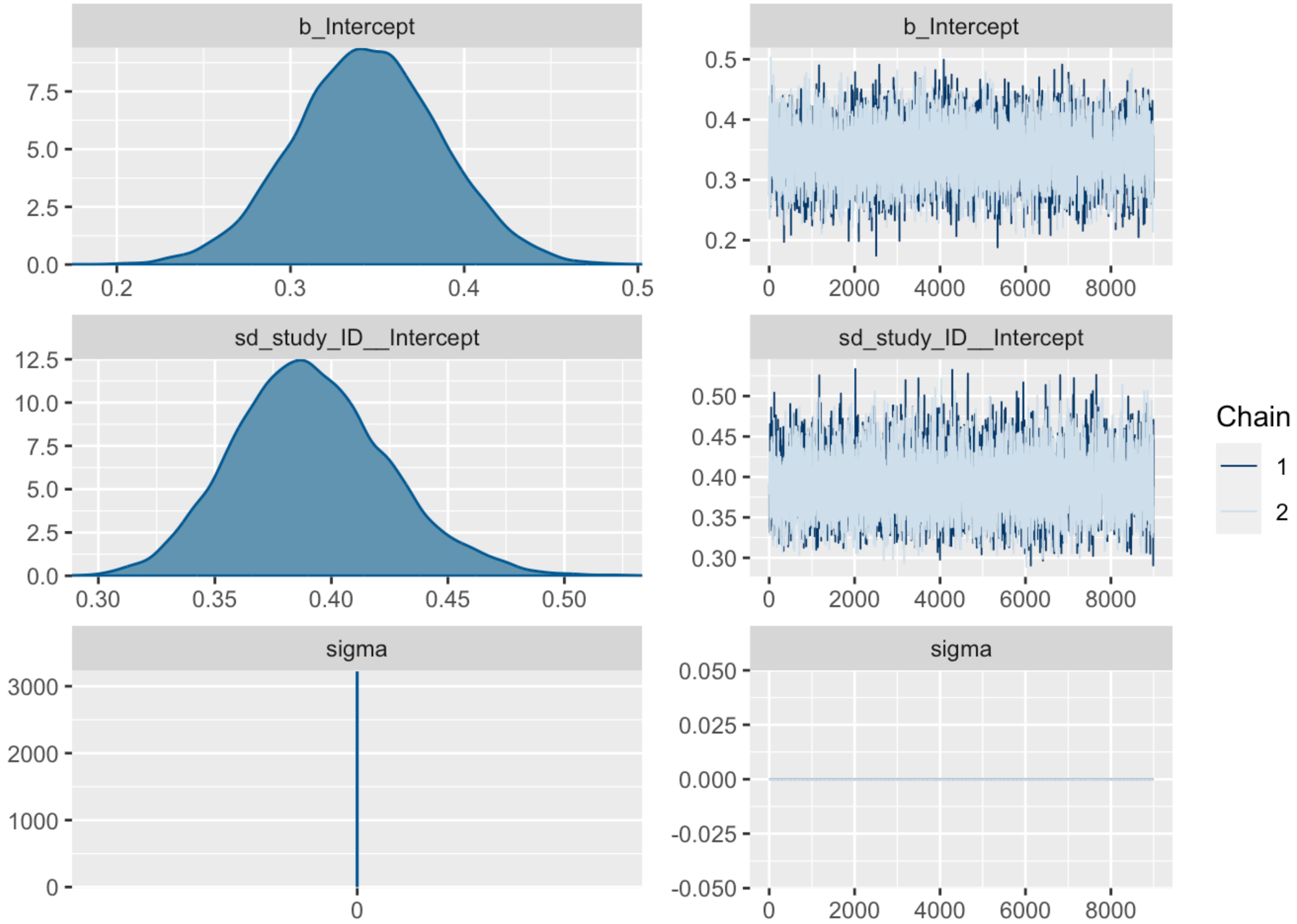
```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 1 finished in 3.0 seconds.
## Chain 2 finished in 4.7 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 3.9 seconds.
## Total execution time: 4.7 seconds.
```

```
pp_check(model_prior_fit, ndraws=100)
```



Plotting and visualizing

```
plot(model_prior_fit)
```



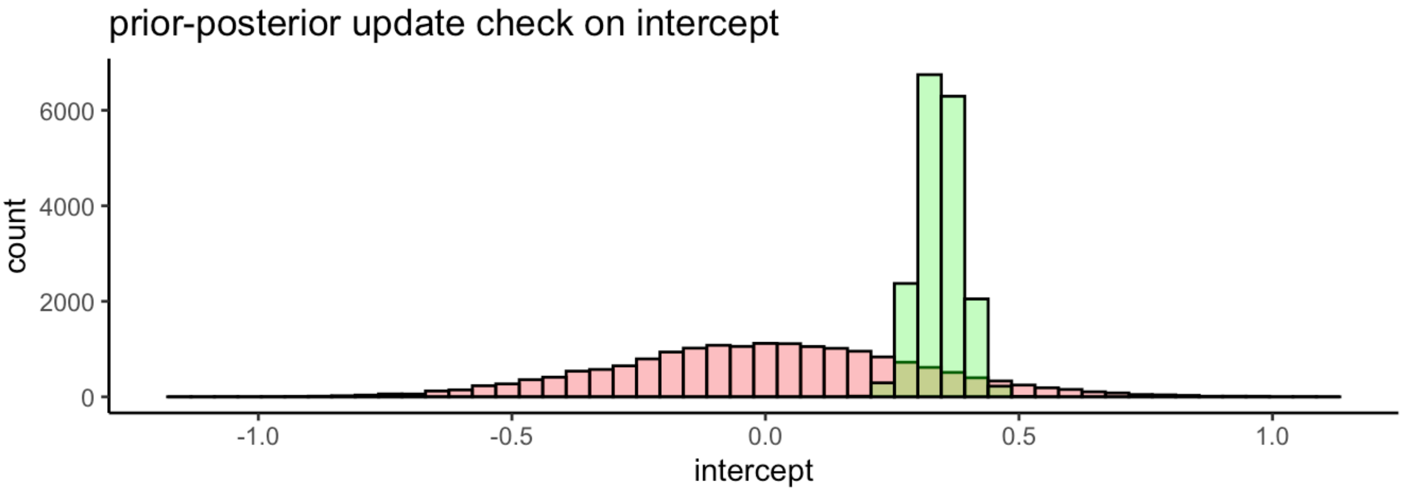

```
summary(model_prior_fit)
```

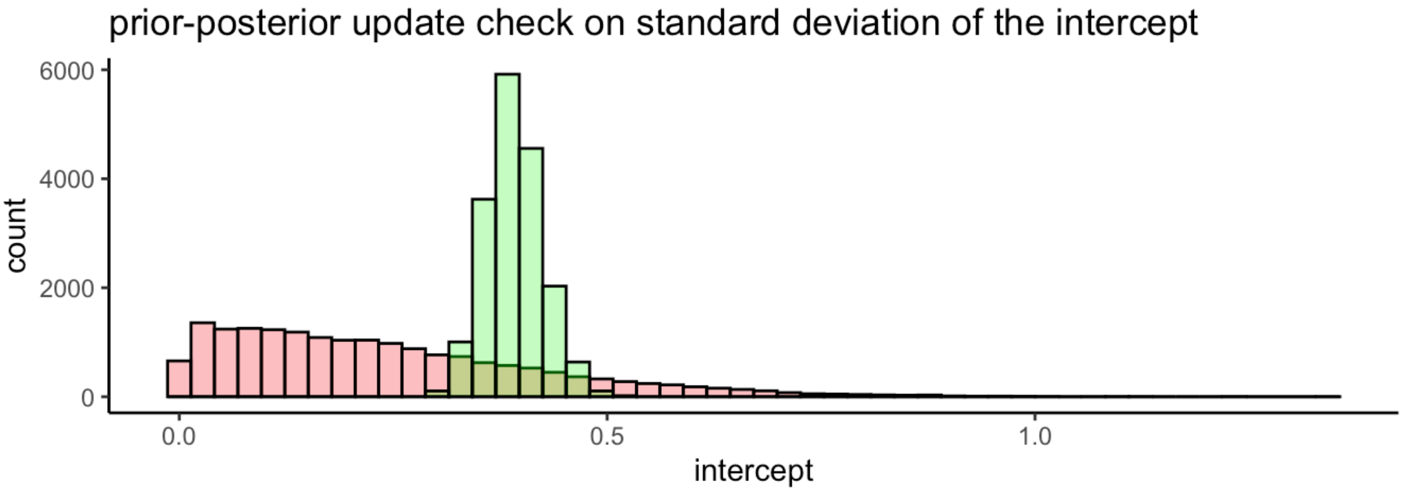
```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: mean_effect_size | se(standard_error) ~ 1 + (1 | study_ID)
##    Data: sim_studies (Number of observations: 100)
##   Draws: 2 chains, each with iter = 10000; warmup = 1000; thin = 1;
##          total post-warmup draws = 18000
##
## Group-Level Effects:
## ~study_ID (Number of levels: 100)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.39      0.03     0.33     0.46 1.00     5268     8430
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.34      0.04     0.26     0.43 1.00     4104     7005
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.00      0.00     0.00     0.00   NA       NA       NA
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Prior posterior update check

Plotting “prior-posterior update check on intercept” and “prior-posterior update check on standard deviation of the intercept”

```
model_posterior <- as_draws_df(model_prior_fit)

plot1 <- ggplot(model_posterior)+
  geom_histogram(aes(prior_Intercept), fill='red', color='black', alpha=0.3, bins=
50)+
  geom_histogram(aes(Intercept), fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on intercept')+
  xlab('intercept')
plot2 <- ggplot(model_posterior)+
  geom_histogram(aes(prior_sd_study_ID), fill='red', color='black', alpha=0.3, bin
s=50)+
  geom_histogram(aes(sd_study_ID__Intercept), fill='green', color='black', alpha=0
.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on standard deviation of the intercept')+
  xlab('intercept')
grid.arrange(plot1, plot2)
```





Simulation of publication bias, the effect of publication bias on our estimate and asses the publication bias (remember to visualize our results)

Simulating the effect size of the publication factors and filtering data for only published studies

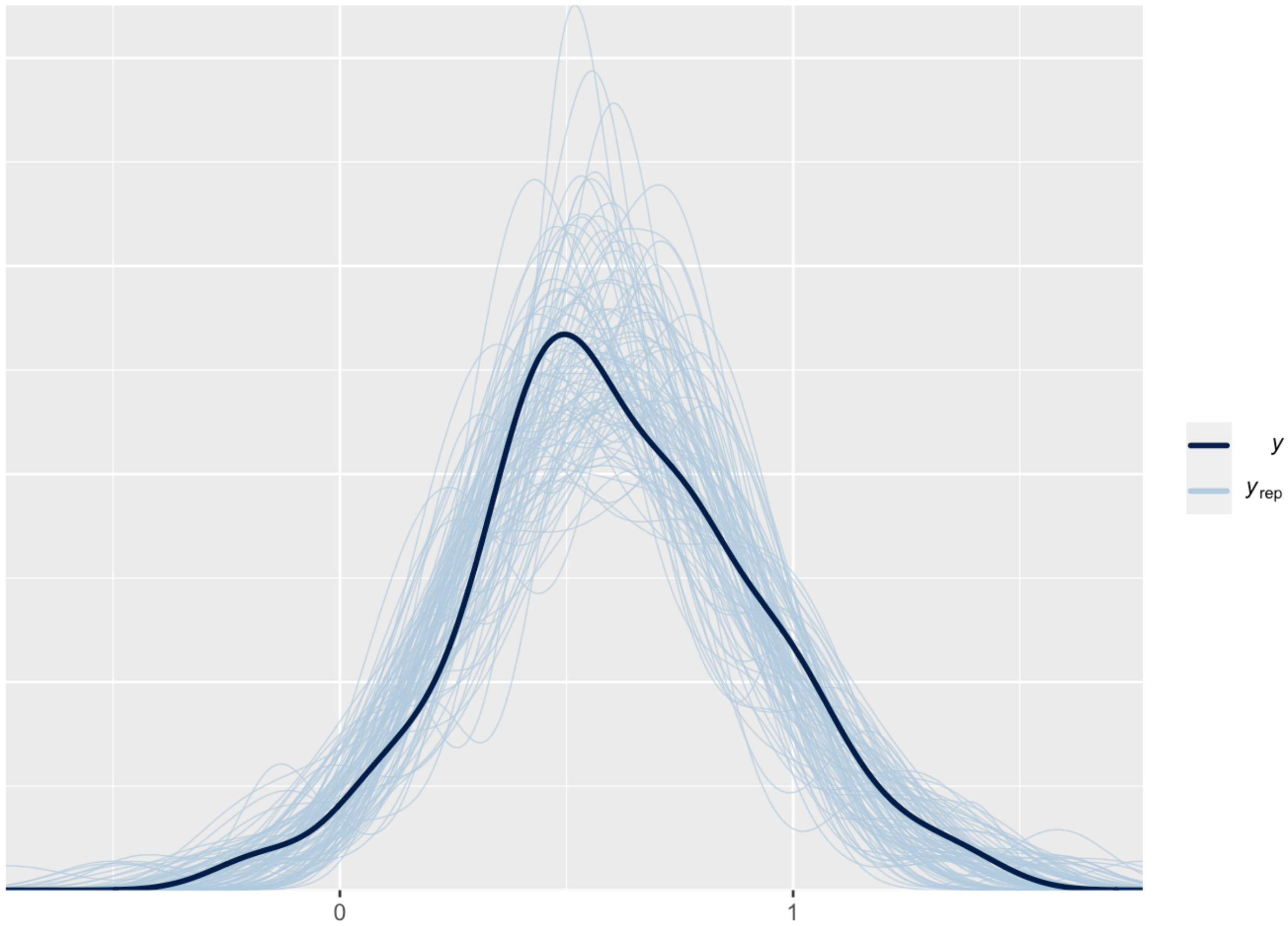
```
set.seed(843)

for (i in seq(nrow(sim_studies))){
  sim_studies$published[i] <-
    ifelse(abs(
      sim_studies$mean_effect_size[i])-(2*sim_studies$standard_error[i])>0
      & sim_studies$mean_effect_size[i]>0,
      rbinom(1,1,0.9), rbinom(1,1,0.1))}

sim_studies <- sim_studies %>%
  mutate(published=as.factor(published))

pub_sim_studies <- dplyr::filter(sim_studies, published==1)
```

Modeling using sample_prior = 'only'

```
pub_model_prior_fit <- brm(
  model_study,
  data = pub_sim_studies,
  prior = priors,
  family = gaussian,
  refresh=0,
  sample_prior = TRUE,
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 2 finished in 2.1 seconds.
## Chain 1 finished in 2.1 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 2.1 seconds.
## Total execution time: 2.2 seconds.
```

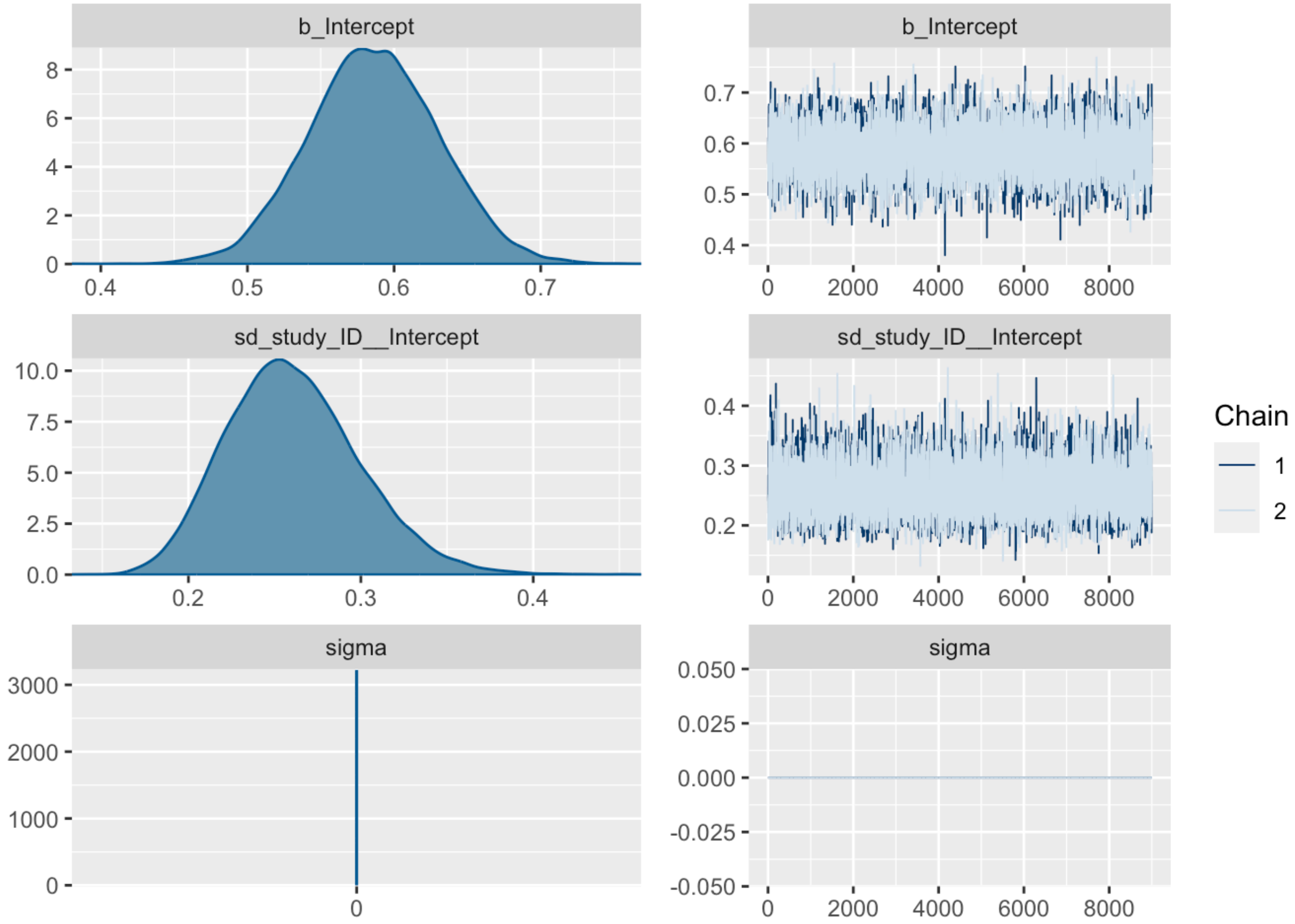
```
pp_check(pub_model_prior_fit, ndraws=100)
```



Ditlev

Potting and assesing and transforming the brmsfit to draws

```
plot(pub_model_prior_fit)
```



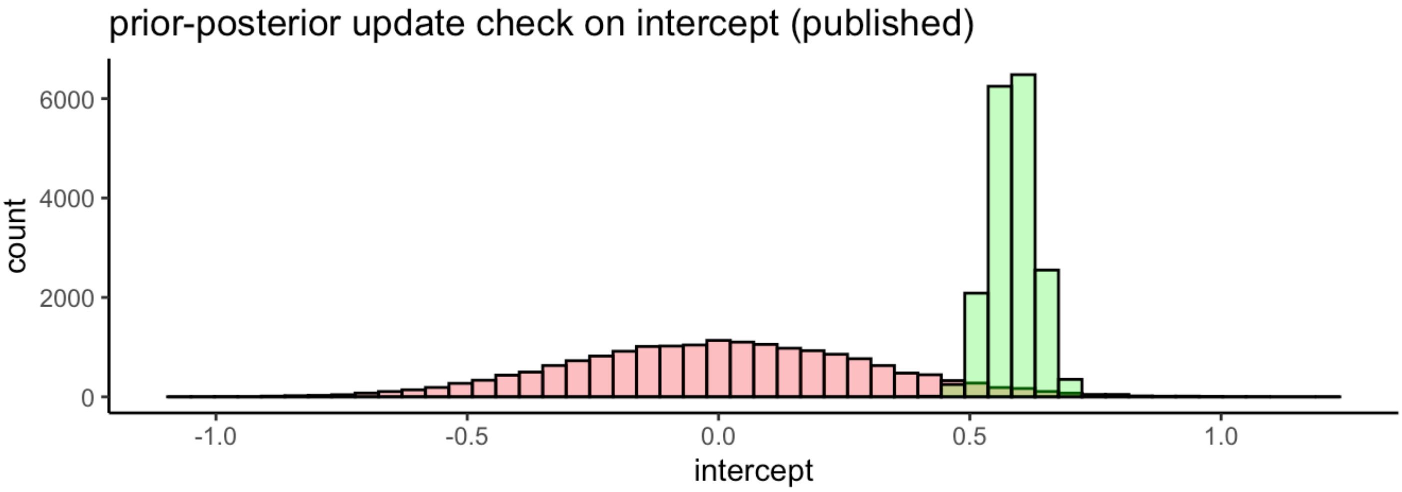

```
summary(pub_model_prior_fit)
```

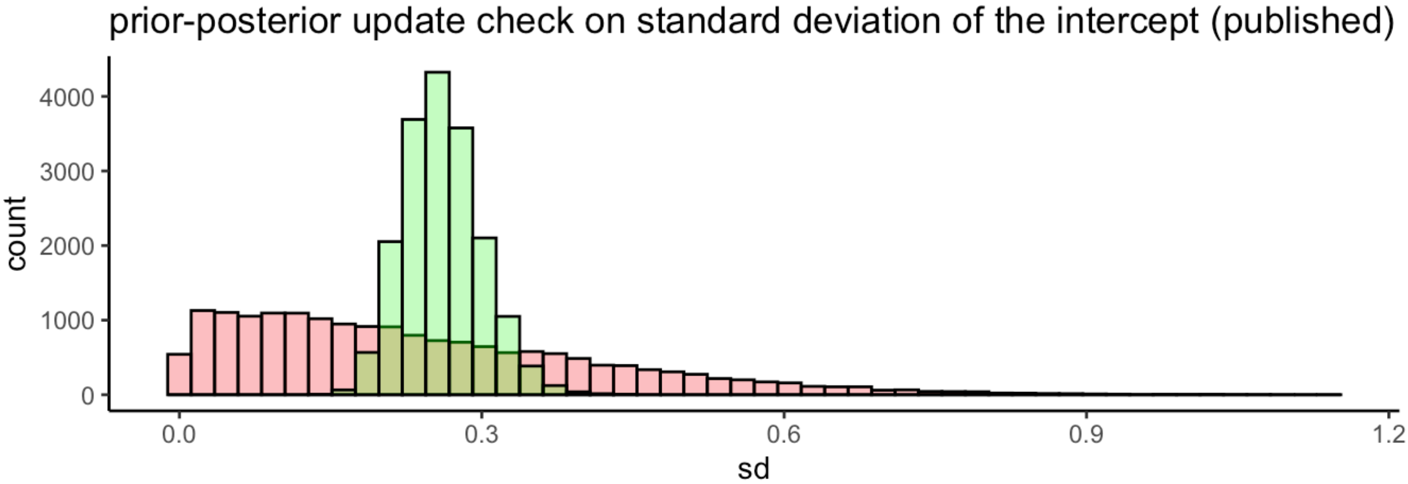
```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: mean_effect_size | se(standard_error) ~ 1 + (1 | study_ID)
##    Data: pub_sim_studies (Number of observations: 48)
##   Draws: 2 chains, each with iter = 10000; warmup = 1000; thin = 1;
##          total post-warmup draws = 18000
##
## Group-Level Effects:
## ~study_ID (Number of levels: 48)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.26      0.04     0.19     0.34 1.00     5900     9863
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.59      0.04     0.50     0.67 1.00     4538     8095
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.00      0.00     0.00     0.00   NA       NA       NA
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
pub_posterior <- as_draws_df(pub_model_prior_fit)
```

Plotting “prior-posterior update check on intercept” and “prior-posterior update check on standard deviation of the intercept”

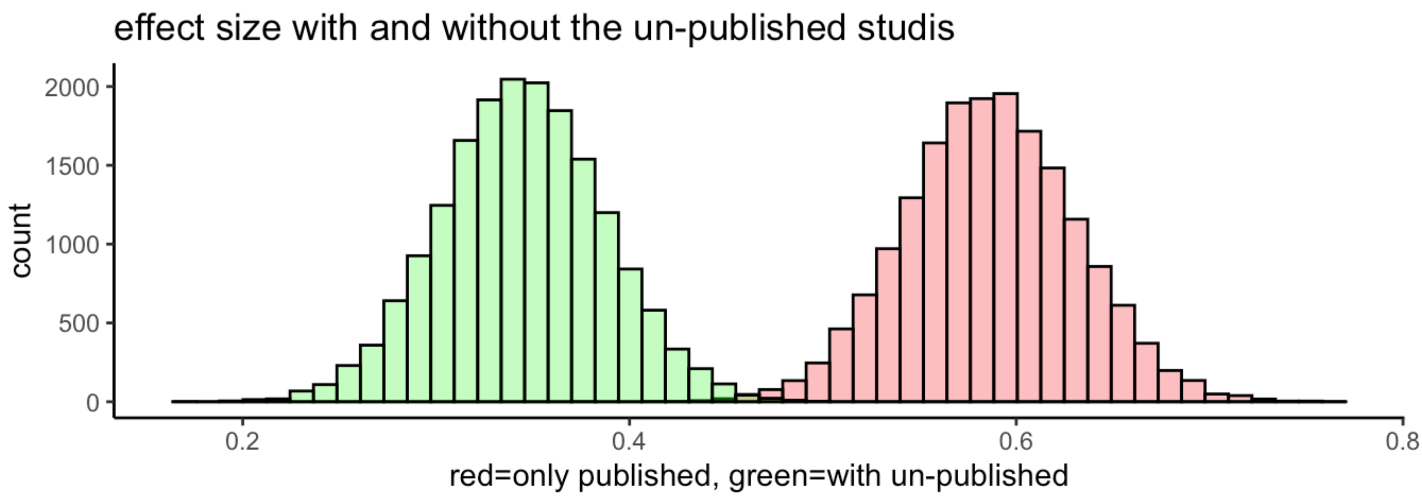
```
pub_plot1 <- ggplot(pub_posterior)+
  geom_histogram(aes(prior_Intercept), fill='red', color='black', alpha=0.3, bins=
50)+
  geom_histogram(aes(Intercept), fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on intercept (published)')+
  xlab('intercept')
pub_plot2 <- ggplot(pub_posterior)+
  geom_histogram(aes(prior_sd_study_ID), fill='red', color='black', alpha=0.3, bin
s=50)+
  geom_histogram(aes(sd_study_ID__Intercept), fill='green', color='black', alpha=0
.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on standard deviation of the intercept (pu
blished)')+
  xlab('sd')
grid.arrange(pub_plot1, pub_plot2)
```

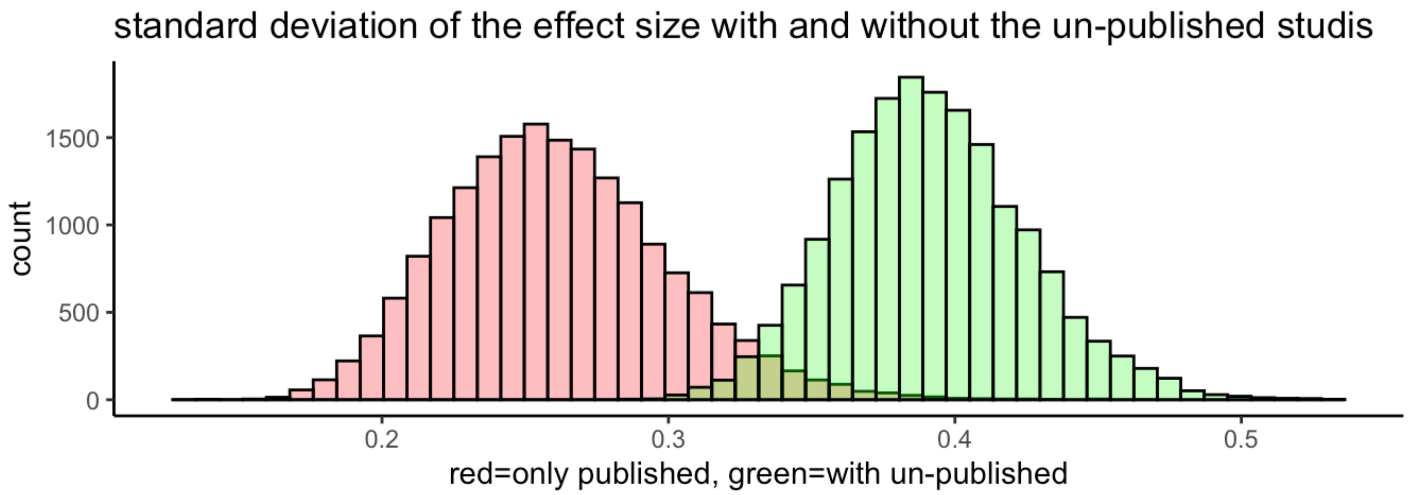




Plotting “effect size with and without the un-published studis” and “tandard deviation of the effect size with and without the un-published studis”

