

Anorexia Nervosa: Symptom-Related Information Alters Decision-Making Policy Despite Outcome Irrelevance

Supplementary Materials

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Participants sample size

We conducted a separate study involving two groups: one of $n = 29$ anorexic patients and one of $n = 124$ healthy controls (the participants in that separate study were distinct from those in the present study). In a PRL task, each participant completed 160 trials per condition, and the content of the pair of images shown in each trial was manipulated. The effect size of the experimental manipulation on the learning rate parameter (the focus of the present study) was found to be 0.54. To determine the sample size needed to detect a similar effect, we carried out a parameter recovery study following the method outlined by Pedersen & Frank (2020). We simulated the data of two groups of 30 participants with different values of α (lower and higher) with a difference of 0.54. The other parameters of the RLDDM model (i.e., a , t , v) were set to the values estimated from the empirical data of the 29 anorexic patients and 124 healthy controls. For the simulation, we used the `hddm.generate.gen_rand_rlddm_data` function of the `hddm` module with following parameters:

```
subjects = 30
trials = 160

data = hddm.generate.gen_rand_rlddm_data(
    a=1.5,
    alpha=0.79, # or 0.25
    scaler=2.25,
    t=0.25,
    size=trials,
    subjs=subjects,
    p_upper=0.7,
    p_lower=0.3,
)
```

We used the `HDDMr1` function of the `hddm` module to estimate the RLDDM parameters based on the simulated data. We repeated this procedure 100 times, and in each iteration, the parameters for the lower and higher values of α were completely separated. These simulations indicate that our study had enough participants and trials to detect the effect size on α observed in the previous study.

A parameter recovery study and a frequentist power analysis are two distinct approaches. However, since Bayesian methods prioritize estimation over hypothesis testing, it is comforting to see that with the current number of participants and trials, the RLDDM model can detect an effect size similar to the one found in a separate study with a different group of participants but with a similar experimental manipulation.

Demographic and psychopathology measures

Age

In our initial statistical analysis, we investigated if there were any differences in age among the groups (AN = Anorexia Nervosa, BN = Bulimia Nervosa, HC = Healthy Controls, RI = participants who were at risk of developing eating disorders but had not received a formal diagnosis).

The mean age and standard deviation by group is shown below.

group	Age	SD
HC	19.77	1.06
AN	21.18	2.41
BN	20.39	1.88
RI	20.36	1.44

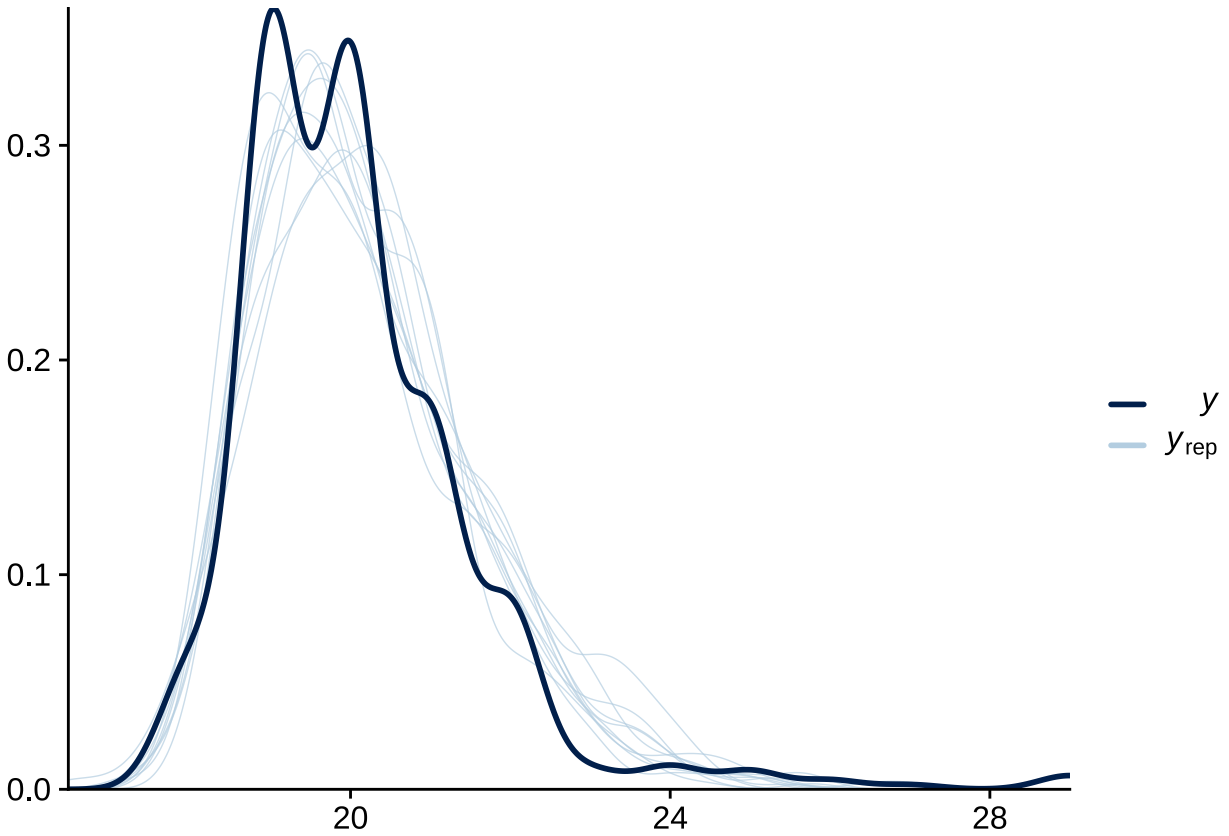
We used a Bayesian regression model to examine the age differences among groups.

```
m1 <- brm(  
  age ~ group,  
  data = quest_param_df,  
  family = skew_normal(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 1 finished in 2.0 seconds.  
## Chain 2 finished in 2.3 seconds.  
## Chain 3 finished in 2.2 seconds.  
## Chain 4 finished in 2.2 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 2.2 seconds.  
## Total execution time: 2.4 seconds.
```

Posterior predictive check

Using 10 posterior draws for ppc type 'dens_overlay' by default.



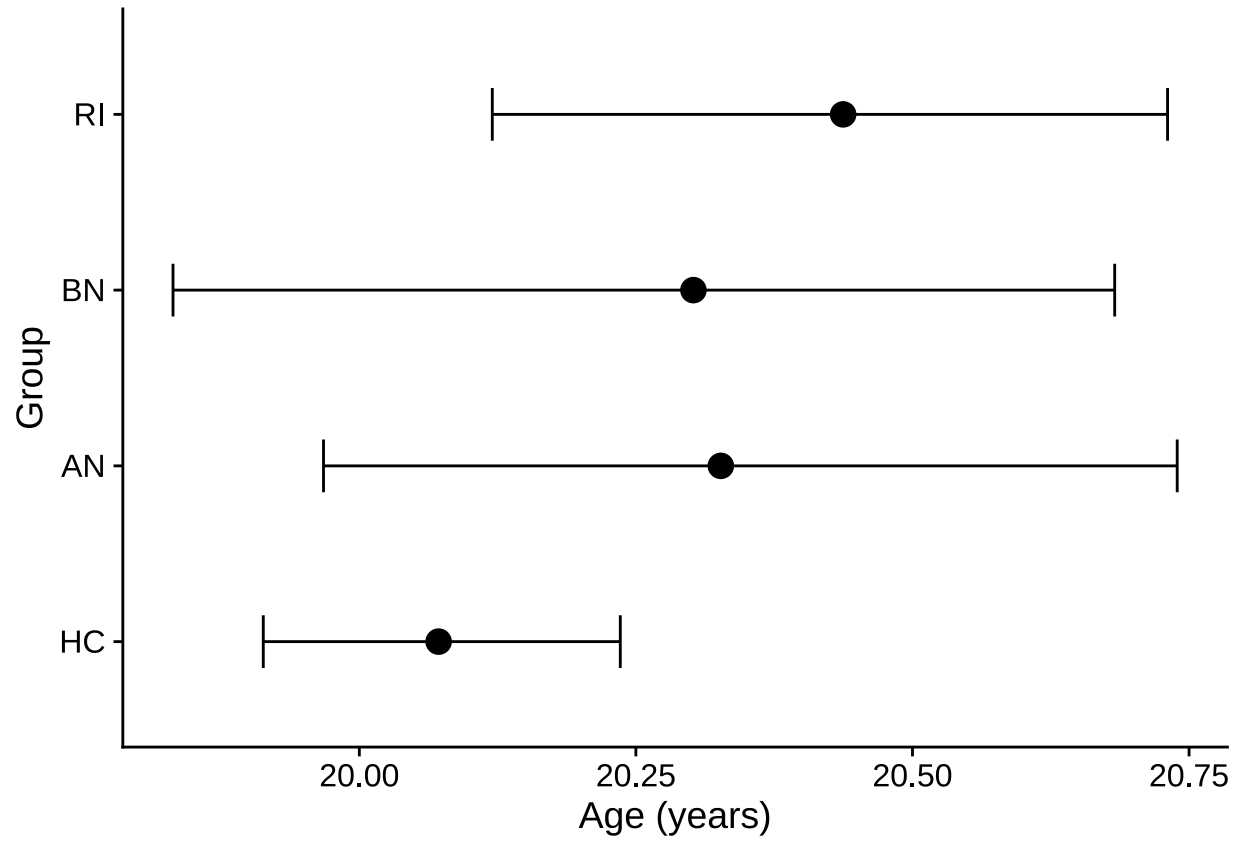
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	20.073	0.082	19.912	20.233
groupAN	0.264	0.234	-0.165	0.747
groupBN	0.219	0.219	-0.236	0.626
groupRI	0.363	0.174	0.015	0.693

The 95% credibility intervals for the difference in age between each group and the HC baseline included zero, indicating that there were no credible differences in age among the groups.

Predicted effect of group on age



Body Mass Index (BMI)

The average Body Mass Index (BMI) values and standard deviations for each group are reported below.

group	BMI	SD
HC	21.62	3.03
AN	16.88	1.55
BN	30.09	5.47
RI	22.41	4.79

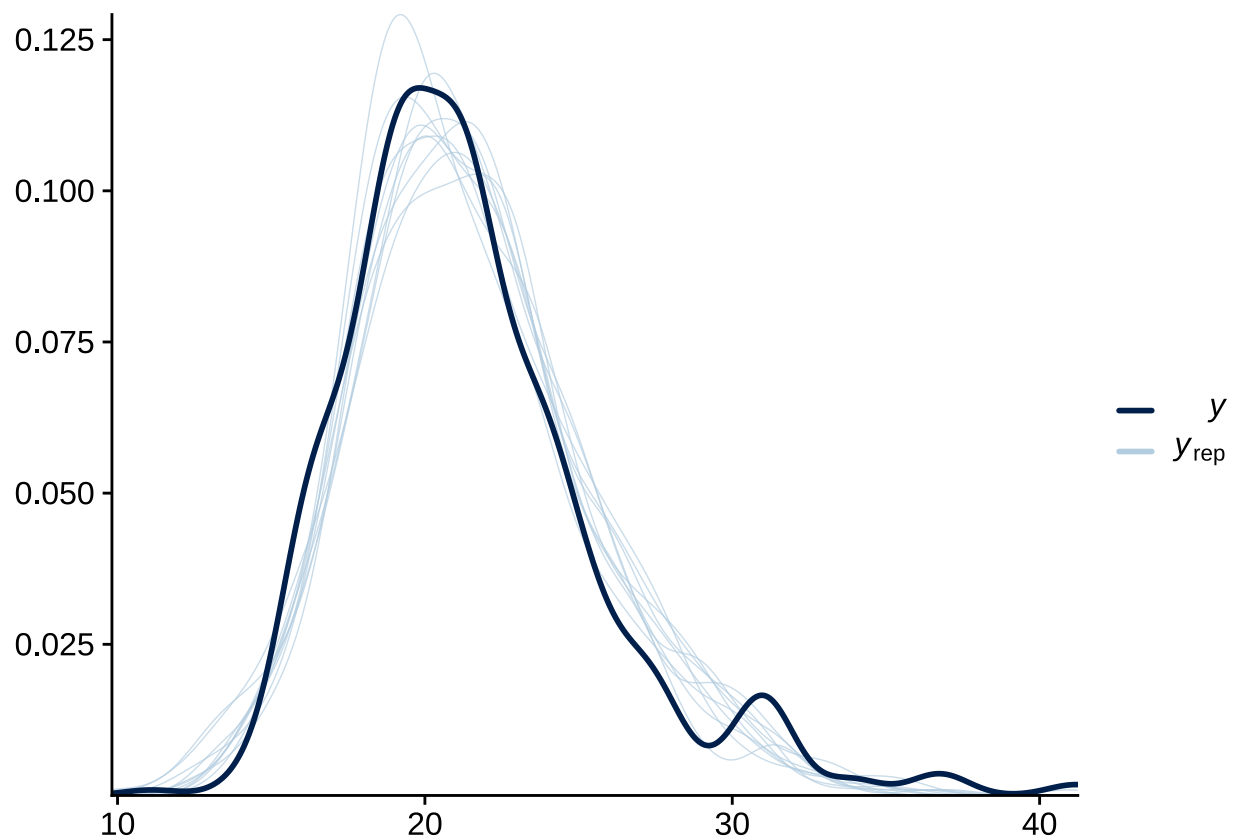
We used a Bayesian regression model to examine the BMI differences among groups.

```
m2 <- brm(  
  bmi ~ group,  
  data = quest_param_df,  
  family = skew_normal(),  
  iter = 4000,  
  cores = 4,  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 parallel chains...  
##  
## Chain 3 finished in 1.9 seconds.  
## Chain 1 finished in 2.0 seconds.  
## Chain 2 finished in 1.9 seconds.  
## Chain 4 finished in 2.0 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.9 seconds.  
## Total execution time: 2.1 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



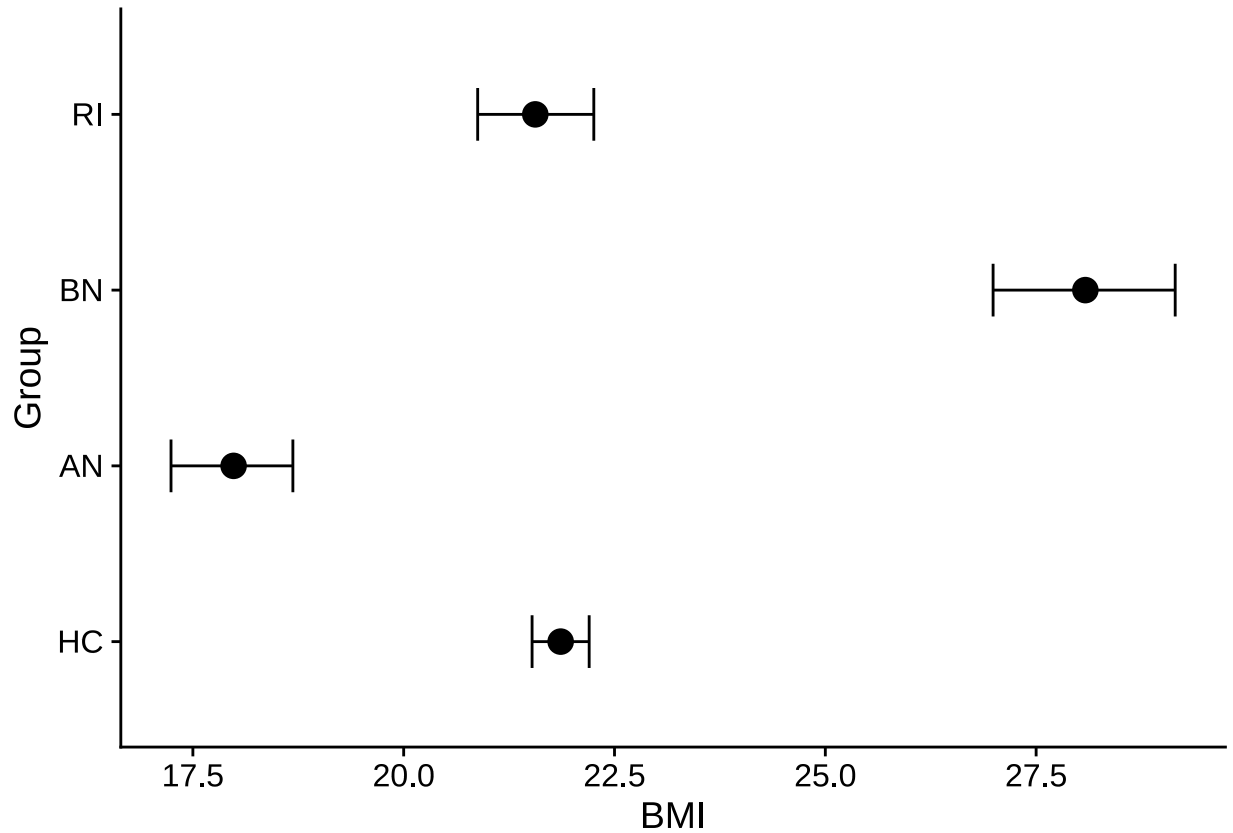
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	21.862	0.173	21.509	22.180
groupAN	-3.885	0.388	-4.655	-3.149
groupBN	6.222	0.579	5.058	7.325
groupRI	-0.299	0.382	-1.041	0.456

The 95% credibility intervals for the difference in age between each group and the HC baseline do not include zero, indicating credible BMI differences between the AN and the HC groups, and between the BN and the HC groups. The at-risk and HC groups did not differ in terms of their average BMI values.

Predicted effect of group on BMI



Rosenberg scale

The average score of the Rosenberg scale as a function of group is shown below.

group	Rosenberg	SD
HC	28.80	5.50
AN	22.42	5.41
BN	20.91	4.91
RI	22.80	5.46

We used a Bayesian regression model to examine the differences in Rosenberg self-esteem scores among groups.