```
plot3 <- ggplot()+
  geom_histogram(aes(pub_posterior$Intercept), fill='red', color='black', alpha=0.
3, bins=50)+
  geom_histogram(aes(model_posterior$Intercept), fill='green', color='black', alph
a=0.3, bins=50)+
  theme_classic()+
  ggtitle('effect size with and without the un-published studis')+
  xlab('red=only published, green=with un-published')
plot4 <- ggplot()+
  geom_histogram(aes(pub_posterior$sd_study_ID__Intercept), fill='red', color='bla
ck', alpha=0.3, bins=50)+
  geom_histogram(aes(model_posterior$sd_study_ID__Intercept), fill='green', color=
'black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('standard deviation of the effect size with and without the un-published
studis')+
  xlab('red=only published, green=with un-published')
grid.arrange(plot3, plot4)
```





Question 2

Loading the data

```
matrix_ma <- read_excel("/Users/patrikmolnar/Desktop/Cognitive Science/Semester 3/
Methods3/Matrix_MetaAnalysis.xlsx")
```

Describing the data

Filtering out NA & NR for SZ

```
matrix_ma_filter_for_analysis <- matrix_ma %>%
  dplyr::filter(AGE_M_SZ!="NR") %>%
  dplyr::filter(AGE_M_SZ!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(AGE_SD_SZ!="NR") %>%
  dplyr::filter(AGE_SD_SZ!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(MALE_SZ!="NR") %>%
  dplyr::filter(MALE_SZ!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(FEMALE_SZ!="NR") %>%
  dplyr::filter(FEMALE_SZ!="NA")
```

Filtering out NA & NR for HC

```
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(AGE_M_HC!="NR") %>%
  dplyr::filter(AGE_M_HC!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(AGE_SD_HC!="NR") %>%
  dplyr::filter(AGE_SD_HC!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(MALE_HC!="NR") %>%
  dplyr::filter(MALE_HC!="NA")
matrix_ma_filter_for_analysis <- matrix_ma_filter_for_analysis %>%
  dplyr::filter(FEMALE_HC!="NR") %>%
  dplyr::filter(FEMALE_HC!="NA")
```

Making the variables numeric for SZ

```
matrix_ma_filter_for_analysis$AGE_M_SZ <- as.numeric(matrix_ma_filter_for_analysis
$AGE_M_SZ)
matrix_ma_filter_for_analysis$AGE_SD_SZ <- as.numeric(matrix_ma_filter_for_analysi
s$AGE_SD_SZ)
matrix_ma_filter_for_analysis$MALE_SZ <- as.numeric(matrix_ma_filter_for_analysis$
MALE_SZ)
matrix_ma_filter_for_analysis$FEMALE_SZ <- as.numeric(matrix_ma_filter_for_analysi
s$FEMALE_SZ)
```

Making the variables numeric for HC

```
matrix_ma_filter_for_analysis$AGE_M_HC <- as.numeric(matrix_ma_filter_for_analysis
$AGE_M_HC)
matrix_ma_filter_for_analysis$AGE_SD_HC <- as.numeric(matrix_ma_filter_for_analysi
s$AGE_SD_HC)
matrix_ma_filter_for_analysis$MALE_HC <- as.numeric(matrix_ma_filter_for_analysis$
MALE_HC)
matrix_ma_filter_for_analysis$FEMALE_HC <- as.numeric(matrix_ma_filter_for_analysi
s$FEMALE_HC)
```

Patrik

Making both tibbles in order to combine them and make them easier for the eye

```
a <- tibble(diagnosis = "SZ",
         mean_sample_size=mean(matrix_ma_filter_for_analysis$SAMPLE_SIZE_SZ),
         mean_numer_of_males=mean(matrix_ma_filter_for_analysis$MALE_SZ),
         mean_number_of_females=mean(matrix_ma_filter_for_analysis$FEMALE_SZ),
         mean_age=mean(matrix_ma_filter_for_analysis$AGE_M_SZ),
         mean_sd_age=mean(matrix_ma_filter_for_analysis$AGE_SD_SZ)
         )

b <- tibble(diagnosis = "HC",
         mean_sample_size=mean(matrix_ma_filter_for_analysis$SAMPLE_SIZE_HC),
         mean_numer_of_males=mean(matrix_ma_filter_for_analysis$MALE_HC),
         mean_number_of_females=mean(matrix_ma_filter_for_analysis$FEMALE_HC),
         mean_age=mean(matrix_ma_filter_for_analysis$AGE_M_HC),
         mean_sd_age=mean(matrix_ma_filter_for_analysis$AGE_SD_HC)
         )
```

Binding the rows together

```
Demographic_overview <- bind_rows(a,b)
```

Showing the tibble

```
Demographic_overview
```

```
## # A tibble: 2 × 6
##   diagnosis mean_sample_size mean_numer_of_males mean_number_o…¹ mean_…² mean_…
³
##   <chr>                <dbl>               <dbl>           <dbl>   <dbl>   <dbl
>
## 1 SZ                    40.5                27.3            14.3    35.9    8.3
9
## 2 HC                    31.2                17.7            14.7    34.9    8.9
2
## # … with abbreviated variable names ¹mean_number_of_females, ²mean_age,
## #   ³mean_sd_age
```

Selceting the relevant variables

```
matrix_pitch <- matrix_ma %>%
  select('StudyID','Article','SAMPLE_SIZE_SZ','SAMPLE_SIZE_HC', 'PITCH_F0SD_HC_M',
'PITCH_F0SD_HC_SD','PITCH_F0SD_SZ_M','PITCH_F0SD_SZ_SD')
```

Filtering out the NA

```
matrix_pitch <- matrix_pitch %>%
  na.omit()
```

Merging diagnosis into one variable

```
matrix_pitch <- matrix_pitch %>%
  mutate(sample_size=(SAMPLE_SIZE_SZ+SAMPLE_SIZE_HC))
```

Creating IDs for the studies

```
matrix_pitch <- matrix_pitch %>%
  mutate(StudyID=as.factor(StudyID))
matrix_pitch <- matrix_pitch %>%
  mutate(StudyID=as.numeric(StudyID))
matrix_pitch <- matrix_pitch %>%
  mutate(StudyID=as.factor(StudyID))
```

Getting normalized results

```
matrix_pitch <- escalc('SMD',
n1i=SAMPLE_SIZE_HC,
n2i=SAMPLE_SIZE_SZ,
m1i = PITCH_F0SD_HC_M,
m2i=PITCH_F0SD_SZ_M,
sd1i = PITCH_F0SD_HC_SD,
sd2i = PITCH_F0SD_SZ_SD,
data = matrix_pitch)
matrix_pitch <- matrix_pitch %>%
  rename(effect_size=yi)
```

Creating a loop to calculate sd effect size and se

```
for (i in seq(nrow(matrix_pitch))){
  matrix_pitch$sd_effect[i] <- sqrt((sum((matrix_pitch$effect_size[i] - mean(matri
x_pitch$effect_size))^2))/length(matrix_pitch))
  matrix_pitch$standard_error[i] <- matrix_pitch$sd_effect[i]/sqrt(matrix_pitch$sa
mple_size)
}
```

Setting model

```
model_matrix <- bf(effect_size|se(standard_error) ~1 + (1|StudyID))
```

Getting priors

```
get_prior(data = matrix_pitch, family = gaussian, model_matrix)
```

```
##                  prior     class      coef   group resp dpar nlpar lb ub
##  student_t(3, 0.3, 2.5) Intercept
##    student_t(3, 0, 2.5)        sd                                  0
##    student_t(3, 0, 2.5)        sd           StudyID                0
##    student_t(3, 0, 2.5)        sd Intercept StudyID                0
##        source
##       default
##       default
##  (vectorized)
##  (vectorized)
```

Setting priors

```
matrix_priors <- c(
  prior(normal( .3, 2.5), class=Intercept),
  prior(normal( 0, 2.5), class=sd))
```

Priors

```
matrix_prior_fit <- brm(
  model_matrix,
  data = matrix_pitch,
  prior = matrix_priors,
  family = gaussian,
  refresh=0,
  sample_prior = 'only',
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 2 finished in 0.4 seconds.
## Chain 1 finished in 0.5 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 0.4 seconds.
## Total execution time: 0.5 seconds.
```

Bryan

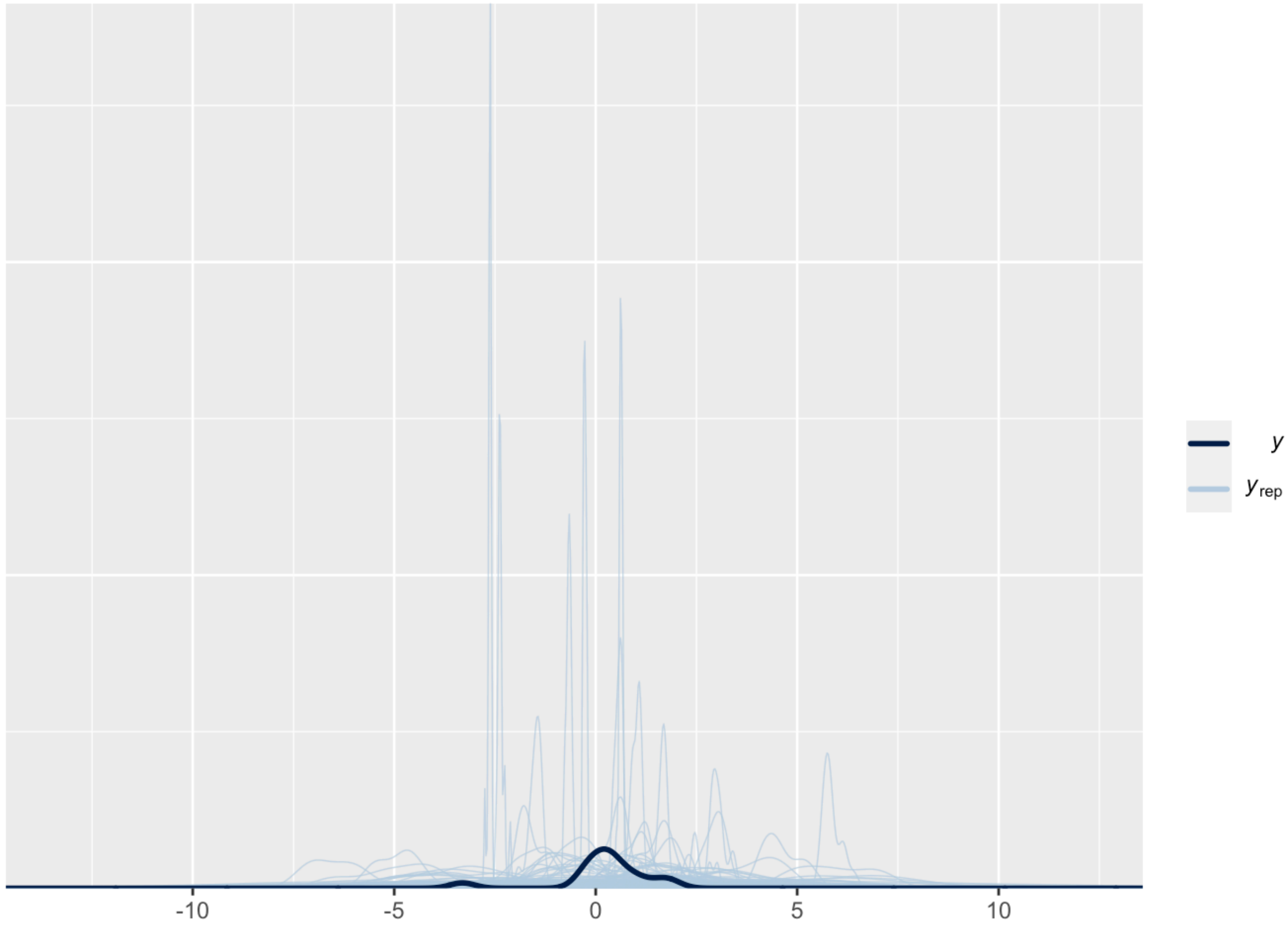
Assesing results

```
matrix_prior_fit
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: effect_size | se(standard_error) ~ 1 + (1 | StudyID)
##    Data: matrix_pitch (Number of observations: 15)
##   Draws: 2 chains, each with iter = 10000; warmup = 1000; thin = 1;
##          total post-warmup draws = 18000
##
## Group-Level Effects:
## ~StudyID (Number of levels: 12)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.98      1.52     0.08     5.62 1.00    14754     8411
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.29      2.51    -4.62     5.09 1.00    26582    13577
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.00      0.00     0.00     0.00   NA       NA       NA
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

PP check

```
pp_check(matrix_prior_fit, ndraws=100)
```



Both data and priors

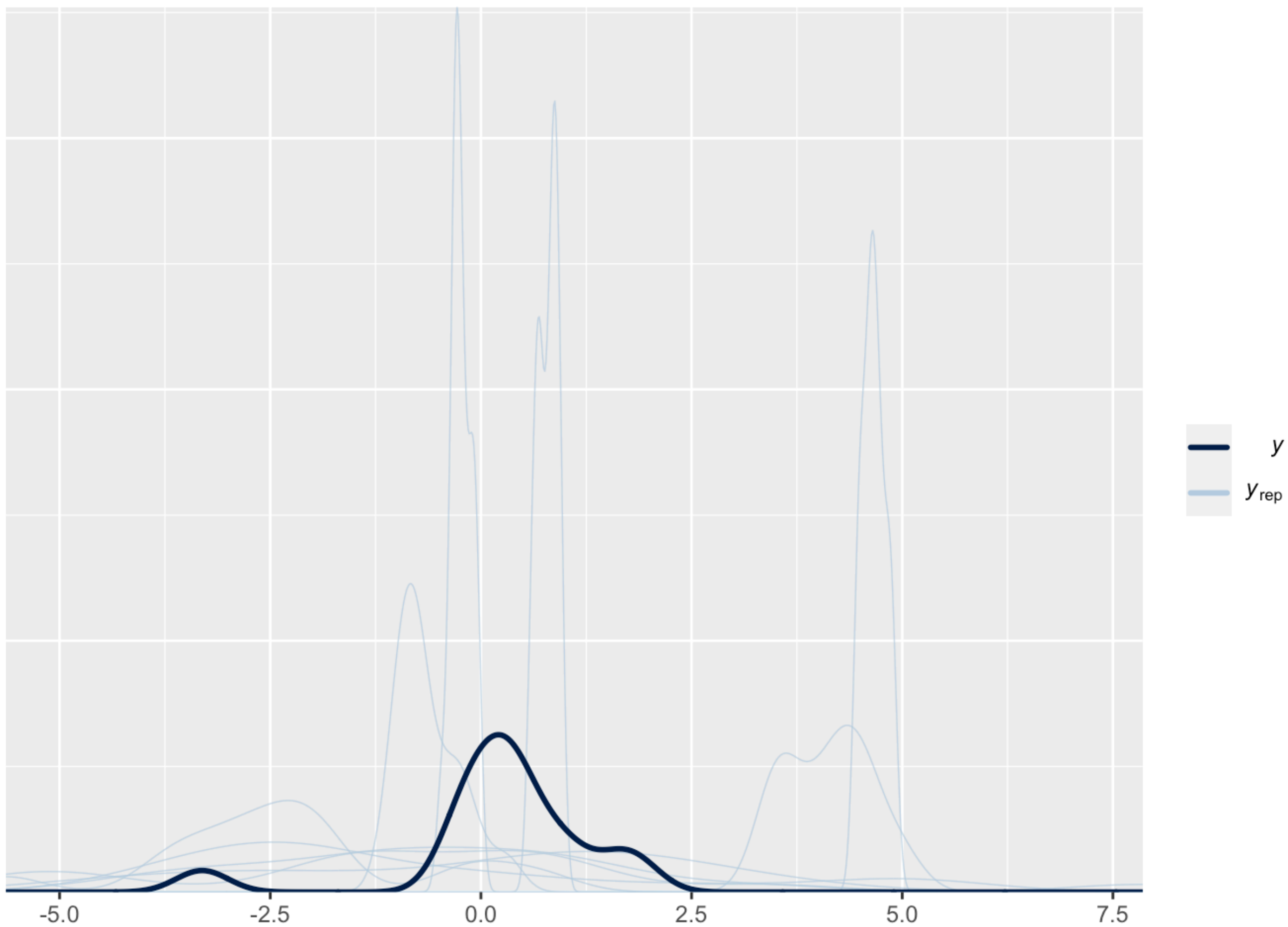
Including both data and priors

```
matrix_fit <- brm(
  model_matrix,
  data = matrix_pitch,
  prior = matrix_priors,
  family = gaussian,
  refresh=0,
  sample_prior = 'only',
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 1 finished in 0.4 seconds.
## Chain 2 finished in 0.6 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 0.5 seconds.
## Total execution time: 0.7 seconds.
```