```
m3 <- brm(  
  ros_tot ~ group,  
  data = ros_df,  
  family = skew_normal(),
```



```
iter = 4000,  
cores = parallel::detectCores(),  
backend = "cmdstan",  
refresh = 0,  
silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
```

```
##
```

```
## Chain 1 finished in 1.1 seconds.
```

```
## Chain 3 finished in 1.0 seconds.
```

```
## Chain 4 finished in 1.1 seconds.
```

```
## Chain 2 finished in 1.1 seconds.
```

```
##
```

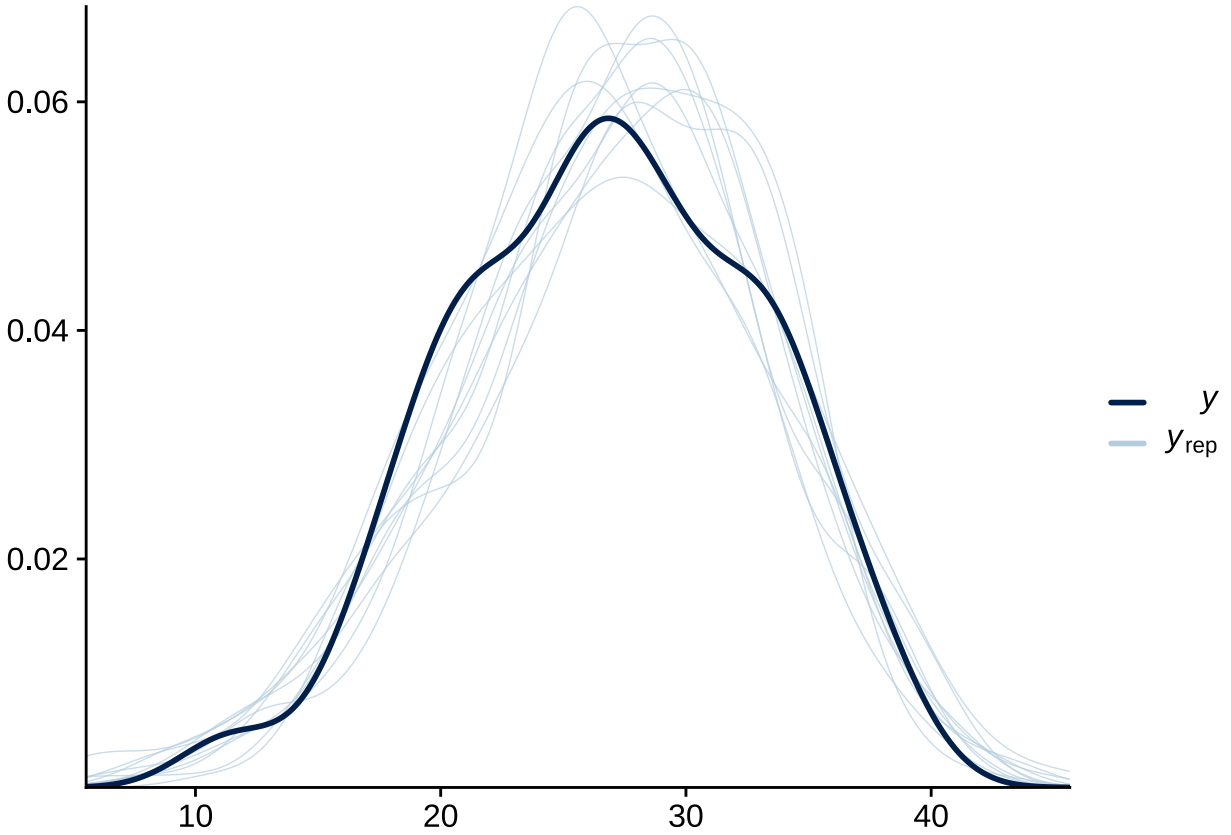
```
## All 4 chains finished successfully.
```

```
## Mean chain execution time: 1.1 seconds.
```

```
## Total execution time: 1.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



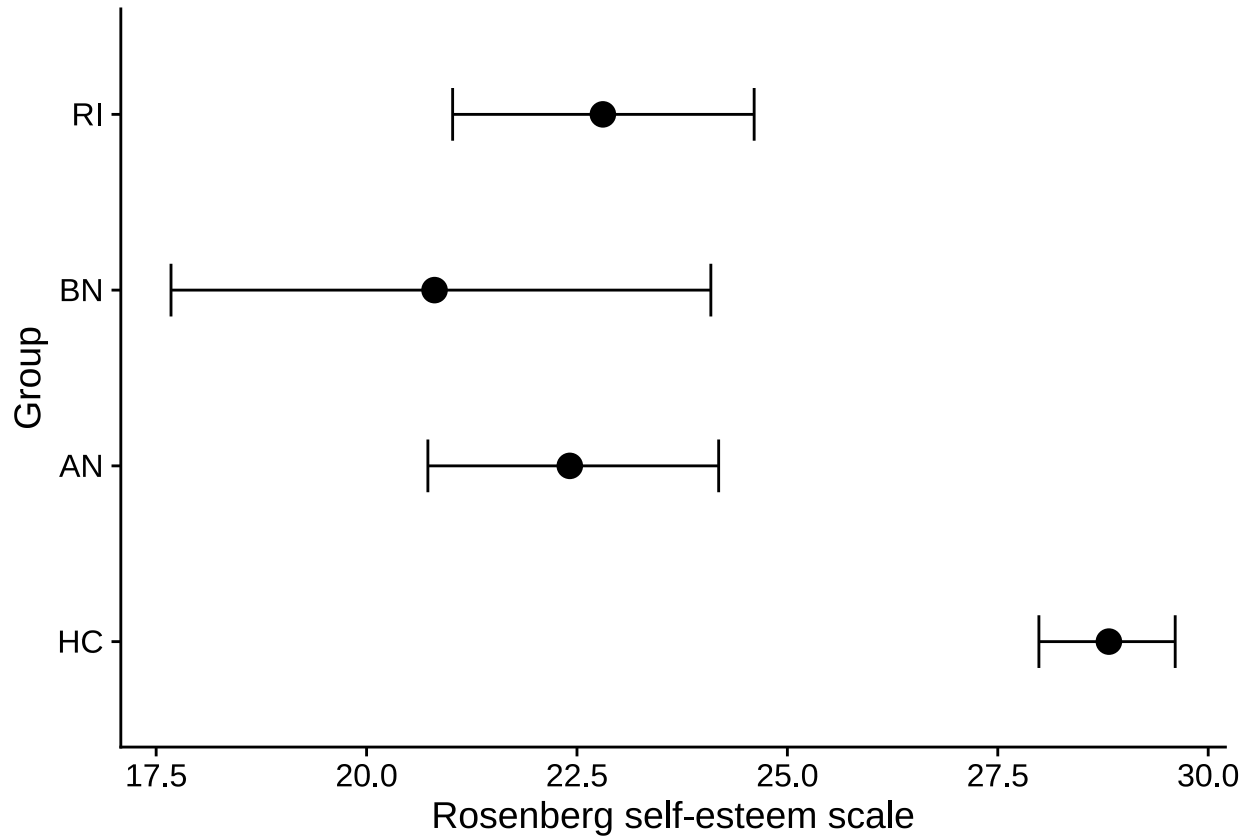
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	28.815	0.411	28.007	29.622
groupAN	-6.391	0.981	-8.244	-4.404
groupBN	-7.991	1.702	-11.353	-4.803
groupRI	-6.002	1.008	-8.020	-4.096

The 95% credibility intervals for the difference in the Rosenberg self-esteem scores between each group and the HC baseline do not include zero, indicating credible differences in the Rosenberg self-esteem scores between the HC and the other groups.

Predicted effect of group on the Rosenberg self-esteem scores



Body Shape Questionnaire-14 (BSQ-14)

The average Body Shape Questionnaire-14 score as a function of group is shown below.

group	BSQ_14	SD
HC	89.90	32.96
AN	145.44	32.58
BN	154.77	33.60
RI	152.79	35.07

We used a Bayesian regression model to examine the BSQ-14 differences among groups.

```
m4 <- brm(  
  ros_tot ~ group,  
  data = ros_df,  
  family = skew_normal(),  
  iter = 4000,
```

```
cores = parallel::detectCores(),  
backend = "cmdstan",  
refresh = 0,  
silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
```

```
##
```

```
## Chain 2 finished in 1.0 seconds.
```

```
## Chain 1 finished in 1.1 seconds.
```

```
## Chain 3 finished in 1.1 seconds.
```

```
## Chain 4 finished in 1.1 seconds.
```

```
##
```

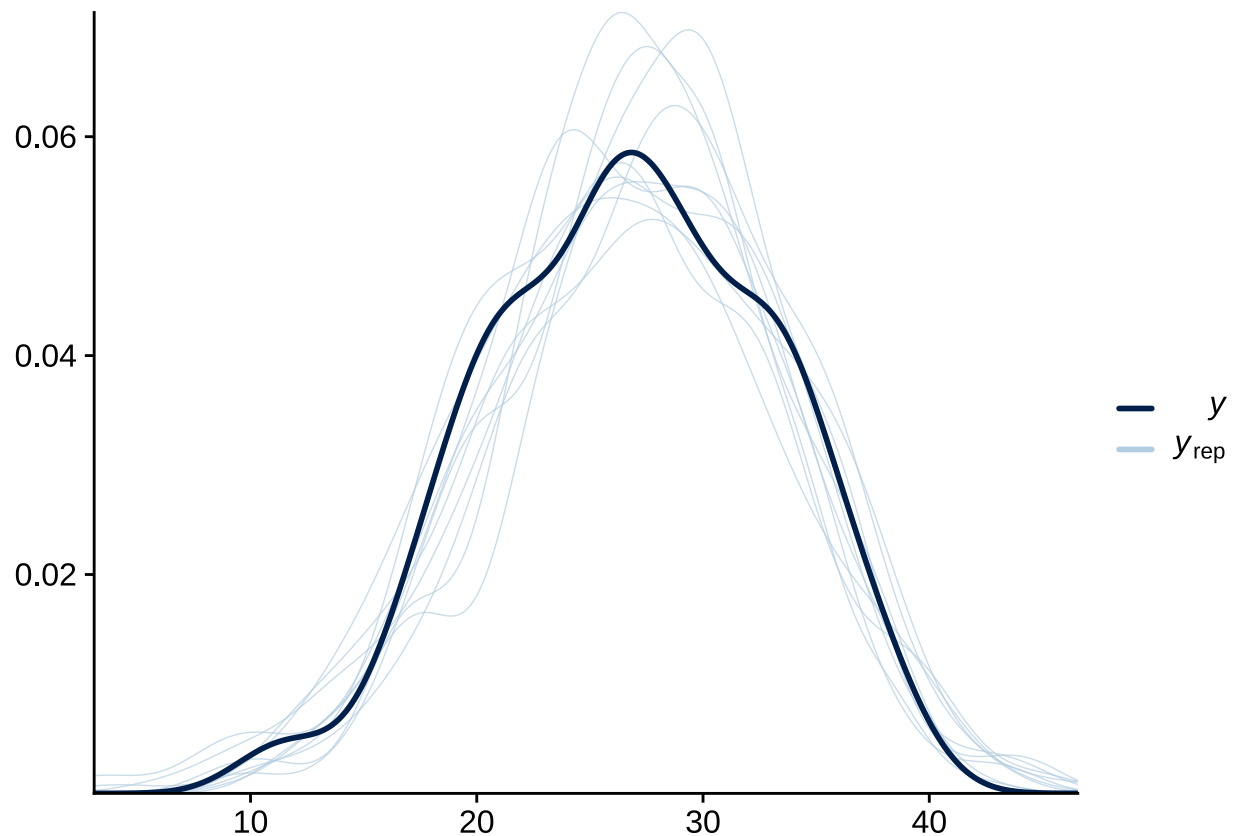
```
## All 4 chains finished successfully.
```

```
## Mean chain execution time: 1.1 seconds.
```

```
## Total execution time: 1.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



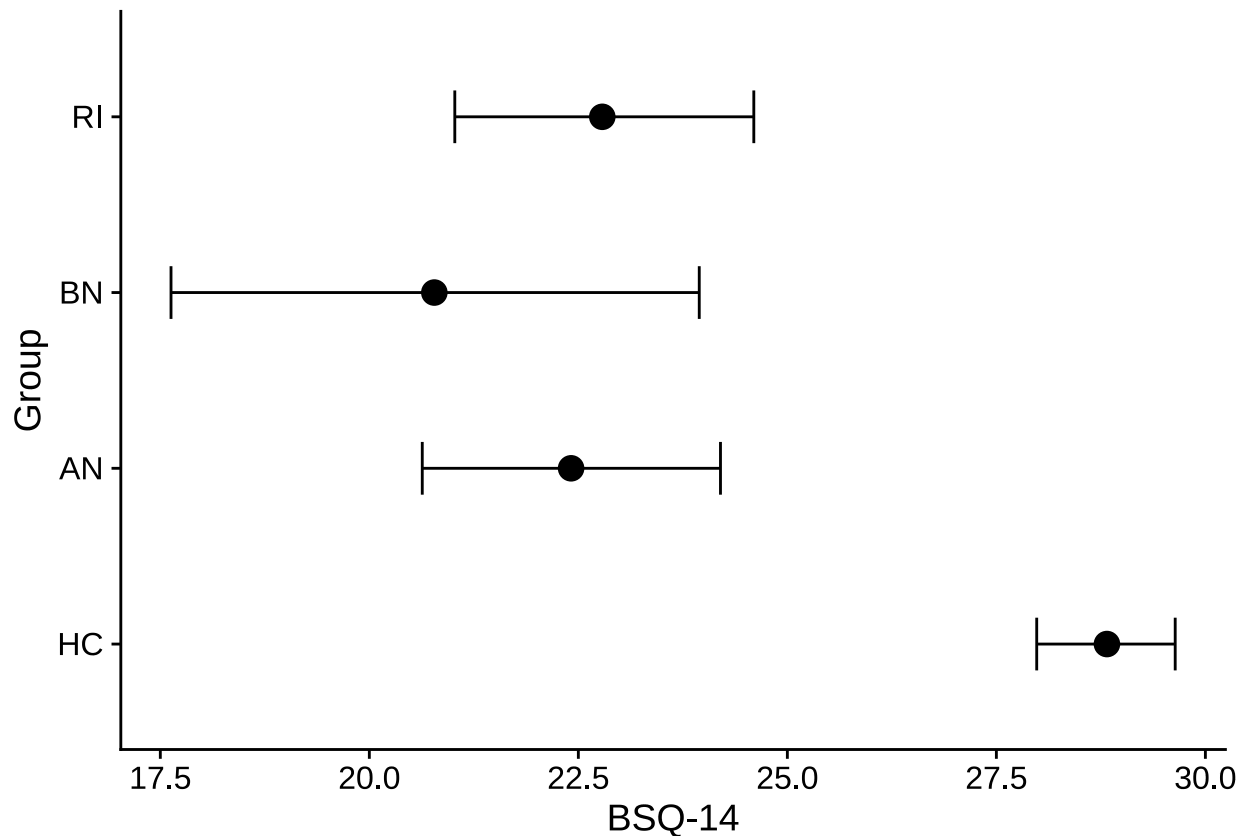
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	28.817	0.414	28.010	29.662
groupAN	-6.410	1.002	-8.438	-4.535
groupBN	-8.029	1.675	-11.209	-4.721
groupRI	-6.021	0.990	-7.948	-4.068

The 95% credibility intervals for the difference in the BSQ-14 scores between each group and the HC baseline do not include zero, indicating credible differences in the BSQ-14 scores between the HC and the other groups.

Predicted effect of group on the BSQ-14 scores



Depression Anxiety Stress Scale-21 (DASS-21)

Average values of the scores on the Stress, Anxiety, and Depression of the DASS-21 scale are shown below.

group	Stress	Anxiety	Depression
HC	9.17	5.30	6.78
AN	13.25	8.56	10.86
BN	10.73	6.73	11.91
RI	12.66	7.69	11.37

Standard deviations of the scores on the Stress, Anxiety, and Depression sub-scales are shown below.

group	SD_stress	SD_anxiety	SD_depression
HC	9.17	5.30	6.78
AN	13.25	8.56	10.86
BN	10.73	6.73	11.91
RI	12.66	7.69	11.37

Stress

We used a Bayesian regression model to examine the DASS-21 Stress differences among groups.

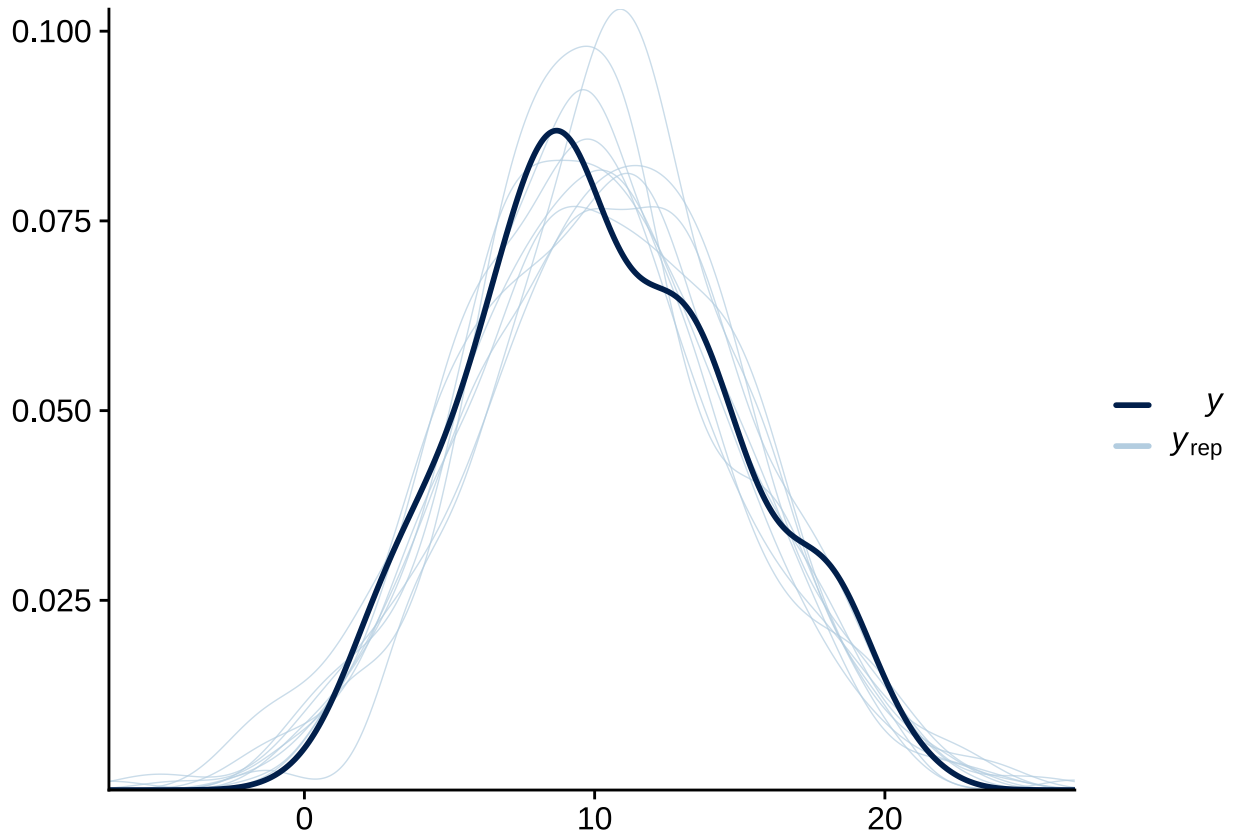
```
m5_s <- brm(  
  dass21_s ~ group,  
  data = dass_df,  
  family = gaussian(),  
  iter = 4000,  
  cores = 4,  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 parallel chains...  
##  
## Chain 1 finished in 0.1 seconds.  
## Chain 2 finished in 0.1 seconds.  
## Chain 3 finished in 0.1 seconds.  
## Chain 4 finished in 0.1 seconds.  
##
```