PP check

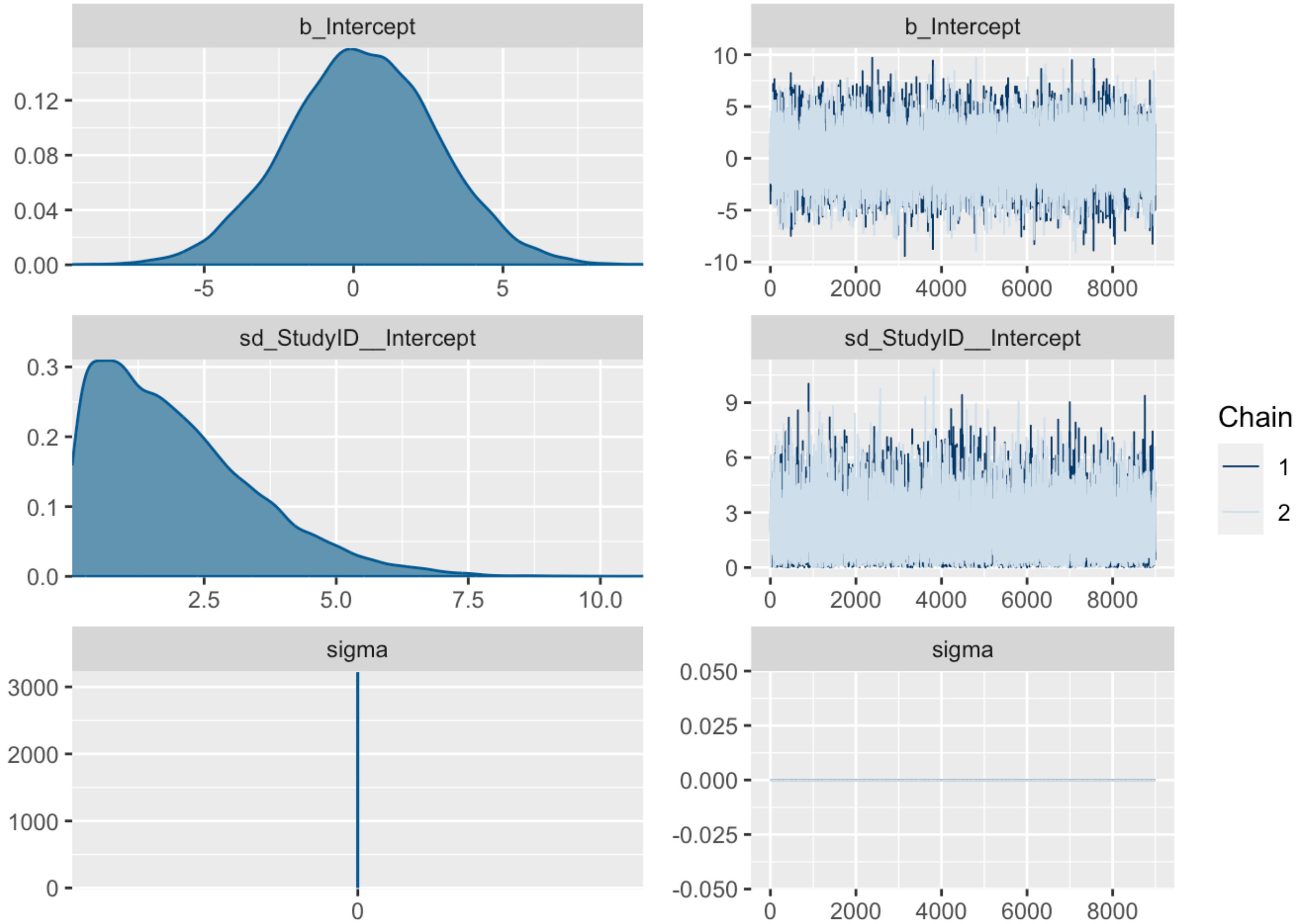
```
pp_check(matrix_fit)
```



Visualize and report

Plotting and assesing the results

```
plot(matrix_fit)
```




```
summary(matrix_fit)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: effect_size | se(standard_error) ~ 1 + (1 | StudyID)
##    Data: matrix_pitch (Number of observations: 15)
##   Draws: 2 chains, each with iter = 10000; warmup = 1000; thin = 1;
##          total post-warmup draws = 18000
##
## Group-Level Effects:
## ~StudyID (Number of levels: 12)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.99      1.51     0.08     5.65 1.00    13897     7399
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.29      2.52    -4.62     5.20 1.00    24126    12836
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.00      0.00     0.00     0.00   NA       NA       NA
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Visualizing and assesing intercepts

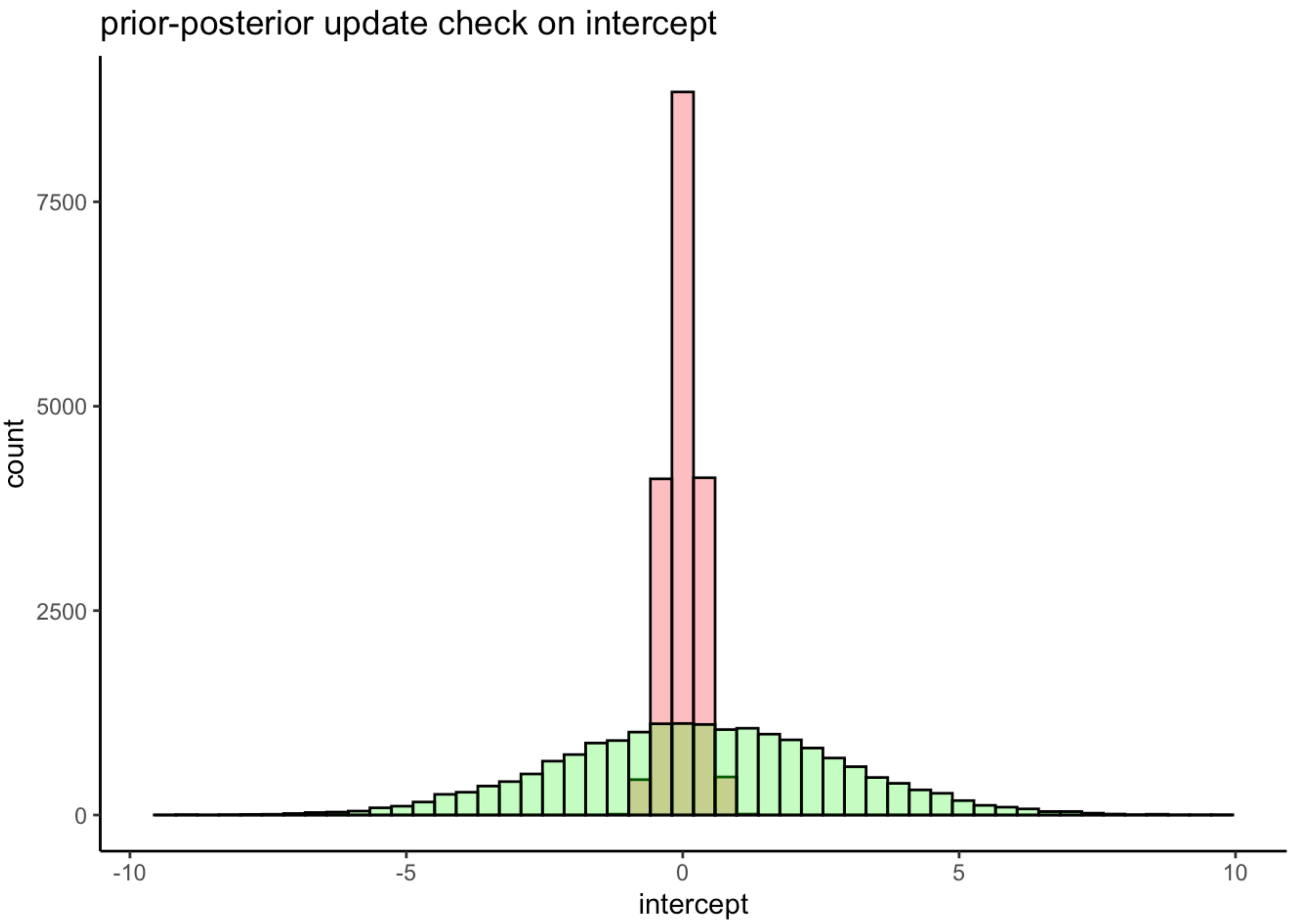
```
matrix_posterior <- as_draws_df(matrix_fit)
plot1 <- ggplot(matrix_posterior)+
  geom_histogram(aes(model_posterior$prior_Intercept), fill='red', color='black',
alpha=0.3, bins=50)+
  geom_histogram(aes(Intercept), fill='green', color='black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on intercept')+
  xlab('intercept')
```

Visualizing standard deviation

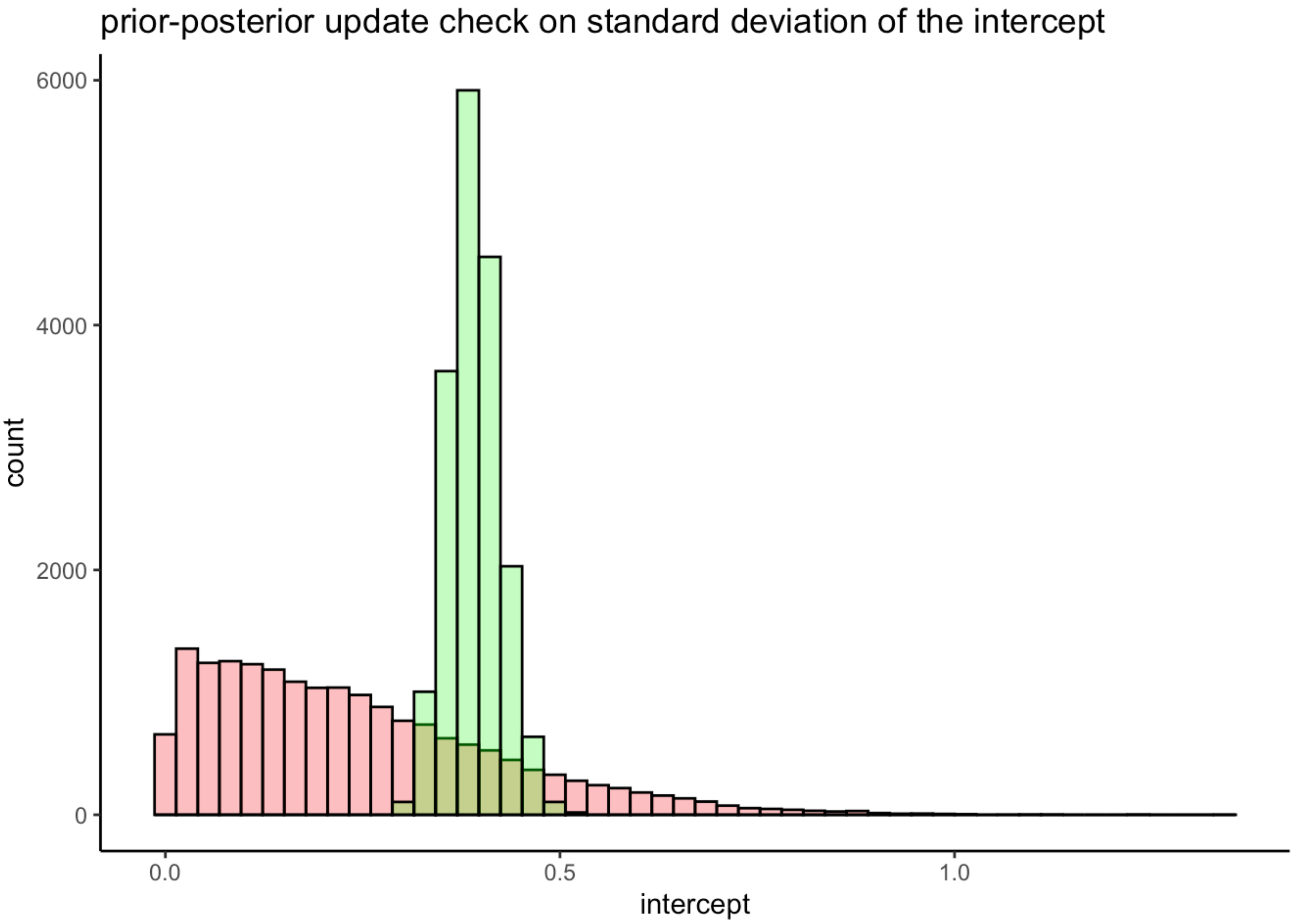
```
plot2 <- ggplot(matrix_posterior)+
  geom_histogram(aes(model_posterior$prior_sd_study_ID), fill='red', color='black'
, alpha=0.3, bins=50)+
  geom_histogram(aes(model_posterior$sd_study_ID__Intercept), fill='green', color=
'black', alpha=0.3, bins=50)+
  theme_classic()+
  ggtitle('prior-posterior update check on standard deviation of the intercept')+
  xlab('intercept')
```

Printing plots

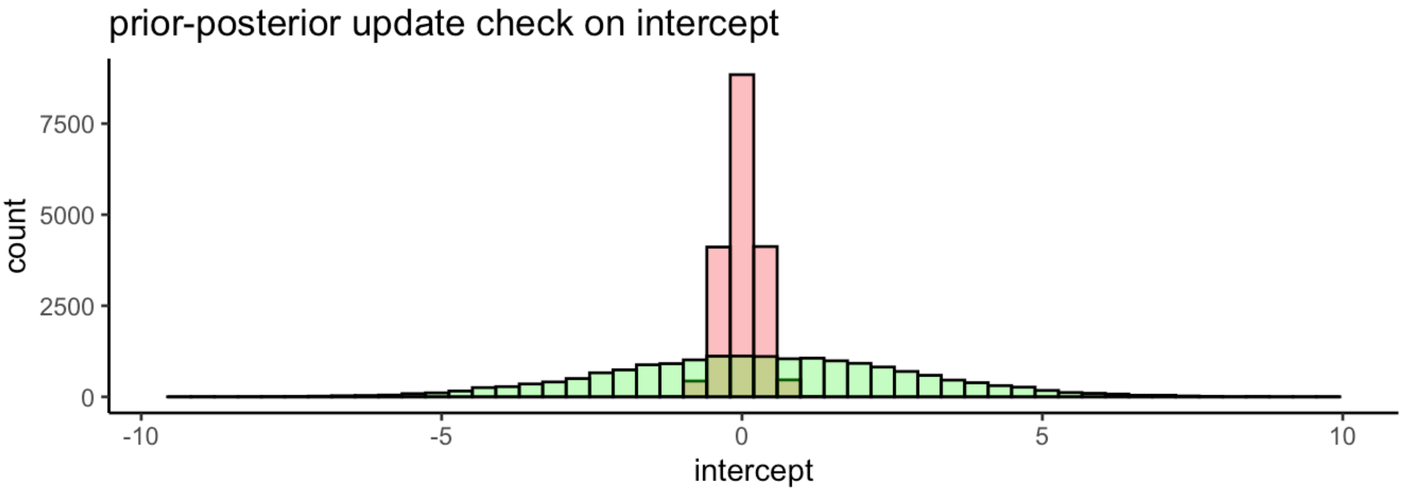
```
plot1
```

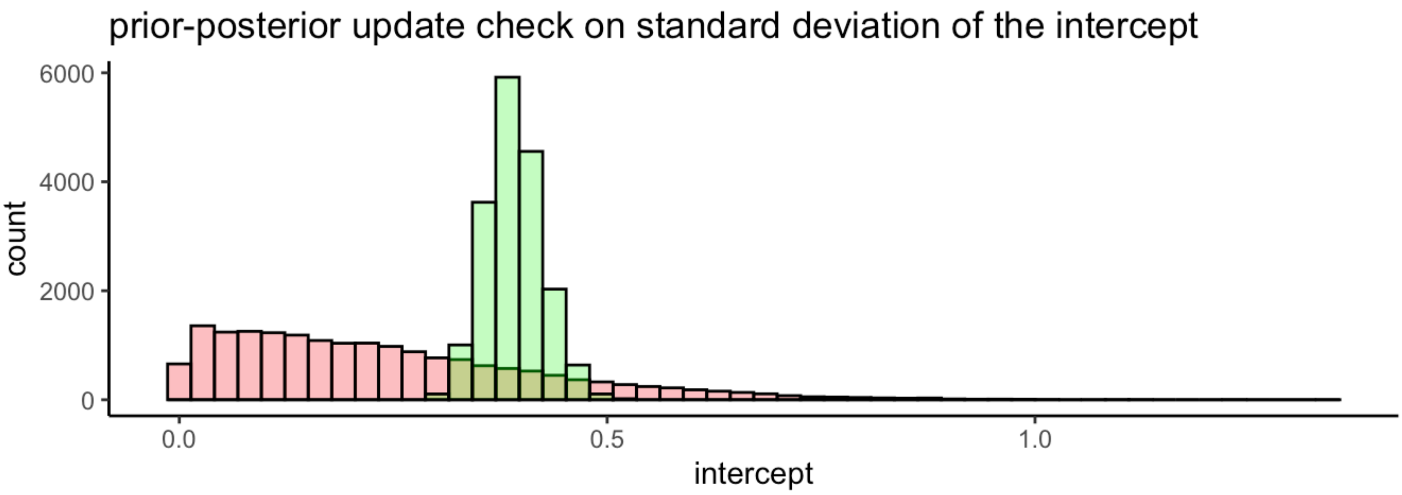

prior-posterior update check on intercept
count
7500
5000
2500
0
-10
-5
0
5
10
intercept

```
plot2
```




```
grid.arrange(plot1, plot2)
```





Influencial studies

Excluding the Cohen et al. (2014) by indexing

```
excluded_matrix <- matrix_pitch %>%
  dplyr::filter(StudyID!=6)
```

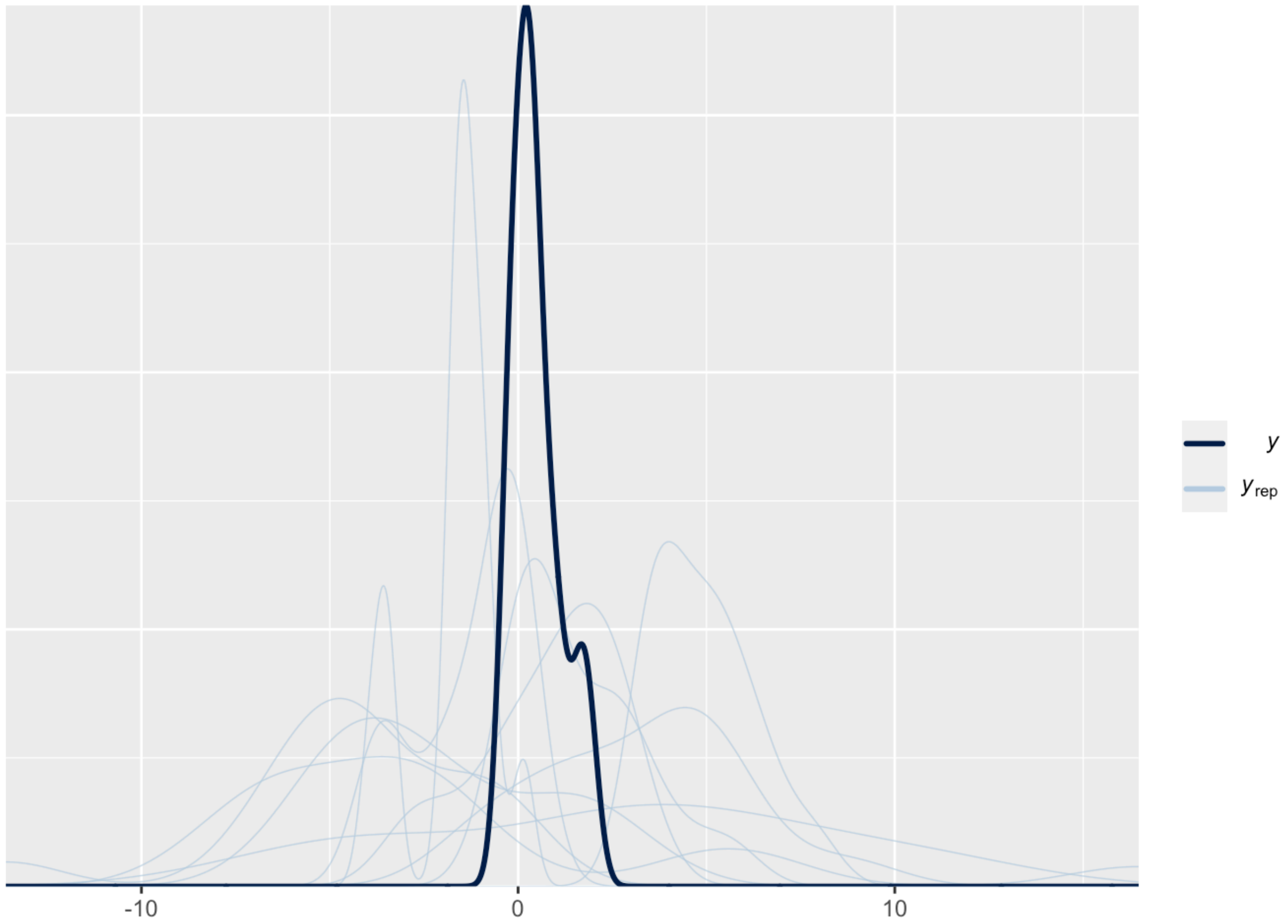
Running the model

```
exclude_matrix_fit <- brm(
  model_matrix,
  data = excluded_matrix,
  prior = matrix_priors,
  family = gaussian,
  refresh=0,
  sample_prior = 'only',
  iter=10000,
  warmup = 1000,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 2,
  cores = 2,
  control = list(
    adapt_delta = 0.99,
    max_treedepth = 20
)
)
```

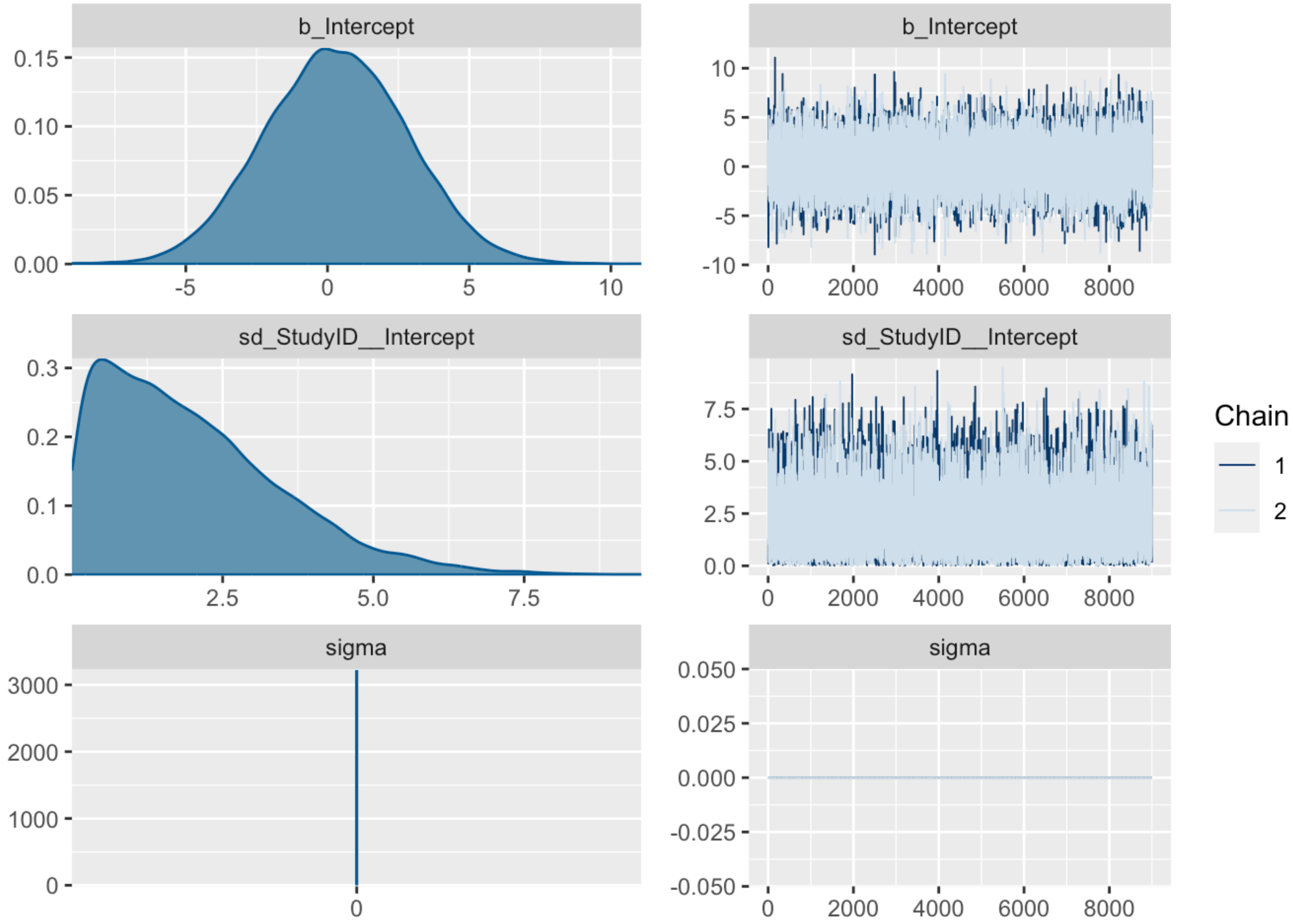
```
## Running MCMC with 2 parallel chains, with 2 thread(s) per chain...
##
## Chain 2 finished in 0.4 seconds.
## Chain 1 finished in 0.5 seconds.
##
## Both chains finished successfully.
## Mean chain execution time: 0.5 seconds.
## Total execution time: 0.6 seconds.
```

Visualizing and plotting

```
pp_check(exclude_matrix_fit)
```




```
plot(exclude_matrix_fit)
```




```
summary(exclude_matrix_fit)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: effect_size | se(standard_error) ~ 1 + (1 | StudyID)
##    Data: excluded_matrix (Number of observations: 14)
##   Draws: 2 chains, each with iter = 10000; warmup = 1000; thin = 1;
##          total post-warmup draws = 18000
##
## Group-Level Effects:
## ~StudyID (Number of levels: 11)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     2.00      1.49     0.09     5.60 1.00    14300     7570
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     0.31      2.52    -4.57     5.20 1.00    22115    13548
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.00      0.00     0.00     0.00   NA       NA       NA
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Assignment_3

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2022-11-09

#Assignment 3

##Part 1 - Simulating data

Use meta analysis reported in Parola et al (2020) to create informed simulated data - 100 pairs of schizophrenia and controls, each participant producing 10 repeated measures (10 trials with their speech recorded), for each recording produce 10 acoustic measures (6 from meta analysis and 4 with random noise)

- Do the same for a baseline data set including only 10 noise variables ##Sara ### seeting up variables

```
###Data simulation
n <- 100
trials <- 10

#Effect sizes definition = Informed effect mean and Skeptic effect mean
IEM <- c(-0.5,-1.26,-.74,1.89,0.25,1.3,0,0,0,0)
SEM <- rep(0,10)

#Defining individual vairability from populationd accross trials measurement error
ISD <- 1
TSD <- 0.5
E <- 0.2
```

Simulating the true effect size for each varibale for all pairs of participants

```
for (i in seq(10)){
  temp_informed <- tibble(
    ID=seq(n),
    TrueEffect = rnorm(n, IEM[i], ISD),
    Variable = paste0("V",i))
  temp_skeptic <- tibble(
    ID=seq(n),
    TrueEffect = rnorm(n, SEM[i], ISD),
    Variable = paste0("V",i))

  if(i==1){
    d_informed_true <- temp_informed
    d_skeptic_true <- temp_skeptic
  } else {
    d_informed_true <-  rbind(d_informed_true, temp_informed)
    d_skeptic_true <- rbind(d_skeptic_true, temp_skeptic)
  }
}
```

Creating one row per trial

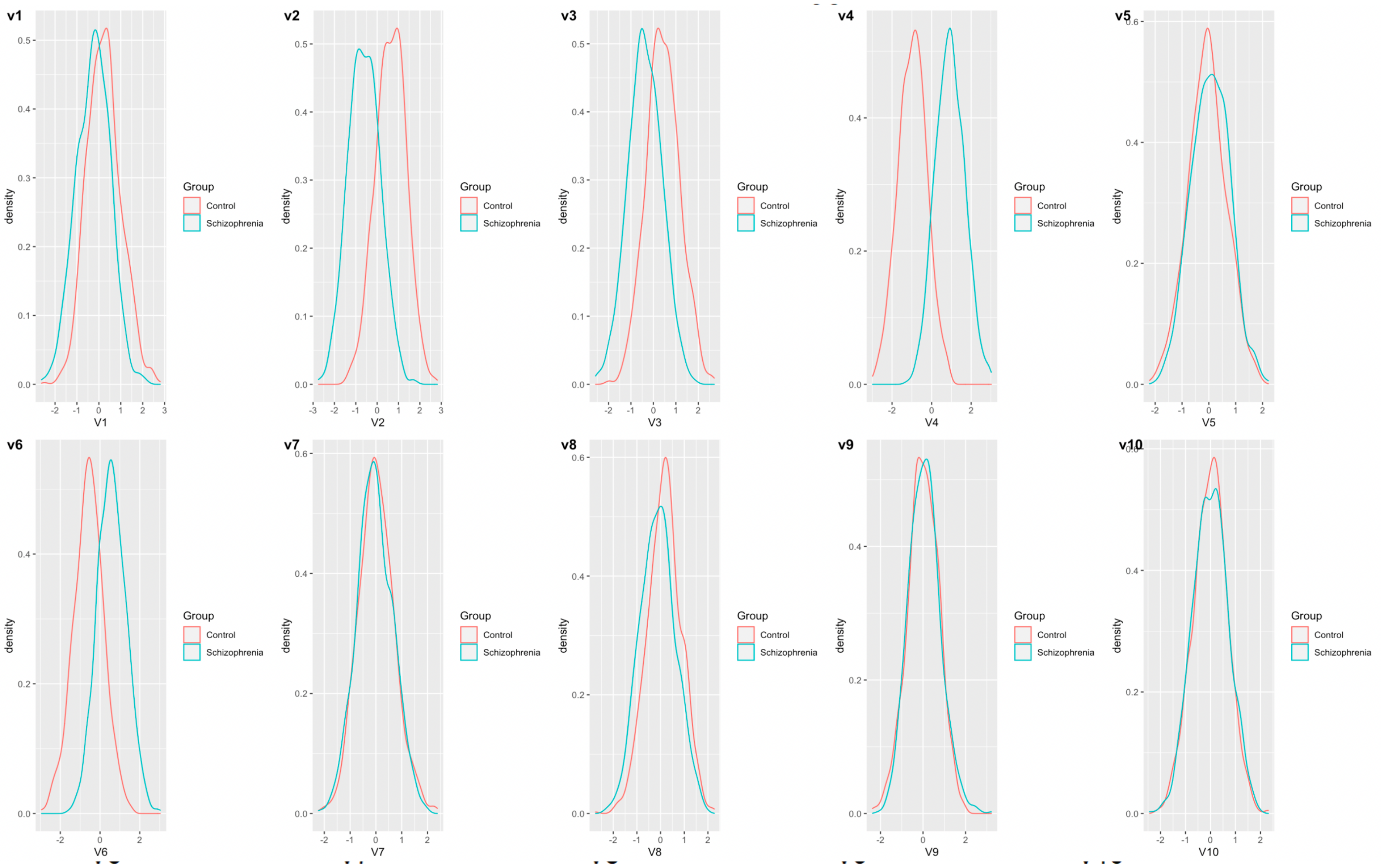
```
d_trial <- tibble(expand_grid(ID=seq(n), Trial = seq(trials), Group = c("Schizophr
enia", "Control")))

d_informed <- merge(d_informed_true, d_trial)
d_skeptic <- merge(d_skeptic_true, d_trial)

for ( i in seq(nrow(d_informed))){
  d_informed$measurement[i] <- ifelse(d_informed$Group[i]=="Schizophrenia",
                                      rnorm(1, rnorm(1, d_informed$TrueEffect[i]/2
, TSD), E),
                                      rnorm(1, rnorm(1, (-d_informed$TrueEffect[i]
)/2, TSD), E))

  d_skeptic$measurement[i] <- ifelse(d_skeptic$Group[i]=="Schizophrenia",
                                      rnorm(1, rnorm(1, d_skeptic$TrueEffect[i]/2,
TSD), E),
                                      rnorm(1, rnorm(1, (-d_skeptic$TrueEffect[i])
/2, TSD), E))
}
```

Transforming the dataframe to a wide format based on the variable

```
d_informed_wide <- d_informed %>%
  mutate(TrueEffect=NULL) %>%
  pivot_wider(names_from = Variable,
              values_from = measurement)
d_skeptic_wide <- d_skeptic %>%
  mutate(TrueEffect=NULL) %>%
  pivot_wider(names_from = Variable,
              values_from = measurement)

Schizo_ID <- d_informed_wide %>%
  filter(Group == 'Schizophrenia')

 control_ID <- d_informed_wide %>%
  filter(Group == 'Control')

control_ID[, 1] <- control_ID[,1] + 100

 d_informed_wide <- rbind(control_ID,Schizo_ID)


 Schizo_ID_skeptic <- d_skeptic_wide %>%
  filter(Group == 'Schizophrenia')

 control_ID_skeptic <- d_skeptic_wide %>%
  filter(Group == 'Control')

 control_ID_skeptic[,1] <- control_ID_skeptic[,1] + 100

 d_skeptic_wide <- rbind(control_ID_skeptic,Schizo_ID_skeptic)
```

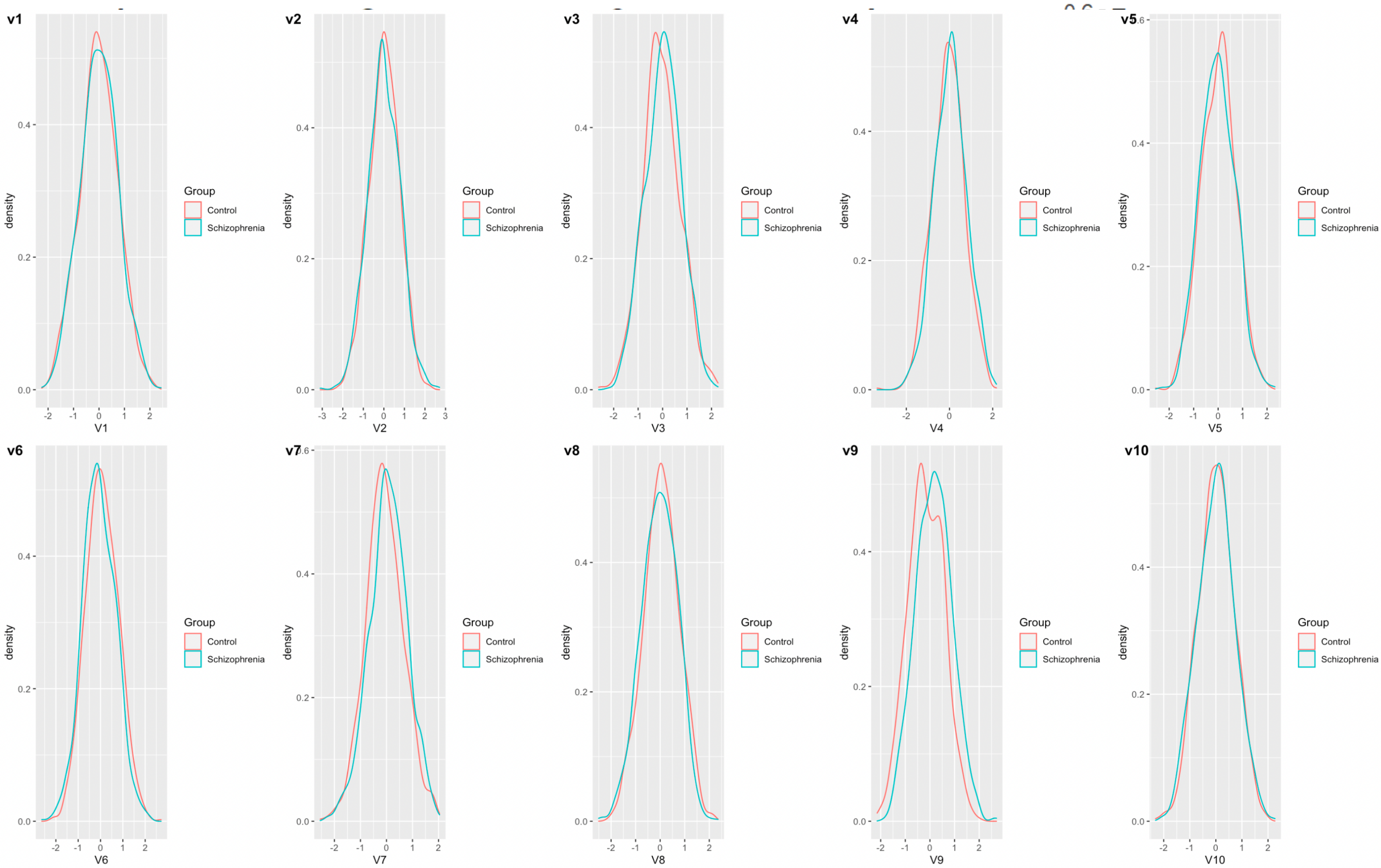
Visualizing the simulated informed data

```
plot1 <- d_informed_wide %>%
  ggplot(aes(x = V1, color = Group))+
  geom_density()

plot2 <- d_informed_wide %>%
  ggplot(aes(x = V2, color = Group))+
  geom_density()

plot3 <- d_informed_wide %>%
  ggplot(aes(x = V3, color = Group))+
  geom_density()

plot4 <- d_informed_wide %>%
  ggplot(aes(x = V4, color = Group))+
  geom_density()

plot5 <- d_informed_wide %>%
  ggplot(aes(x = V5, color = Group))+
  geom_density()

plot6 <- d_informed_wide %>%
  ggplot(aes(x = V6, color = Group))+
  geom_density()

plot7 <- d_informed_wide %>%
  ggplot(aes(x = V7, color = Group))+
  geom_density()

plot8 <- d_informed_wide %>%
  ggplot(aes(x = V8, color = Group))+
  geom_density()

plot9 <- d_informed_wide %>%
  ggplot(aes(x = V9, color = Group))+
  geom_density()

plot10 <- d_informed_wide %>%
  ggplot(aes(x = V10, color = Group))+
  geom_density()

cowplot::plot_grid(plot1, plot2, plot3, plot4, plot5, plot6, plot7, plot8, plot9,
plot10,
          labels = c("v1", "v2", "v3",'v4','v5','v6','v7','v8','v9','v10'),
          ncol = 5, nrow = 2)
```



Visualizing the simulated data for skeptical data frame

```
plot1_s <- d_skeptic_wide %>%
  ggplot(aes(x = V1, color = Group))+
  geom_density()

plot2_s <- d_skeptic_wide %>%
  ggplot(aes(x = V2, color = Group))+
  geom_density()

plot3_s <- d_skeptic_wide %>%
  ggplot(aes(x = V3, color = Group))+
  geom_density()

plot4_s <- d_skeptic_wide %>%
  ggplot(aes(x = V4, color = Group))+
  geom_density()

plot5_s <- d_skeptic_wide %>%
  ggplot(aes(x = V5, color = Group))+
  geom_density()

plot6_s <- d_skeptic_wide %>%
  ggplot(aes(x = V6, color = Group))+
  geom_density()

plot7_s <- d_skeptic_wide %>%
  ggplot(aes(x = V7, color = Group))+
  geom_density()

plot8_s <- d_skeptic_wide %>%
  ggplot(aes(x = V8, color = Group))+
  geom_density()

plot9_s <- d_skeptic_wide %>%
  ggplot(aes(x = V9, color = Group))+
  geom_density()

plot10_s <- d_skeptic_wide %>%
  ggplot(aes(x = V10, color = Group))+
  geom_density()

cowplot::plot_grid(plot1_s, plot2_s, plot3_s, plot4_s, plot5_s, plot6_s, plot7_s,
plot8_s, plot9_s, plot10_s,
          labels = c("v1", "v2", "v3",'v4','v5','v6','v7','v8','v9','v10'),
          ncol = 5, nrow = 2)
```



##Patrik ##Part 2 - Machine larning pipeline on simulated data Build a machine leaning pipeline (separately on the 2 datasets) - create a data budget (e.g., balanced training and test sets) pree-process the data (e.g., scaling the features) - fit and assess a classification algorithm on the training data (e.g., bayesian multilevel logistic regression) - assess performance on the test set - discuss whether performance and feature importance is as expected

Data budget (splitting) and pree-processing (scaling)

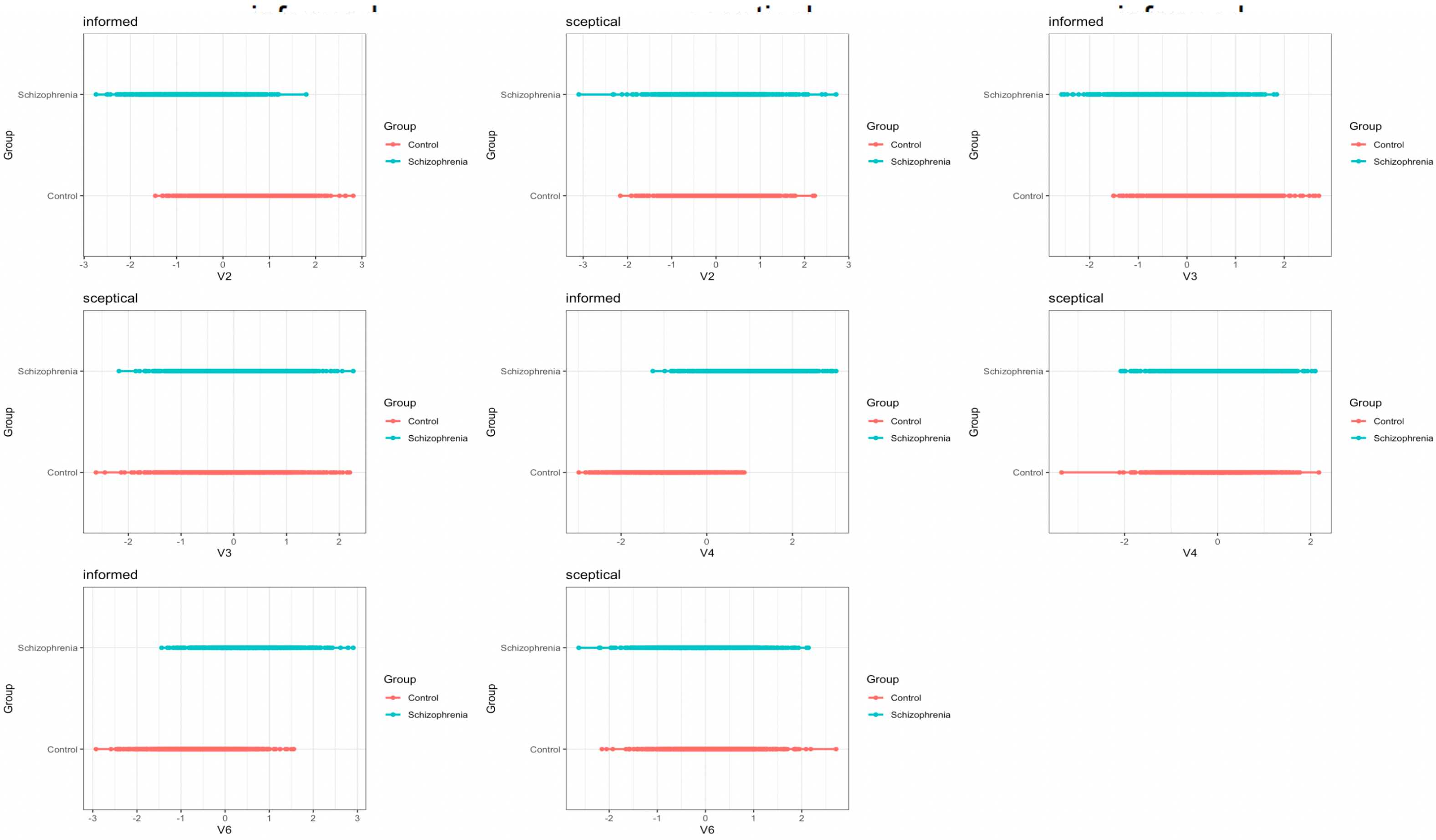
```
set.seed(260)


d_informed_wide <- d_informed_wide %>%
  mutate(pair_ID=ID) %>%
  mutate(pair_ID= ifelse(ID>100, ID-100, ID))

d_skeptic_wide <- d_skeptic_wide %>%
  mutate(pair_ID=ID) %>%
  mutate(pair_ID= ifelse(ID>100, ID-100, ID))

split_inf <- initial_split(d_informed_wide, prop = 4/5)

train_informed <- training(split_inf)
test_informed <- testing(split_inf)
```

```
split_skep <- initial_split(d_skeptic_wide, prop = 4/5)
train_skeptic <- training(split_skep)
test_skeptic <- testing(split_skep)

train_informed$ID <- as.factor(train_informed$ID)
train_skeptic$ID <- as.factor(train_skeptic$ID)

test_informed$ID <- as.factor(test_informed$ID)
test_skeptic$ID <- as.factor(test_skeptic$ID)

train_informed$pair_ID <- as.factor(train_informed$pair_ID)
train_skeptic$pair_ID <- as.factor(train_skeptic$pair_ID)

test_informed$pair_ID <- as.factor(test_informed$pair_ID)
test_skeptic$pair_ID <- as.factor(test_skeptic$pair_ID)

train_informed$Trial <- as.factor(train_informed$Trial)
train_skeptic$Trial <- as.factor(train_skeptic$Trial)

test_informed$Trial <- as.factor(test_informed$Trial)
test_skeptic$Trial <- as.factor(test_skeptic$Trial)


rec_informed <- train_informed %>%
  recipe(Group~.) %>%
  update_role(ID, new_role = 'ID') %>%
  step_scale(all_numeric()) %>%
  step_center(all_numeric()) %>%
  prep(training=train_informed, retain=TRUE)

rec_skeptic <- train_skeptic %>%
  recipe(Group~.) %>%
  update_role(ID, new_role = 'ID') %>%
  step_scale(all_numeric()) %>%
  step_center(all_numeric()) %>%
  prep(training=train_informed, retain=TRUE)


train_informed_s <- juice(rec_informed)
test_informed_s <- bake(rec_informed, new_data = test_informed)

train_skeptic_s <- juice(rec_skeptic)
test_skeptic_s <- bake(rec_skeptic, new_data = test_skeptic)
```

Visual inspection of the data

```
plot_i2 <- ggplot(train_informed, aes(V2, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("informed")

plot_s2 <- ggplot(train_skeptic, aes(V2, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("sceptical")

plot_i3 <- ggplot(train_informed, aes(V3, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("informed")

plot_s3 <- ggplot(train_skeptic, aes(V3, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("sceptical")

plot_i4 <- ggplot(train_informed, aes(V4, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("informed")

plot_s4 <- ggplot(train_skeptic, aes(V4, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("sceptical")

plot_i6 <- ggplot(train_informed, aes(V6, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("informed")

plot_s6 <- ggplot(train_skeptic, aes(V6, Group, colour=Group))+
  geom_point()+
  geom_smooth(method = "glm", se=FALSE)+
  theme_bw()+
  ggtitle("sceptical")

plot_grid(plot_i2, plot_s2, plot_i3, plot_s3, plot_i4, plot_s4, plot_i6, plot_s6)
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



fit and asses a classification algorithm on training data (Baysian)

```
##Setting up the model
PR_f0 <-bf(Group~1+V1+V2+V3+V4+V5+V6+V7+V8+V9+V10)

PR_f1 <-bf(Group~1+V1+V2+V3+V4+V5+V6+V7+V8+V9+V10+(1|ID))

get_prior(PR_f0, train_informed_s, family = bernoulli)
```

```
##                prior     class coef group resp dpar nlpar lb ub       source
##               (flat)         b                                       default
##               (flat)         b   V1                             (vectorized)
##               (flat)         b  V10                             (vectorized)
##               (flat)         b   V2                             (vectorized)
##               (flat)         b   V3                             (vectorized)
##               (flat)         b   V4                             (vectorized)
##               (flat)         b   V5                             (vectorized)
##               (flat)         b   V6                             (vectorized)
##               (flat)         b   V7                             (vectorized)
##               (flat)         b   V8                             (vectorized)
##               (flat)         b   V9                             (vectorized)
##  student_t(3, 0, 2.5) Intercept                                      default
```

```
get_prior(PR_f1, train_informed_s, family = bernoulli)
```

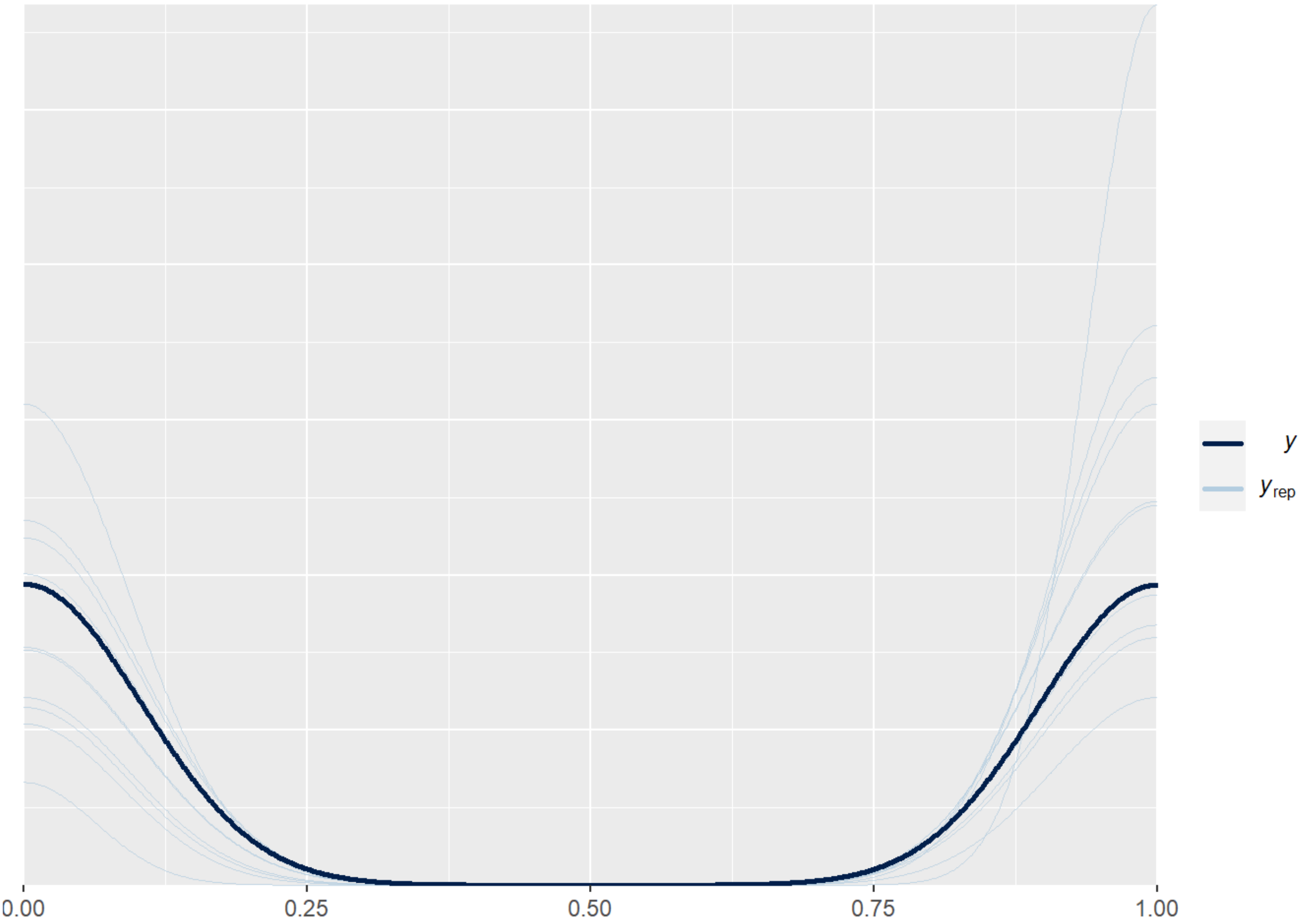
```
##                prior     class      coef group resp dpar nlpar lb ub
##               (flat)         b
##               (flat)         b        V1
##               (flat)         b       V10
##               (flat)         b        V2
##               (flat)         b        V3
##               (flat)         b        V4
##               (flat)         b        V5
##               (flat)         b        V6
##               (flat)         b        V7
##               (flat)         b        V8
##               (flat)         b        V9
##  student_t(3, 0, 2.5) Intercept
##  student_t(3, 0, 2.5)        sd                                 0
##  student_t(3, 0, 2.5)        sd              ID                 0
##  student_t(3, 0, 2.5)        sd Intercept    ID                 0
##        source
##       default
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##       default
##       default
##  (vectorized)
##  (vectorized)
```

Setting priors

```
PR_p0 <- c(
  prior(normal(0, 1), class=Intercept),
  prior(normal(0, 0.3), class=b)
)

PR_p1 <- c(
  prior(normal(0, 1), class=Intercept),
  prior(normal(0, 0.3), class=sd),
  prior(normal(0, 0.3), class=b)
)
```

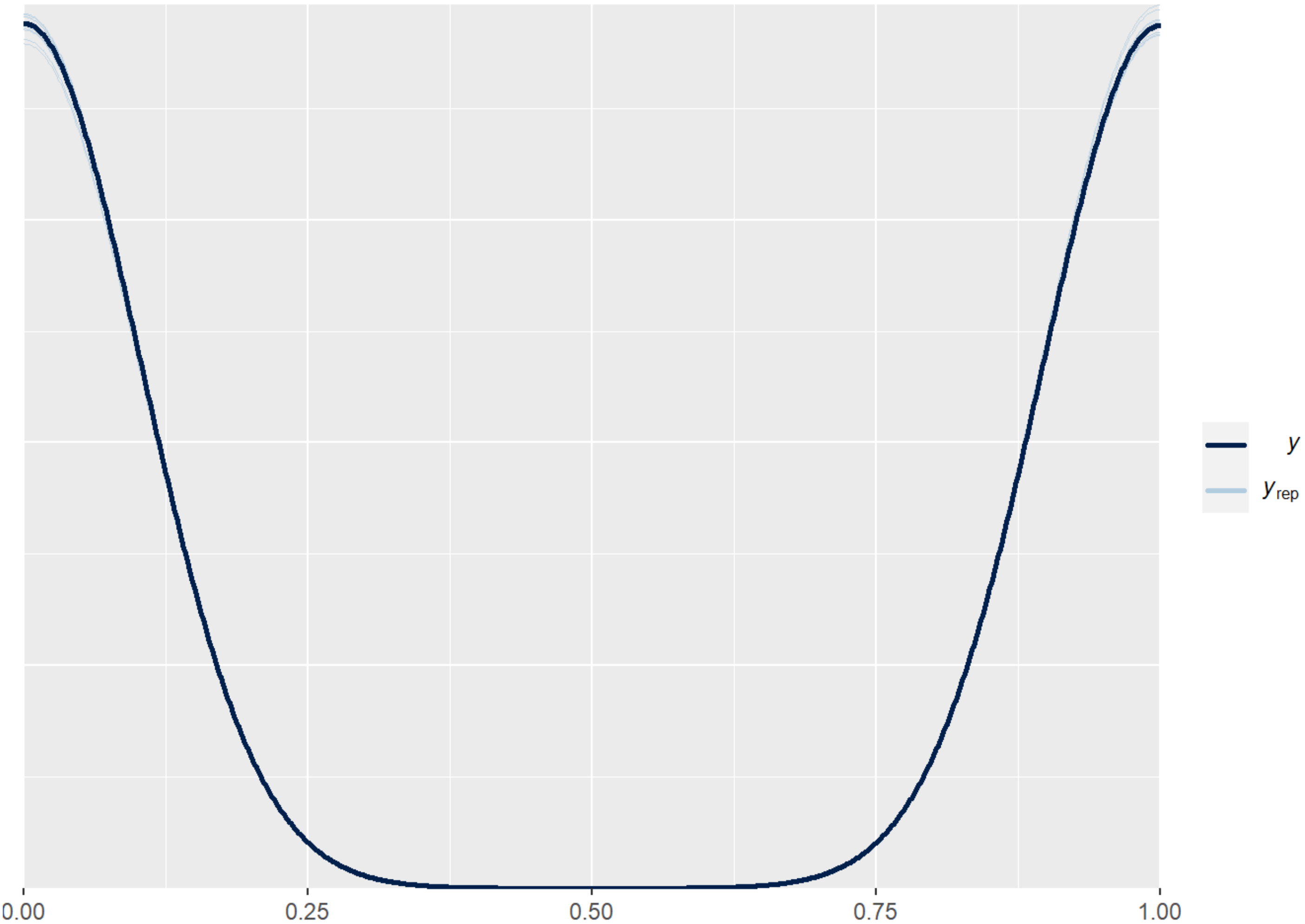
Fitting the first model on both the skeptical and informed data