```
## All 4 chains finished successfully.  
## Mean chain execution time: 0.1 seconds.  
## Total execution time: 0.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



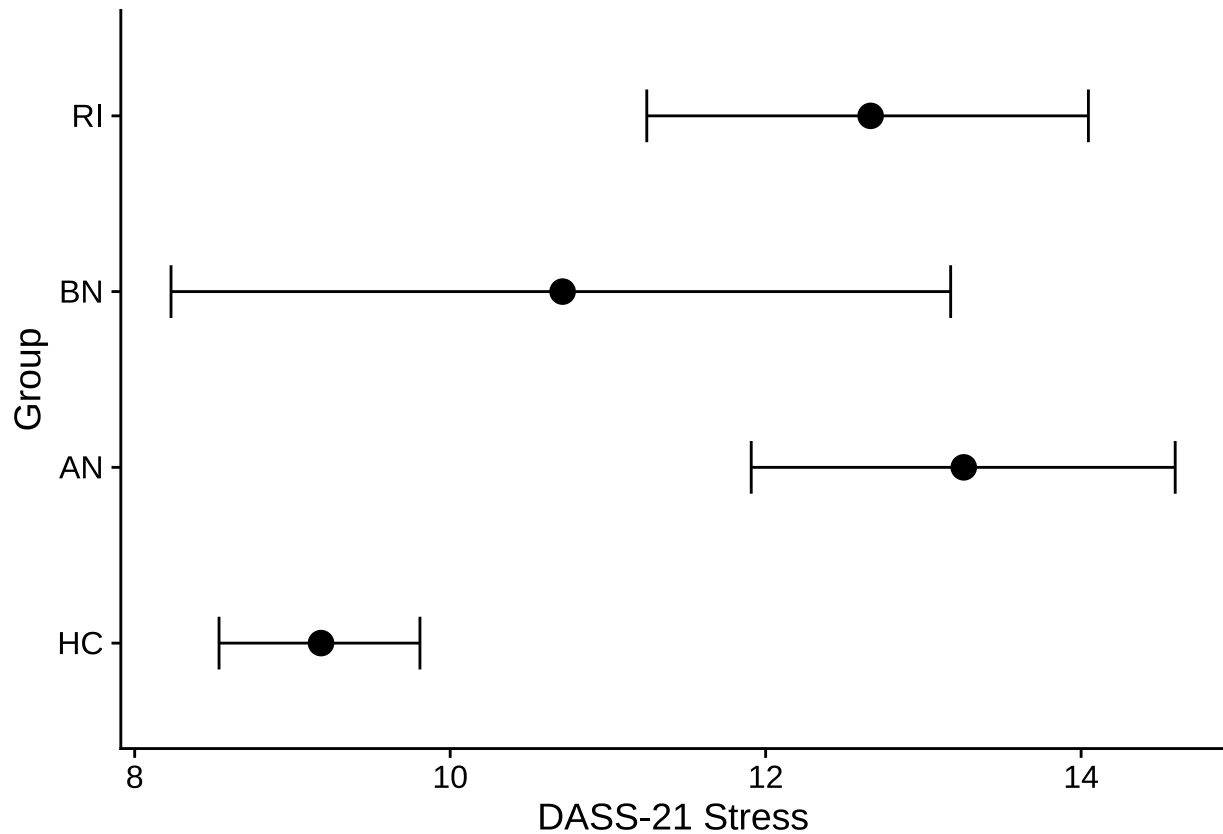
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	9.176	0.326	8.546	9.814
groupAN	4.082	0.764	2.591	5.582
groupBN	1.553	1.311	-0.961	4.119
groupRI	3.484	0.783	2.013	5.070

The 95% credibility intervals for the difference in the DASS-21 Stress scores between the AN and RI groups, on the one side, and the HC baseline, on the other, do not include zero, indicating credible differences in the DASS-21 Stress between the HC and the other two groups. We found no credible difference in the average DASS-21 Stress score between the HC and BC groups.

Predicted effect of group on the DASS-21 Stress scores



Anxiety

We used a Bayesian regression model to examine the DASS-21 Anxiety differences among groups.

```
m5_a <- brm(  
  dass21_a ~ group,  
  data = dass_df,  
  family = skew_normal(),  
  iter = 4000,  
  cores = 4,  
  backend = "cmdstan",
```

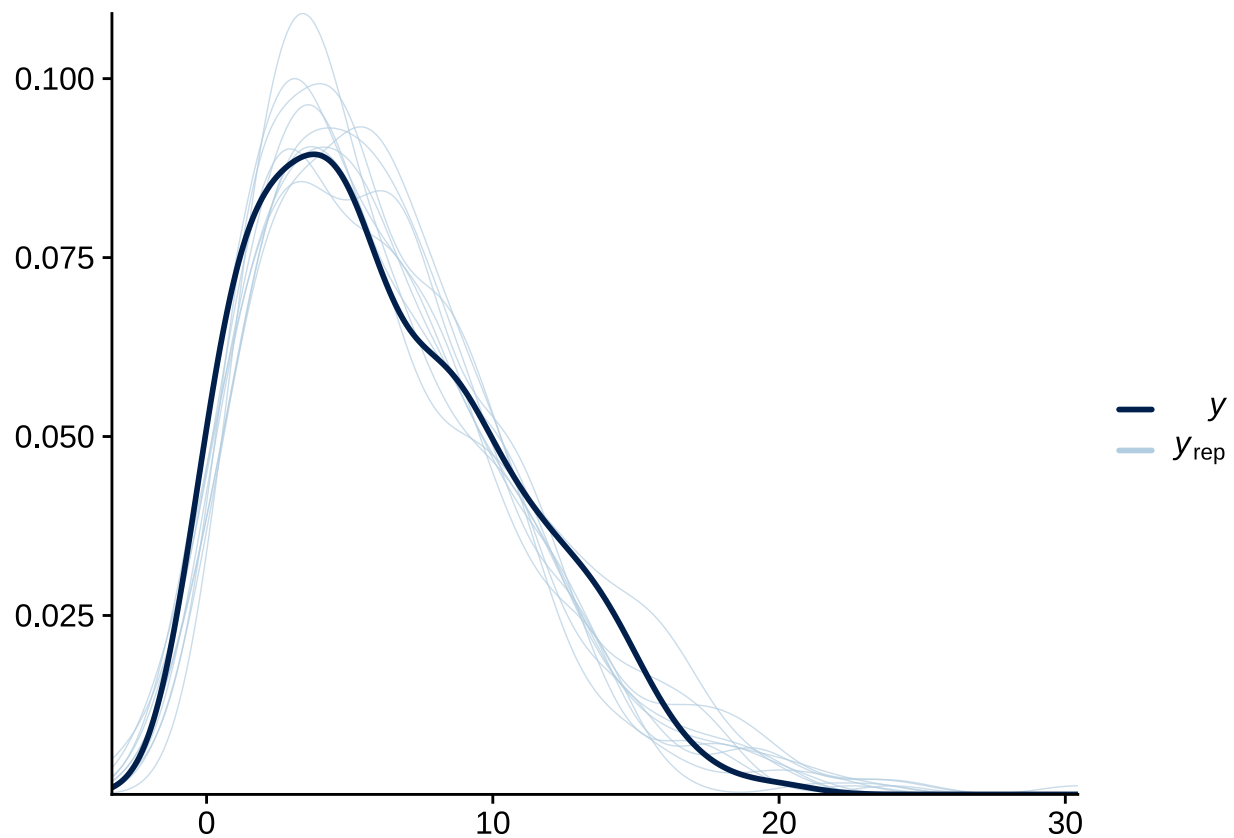


```
refresh = 0,  
silent = TRUE  
)
```

```
## Running MCMC with 4 parallel chains...  
##  
## Chain 2 finished in 1.5 seconds.  
## Chain 4 finished in 1.6 seconds.  
## Chain 3 finished in 1.7 seconds.  
## Chain 1 finished in 1.8 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.6 seconds.  
## Total execution time: 1.9 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



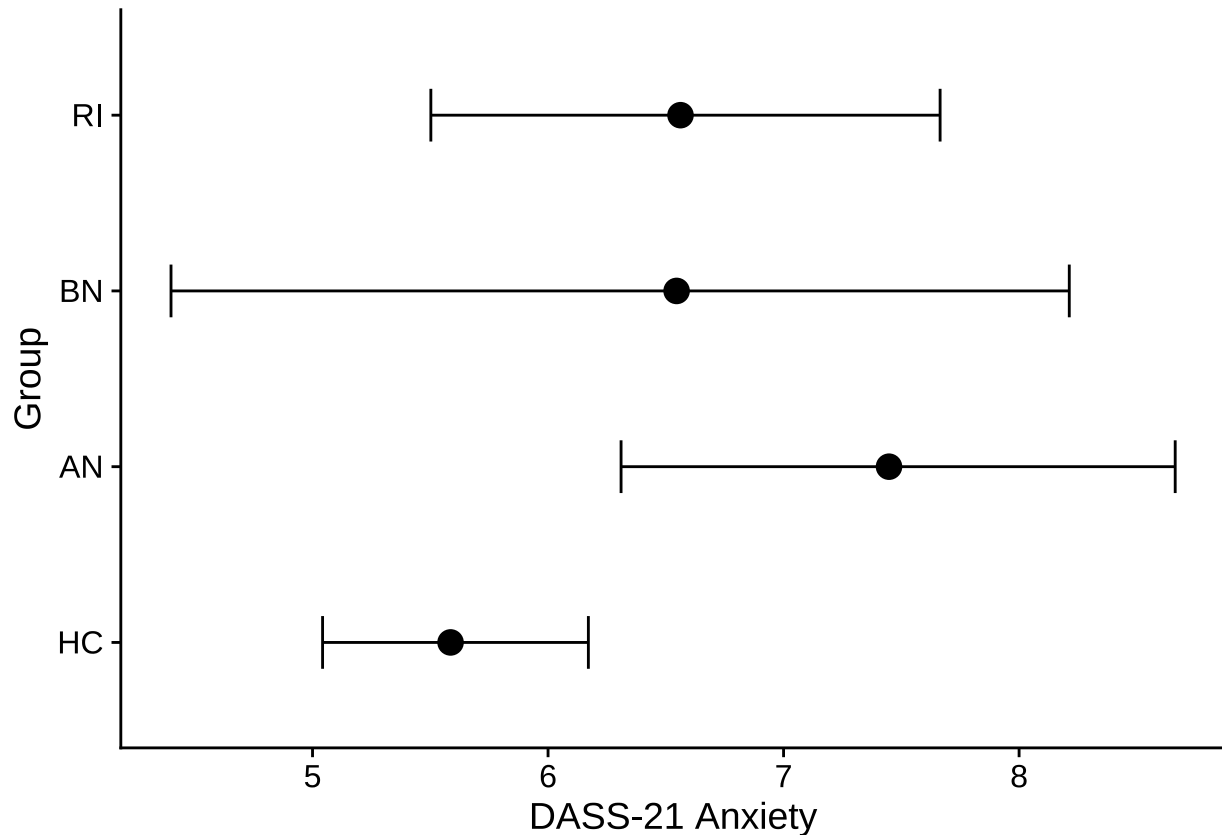
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	5.591	0.292	5.044	6.172
groupAN	1.864	0.629	0.582	3.079
groupBN	0.893	0.980	-1.113	2.718
groupRI	0.981	0.565	-0.133	2.127

The 95% credibility intervals for the difference in the DASS-21 Anxiety scores between the AN and the HC baseline do not include zero, indicating credible differences in the DASS-21 Anxiety between the two groups. We found no credible difference in the average DASS-21 Anxiety score between the HC and BC groups, nor between the HC and the RI groups.

Predicted effect of group on the DASS-21 Anxiety scores



Depression

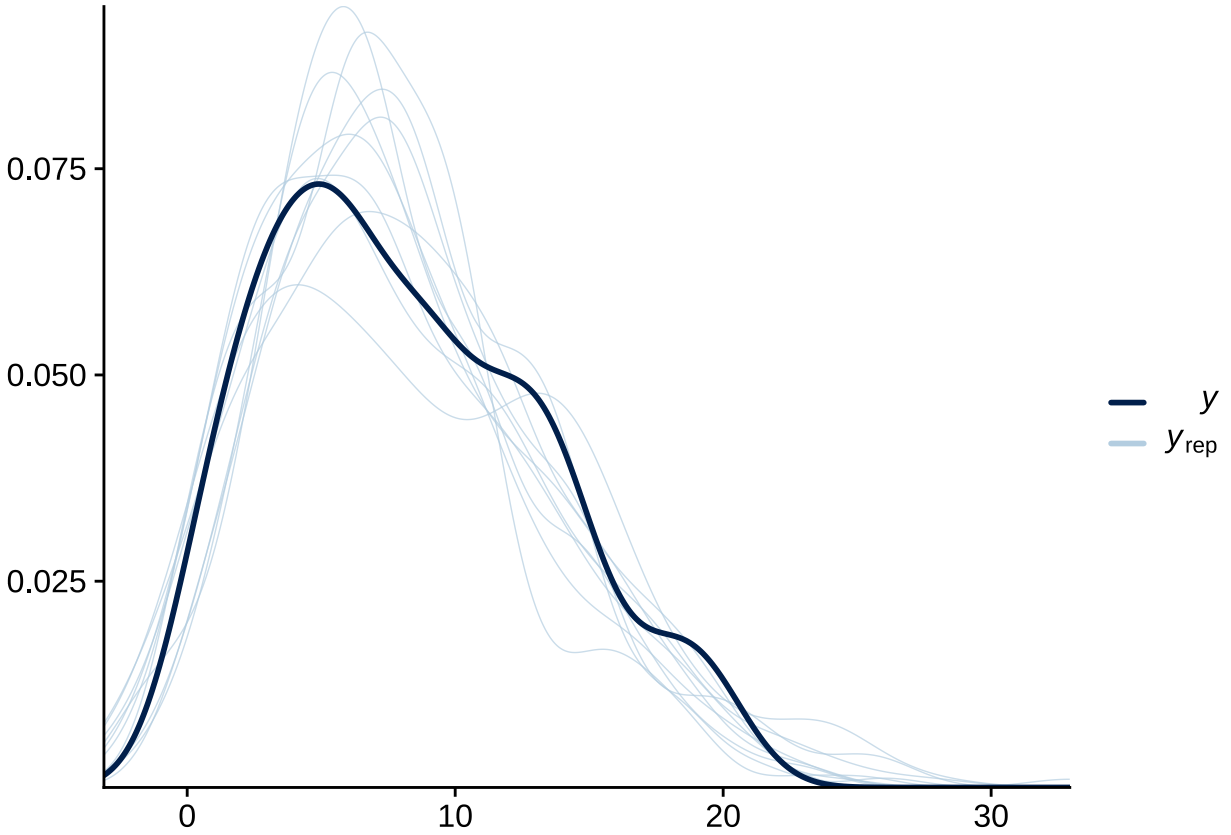
We used a Bayesian regression model to examine the DASS-21 Depression differences among groups.

```
m5_d <- brm(  
  dass21_d ~ group,  
  data = dass_df,  
  family = skew_normal(),  
  iter = 4000,  
  cores = 4,  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 parallel chains...  
##  
## Chain 2 finished in 1.5 seconds.  
## Chain 3 finished in 1.5 seconds.  
## Chain 4 finished in 1.4 seconds.  
## Chain 1 finished in 1.5 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.5 seconds.  
## Total execution time: 1.6 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



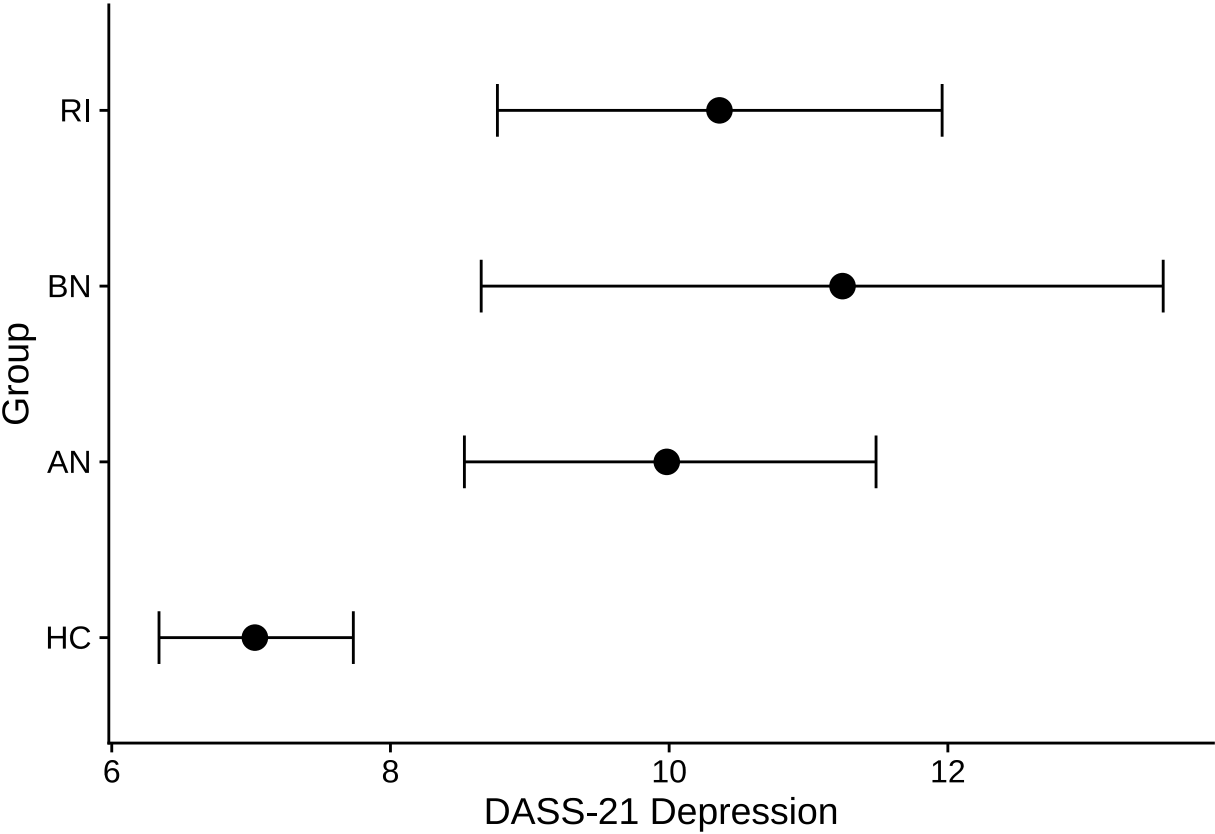
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	7.027	0.356	6.338	7.729
groupAN	2.962	0.820	1.325	4.545
groupBN	4.183	1.266	1.632	6.674
groupRI	3.337	0.893	1.498	4.968

The 95% credibility intervals for the difference in the DASS-21 Depression scores between the AN, BN, and RI groups, on the one side, and the HC baseline, on the other, do not include zero, indicating credible differences in the DASS-21 Anxiety between the baseline group and the other groups.

Predicted effect of group on the DASS-21 Depression scores



Social Interaction Anxiety Scale (SIAS)

group	SIAS	SD
HC	28.03	13.07
AN	37.31	15.44
BN	34.64	15.19
RI	37.31	17.09

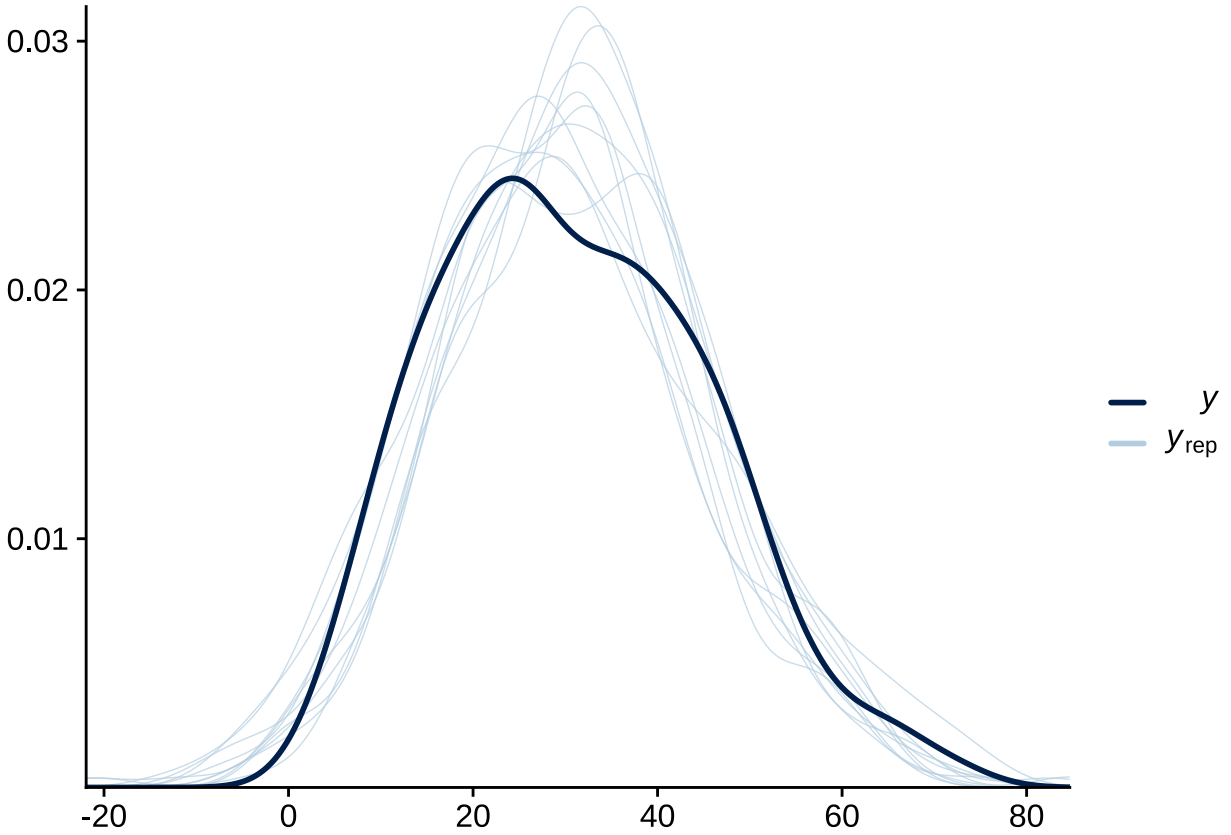
We used a Bayesian regression model to examine the SIAS score differences among groups.

```
m6 <- brm(  
  sias_tot ~ group,  
  data = sias_df,  
  family = skew_normal(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 1 finished in 1.5 seconds.  
## Chain 2 finished in 1.6 seconds.  
## Chain 3 finished in 1.7 seconds.  
## Chain 4 finished in 1.6 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.6 seconds.  
## Total execution time: 1.8 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



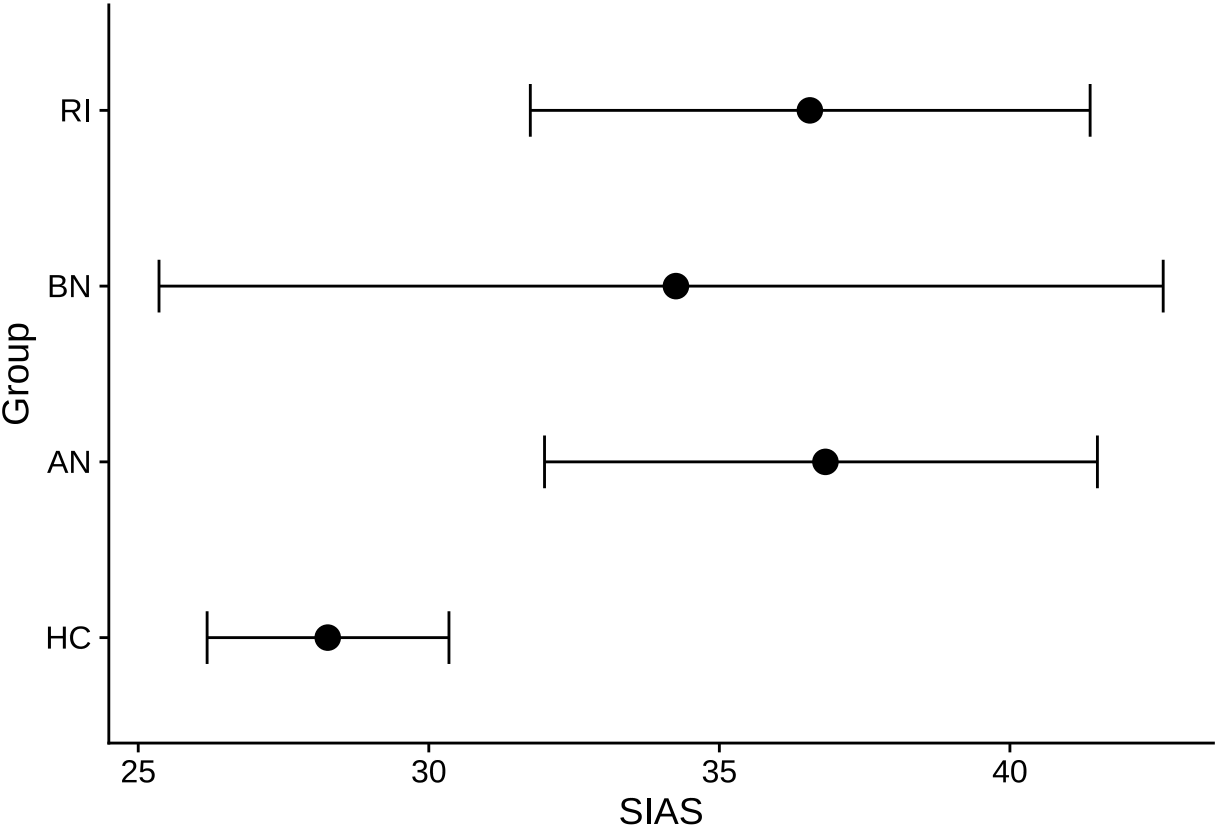
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	28.260	1.067	26.137	30.276
groupAN	8.549	2.660	3.255	13.608
groupBN	5.890	4.587	-2.925	14.882
groupRI	8.291	2.742	2.982	13.685

The 95% credibility intervals for the difference in the SIAS scores between the AN and RI groups, on the one side, and the HC baseline, on the other do not include zero, indicating credible differences in the SIAS scores between the HC and these two groups. We found no credible difference in the average SIAS scores between the BN and the HC groups.

Predicted effect of group on the SIAS scores



Multidimensional Perfectionism Scale (MPS)

The average scores on the sub-scales of Concerns over Mistakes and Doubts (CMD), Parental Expectations and Criticism (PEC), Personal Standards (PS), and Organization (O) of the MPS as a function of group are shown below.

group	MPS_cmd	MPS_ps	MPS_pepc	MPS_or
HC	38.28	22.01	21.20	22.23
AN	45.19	25.58	21.72	23.47
BN	44.91	23.55	21.36	23.00
RI	48.74	25.89	25.69	22.80

The standard deviations on the sub-scales of Concerns over Mistakes and Doubts (CMD), Parental Expectations and Criticism (PEC), Personal Standards (PS), and Organization (O) of the MPS as a function of group are shown below.

group	SD_cmd	SD_ps	SD_pepc	SD_or
HC	8.66	4.97	7.09	4.73
AN	8.43	5.52	8.00	5.63
BN	9.43	5.39	5.35	5.08
RI	8.66	5.89	7.61	5.76

Concerns over Mistakes and Doubts

We used a Bayesian regression model to examine the MPS CMD score differences among groups.

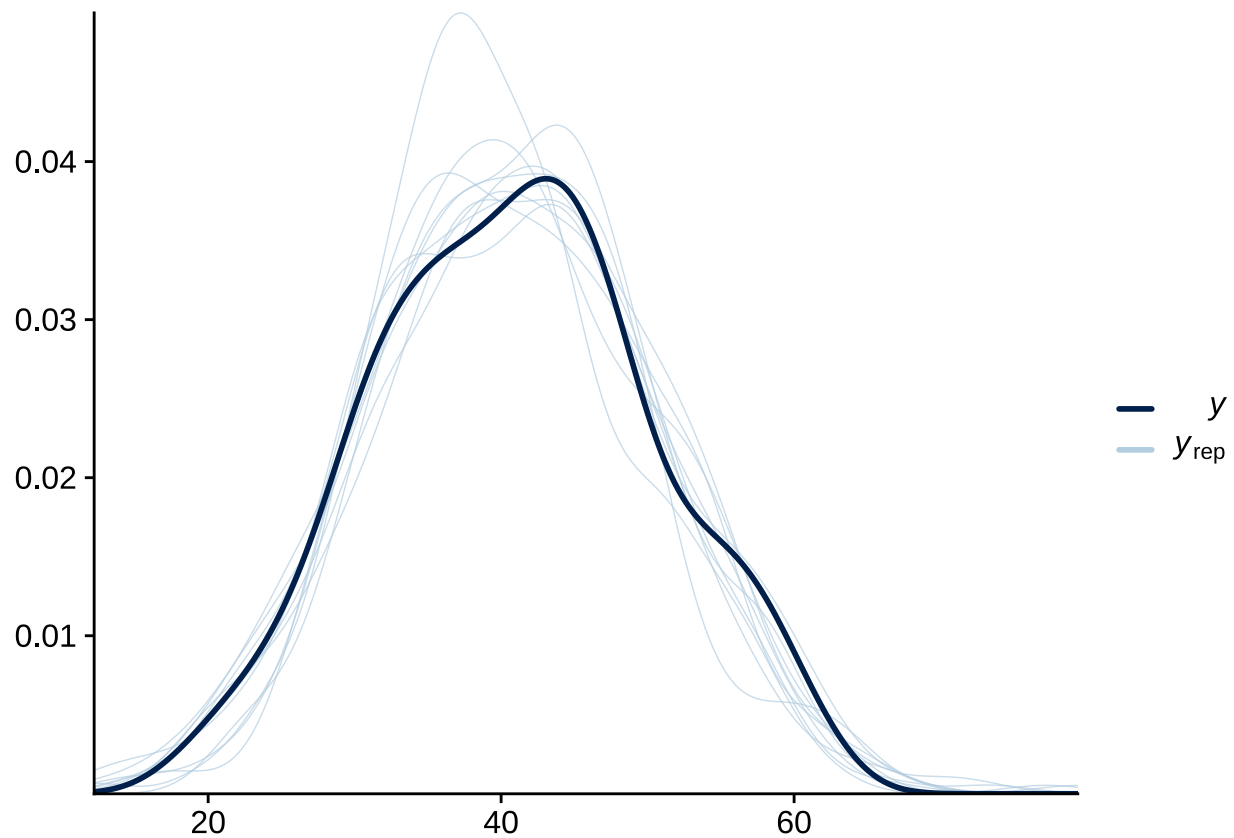
```
m7_cmd <- brm(  
  mps_cmd ~ group,  
  data = mps_df,  
  family = gaussian(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 1 finished in 0.1 seconds.  
## Chain 2 finished in 0.1 seconds.  
## Chain 3 finished in 0.1 seconds.
```

```
## Chain 4 finished in 0.1 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 0.1 seconds.  
## Total execution time: 0.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



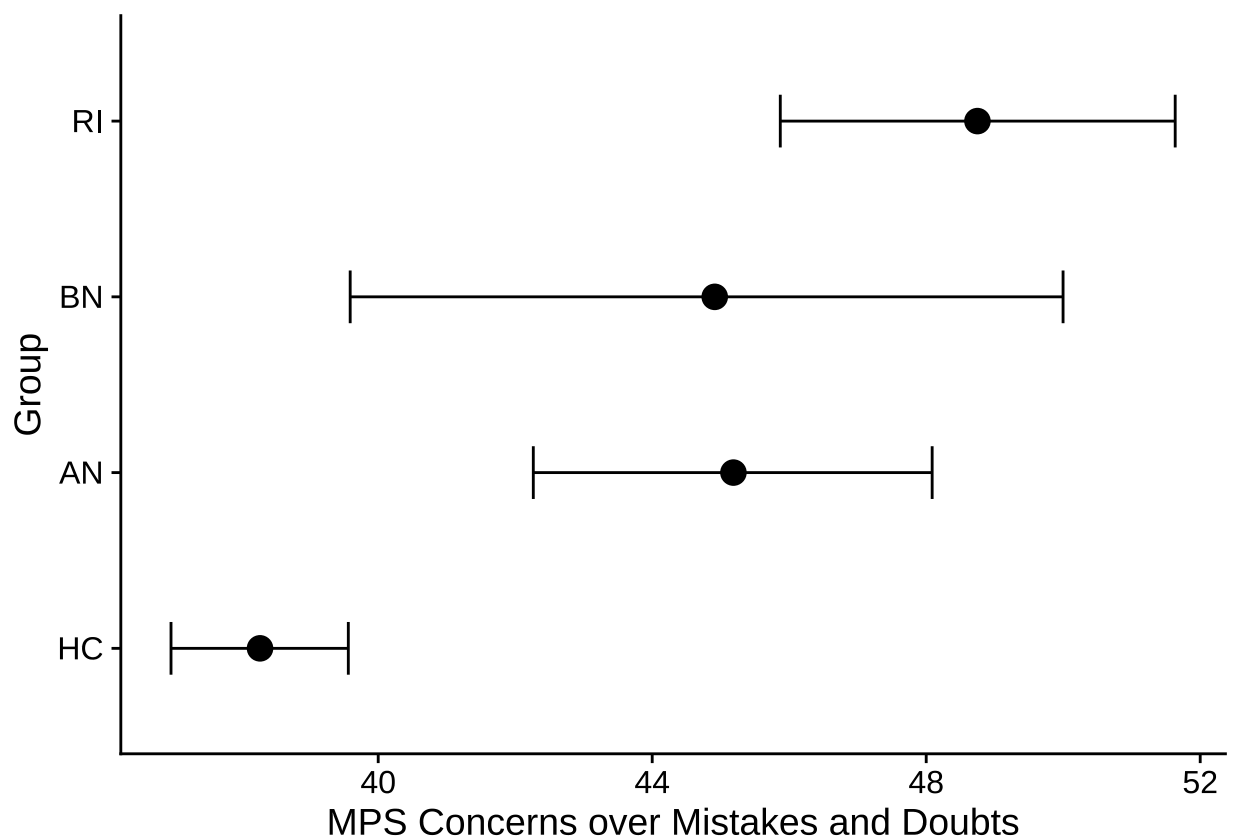
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	38.279	0.654	36.996	39.579
groupAN	6.908	1.603	3.917	10.130
groupBN	6.633	2.728	1.360	11.986
groupRI	10.467	1.625	7.179	13.529

The 95% credibility intervals for the difference in the SIAS scores between the HC and the other groups do not include zero, indicating credible differences in the MPS-CMD scores between the HC and the other groups.

Predicted effect of group on the MPS Concerns over Mistakes and Doubts



Parental Expectations and Criticism

We used a Bayesian regression model to examine the MPS PEC score differences among groups.