```
##Model fit on priors
pr_m0_inf <- brm(
  PR_f0,
  data = train_informed_s,
  prior = PR_p0,
  family = bernoulli,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)


#pp_check(pr_m0_inf)

pr_m0_skep <- brm(
  PR_f0,
  data = train_skeptic_s,
  prior = PR_p0,
  family = bernoulli,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)


pp_check(pr_m0_skep)
```

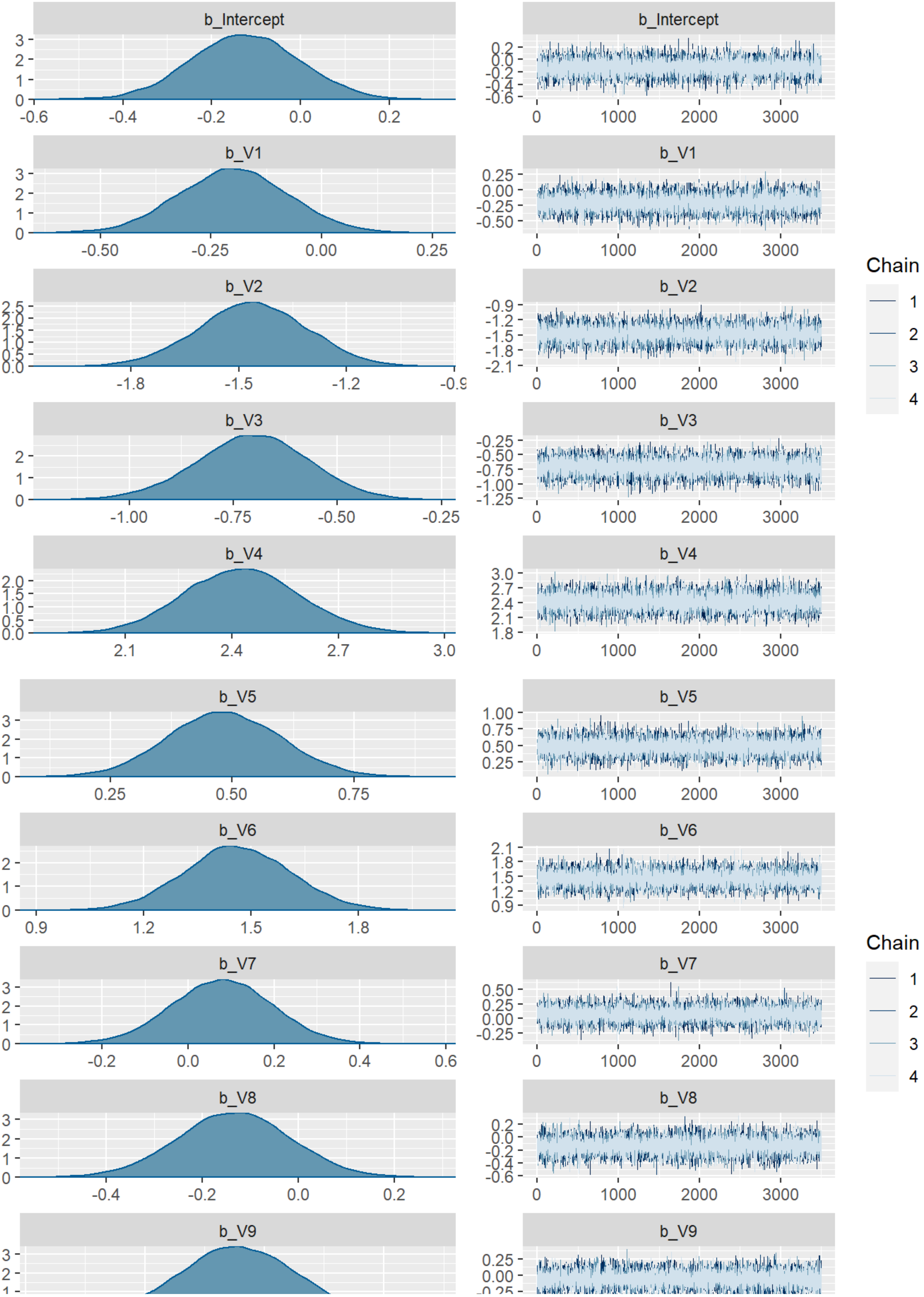


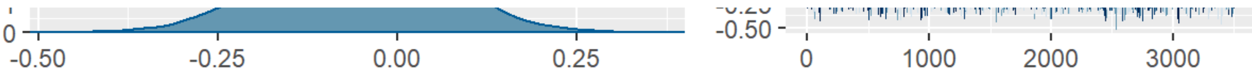
##Bryan

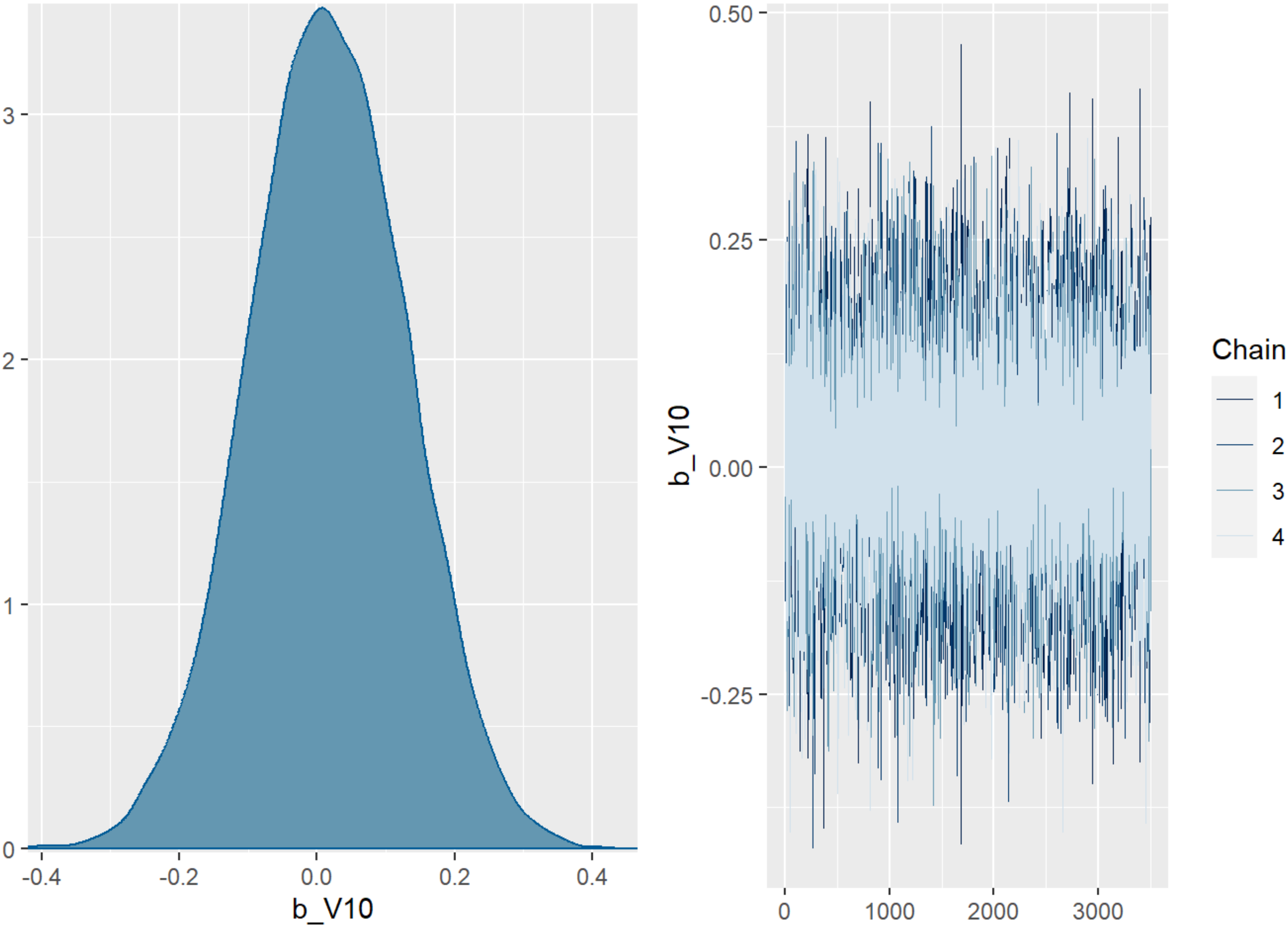
```
##Model fit on informed data
pr_m0_fit_inf <- brm(
  PR_f0,
  data = train_informed_s,
  prior = PR_p0,
  family = bernoulli,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m0_fit_inf)
```




```
plot(pr_m0_fit_inf)
```

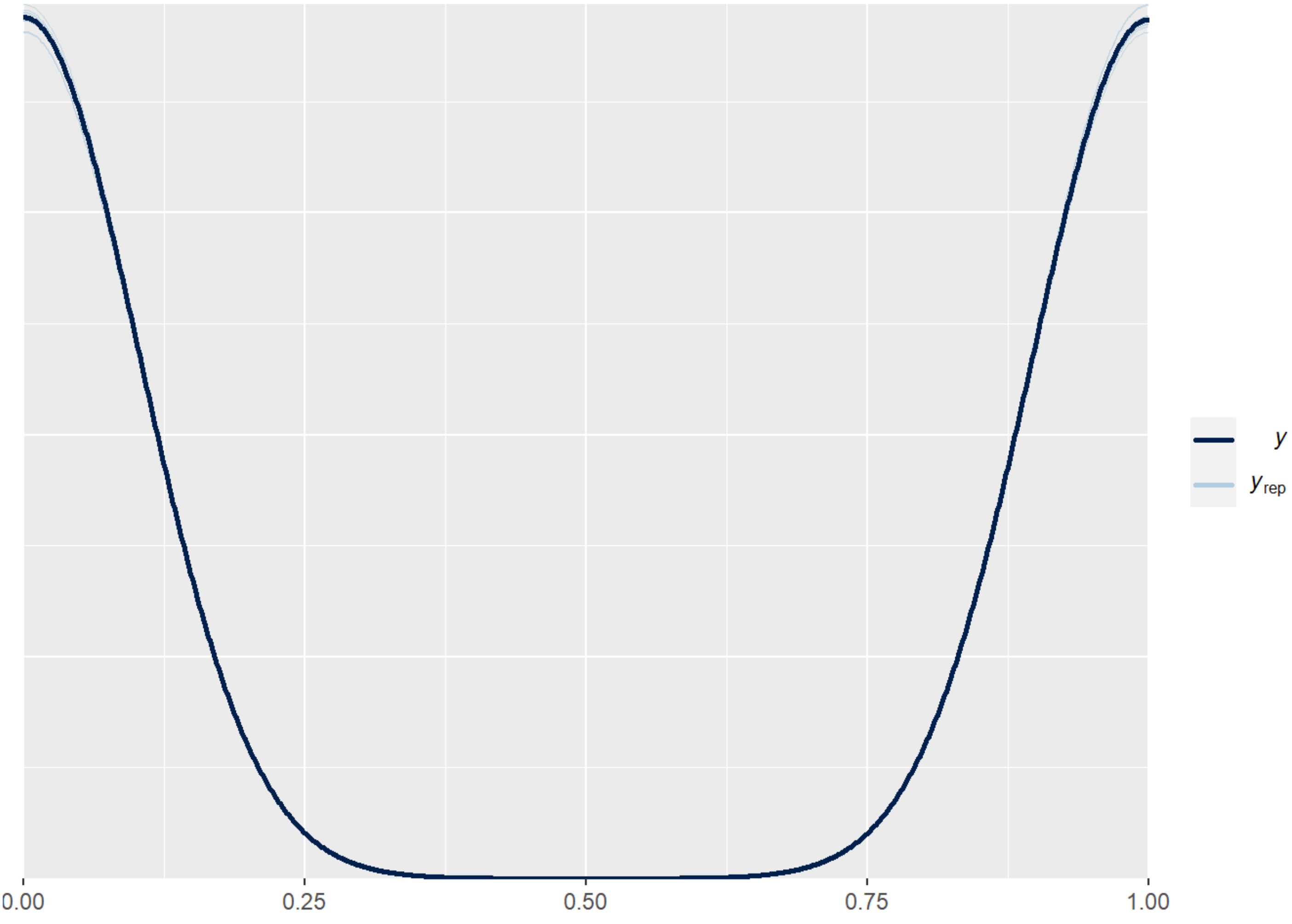

b_Intercept
b_V1
b_V2
b_V3
b_V4
b_V5
b_V6
b_V7
b_V8
b_V9
Chain
1
2
3
4
Chain
1
2
3
4
0
1000
2000
3000



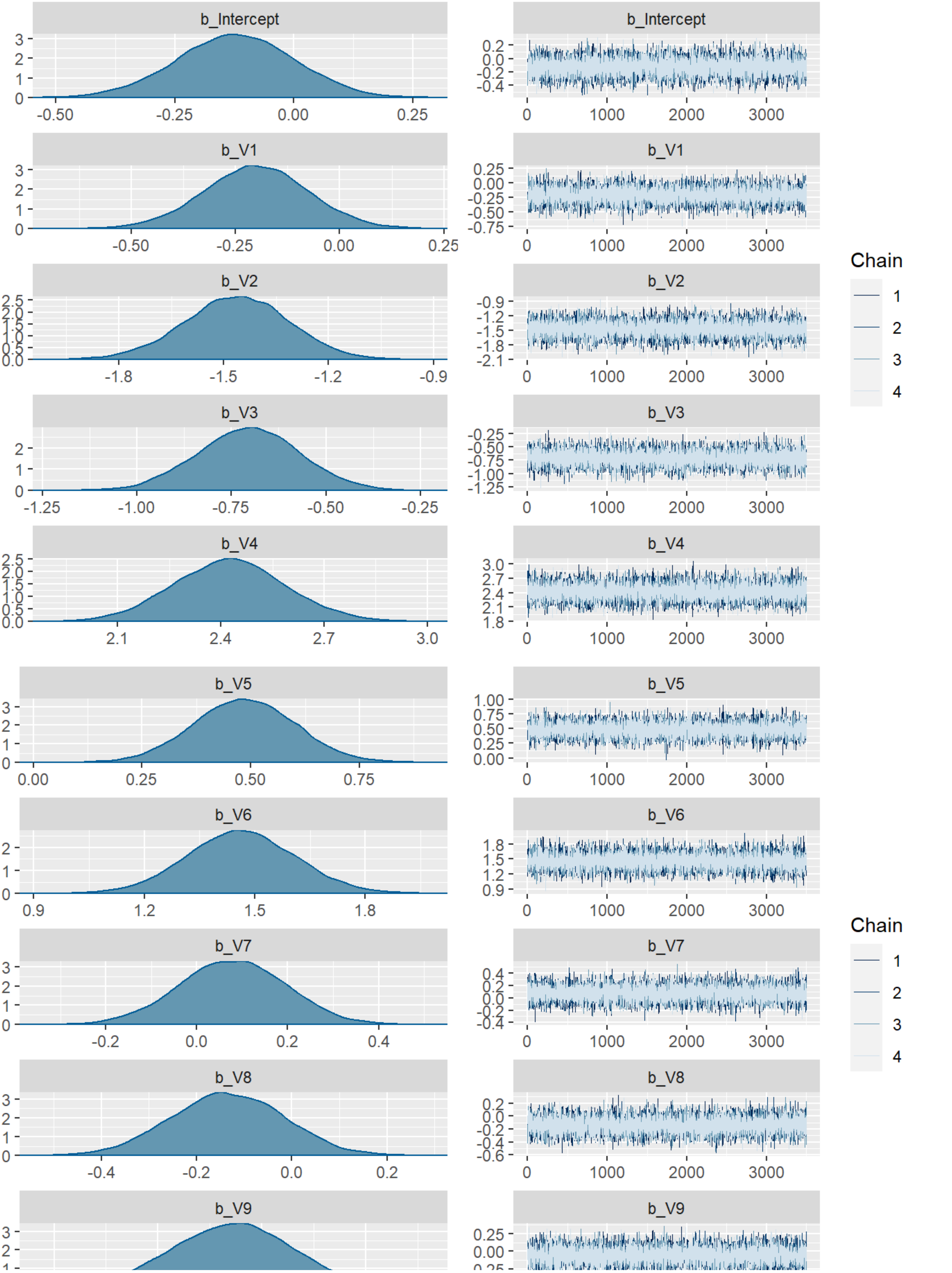


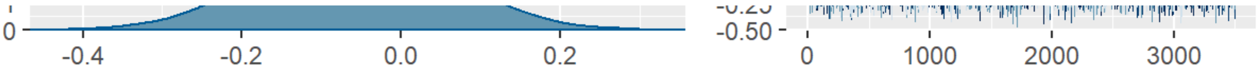

```
summary(pr_m0_fit_inf)
```

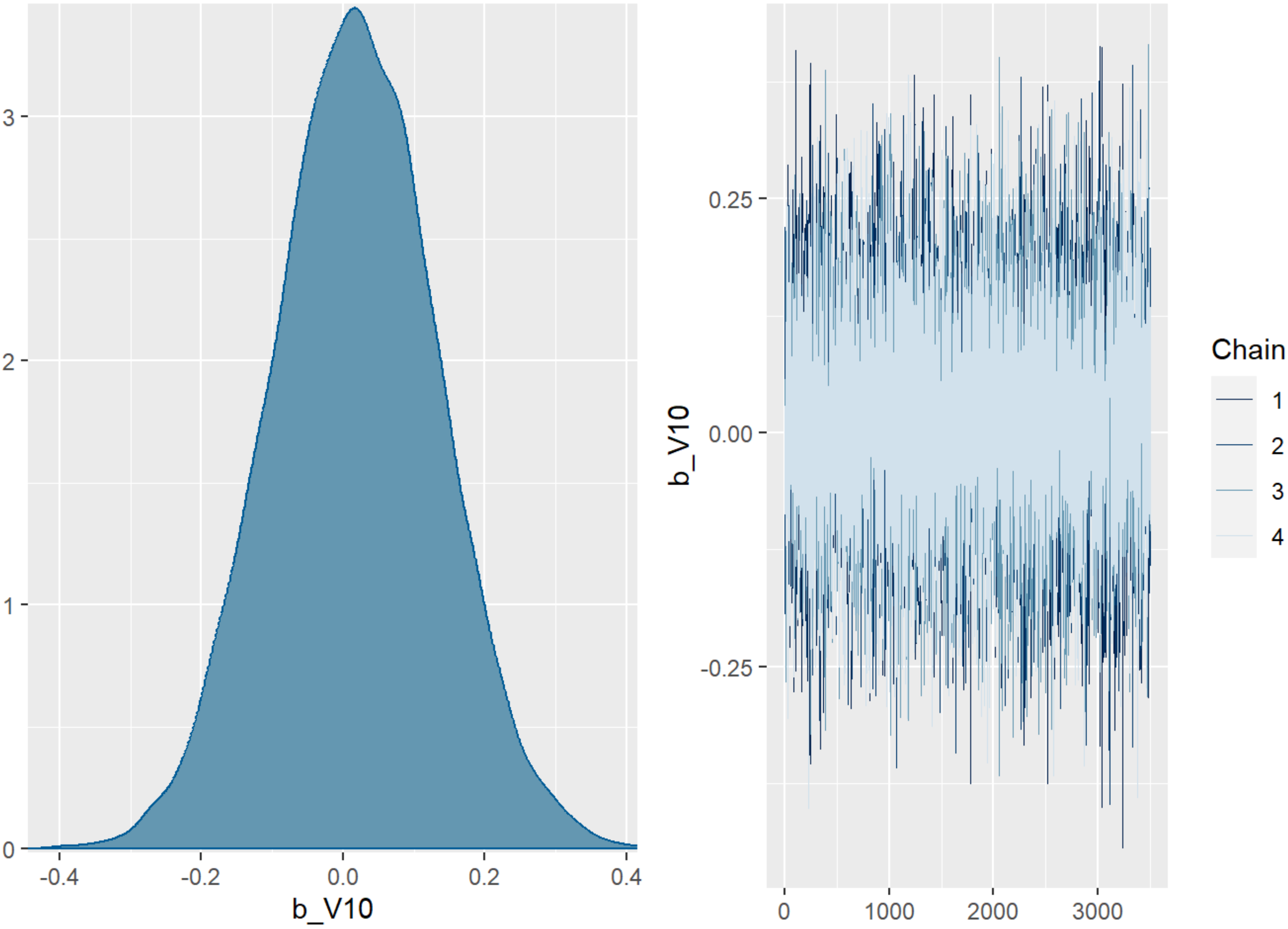
```
##Model fit on skeptical data
pr_m0_fit_skep <- brm(
  PR_f0,
  data = train_skeptic_s,
  prior = PR_p0,
  family = bernoulli,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m0_fit_skep)
```