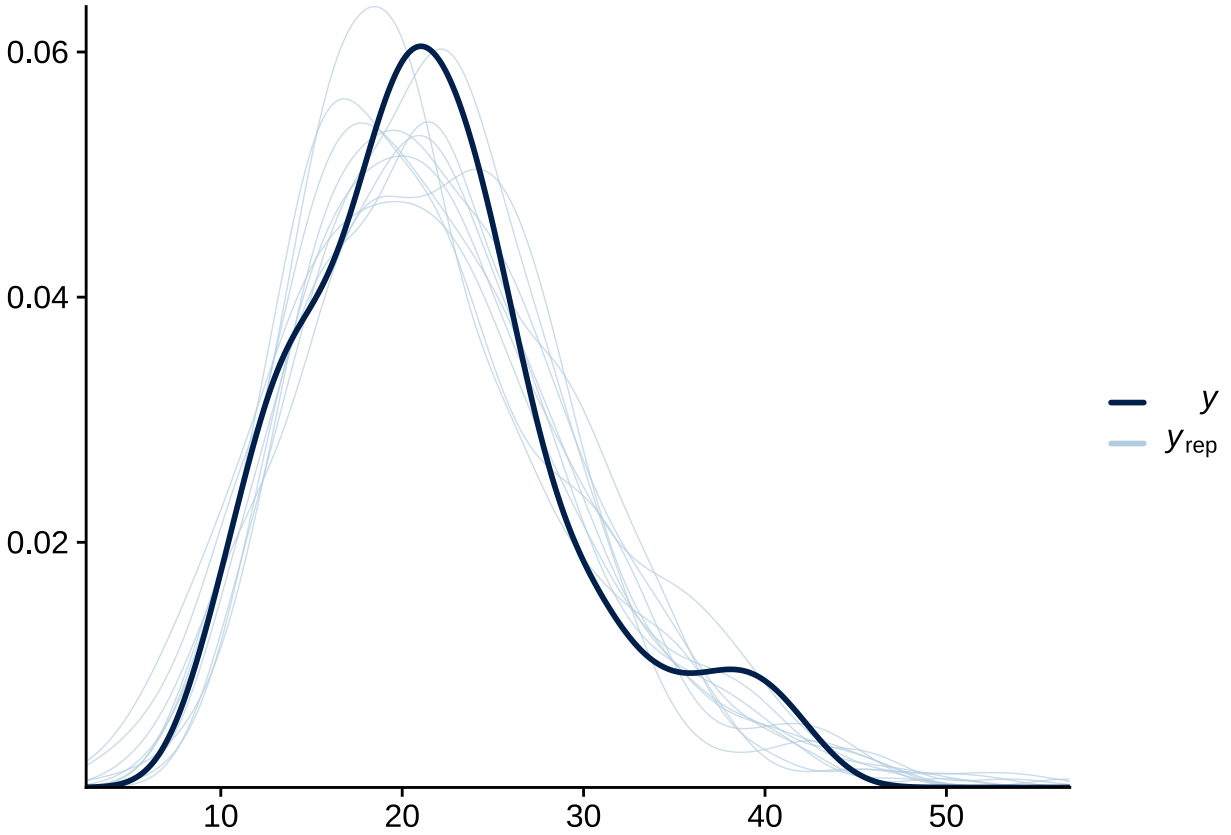
```
m7_pec <- brm(
  mps_pepc ~ group,
```

```
data = mps_df,  
family = skew_normal(),  
iter = 4000,  
cores = parallel::detectCores(),  
backend = "cmdstan",  
refresh = 0,  
silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 1 finished in 1.1 seconds.  
## Chain 2 finished in 1.1 seconds.  
## Chain 3 finished in 1.1 seconds.  
## Chain 4 finished in 1.2 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.1 seconds.  
## Total execution time: 1.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



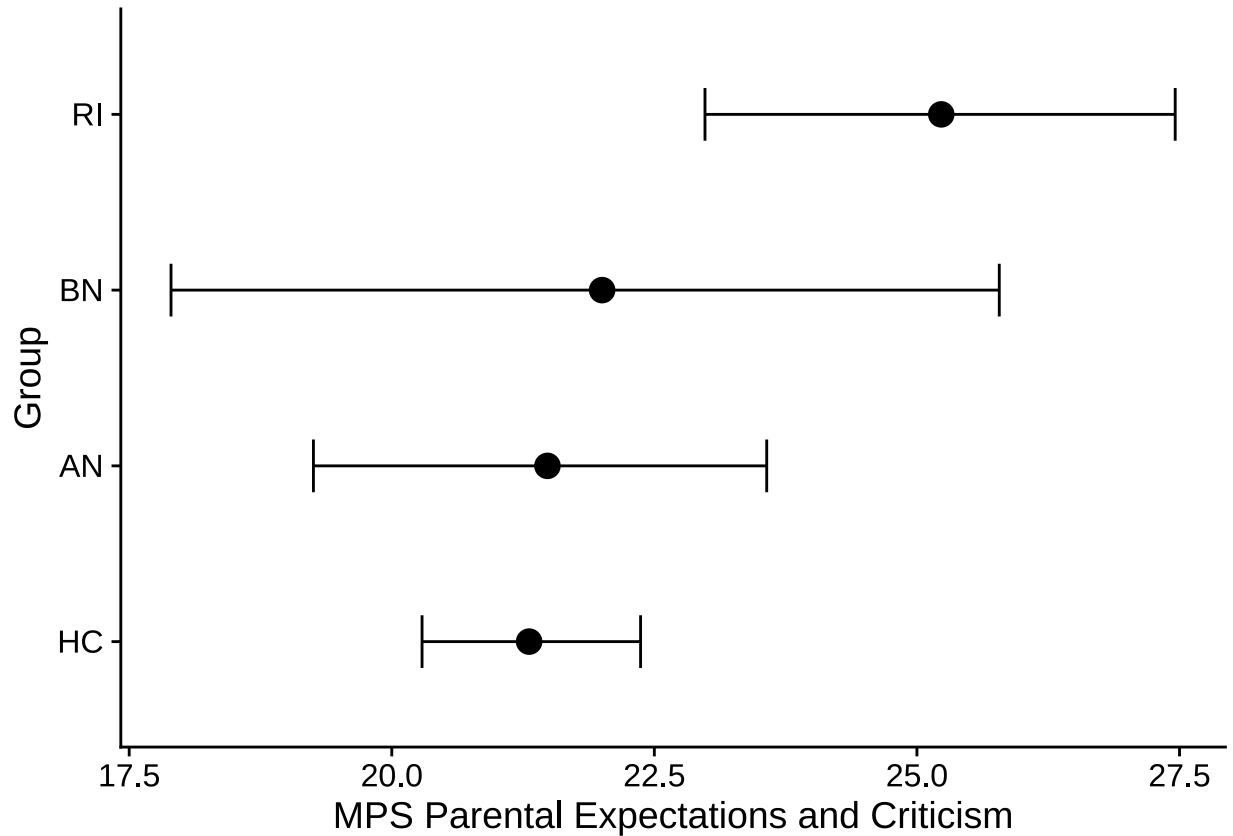
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	21.311	0.531	20.324	22.399
groupAN	0.155	1.176	-2.191	2.456
groupBN	0.666	2.066	-3.226	4.836
groupRI	3.925	1.211	1.675	6.431

The 95% credibility intervals for the difference in the MPS-PEC scores between the HC and the RI group do not include zero, indicating credible differences in Parental Expectations and Criticism between these two groups. We found no credible difference in MPS-PEC between the HC group, on the one side, and the AN and BN groups, on the other.

Predicted effect of group on the MPS Parental Expectations and Criticism



Personal Standards

We used a Bayesian regression model to examine the MPS PS score differences among groups.

```
m7_ps <- brm(  
  mps_ps ~ group,  
  data = mps_df,  
  family = gaussian(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
```

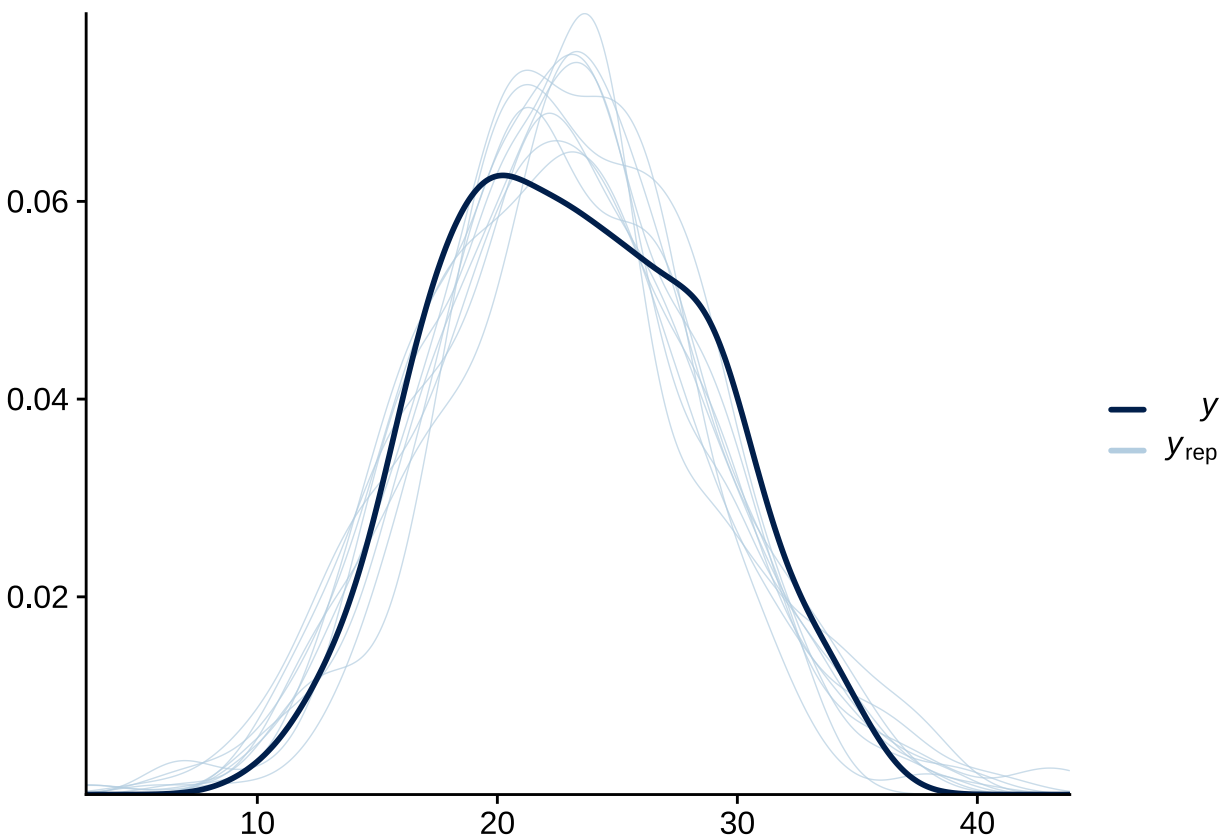
```
##
```

```
## Chain 1 finished in 0.1 seconds.
```

```
## Chain 2 finished in 0.1 seconds.  
## Chain 3 finished in 0.1 seconds.  
## Chain 4 finished in 0.1 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 0.1 seconds.  
## Total execution time: 0.2 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



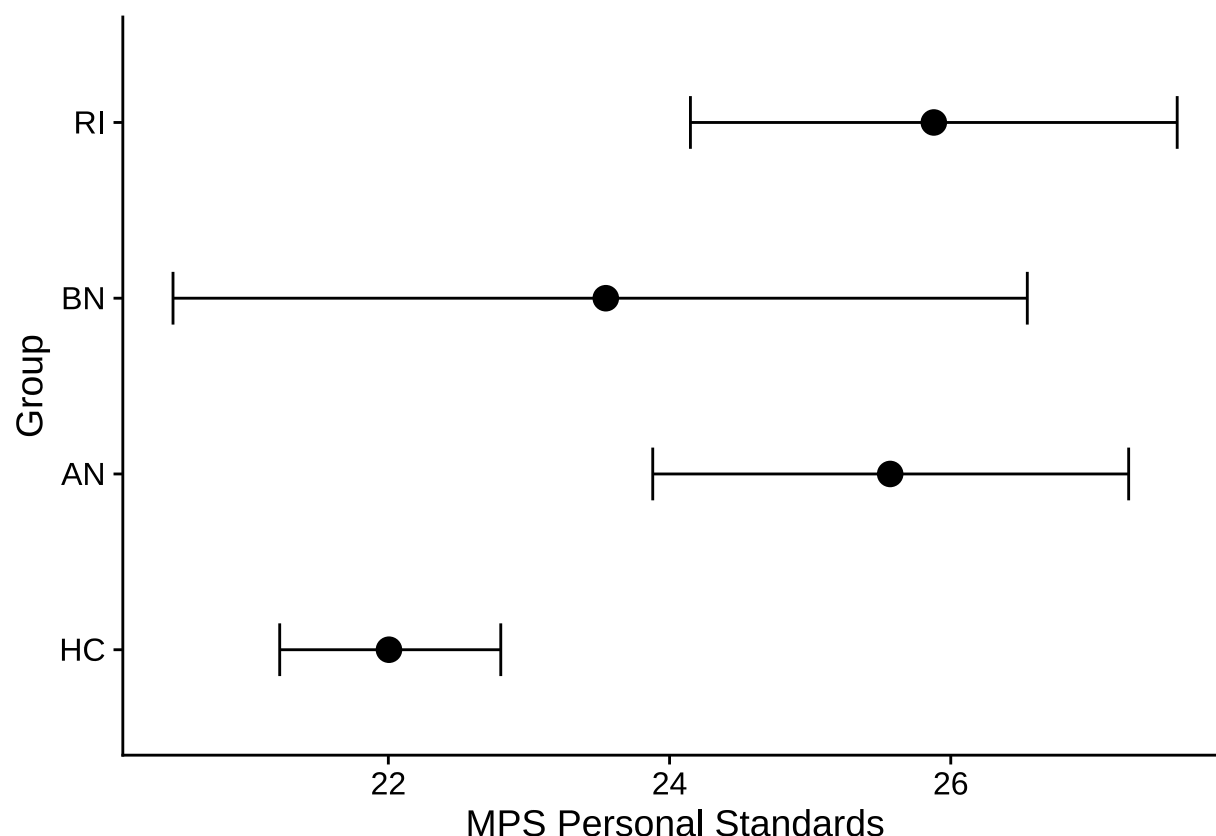
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	22.010	0.399	21.243	22.810
groupAN	3.566	0.960	1.642	5.435
groupBN	1.529	1.624	-1.583	4.682
groupRI	3.869	0.969	2.012	5.764

The 95% credibility intervals for the difference in the MPS-PS scores between the HC group, on the one side, and the AN and RI groups, on the other, do not include zero, indicating credible differences in Personal standards between these groups. We found no credible difference in MPS-PS between the HC group and the BN groups.

Predicted effect of group on the MPS Personal Standards scores



Organization

We used a Bayesian regression model to examine the MPS-O score differences among groups.

```
m7_or <- brm(
  mps_or ~ group,
```

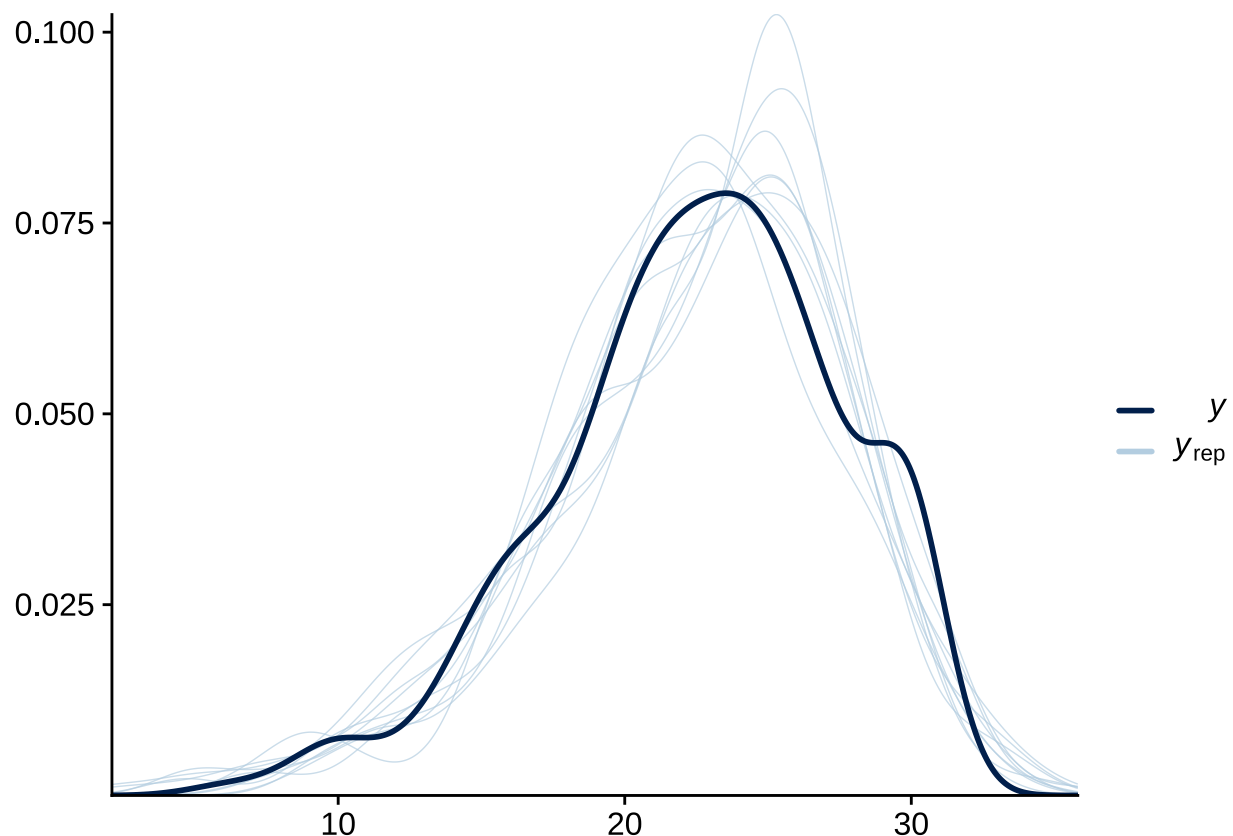


```
data = mps_df,  
family = skew_normal(),  
iter = 4000,  
cores = parallel::detectCores(),  
backend = "cmdstan",  
refresh = 0,  
silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 3 finished in 1.2 seconds.  
## Chain 1 finished in 1.3 seconds.  
## Chain 2 finished in 1.3 seconds.  
## Chain 4 finished in 1.3 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 1.3 seconds.  
## Total execution time: 1.4 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



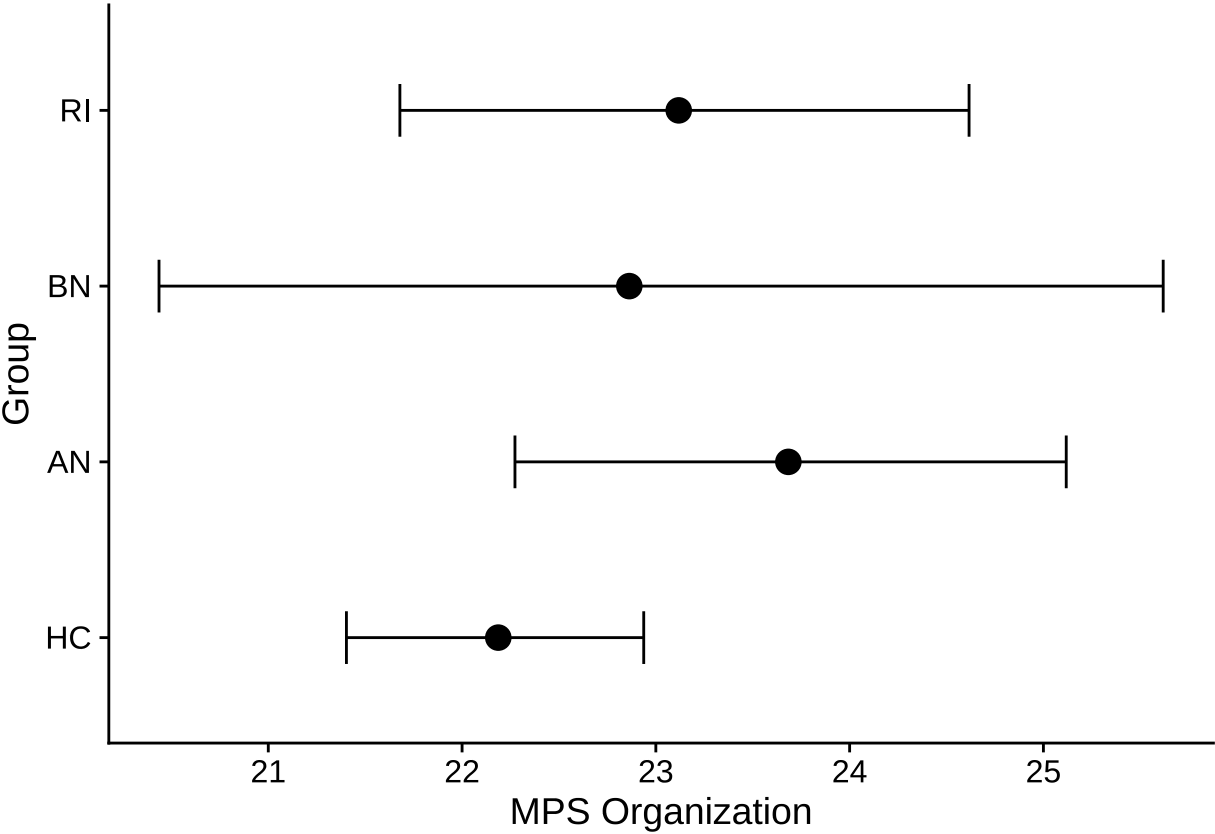
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	22.182	0.387	21.448	22.968
groupAN	1.503	0.787	-0.070	2.996
groupBN	0.723	1.360	-1.832	3.493
groupRI	0.949	0.827	-0.578	2.658

The 95% credibility intervals for the difference in the MPS-O scores between the HC group, on the one side, and the AN, BN, and RI groups, on the other, do include zero, indicating that there are no credible differences in Organization between these groups.

Predicted effect of group on the MPS Organization scores



Eating Attitude Test-26 (EAT-26)

The average scores on the Dieting Scale, the Bulimia and Food Preoccupation Scale, and the Oral Control Scale as a function of group are shown below. The average scores of each sub-scale and of the EAT-26 total score, as a function of group, are shown below together with the standard deviations.

group	EAT26_dieting	EAT26_bulimia	EAT26_oralcontrol	EAT26_tot
HC	2.47	0.57	1.10	4.14
AN	19.67	7.06	9.14	35.86
BN	19.09	7.64	5.64	32.36
RI	15.51	6.46	3.63	25.60

group	SD_dieting	SD_bulimia	SD_oralcontrol	SD_tot
HC	3.25	1.31	1.81	4.45
AN	10.60	3.70	5.91	17.96
BN	13.60	4.78	7.49	23.15
RI	7.85	3.81	3.83	12.45

Dieting

We used a Bayesian regression model to examine the EAT-26 Dieting score differences among groups.

```
m8_d <- brm(
  dieting ~ group,
  data = eat26_df,
  family = hurdle_lognormal(),
  iter = 4000,
  cores = parallel::detectCores(),
  backend = "cmdstan",
  refresh = 0,
  silent = TRUE
)

## Running MCMC with 4 chains, at most 8 in parallel...
##
## Chain 1 finished in 0.8 seconds.
## Chain 2 finished in 0.8 seconds.
## Chain 3 finished in 0.8 seconds.
## Chain 4 finished in 0.8 seconds.
##
## All 4 chains finished successfully.
```

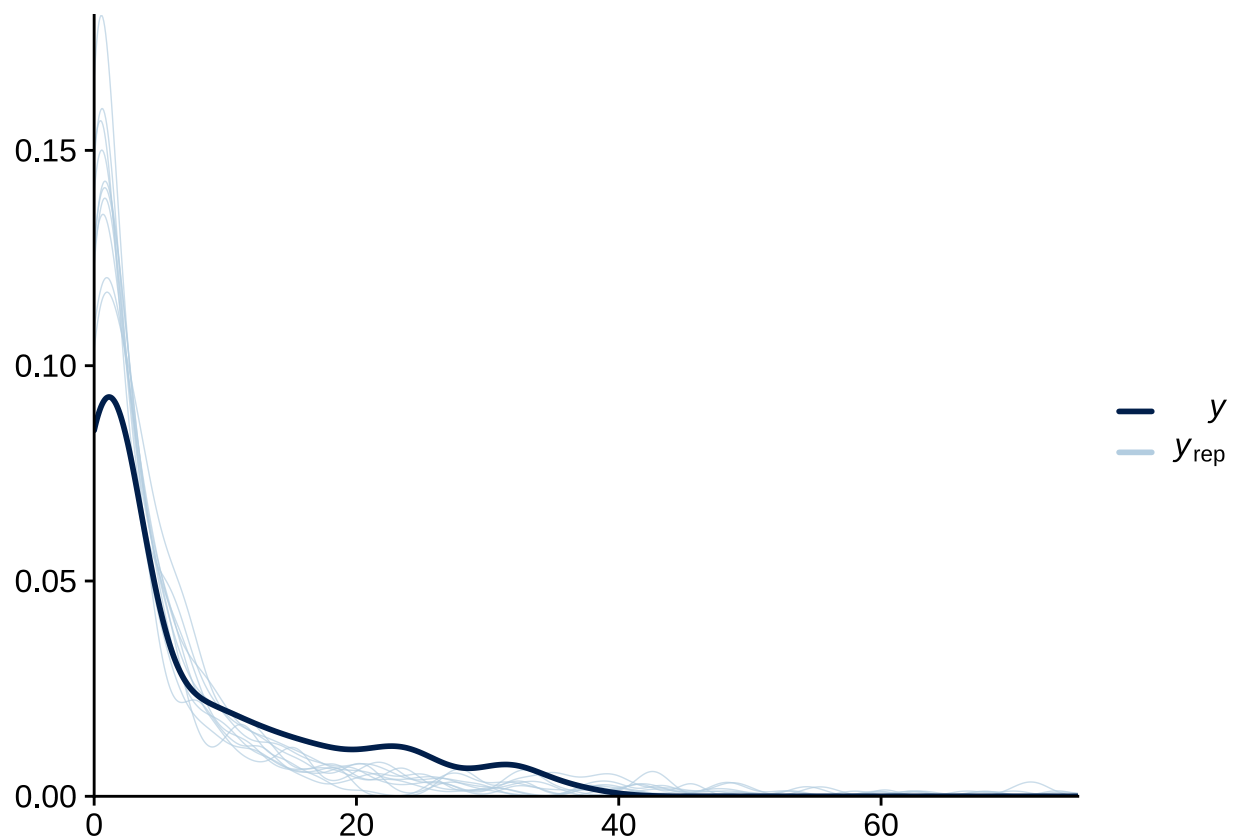
```
## Mean chain execution time: 0.8 seconds.
```

```
## Total execution time: 0.9 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```

```
## Warning: Removed 18 rows containing non-finite values (`stat_density()`).
```



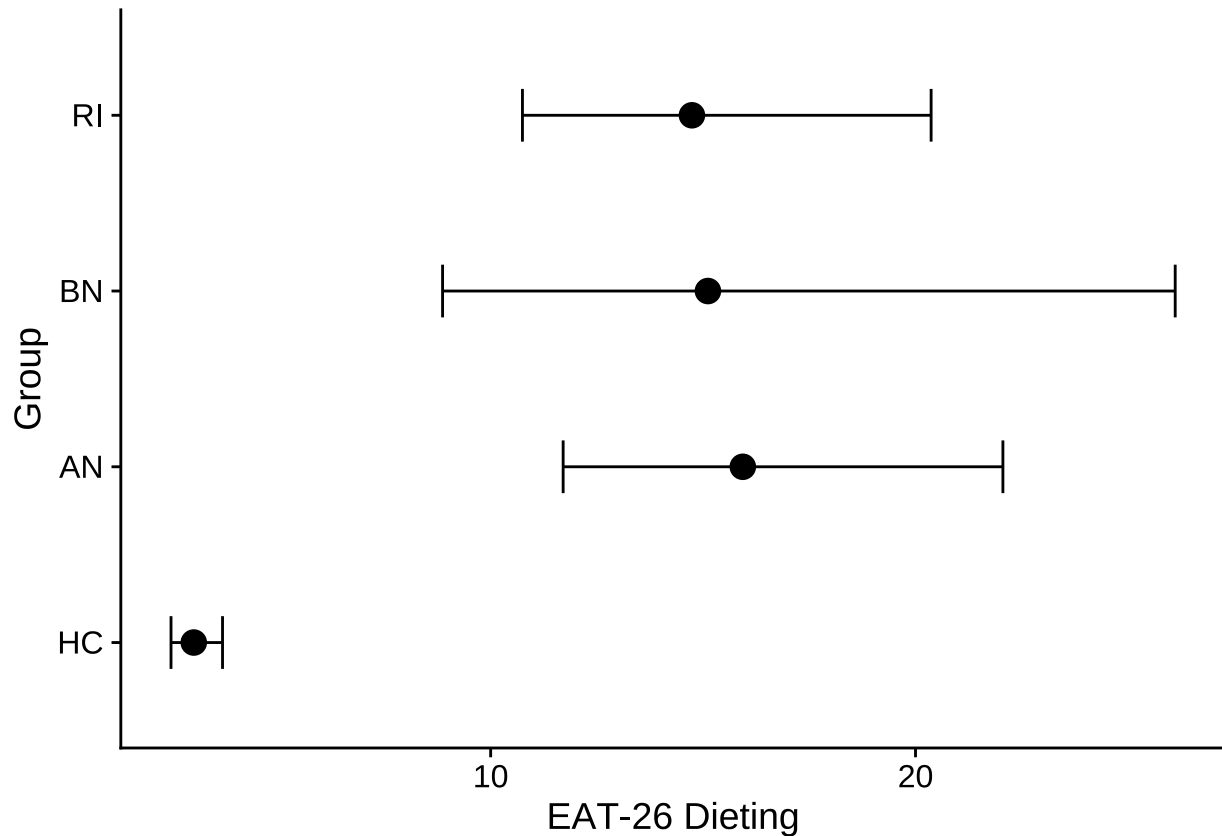
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.979	0.084	0.820	1.150
groupAN	1.666	0.171	1.327	2.000
groupBN	1.616	0.285	1.047	2.159
groupRI	1.587	0.176	1.250	1.941

The 95% credibility intervals for the difference in the EAT-26 Dieting scores between the HC group, on the one side, and the AN, BN, and RI groups, on the other, do not include zero, indicating a credible elevation in the EAT-26 Dieting scores of the AN, BN, and RI groups with respect to the HC group.

Predicted effect of group on the EAT-26 Dieting scores



Bulimia and Food Preoccupation

We used a Bayesian regression model to examine the EAT-26 Bulimia and Food Preoccupation score differences among groups.

```
m8_b <- brm(  
  bulimia ~ group,  
  data = eat26_df,  
  family = hurdle_lognormal(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
)
```

```
silent = TRUE
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
```

```
##
```

```
## Chain 1 finished in 0.8 seconds.
```

```
## Chain 2 finished in 0.8 seconds.
```

```
## Chain 3 finished in 0.8 seconds.
```

```
## Chain 4 finished in 0.8 seconds.
```

```
##
```

```
## All 4 chains finished successfully.
```

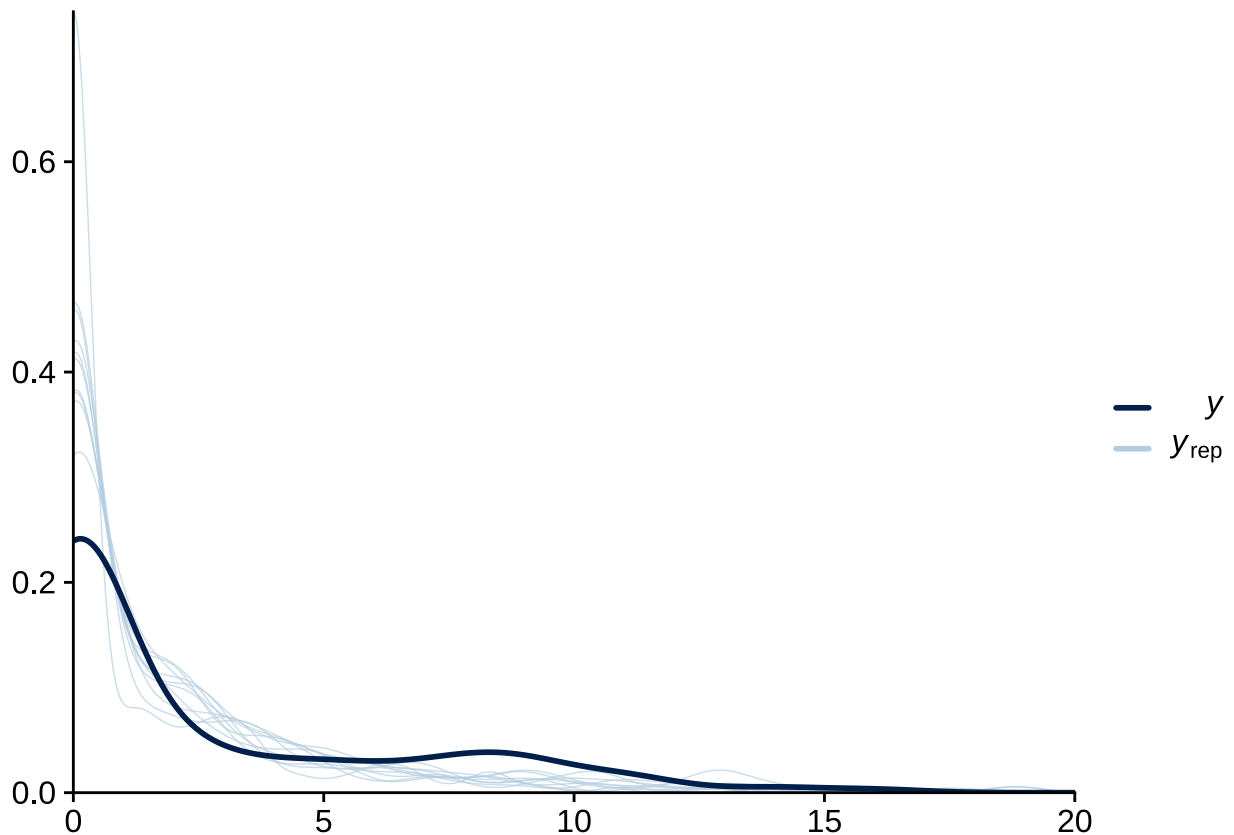
```
## Mean chain execution time: 0.8 seconds.
```

```
## Total execution time: 0.9 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_density()`).
```



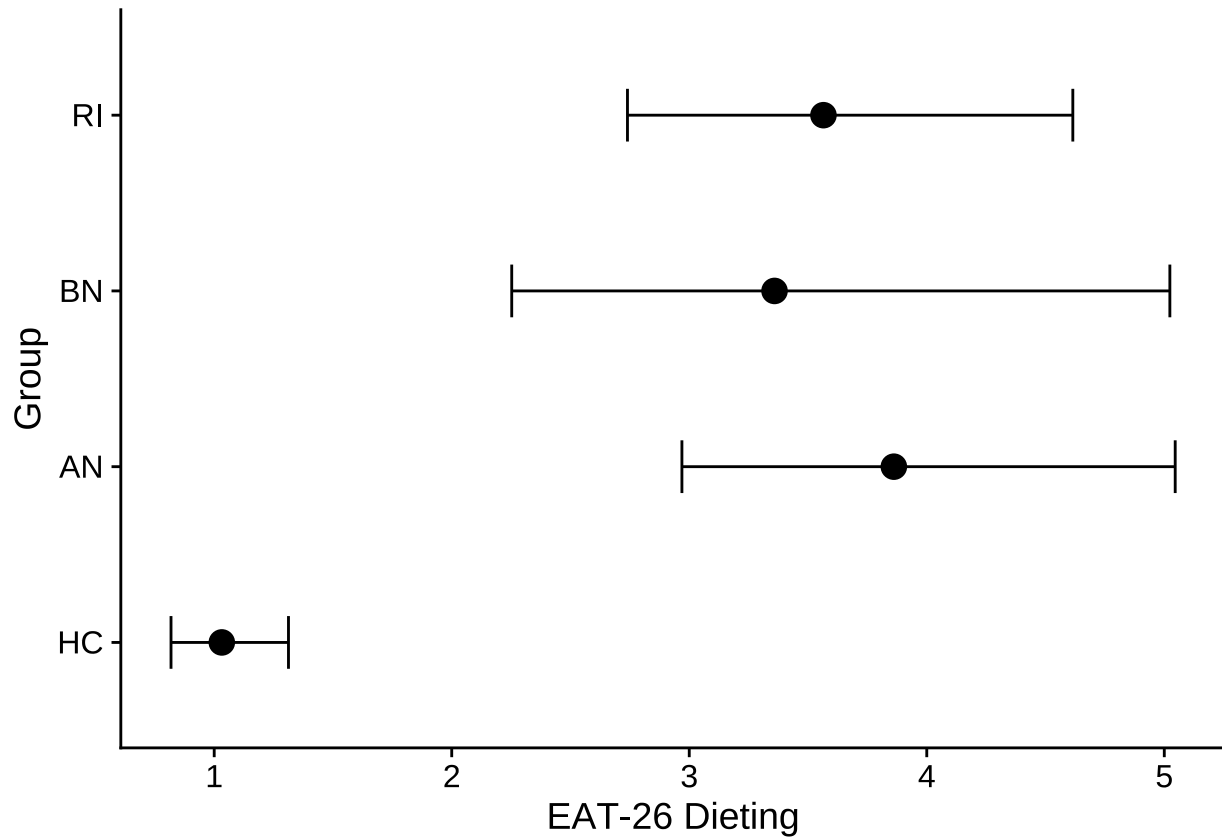
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.586	0.097	0.395	0.773
groupAN	1.319	0.149	1.048	1.633
groupBN	1.181	0.214	0.766	1.610
groupRI	1.238	0.151	0.939	1.529

The 95% credibility intervals for the difference in the EAT-26 Bulimia and Food Preoccupation scores between the HC group, on the one side, and the AN, BN, and RI groups, on the other, do not include zero, indicating a credible elevation in the EAT-26 Bulimia and Food Preoccupation scores of the clinical and at-risk groups with respect to the HC group.