```
plot(pr_m0_fit_skep)
```


b_Intercept
b_V1
b_V2
b_V3
b_V4
b_V5
b_V6
b_V7
b_V8
b_V9
Chain
1
2
3
4

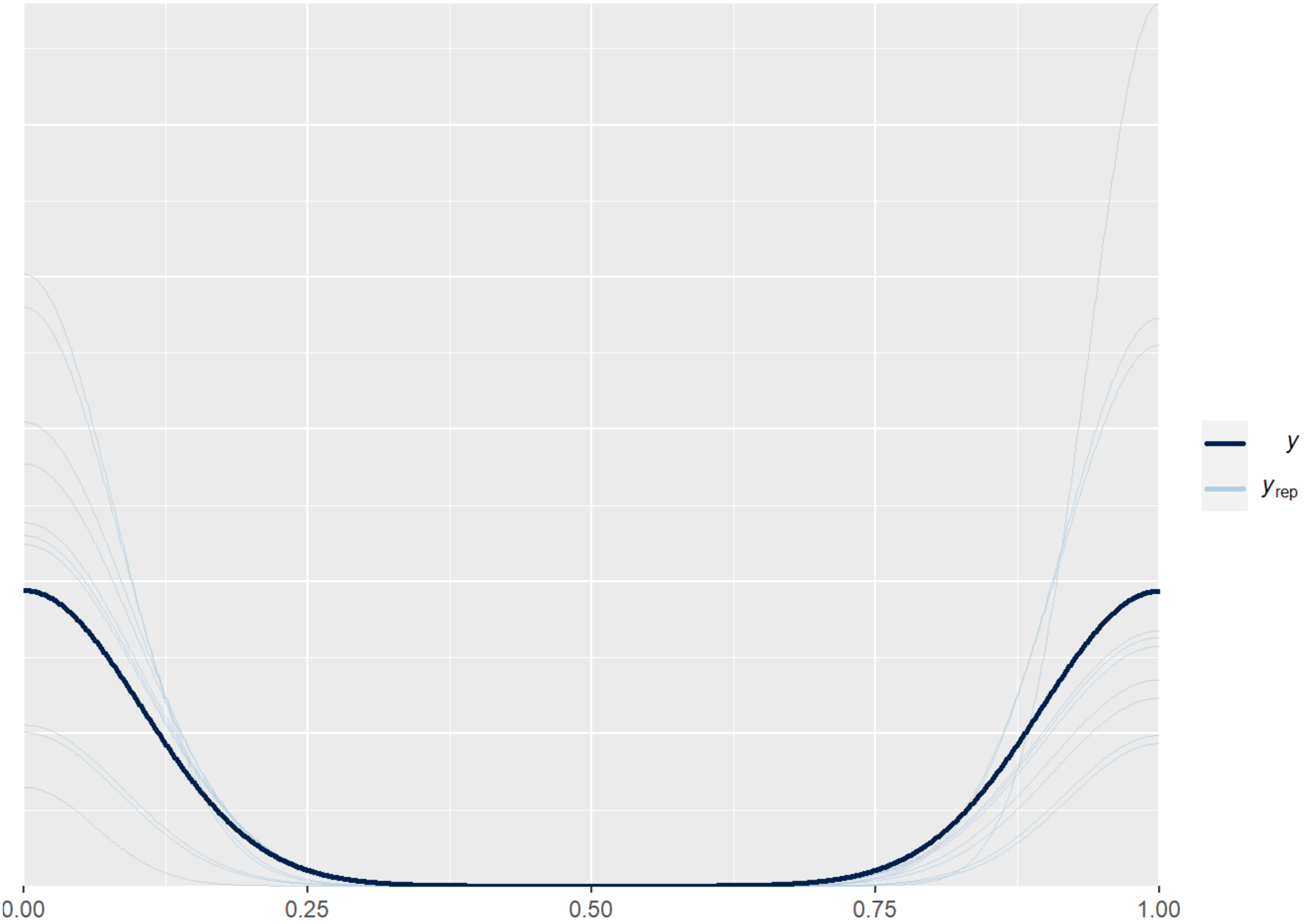




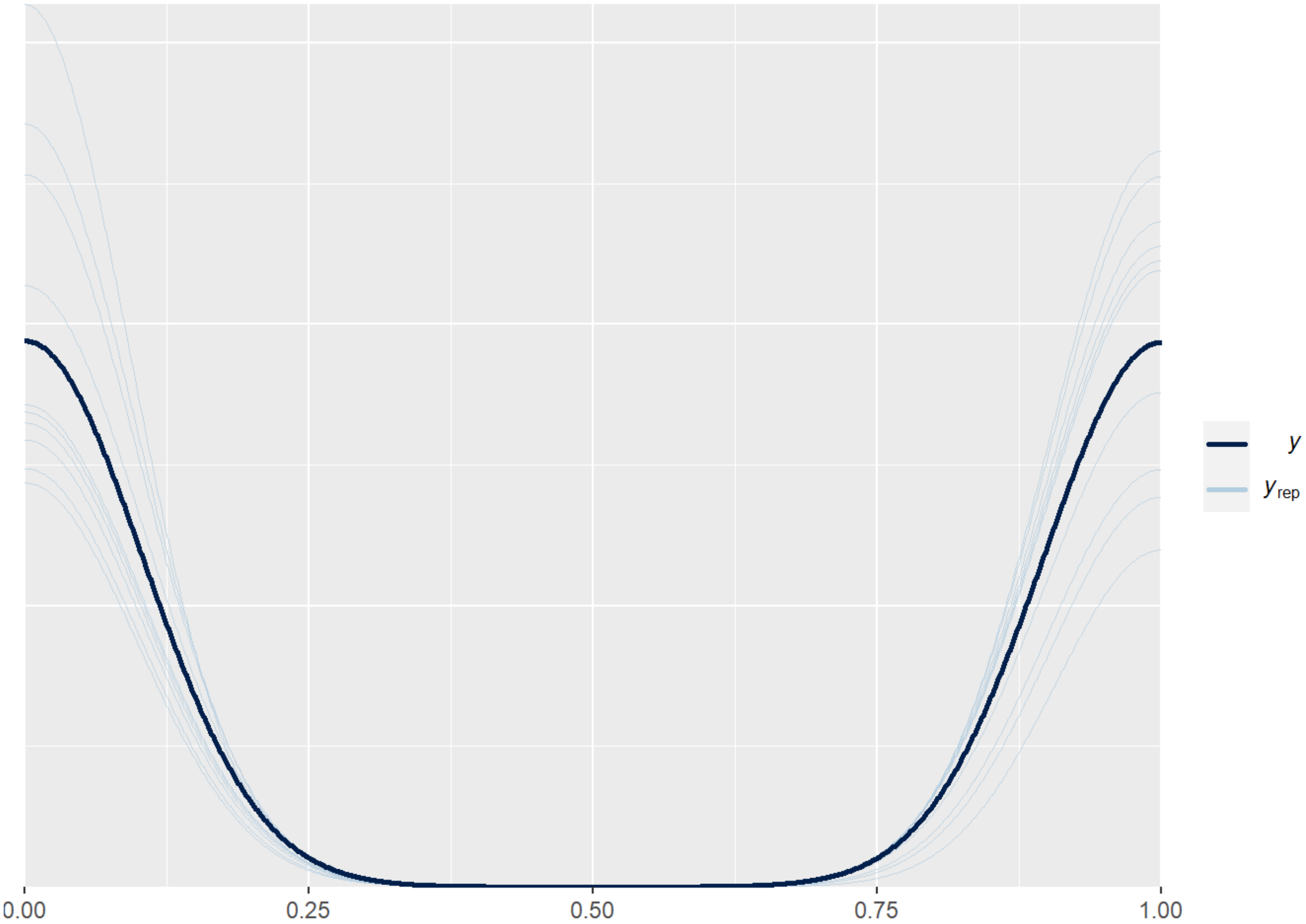

```
summary(pr_m0_fit_skep)
```

Fitting the second model on skeptical and informed data

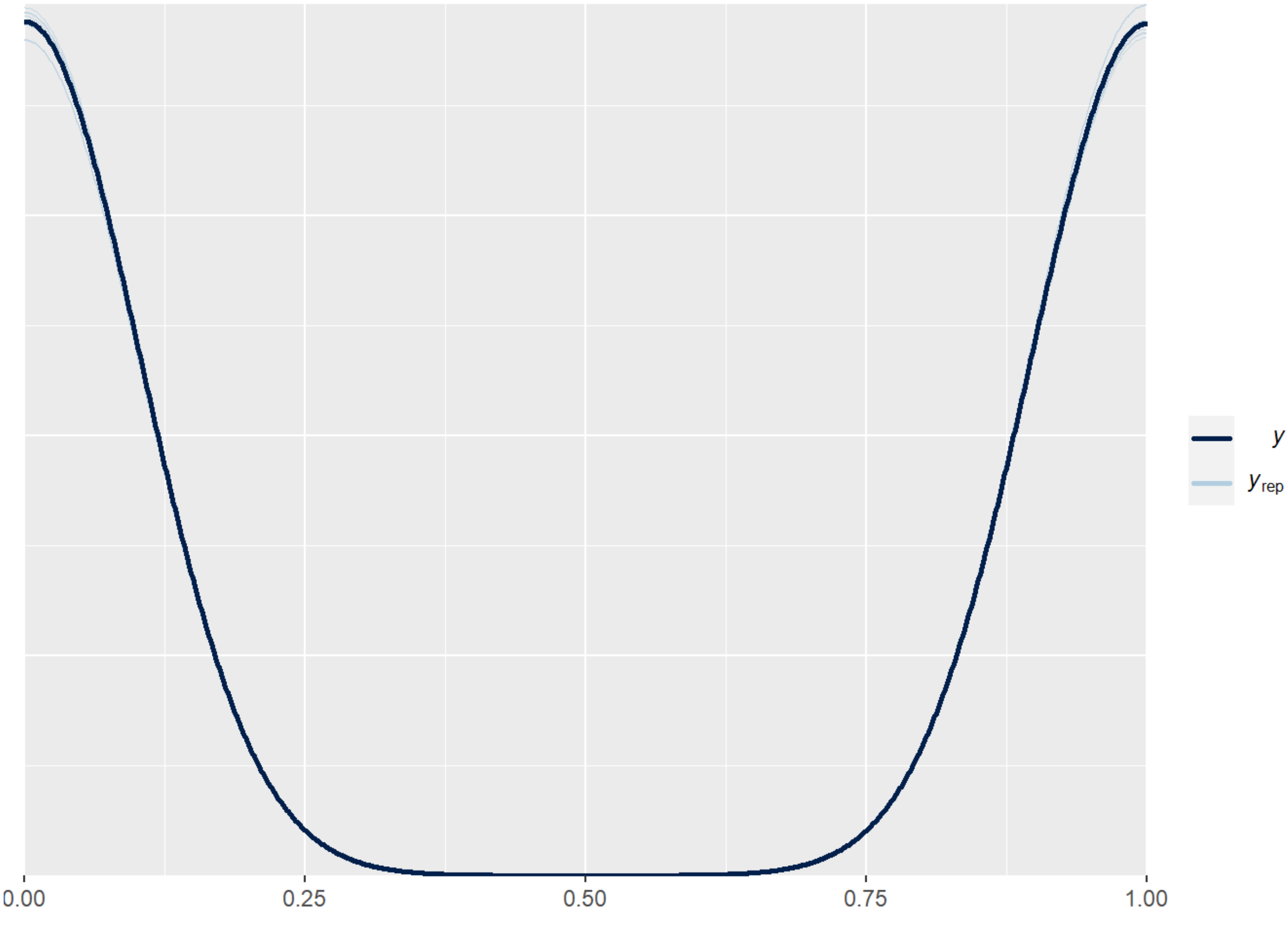
```
##Second model fit on priors
pr_m1_inf <- brm(
  PR_f1,
  data = train_informed_s,
  prior = PR_p1,
  family = bernoulli,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)


pp_check(pr_m1_inf)
```



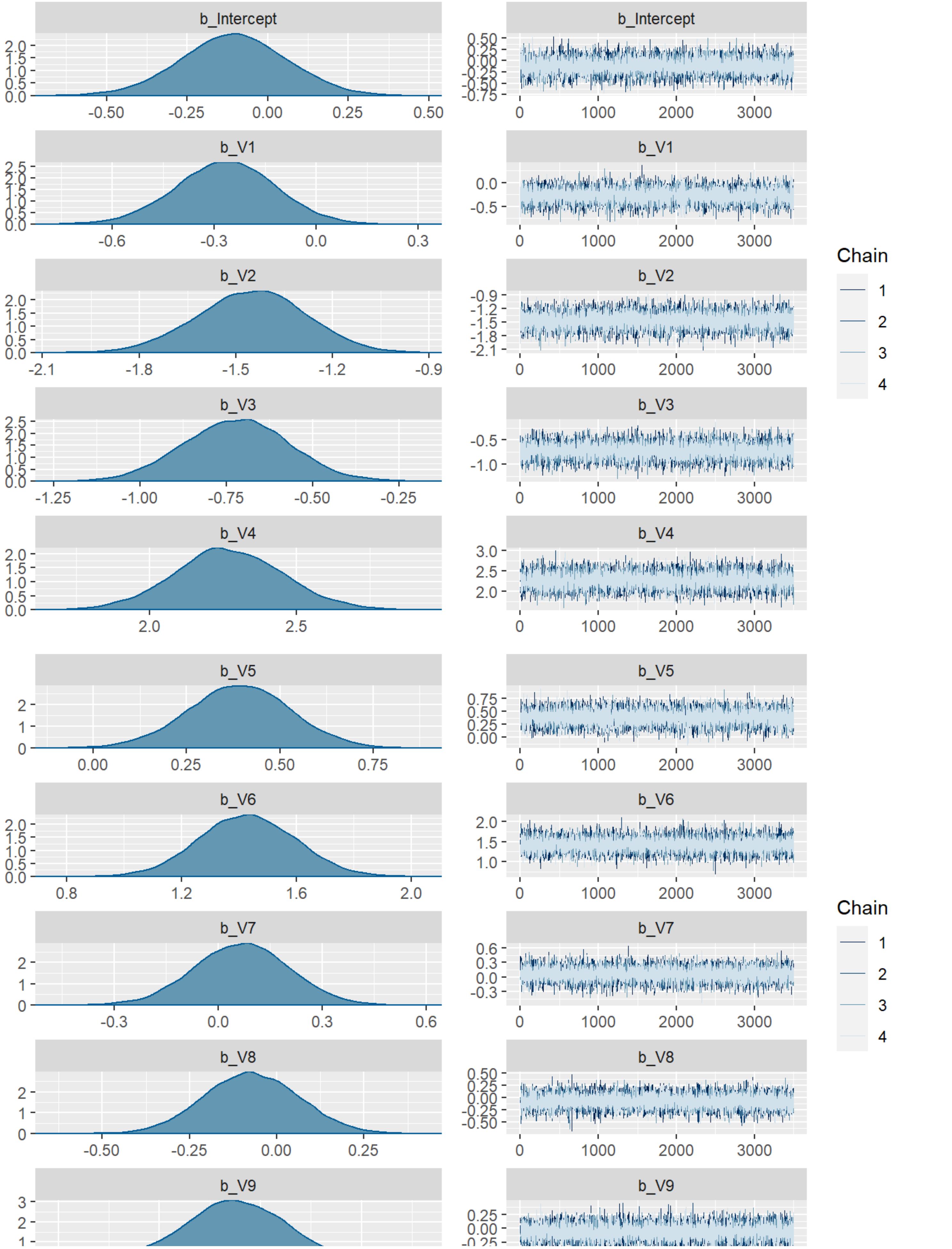
```
pr_m1_skep <- brm(
  PR_f1,
  data = train_skeptic_s,
  prior = PR_p1,
  family = bernoulli,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)


pp_check(pr_m1_skep)
```

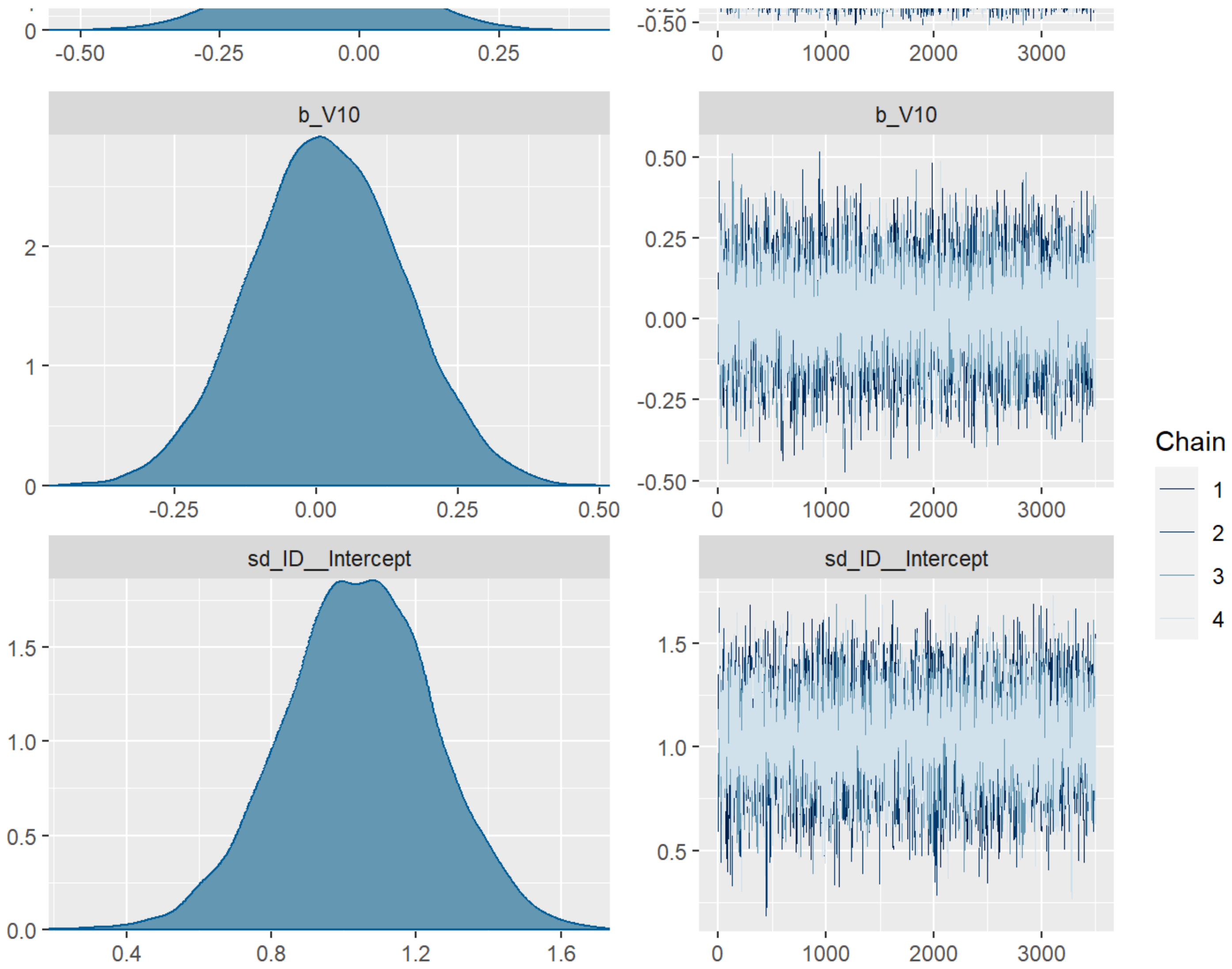


```
##second model fit on informed data
pr_m1_fit_inf <- brm(
  PR_f1,
  data = train_informed_s,
  prior = PR_p1,
  family = bernoulli,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m1_fit_inf)
```



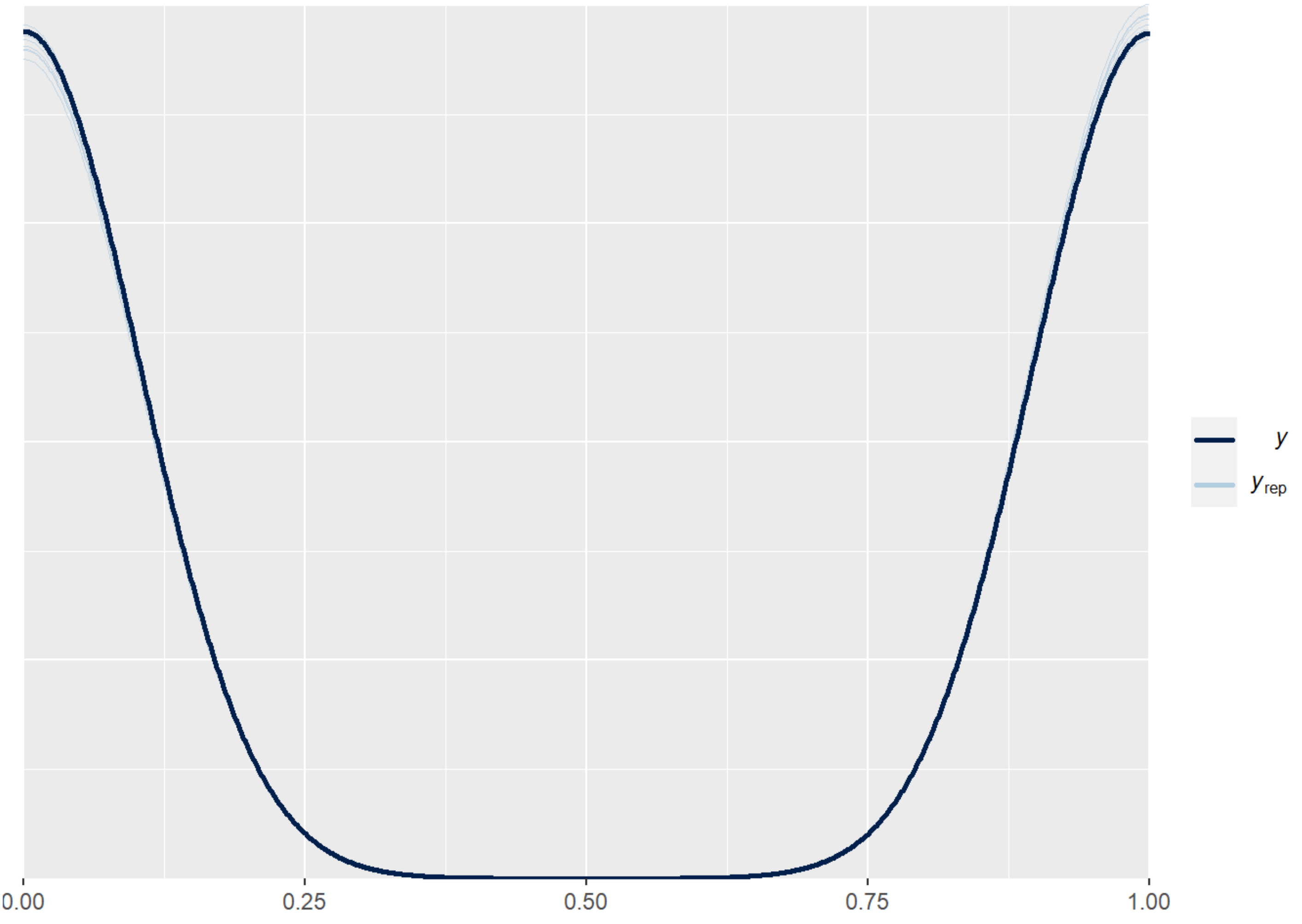

```
plot(pr_m1_fit_inf)
```


b_Intercept
b_Intercept
b_V1
b_V1
b_V2
b_V2
b_V3
b_V3
b_V4
b_V4
b_V5
b_V5
b_V6
b_V6
b_V7
b_V7
b_V8
b_V8
b_V9
b_V9
Chain
1
2
3
4
Chain
1
2
3
4

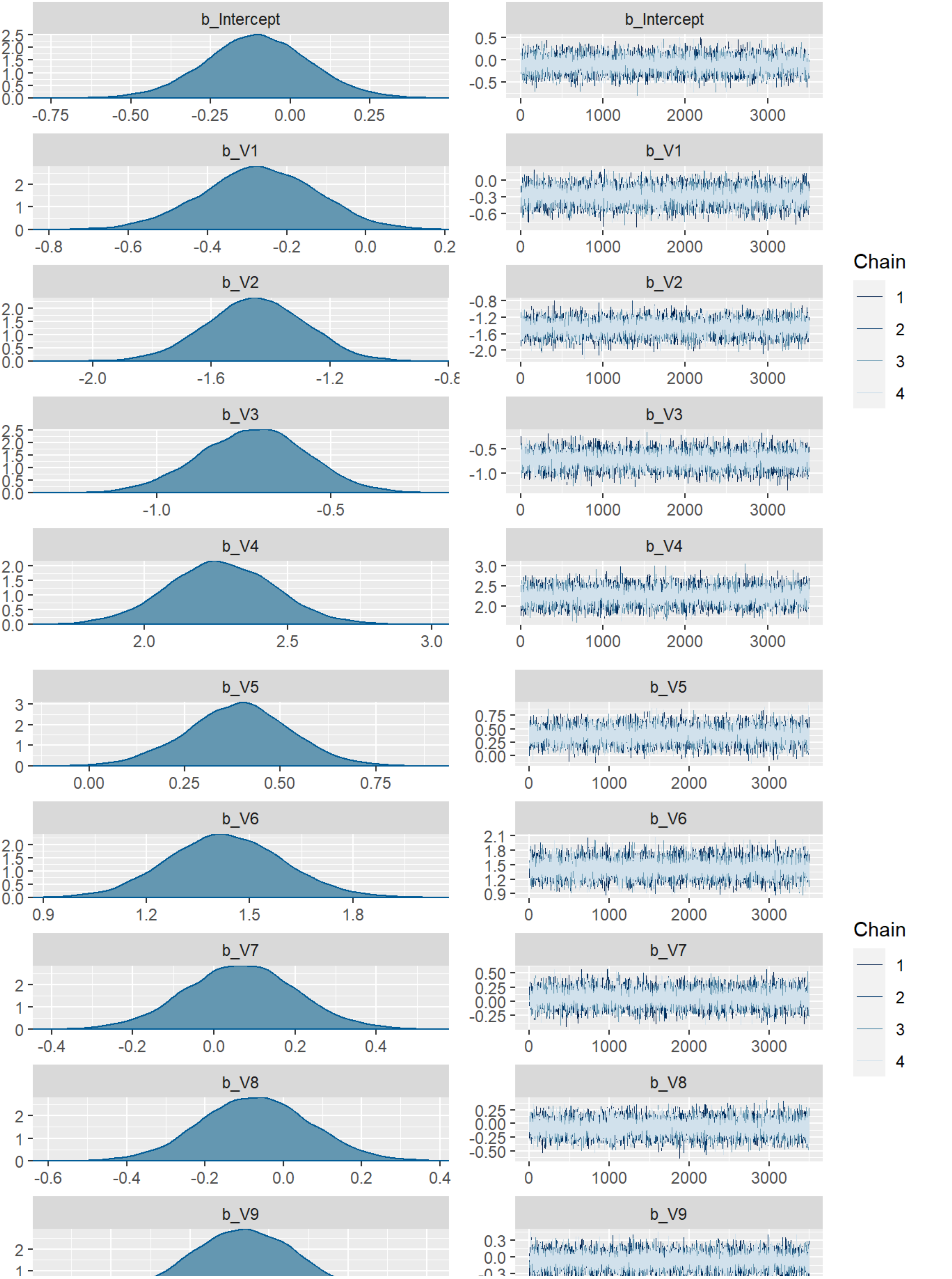


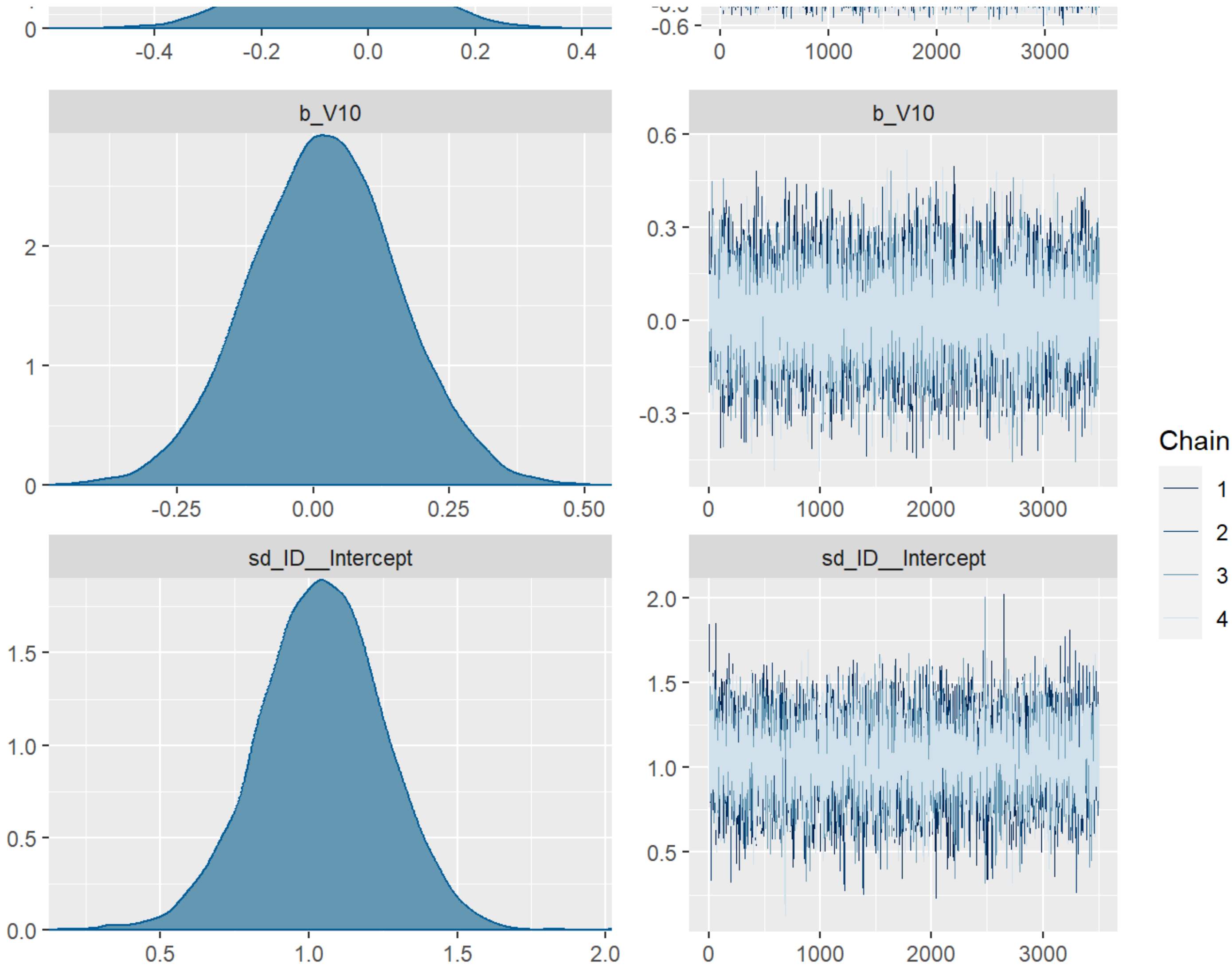

```
summary(pr_m1_fit_inf)
```

```
## second model fit on skeptical data
pr_m1_fit_skep <- brm(
  PR_f1,
  data = train_skeptic_s,
  prior = PR_p1,
  family = bernoulli,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m1_fit_skep)
```




```
plot(pr_m1_fit_skep)
```


b_Intercept
b_Intercept
b_V1
b_V1
b_V2
b_V2
b_V3
b_V3
b_V4
b_V4
b_V5
b_V5
b_V6
b_V6
b_V7
b_V7
b_V8
b_V8
b_V9
b_V9
Chain
1
2
3
4
Chain
1
2
3
4




```
summary(pr_m1_fit_skep)
```

##Ditlev ### Asses performance on test data

```
train_informed_s$PredictionsPerc0 <- predict(pr_m0_fit_inf)[, 1]
train_informed_s$Prediction0[train_informed_s$PredictionsPerc0 > 0.5] <- "Schizoph
renia"
```

```
## Warning: Unknown or uninitialised column: `Prediction0`.
```

```
train_informed_s$Prediction0[train_informed_s$PredictionsPerc0 <= 0.5] <- "Control
"


train_informed_s$PredictionsPerc1 <- predict(pr_m1_fit_inf)[, 1]
train_informed_s$Prediction1[train_informed_s$PredictionsPerc1 > 0.5] <- "Schizoph
renia"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
train_informed_s$Prediction1[train_informed_s$PredictionsPerc1 <= 0.5] <- "Control
"


train_skeptic_s$PredictionsPerc0 <- predict(pr_m0_fit_skep)[, 1]
train_skeptic_s$Prediction0[train_skeptic_s$PredictionsPerc0 > 0.5] <- "Schizophre
nia"
```

```
## Warning: Unknown or uninitialised column: `Prediction0`.
```

```
train_skeptic_s$Prediction0[train_skeptic_s$PredictionsPerc0 <= 0.5] <- "Control"

train_skeptic_s$PredictionsPerc1 <- predict(pr_m1_fit_skep)[, 1]
train_skeptic_s$Prediction1[train_skeptic_s$PredictionsPerc1 > 0.5] <- "Schizophre
nia"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
train_skeptic_s$Prediction1[train_skeptic_s$PredictionsPerc1 <= 0.5] <- "Control"

train_informed_s <- train_informed_s %>%
  mutate(
    Group = as.factor(Group),
    Prediction0 = as.factor(Prediction0),
    Prediction1 = as.factor(Prediction1)
  )

train_skeptic_s <- train_skeptic_s %>%
  mutate(
    Group = as.factor(Group),
    Prediction0 = as.factor(Prediction0),
    Prediction1 = as.factor(Prediction1)
  )


test_informed_s$PredictionsPerc0 <- predict(pr_m0_fit_inf, newdata = test_informed
_s, allow_new_levels = T)[, 1]
test_informed_s$Prediction0[test_informed_s$PredictionsPerc0 > 0.5] <- "Schizophre
nia"
```

```
## Warning: Unknown or uninitialised column: `Prediction0`.
```

```
test_informed_s$Prediction0[test_informed_s$PredictionsPerc0 <= 0.5] <- "Control"


test_informed_s$PredictionsPerc1 <- predict(pr_m1_fit_inf, newdata = test_informed
_s, allow_new_levels = T)[, 1]
test_informed_s$Prediction1[test_informed_s$PredictionsPerc1 > 0.5] <- "Schizophre
nia"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
test_informed_s$Prediction1[test_informed_s$PredictionsPerc1 <= 0.5] <- "Control"


test_skeptic_s$PredictionsPerc0 <- predict(pr_m0_fit_skep, newdata = test_informed
_s, allow_new_levels = T)[, 1]
test_skeptic_s$Prediction0[test_skeptic_s$PredictionsPerc0 > 0.5] <- "Schizophreni
a"
```

```
## Warning: Unknown or uninitialised column: `Prediction0`.
```

```
test_skeptic_s$Prediction0[test_skeptic_s$PredictionsPerc0 <= 0.5] <- "Control"

test_skeptic_s$PredictionsPerc1 <- predict(pr_m1_fit_skep, newdata = test_informed
_s, allow_new_levels = T)[, 1]
test_skeptic_s$Prediction1[test_skeptic_s$PredictionsPerc1 > 0.5] <- "Schizophreni
a"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
test_skeptic_s$Prediction1[test_skeptic_s$PredictionsPerc1 <= 0.5] <- "Control"

test_informed_s <- test_informed_s %>%
  mutate(
    Group = as.factor(Group),
    Prediction0 = as.factor(Prediction0),
    Prediction1 = as.factor(Prediction1)
  )

test_skeptic_s <- test_skeptic_s %>%
  mutate(
    Group = as.factor(Group),
    Prediction0 = as.factor(Prediction0),
    Prediction1 = as.factor(Prediction1)
  )
```

```
confusionMatrix(train_skeptic_s$Group, train_skeptic_s$Prediction0)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction      Control Schizophrenia
##   Control           778            23
##   Schizophrenia      15           784
##
##                Accuracy : 0.9762
##                  95% CI : (0.9675, 0.9831)
##     No Information Rate : 0.5044
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9525
##
##  Mcnemar's Test P-Value : 0.2561
##
##             Sensitivity : 0.9811
##             Specificity : 0.9715
##          Pos Pred Value : 0.9713
##          Neg Pred Value : 0.9812
##              Prevalence : 0.4956
##          Detection Rate : 0.4863
##    Detection Prevalence : 0.5006
##       Balanced Accuracy : 0.9763
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(test_skeptic_s$Group, test_skeptic_s$Prediction0)
```

```
## Confusion Matrix and Statistics
##
##               Reference
## Prediction      Control Schizophrenia
##   Control           198             9
##   Schizophrenia       5           188
##
##                Accuracy : 0.965
##                  95% CI : (0.942, 0.9807)
##     No Information Rate : 0.5075
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.93
##
##  Mcnemar's Test P-Value : 0.4227
##
##             Sensitivity : 0.9754
##             Specificity : 0.9543
##          Pos Pred Value : 0.9565
##          Neg Pred Value : 0.9741
##              Prevalence : 0.5075
##          Detection Rate : 0.4950
##    Detection Prevalence : 0.5175
##       Balanced Accuracy : 0.9648
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(train_skeptic_s$Group, train_skeptic_s$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction      Control Schizophrenia
##   Control           797             4
##   Schizophrenia       2           797
##
##                Accuracy : 0.9962
##                  95% CI : (0.9919, 0.9986)
##     No Information Rate : 0.5006
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9925
##
##  Mcnemar's Test P-Value : 0.6831
##
##             Sensitivity : 0.9975
##             Specificity : 0.9950
##          Pos Pred Value : 0.9950
##          Neg Pred Value : 0.9975
##              Prevalence : 0.4994
##          Detection Rate : 0.4981
##    Detection Prevalence : 0.5006
##       Balanced Accuracy : 0.9963
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(test_skeptic_s$Group, test_skeptic_s$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction      Control Schizophrenia
##   Control           199             8
##   Schizophrenia       2           191
##
##                Accuracy : 0.975
##                  95% CI : (0.9545, 0.9879)
##     No Information Rate : 0.5025
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.95
##
##  Mcnemar's Test P-Value : 0.1138
##
##             Sensitivity : 0.9900
##             Specificity : 0.9598
##          Pos Pred Value : 0.9614
##          Neg Pred Value : 0.9896
##              Prevalence : 0.5025
##          Detection Rate : 0.4975
##    Detection Prevalence : 0.5175
##       Balanced Accuracy : 0.9749
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(train_informed_s$Group, train_informed_s$Prediction0)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction      Control Schizophrenia
##   Control           777            24
##   Schizophrenia      15           784
##
##                Accuracy : 0.9756
##                  95% CI : (0.9668, 0.9826)
##     No Information Rate : 0.505
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9513
##
##  Mcnemar's Test P-Value : 0.2002
##
##             Sensitivity : 0.9811
##             Specificity : 0.9703
##          Pos Pred Value : 0.9700
##          Neg Pred Value : 0.9812
##              Prevalence : 0.4950
##          Detection Rate : 0.4856
##    Detection Prevalence : 0.5006
##       Balanced Accuracy : 0.9757
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(test_informed_s$Group, test_informed_s$Prediction0)
```

```
## Confusion Matrix and Statistics
##
##                 Reference
## Prediction      Control Schizophrenia
##   Control           198             1
##   Schizophrenia       5           196
##
##                Accuracy : 0.985
##                  95% CI : (0.9676, 0.9945)
##     No Information Rate : 0.5075
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.97
##
##  Mcnemar's Test P-Value : 0.2207
##
##             Sensitivity : 0.9754
##             Specificity : 0.9949
##          Pos Pred Value : 0.9950
##          Neg Pred Value : 0.9751
##              Prevalence : 0.5075
##          Detection Rate : 0.4950
##    Detection Prevalence : 0.4975
##       Balanced Accuracy : 0.9851
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(train_informed_s$Group, train_informed_s$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##                 Reference
## Prediction      Control Schizophrenia
##   Control           797             4
##   Schizophrenia       2           797
##
##                Accuracy : 0.9962
##                  95% CI : (0.9919, 0.9986)
##     No Information Rate : 0.5006
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9925
##
##  Mcnemar's Test P-Value : 0.6831
##
##             Sensitivity : 0.9975
##             Specificity : 0.9950
##          Pos Pred Value : 0.9950
##          Neg Pred Value : 0.9975
##              Prevalence : 0.4994
##          Detection Rate : 0.4981
##    Detection Prevalence : 0.5006
##       Balanced Accuracy : 0.9963
##
##        'Positive' Class : Control
##
```

```
confusionMatrix(test_informed_s$Group, test_informed_s$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction      Control Schizophrenia
##   Control           199             0
##   Schizophrenia       2           199
##
##                Accuracy : 0.995
##                  95% CI : (0.9821, 0.9994)
##     No Information Rate : 0.5025
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.99
##
##  Mcnemar's Test P-Value : 0.4795
##
##             Sensitivity : 0.9900
##             Specificity : 1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 0.9900
##              Prevalence : 0.5025
##          Detection Rate : 0.4975
##    Detection Prevalence : 0.4975
##       Balanced Accuracy : 0.9950
##
##        'Positive' Class : Control
##
```

Discuss whether performance and feature importance is as expected

##Part 3 - Applying the machine learning pipeline to empirical data

```
real_data <- read_csv("assignment_3_data.csv")
```

```
## Rows: 1889 Columns: 398
## ── Column specification ────────────────────────────────────────────────────────
─
## Delimiter: ","
## chr   (5): NewID, Diagnosis, Language, Gender, Trial
## dbl (393): PatID, Corpus, Duration_Praat, F0_Mean_Praat, F0_SD_Praat, Intens...
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this messag
e.
```

```
real_data <- real_data %>%
  select(-Language) %>%
  select(-Corpus) %>%
  select(-NewID)
```

Apply your machine learning pipeline to the empirical data

Warning: in simulated data you only have 10 features, now you have many more - Consider the impact a higher number of features will have on your ML inference and decide if you want to cut down the number of features before running the pipeline (alternatibvely expand the pipeline to add feature selection)

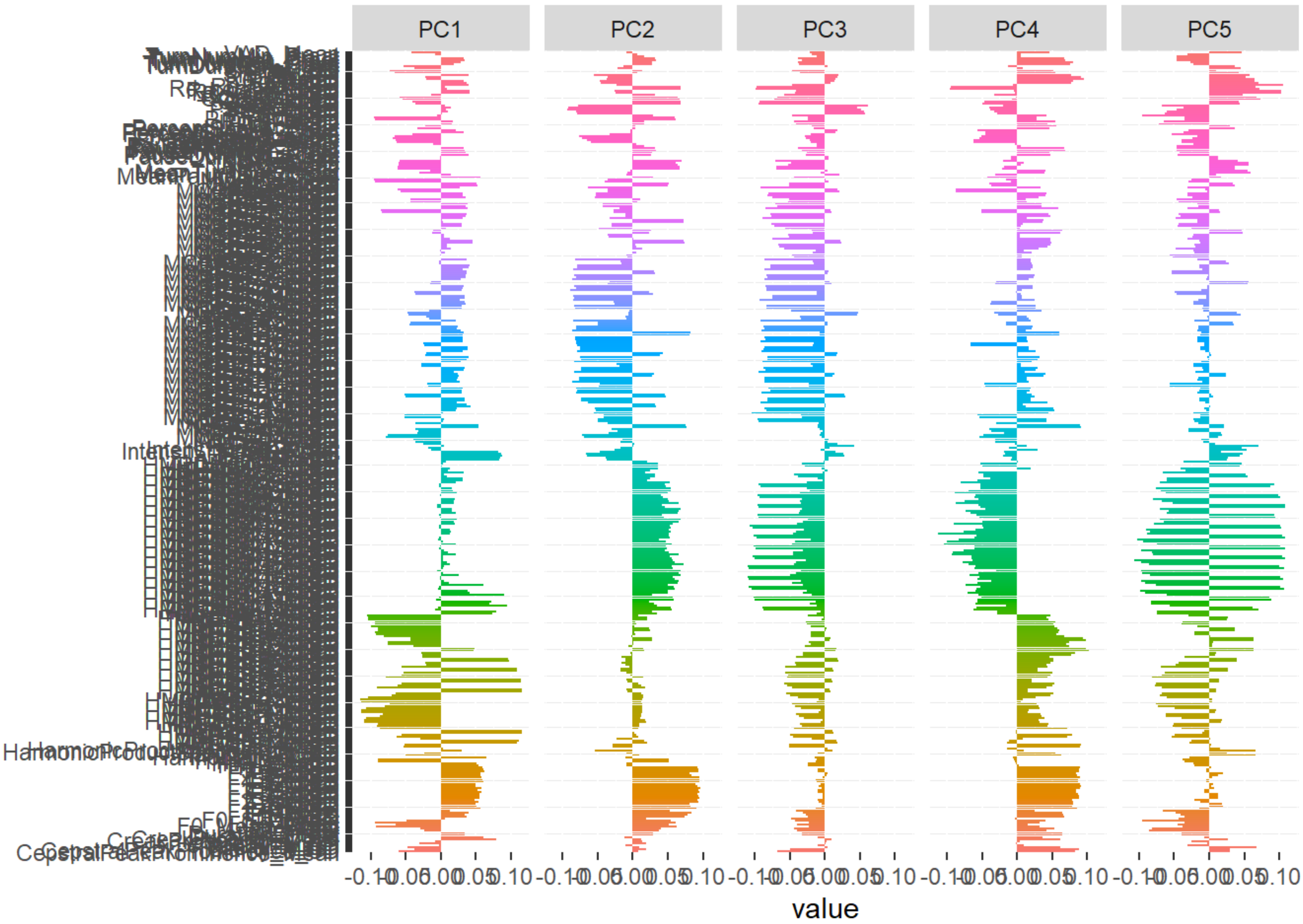
data budgeting and pree-processing of the data

```
set.seed(304)

split_real_data <- initial_split(real_data, prop = 4/5, strata = Gender)

train_data <- training(split_real_data)
test_data <- testing(split_real_data)

train_data <- train_data %>%
  select(-Gender) %>%
  select(-Trial)

test_data <- test_data %>%
  select(-Gender) %>%
  select(-Trial)

train_data$PatID <- as.factor(train_data$PatID)

test_data$PatID <- as.factor(test_data$PatID)
```

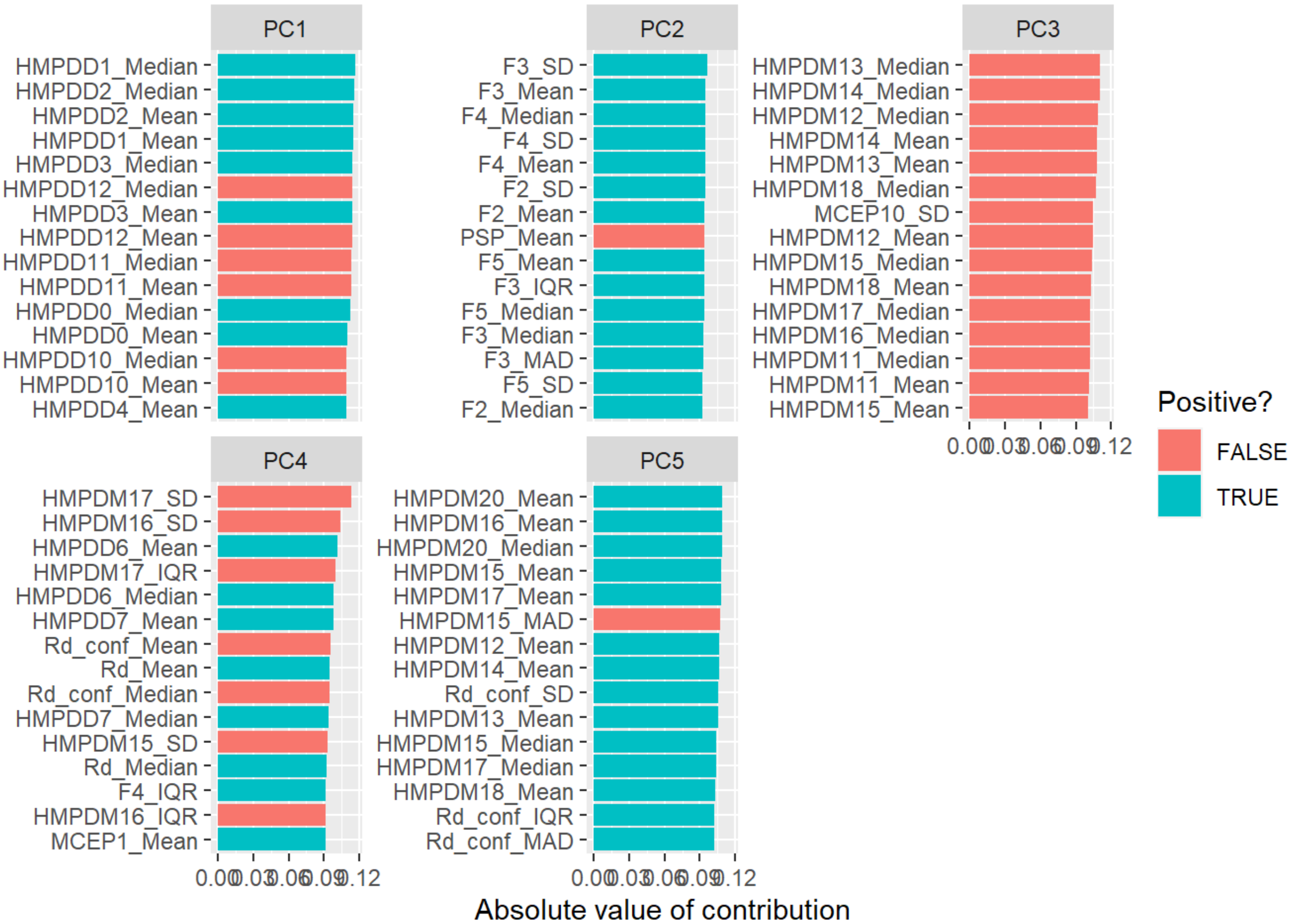
```
recipe_real <- train_data %>%
  recipe(Diagnosis~.) %>%
  update_role(PatID, new_role = 'PatID') %>%
  step_scale(all_numeric()) %>%
  step_center(all_numeric()) %>%
  prep(training=train_data, retain=TRUE)

train_data_s <- juice(recipe_real)
test_data_s <- bake(recipe_real, new_data = test_data)
```

Principle component analysis

```
pca_recipe <- recipe(Diagnosis~., data = train_data_s) %>%
  update_role(PatID, new_role = "id") %>%
  step_pca(all_numeric(), id = "pca")%>%
  prep()

tidy_pca <- tidy(pca_recipe, 1)

bake_pca <- bake(pca_recipe, train_data_s)

pca_b_test <- bake(pca_recipe, test_data_s)

tidy_pca %>%
  filter(component %in% paste0("PC", 1:5)) %>%
  mutate(component = fct_inorder(component)) %>%
  ggplot(aes(value, terms, fill = terms)) +
  geom_col(show.legend = FALSE) +
  facet_wrap(~component, nrow = 1) +
  labs(y = NULL)
```



```
tidy_pca %>%
  filter(component %in% paste0("PC", 1:5)) %>%
  group_by(component) %>%
  top_n(15, abs(value)) %>%
  ungroup() %>%
  mutate(terms = reorder_within(terms, abs(value), component)) %>%
  ggplot(aes(abs(value), terms, fill = value > 0)) +
  geom_col() +
  facet_wrap(~component, scales = "free_y") +
  scale_y_reordered() +
  labs(
    x = "Absolute value of contribution",
    y = NULL, fill = "Positive?"
  )
```



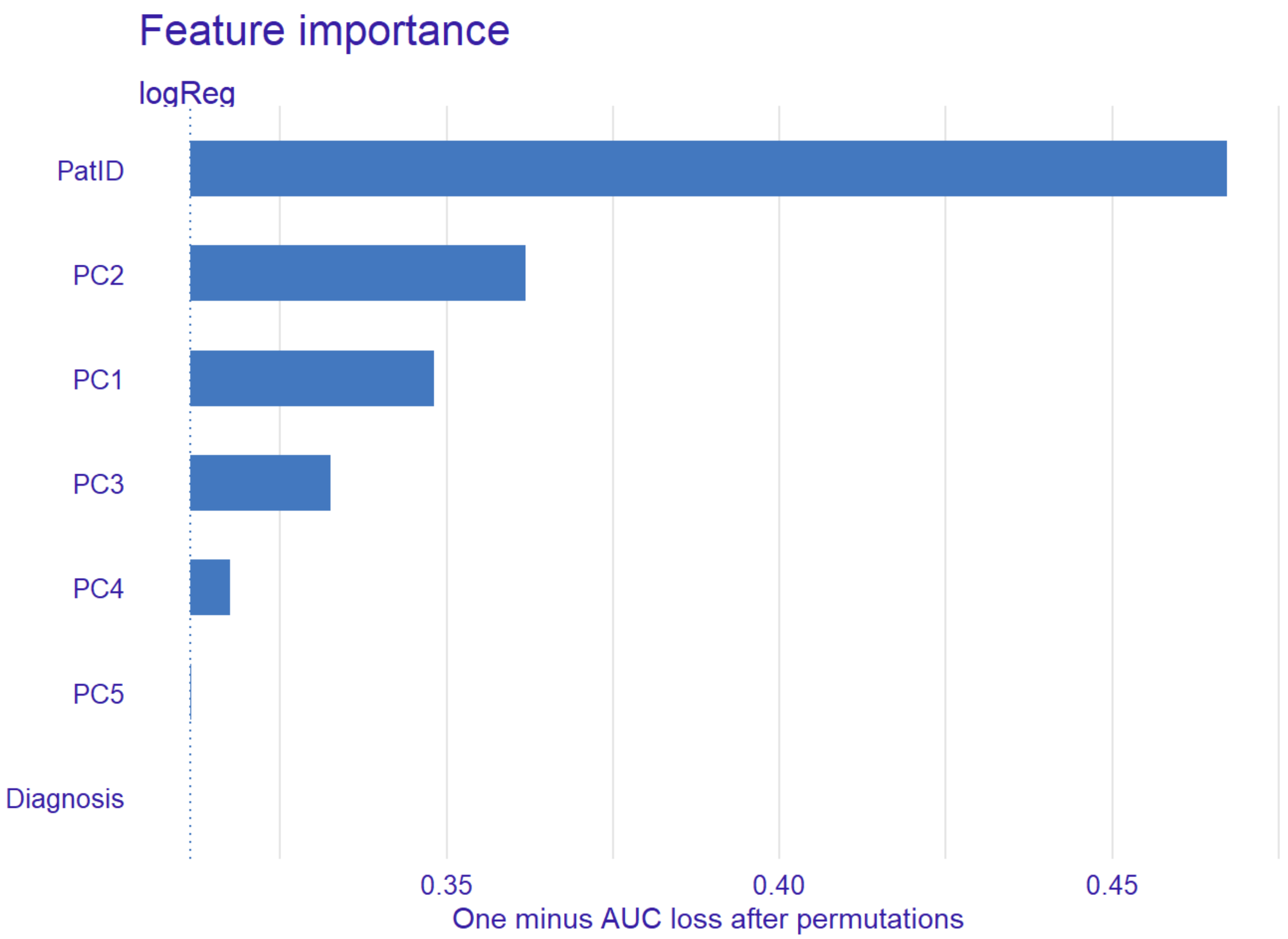