Predicted effect of group on the EAT-26 Dieting scores



Oral Control

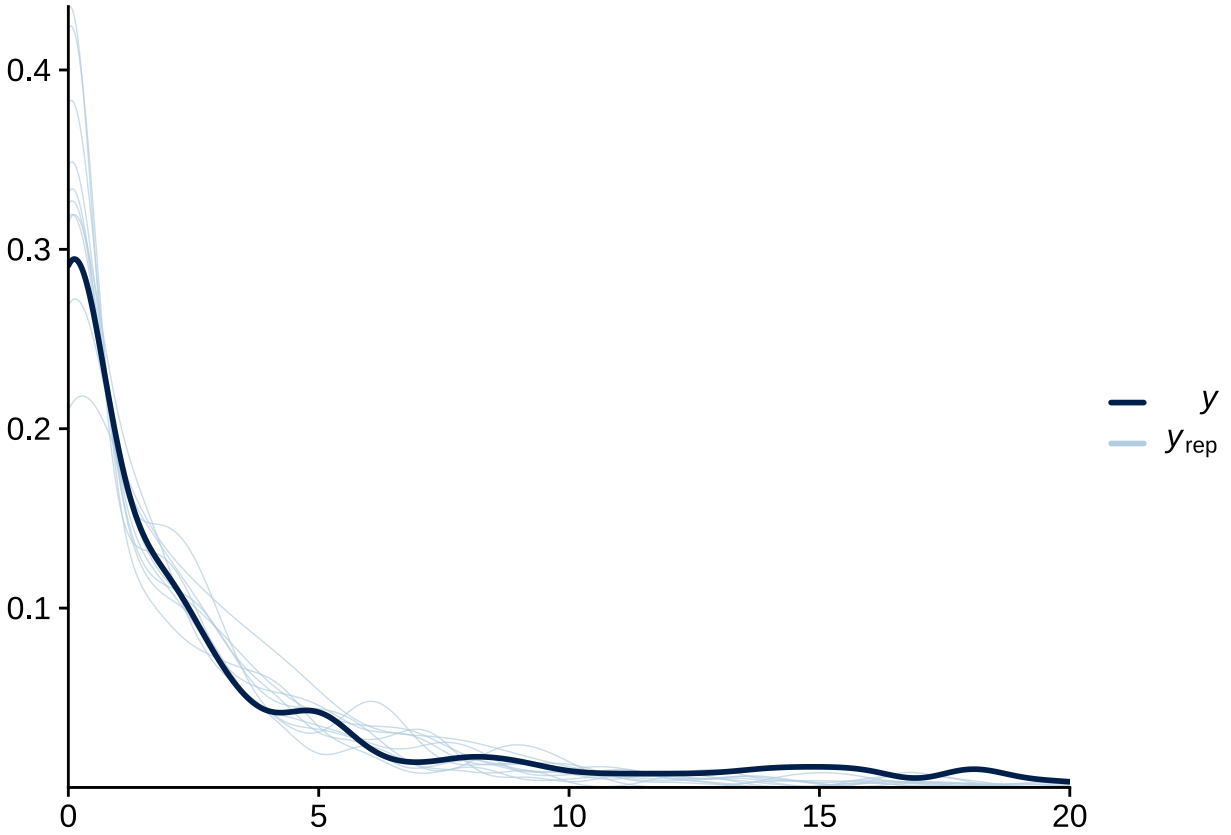
We used a Bayesian regression model to examine the EAT-26 Oral Control score differences among groups.

```
m8_oc <- brm(  
  oral_control ~ group,  
  data = eat26_df,  
  family = hurdle_lognormal(),  
  iter = 4000,  
  cores = parallel::detectCores(),  
  backend = "cmdstan",  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...  
##  
## Chain 1 finished in 0.8 seconds.  
## Chain 2 finished in 0.8 seconds.  
## Chain 3 finished in 0.8 seconds.  
## Chain 4 finished in 0.8 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 0.8 seconds.  
## Total execution time: 0.9 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.  
## Warning: Removed 36 rows containing non-finite values (`stat_density()`).
```



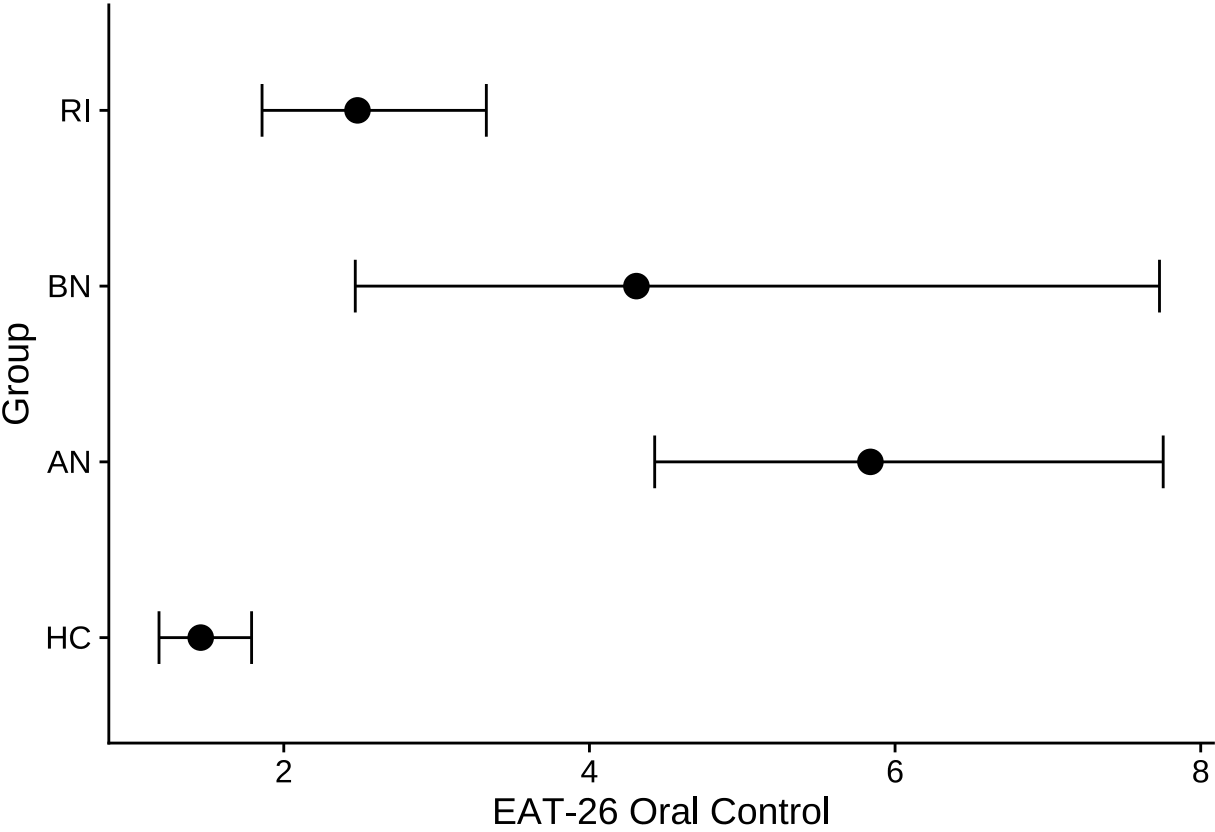
Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.692	0.083	0.530	0.851
groupAN	1.389	0.154	1.089	1.689
groupBN	1.086	0.291	0.532	1.684
groupRI	0.534	0.159	0.232	0.854

The 95% credibility intervals for the difference in the EAT-26 Oral Control scores between the HC group, on the one side, and the AN, BN, and RI groups, on the other, do not include zero, indicating a credible elevation in the EAT-26 Oral Control scores of the clinical and at-risk groups with respect to the HC group.

Predicted effect of group on the EAT-26 Oral Control



Participants Sample Size

Outcome-irrelevant learning: spatial-motor associations

In order to investigate whether the likelihood of selecting ‘stay’ was greater for ‘same’ versus ‘flipped’ response/key mapping, when contrasting rewarded and unrewarded responses, we reproduced the statistical evaluations conducted by Shahar et al. (2019) and Ben-Artzi et al. (2022). First, we employed a 3-way interaction model that permitted the modulation of the interaction between ‘same/flipped’ response/key mapping \times previously rewarded/unrewarded responses to vary across different groups.

Three-way interaction

```
priors_0 <- c(
  set_prior("student_t(3, 0, 0.2)", class = "b", coef = "Intercept"),
  set_prior("student_t(3, 0, 0.2)", class = "b"),
  set_prior("student_t(3, 0, 0.2)", class = "sd"),
  set_prior("lkj(1)", class = "cor"),
  set_prior("gamma(0.01, 0.01)", class = "phi"),
  set_prior("beta(2, 2)", class = "coi"),
  set_prior("beta(2, 2)", class = "zoi")
)

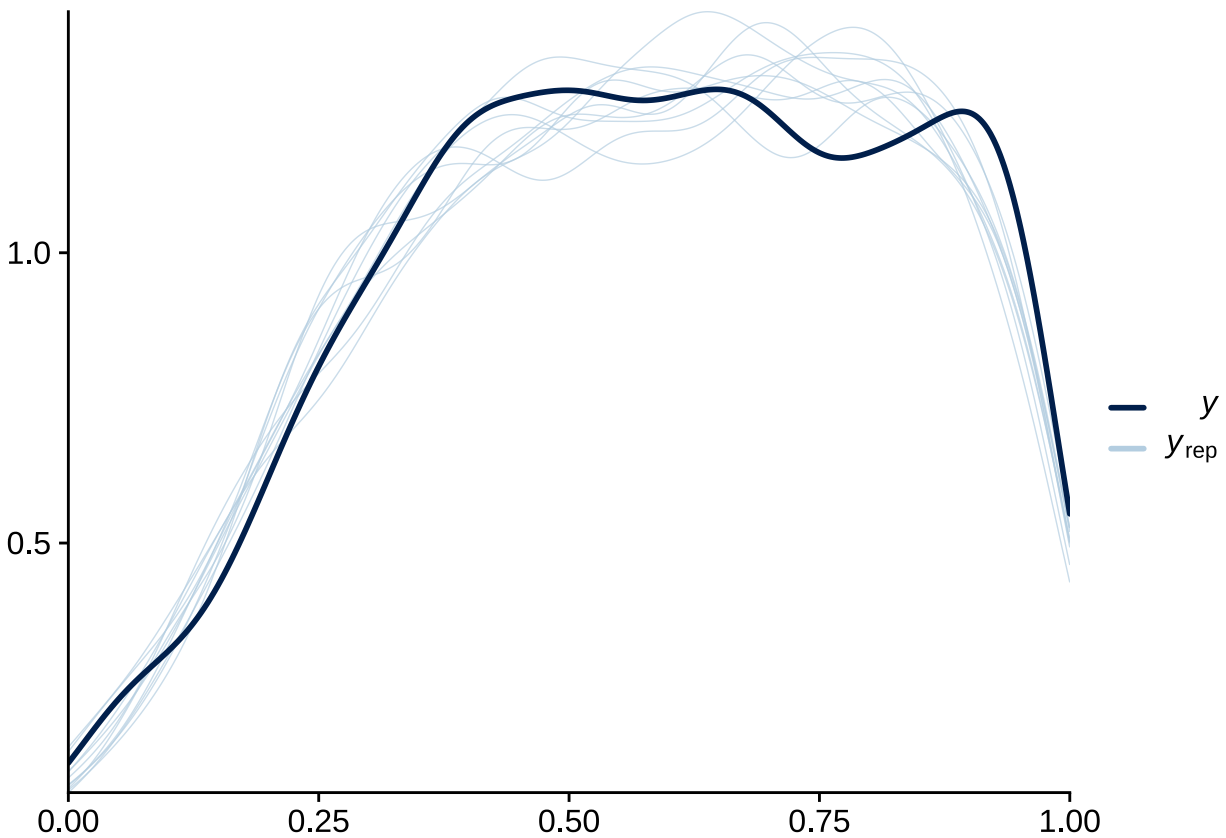
mod_0 <- brm(
  stay ~ 0 + Intercept + mapping * feedback * diagnosis +
    (1 + mapping * feedback | subj_code),
  family = zero_one_inflated_beta(),
  backend = "cmdstanr",
  data = bysubj_ed,
  prior = priors_0,
  iter = 2000,
  refresh = 0,
  silent = TRUE
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
##
## Chain 3 finished in 119.0 seconds.
## Chain 1 finished in 120.3 seconds.
## Chain 2 finished in 123.5 seconds.
## Chain 4 finished in 126.5 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 122.3 seconds.
## Total execution time: 126.7 seconds.
```

```
mod_0 <- add_criterion(mod_0, "loo")
```

Posterior predictive check

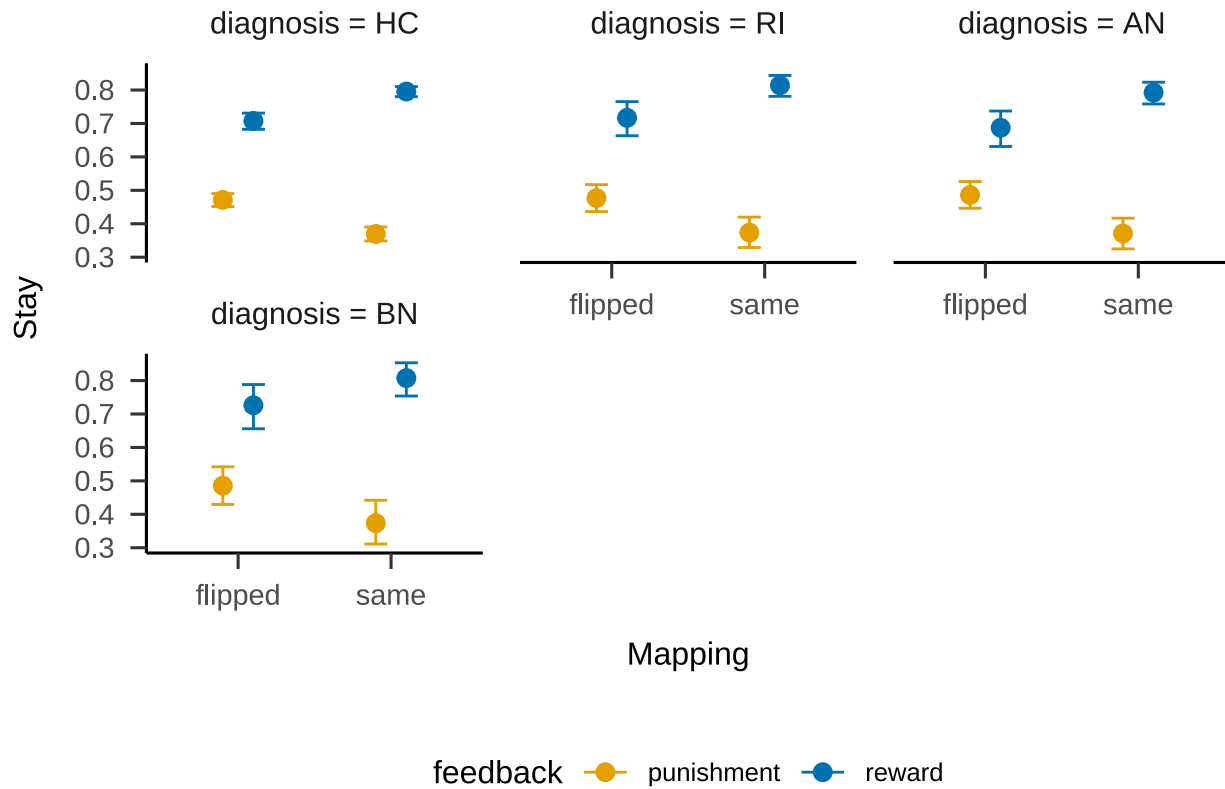
```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	-0.125	0.040	-0.202	-0.046
mappingsame	-0.425	0.055	-0.538	-0.322
feedbackreward	1.011	0.079	0.859	1.169
diagnosisRI	0.025	0.084	-0.136	0.197
diagnosisAN	0.061	0.085	-0.098	0.230
diagnosisBN	0.058	0.116	-0.170	0.289
mappingsame:feedbackreward	0.907	0.066	0.778	1.035
mappingsame:diagnosisRI	-0.006	0.114	-0.240	0.205
mappingsame:diagnosisAN	-0.056	0.112	-0.276	0.160
mappingsame:diagnosisBN	-0.039	0.149	-0.330	0.251
feedbackreward:diagnosisRI	0.019	0.152	-0.289	0.293
feedbackreward:diagnosisAN	-0.159	0.158	-0.485	0.143
feedbackreward:diagnosisBN	0.034	0.178	-0.332	0.388
mappingsame:feedbackreward:diagnosisRI	0.082	0.130	-0.174	0.326
mappingsame:feedbackreward:diagnosisAN	0.136	0.129	-0.104	0.404
mappingsame:feedbackreward:diagnosisBN	0.028	0.160	-0.275	0.368



This model failed to yield convincing evidence of a 3-way interaction, prompting us to simplify

it by disregarding variations across groups.