```
??reorder_within
```

```
## starting httpd help server ... done
```

##Manuela ### feature selection

```
d_data <- bake_pca %>%
  mutate(PatID = NULL, Trail = NULL, NewID = NULL, Gender = NULL, Language = NULL,
Corpus = NULL)

LogisticRegression_train<- logistic_reg() %>%
  set_mode('classification') %>%
  set_engine('glm') %>%
  fit(Diagnosis ~ . , data = bake_pca)
```

```
explainer_lm <-
  explain_tidymodels(
    LogisticRegression_train,
    data = bake_pca,
    y = as.numeric(d_data$Diagnosis) -1,
    label = 'logReg',
    verbose = FALSE
  )

explainer_lm %>% model_parts() %>%  plot(show_boxplots = FALSE) + ggtitle('Feature
importance', '')
```



fit and assess a classification algorithm on the training data

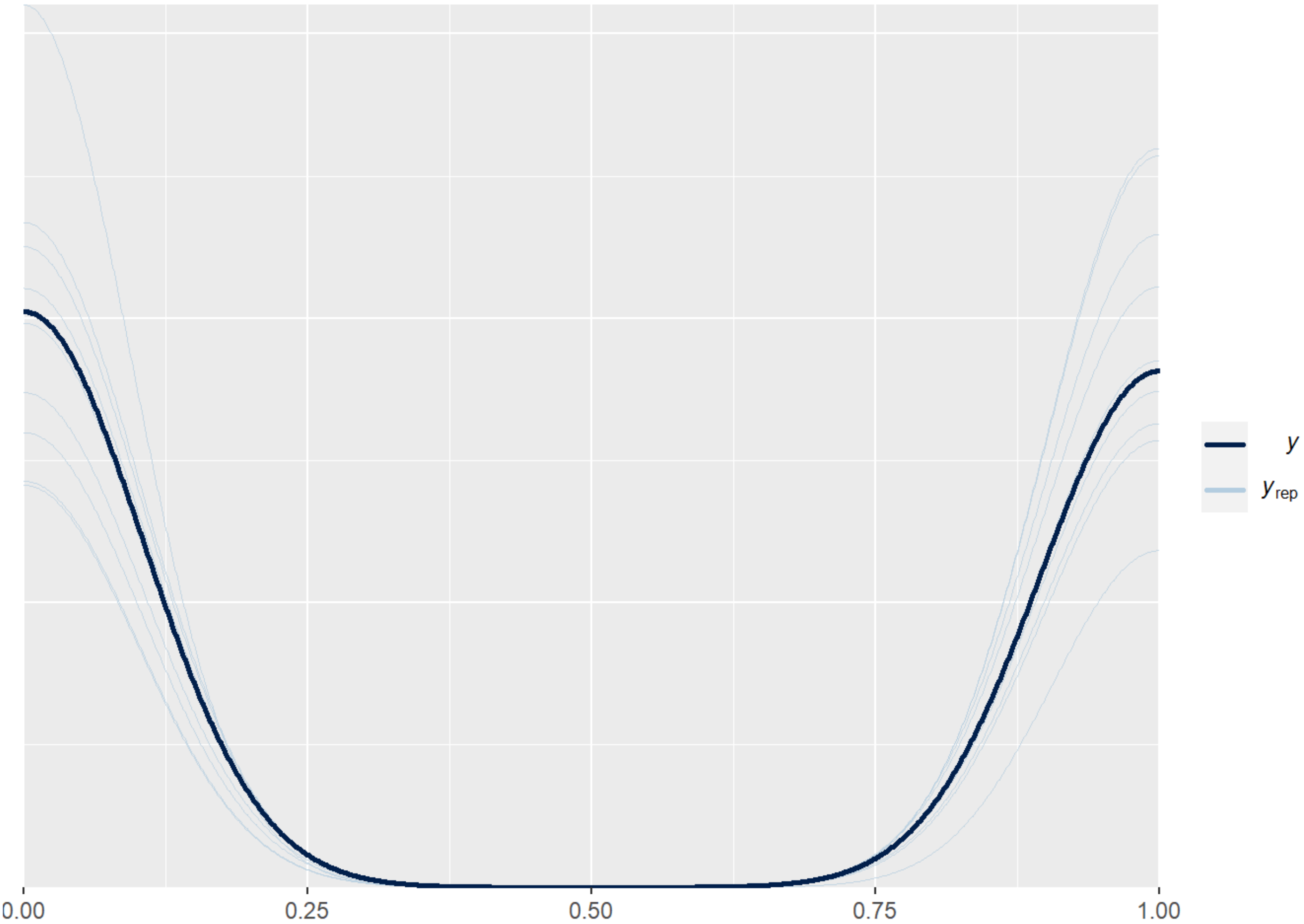
```
form1 <- bf(Diagnosis~1+PC2+PC1+PC3+PC4+(1|PatID))
get_prior(form1, bake_pca, family = bernoulli)
```

```
##                  prior     class      coef group resp dpar nlpar lb ub
##                 (flat)         b                                      
##                 (flat)         b       PC1                            
##                 (flat)         b       PC2                            
##                 (flat)         b       PC3                            
##                 (flat)         b       PC4                            
##  student_t(3, 0, 2.5) Intercept                                       
##  student_t(3, 0, 2.5)        sd                                  0    
##  student_t(3, 0, 2.5)        sd           PatID                  0    
##  student_t(3, 0, 2.5)        sd Intercept PatID                  0    
##        source
##       default
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##       default
##       default
##  (vectorized)
##  (vectorized)
```

```
prior_f1 <- c(
  prior(normal(0, 1), class=Intercept),
  prior(normal(0, 1), class=sd),
  prior(normal(0, 0.3), class=b)
)
```

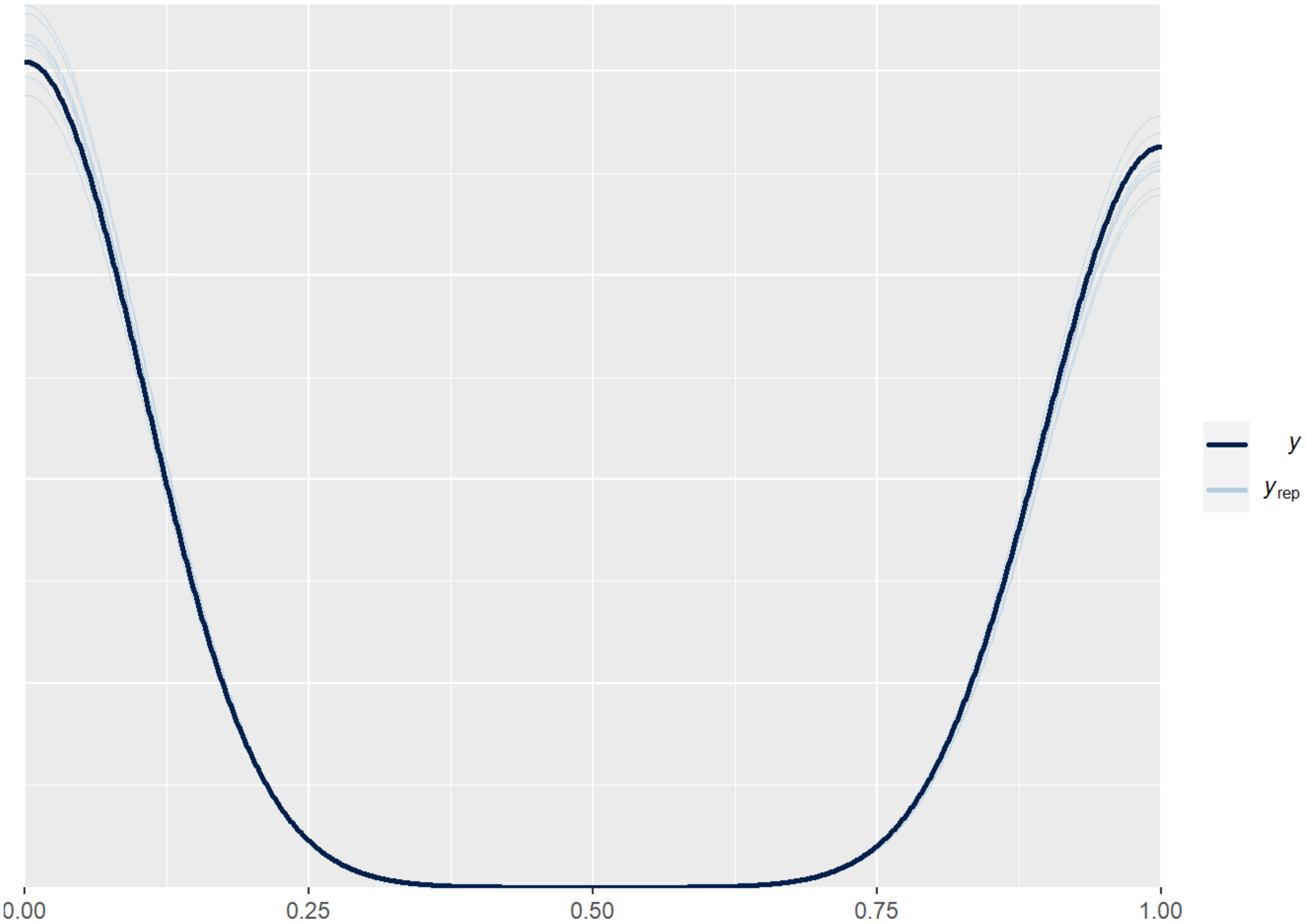
Fitting the model with only the priors

```
pr_m1 <- brm(
  form1,
  data = bake_pca,
  prior = prior_f1,
  family = bernoulli,
  refresh=0,
  sample_prior = 'only',
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m1)
```

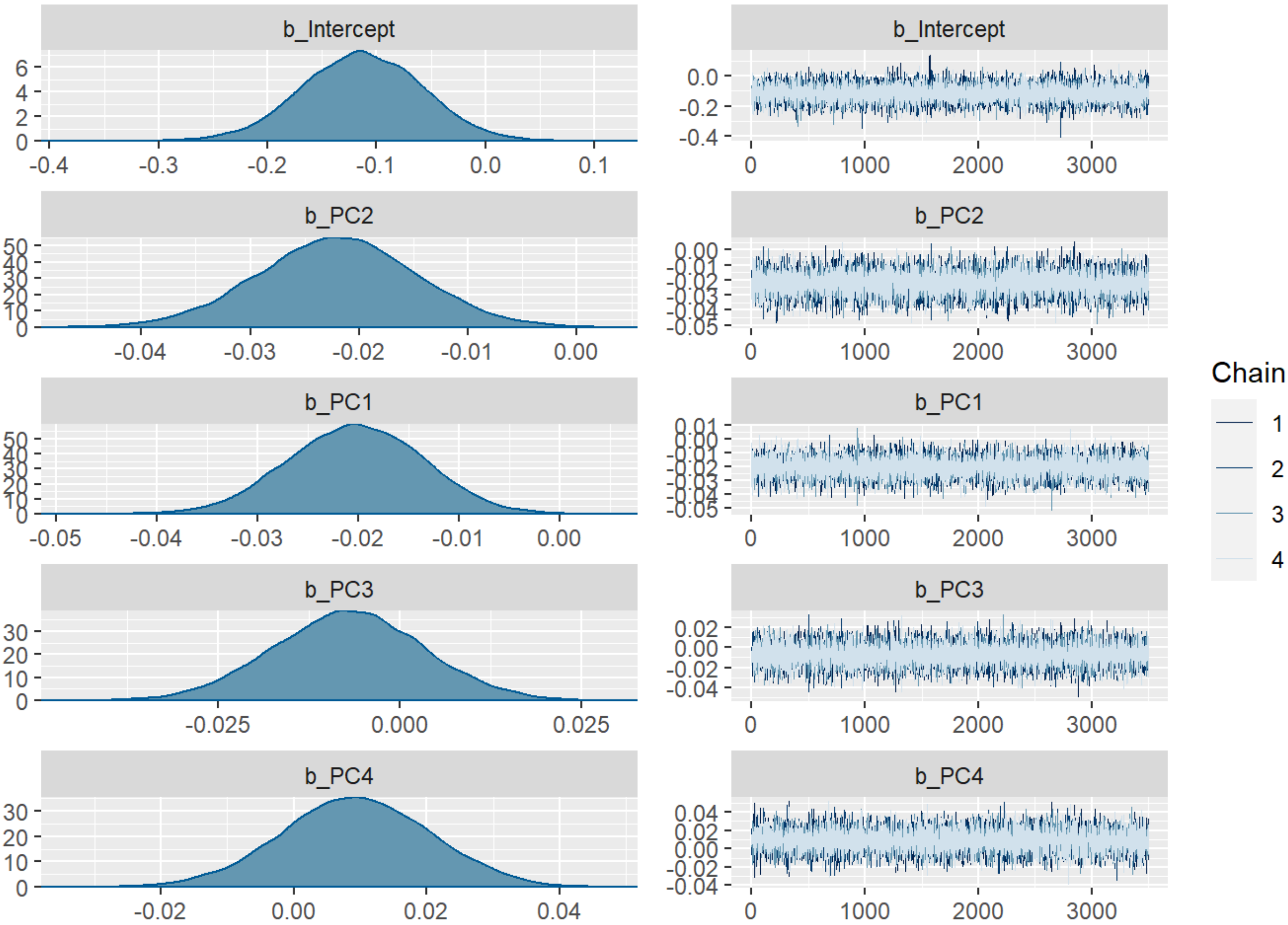


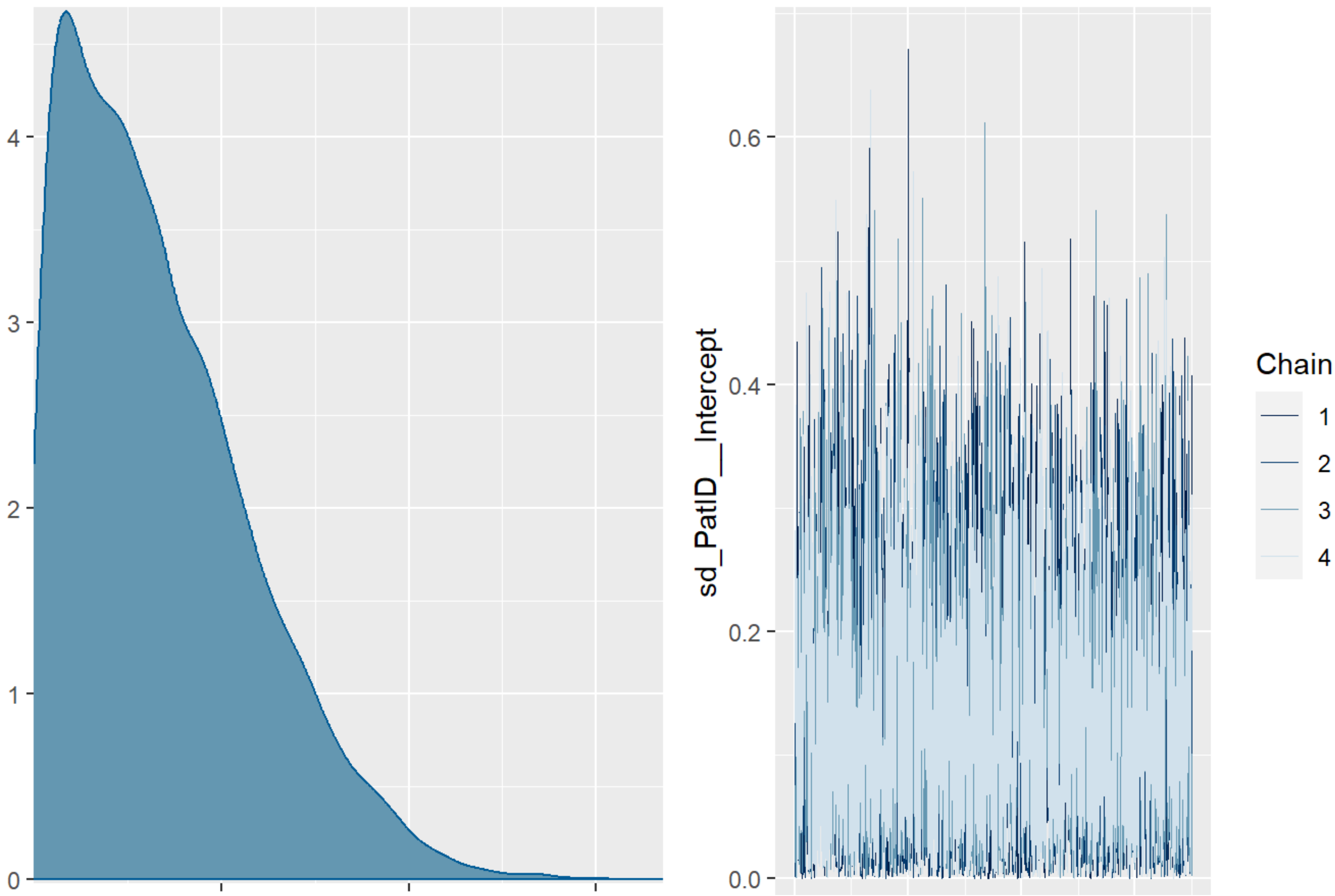
Fitting model on the data

```
pr_m1_fit <- brm(
  form1,
  data = bake_pca,
  prior = prior_f1,
  family = bernoulli,
  refresh=0,
  sample_prior = TRUE,
  iter=6000,
  warmup = 2500,
  backend = "cmdstanr",
  threads = threading(2),
  chains = 4,
  cores = 4,
  control = list(
    adapt_delta = 0.9,
    max_treedepth = 20)
)

pp_check(pr_m1_fit)
```




```
plot(pr_m1_fit)
```

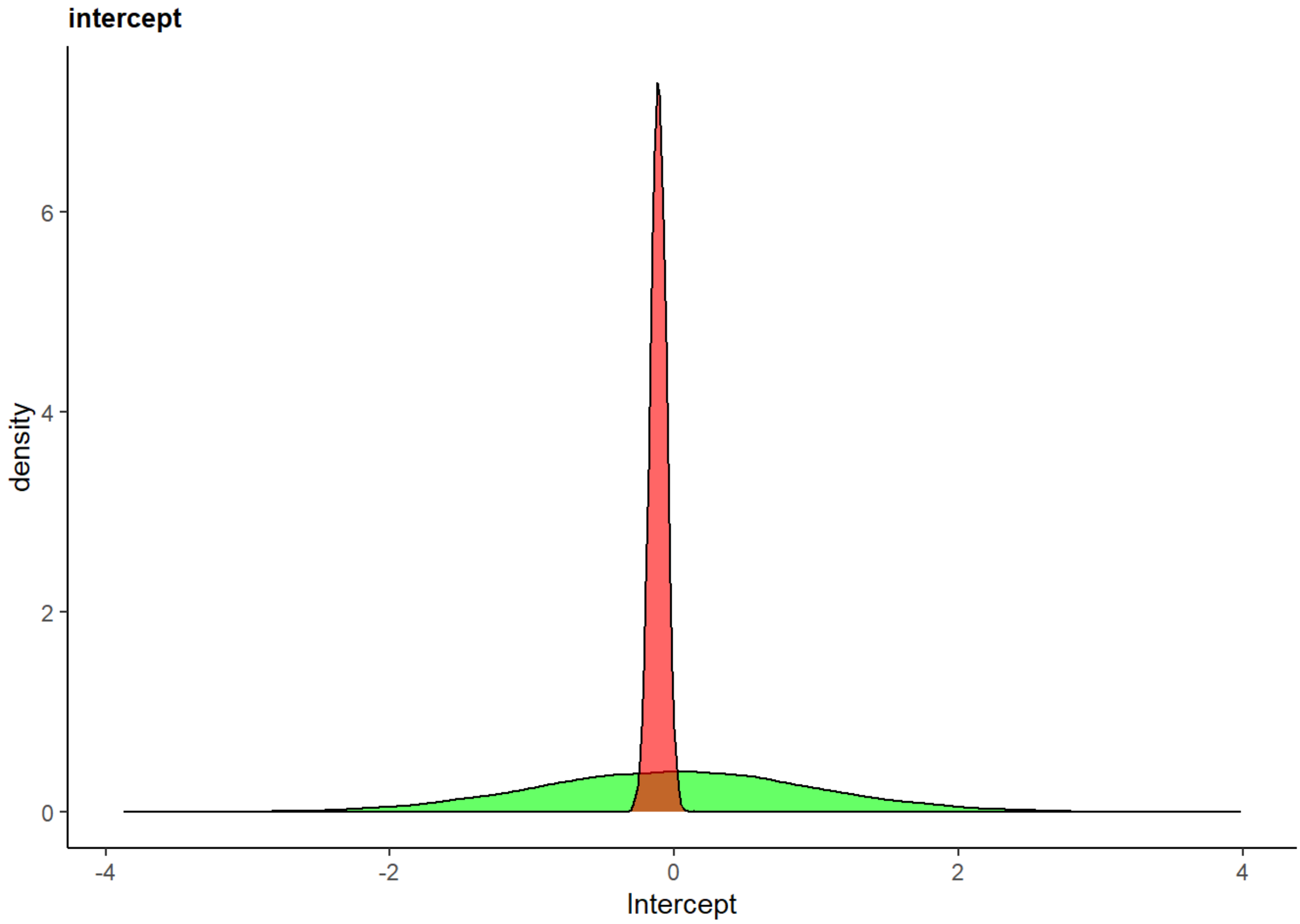

b_Intercept
b_Intercept
b_PC2
b_PC2
b_PC1
b_PC1
b_PC3
b_PC3
b_PC4
b_PC4
Chain
1
2
3
4


sd_PatID__Intercept
Chain
1
2
3
4


```
summary(pr_m1_fit)
```

Prior posterior update check

```
Posterior_f1 <- as_draws_df(pr_m1_fit)

ggplot(Posterior_f1) +
  geom_density(aes(prior_Intercept), fill="green", color="black",alpha=0.6) +
  geom_density(aes(b_Intercept), fill="red", color="black",alpha=0.6) +
  xlab('Intercept') +
  theme_classic()+
  ggtitle("intercept")+
      theme(plot.title = element_text(size = 10, face = "bold"))
```



assess performance on the test set

```
bake_pca$PredictionsPerc1 <- predict(pr_m1_fit)[, 1]

bake_pca$Prediction1[bake_pca$PredictionsPerc1 > 0.5] <- "SCZ"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
bake_pca$Prediction1[bake_pca$PredictionsPerc1 <= 0.5] <- "CT"

bake_pca <- bake_pca %>%
  mutate(
    Diagnosis = as.factor(Diagnosis),
    Prediction1 = as.factor(Prediction1))

pca_b_test$PredictionsPerc1 <- predict(pr_m1_fit, newdata = pca_b_test, allow_new_
levels = T)[, 1]



pca_b_test$Prediction1[pca_b_test$PredictionsPerc1 > 0.5] <- "SCZ"
```

```
## Warning: Unknown or uninitialised column: `Prediction1`.
```

```
pca_b_test$Prediction1[pca_b_test$PredictionsPerc1 <= 0.5] <- "CT"

pca_b_test <- pca_b_test %>%
  mutate(
    Diagnosis = as.factor(Diagnosis),
    Prediction1 = as.factor(Prediction1)
  )
```

Accuracy

```
confusionMatrix(bake_pca$Diagnosis, bake_pca$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  CT SCZ
##        CT  545 251
##        SCZ 444 270
##
##                Accuracy : 0.5397
##                  95% CI : (0.5142, 0.5651)
##     No Information Rate : 0.655
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.0637
##
##  Mcnemar's Test P-Value : 3.265e-13
##
##             Sensitivity : 0.5511
##             Specificity : 0.5182
##          Pos Pred Value : 0.6847
##          Neg Pred Value : 0.3782
##              Prevalence : 0.6550
##          Detection Rate : 0.3609
##    Detection Prevalence : 0.5272
##       Balanced Accuracy : 0.5346
##
##        'Positive' Class : CT
##
```

```
confusionMatrix(pca_b_test$Diagnosis, pca_b_test$Prediction1)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  CT SCZ
##        CT  115  78
##        SCZ 104  82
##
##                Accuracy : 0.5198
##                  95% CI : (0.4682, 0.5711)
##     No Information Rate : 0.5778
##     P-Value [Acc > NIR] : 0.99011
##
##                   Kappa : 0.0368
##
##  Mcnemar's Test P-Value : 0.06386
##
##             Sensitivity : 0.5251
##             Specificity : 0.5125
##          Pos Pred Value : 0.5959
##          Neg Pred Value : 0.4409
##              Prevalence : 0.5778
##          Detection Rate : 0.3034
##    Detection Prevalence : 0.5092
##       Balanced Accuracy : 0.5188
##
##        'Positive' Class : CT
##
```

###discuss whether performance and feature importance is as expected