```
bcpriors <- get_prior(
  stay ~ 0 + Intercept + mapping * feedback +
    (1 + mapping * feedback | subj_code),
  family = zero_one_inflated_beta(),
  data = bysubj_ed
)

priors_1 <- c(
  set_prior("student_t(3, 0, 0.2)", class = "b", coef = "Intercept"),
  set_prior("student_t(3, 0, 0.2)", class = "b"),
  set_prior("student_t(3, 0, 0.2)", class = "sd"),
  set_prior("lkj(1)", class = "cor"),
  set_prior("gamma(0.01, 0.01)", class = "phi"),
  set_prior("beta(2, 2)", class = "coi"),
  set_prior("beta(2, 2)", class = "zoi")
)

mod_1 <- brm(
  stay ~ 0 + Intercept + mapping * feedback +
    (1 + mapping * feedback | subj_code),
  family = zero_one_inflated_beta(),
  backend = "cmdstanr",
  data = bysubj_ed,
  prior = priors_1,
  iter = 2000,
  refresh = 0,
  silent = TRUE,
  save_pars = save_pars(all = TRUE)
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
##
## Chain 3 finished in 119.1 seconds.
## Chain 1 finished in 119.2 seconds.
## Chain 2 finished in 119.4 seconds.
## Chain 4 finished in 160.9 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 129.7 seconds.
```

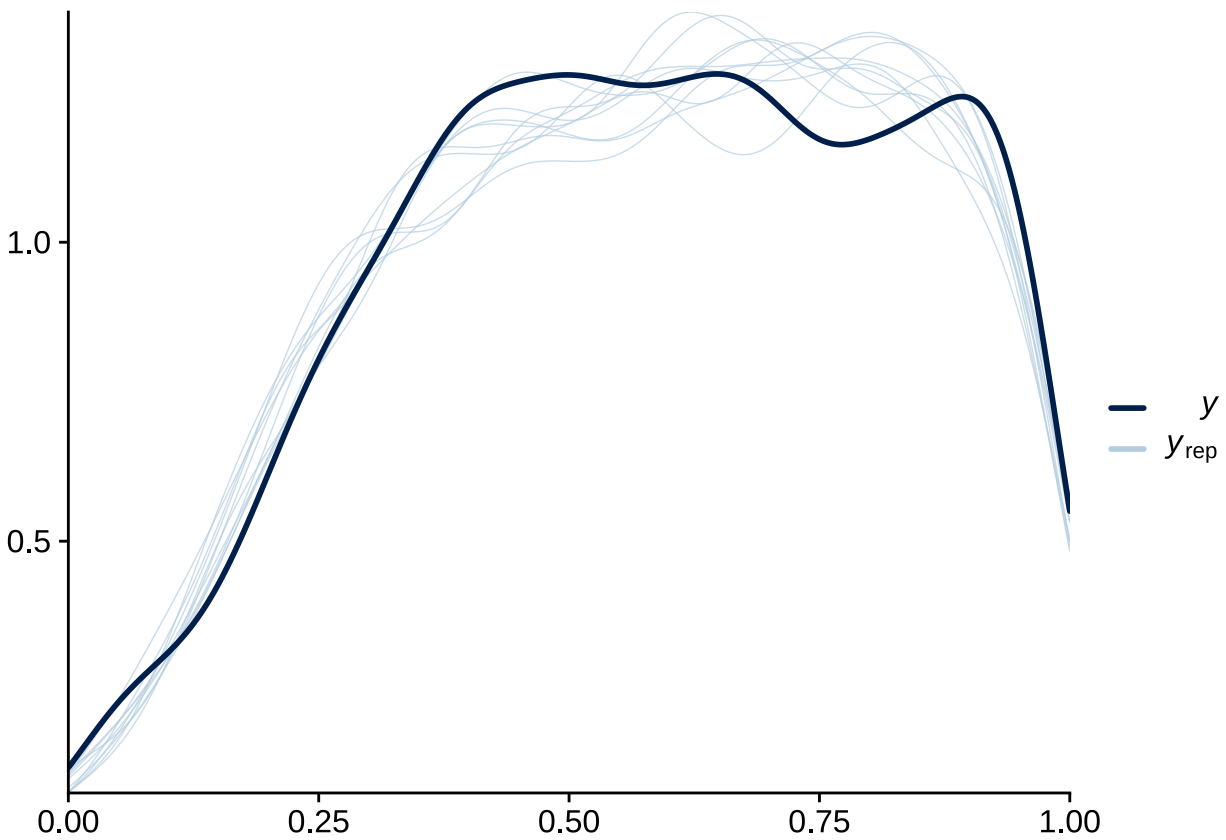


```
## Total execution time: 161.0 seconds.
```

```
mod_1 <- add_criterion(mod_1, "loo")
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```

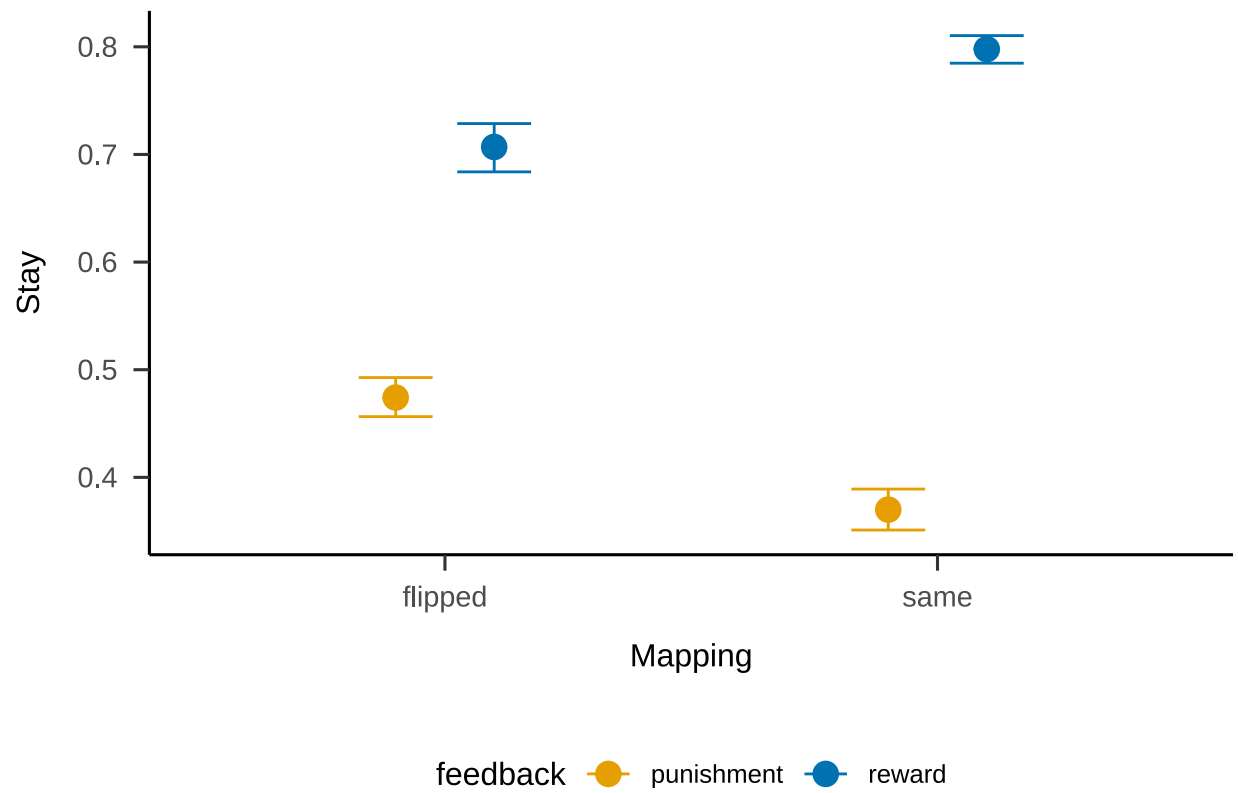


Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	-0.113	0.037	-0.185	-0.039
mappingsame	-0.434	0.050	-0.531	-0.339
feedbackreward	0.996	0.075	0.844	1.133
mappingsame:feedbackreward	0.933	0.062	0.802	1.046

The following figure, which describes the predicted marginal effects, replicates Fig. 2C of Shahar et al. (2019).



Data Analysis of the Probabilistic Reversal Learning Task

Tasks were programmed in MATLAB (MathWorks) using Psychtoolbox extensions (Brainard, 1997). Task structure is detailed in the main text methods. For all tasks, trials were interleaved by an inter-trial interval (ITI) drawn from a uniform distribution ITI uniform (0.7s, 1s). During the ITI a fixation cross was displayed (.65o visual angle) to draw attention to the center of the screen. Next, stimuli were displayed on screen until a response was made or until a time deadline (3 seconds, learnt by the participant during practice trials) was reached. Overall, only 583 trials were lost due to time-outs (~0.58% of the total database).
TODO

Decision Process (RLDDM)

We utilized a reinforcement learning drift diffusion model [RLDDM; Pedersen & Frank (2020)] to investigate the impact of illness-related information, which was irrelevant to the outcome, on decision-making. The RLDDM consists of two key components: one describes how reward feedback is employed to update value expectations and the other describes how an agent uses these expectations to arrive at a decision. The first component characterizes the learning process in terms of the delta learning rule (Rescorla, 1972):

$$Q_{a,i} = Q_{a,i-1} + \alpha(I_{a,i-1} - Q_{a,i-1}).$$

Here, Q refers to the expected values for option a on trial i , I represents the reward (with values 1 or 0), and α is the leaning rate, which scales the difference between the expected and actual rewards.

The second component describes the selection rule for reinforced options. Typically, a softmax function is used, where the probability of selecting option a depends on its expected value relative to other options n , scaled by the inverse temperature parameter β :

$$p_{a,i} = \frac{e^{\beta Q_{a,i}}}{\sum_{j=1}^n e^{\beta Q_{j,i}}}.$$

In the RLDDM, instead, this second component of decision-making is replaced by a Drift-Diffusion Model [DDM; Ratcliff & McKoon (2008)] which assumes a stochastic accumulation of evidence on each trial. A drift rate parameter (v) describes the rate of (noisy) evidence accumulation; a decision threshold parameter (a) represents the amount of evidence needed to make a decision; a non-decision time parameter (t) accounts for the time devoted to sensory processing, motor preparation, and motor output, and a starting point parameter (z) accounts for any predispositions in the initial decision variable towards either boundary.

We analyzed the data using the HDDM Python toolbox (Wiecki et al., 2013), which implements

the RLDDM and uses a hierarchical Bayesian approach to compute the posterior distribution of group and individual parameters (for a detailed description of the model, see Pedersen & Frank, 2020). The Bayesian posterior estimations of the RLDDM rely on informative priors obtained from a prior meta-analysis (Wiecki et al., 2013) for the DDM aspect of the model. On the other hand, non-informative broad normal distributions, centered at 0.5 after transformation, are used for the learning rate parameters (positive and negative).

Biased choices

We examined the PRL blocks where a food image was paired with a neutral image.

The proportion of times the target image was chosen, for each group, is shown below.

```
## group_by: one grouping variable (di)
```

```
## summarise: now 4 rows and 2 columns, ungrouped
```

di	m
HC	0.480
AN	0.447
BN	0.493
RI	0.474

The proportions were analyzed with a robust Bayesian regression model (a Beta model produced similar results).

```
priors <- c(  
  set_prior("student_t(4, 0, 2.5)", class = "b")  
)
```

```
bmod_02 <- brm(  
  bf(y ~ di, sigma ~ di),  
  data = bysubj_freq,  
  family = student(),  
  control = list(adapt_delta = 0.99),  
  prior = priors,  
  backend = "cmdstan",  
  warmup = 1000,  
  iter = 5000,  
  cores = parallel::detectCores(),  
  seed = "12345",  
  chains = 4,  
  refresh = 0,  
  silent = TRUE  
)
```

```
## Running MCMC with 4 chains, at most 8 in parallel...
```

```
##
```

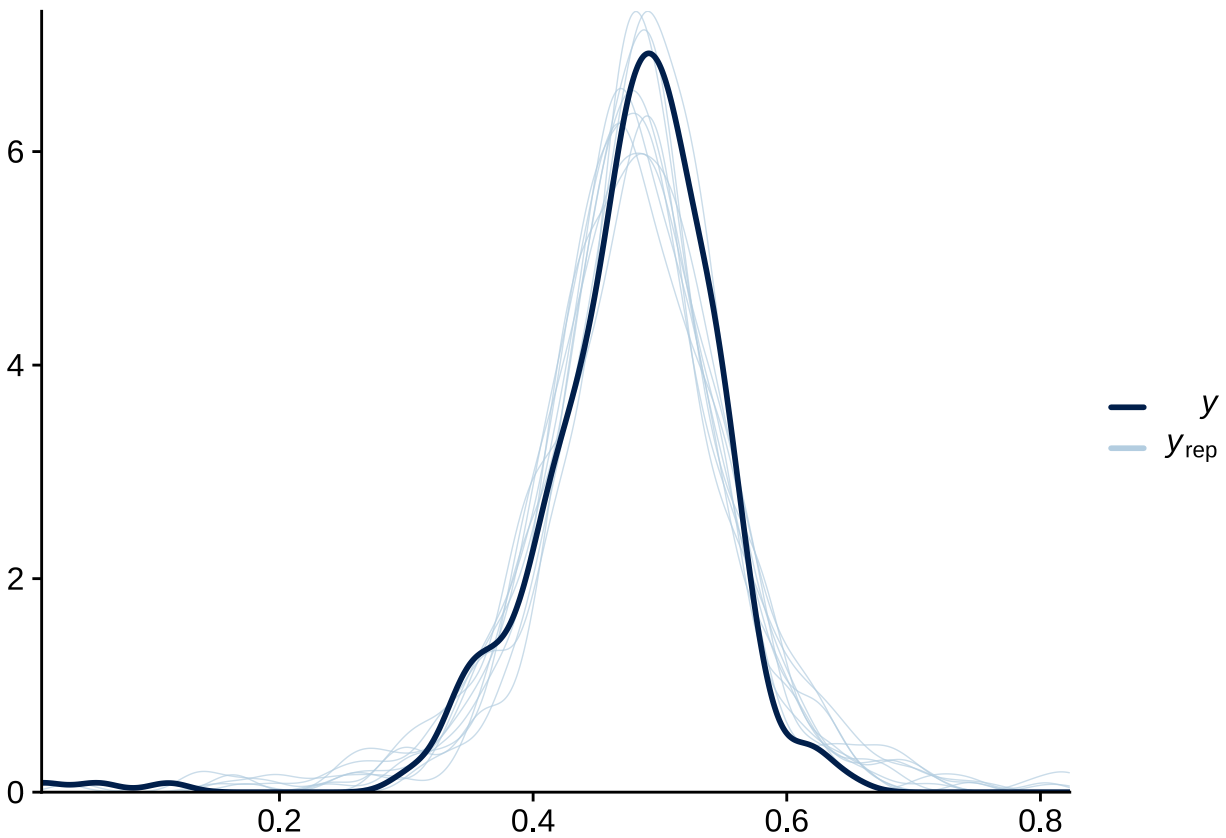
```
## Chain 3 finished in 4.3 seconds.
```

```
## Chain 4 finished in 4.4 seconds.
```

```
## Chain 1 finished in 5.1 seconds.  
## Chain 2 finished in 5.6 seconds.  
##  
## All 4 chains finished successfully.  
## Mean chain execution time: 4.9 seconds.  
## Total execution time: 5.8 seconds.
```

Posterior predictive check

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



Model's coefficients

The estimations obtained for the model are summarized in Table below, which includes the mean, the standard error, and the lower and upper bounds of the 95% credible interval of the posterior distribution for each parameter.

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.482	0.004	0.474	0.491
sigma_(Intercept)	-2.968	0.081	-3.135	-2.815
diAN	-0.009	0.017	-0.044	0.024
diBN	0.014	0.023	-0.034	0.059
diRI	-0.007	0.012	-0.031	0.016
sigma_diAN	0.471	0.220	0.053	0.901
sigma_diBN	0.249	0.279	-0.277	0.825
sigma_diRI	0.215	0.147	-0.069	0.505

Contrasts were obtained with the `emmeans` function of the `emmeans` package:

contrast	estimate	lower.HPD	upper.HPD
AN - HC	-0.008	-0.044	0.024
BN - HC	0.014	-0.034	0.059
BN - AN	0.022	-0.033	0.079
RI - HC	-0.007	-0.031	0.016
RI - AN	0.000	-0.038	0.042
RI - BN	-0.021	-0.070	0.030

Comorbidity

Individuals with eating disorders are prone to exhibiting not only eating-related pathologies, but also other comorbidities like mood and anxiety disorders. Here, we report the outcomes of the application of model M7 to the patient data, wherein patients were categorized into two groups based on the presence or absence of comorbidities.

```
m = hddm.HDDMr1(
    data,
    depends_on={
        "a": ["diag_cat", "comorbidity", "stim"],
        "v": ["diag_cat", "comorbidity", "stim"],
        "t": ["diag_cat", "comorbidity", "stim"],
        "alpha": ["diag_cat", "comorbidity", "stim"],
        "pos_alpha": ["diag_cat", "comorbidity", "stim"],
    },
    dual=True,
    p_outlier=0.05,
    informative=True
)
```

In each instance, the 95% credibility interval encompassed zero, thus indicating a lack of credible evidence for any differences in the RLDDM parameters between patients with and without comorbid diagnoses.

Parameter a

For anorexic patients, the difference in the posterior estimates of the a parameter for the two groups, $a_{\text{comorbidity present}} - a_{\text{comorbidity absent}}$, was 0.050, 95% CI [-0.124, 0.220] in the “food” condition; the difference in the posterior estimates of the a parameter for the two groups, $a_{\text{comorbidity present}} - a_{\text{comorbidity absent}}$, was 0.097, 95% CI [-0.072, 0.256] in the “neutral” condition.

For bulimic patients, the difference in the posterior estimates of the a parameter for the two groups, $a_{\text{comorbidity present}} - a_{\text{comorbidity absent}}$, was 0.116, 95% CI [-0.195, 0.396] in the “food” condition; the difference in the posterior estimates of the a parameter for the two groups, $a_{\text{comorbidity present}} - a_{\text{comorbidity absent}}$, was 0.065, 95% CI [-0.258, 0.382] in the “neutral” condition.

Parameter α^-

For anorexic patients, the difference in the posterior estimates of the α^- parameter for the two groups, $\alpha^-_{\text{comorbidity present}} - \alpha^-_{\text{comorbidity absent}}$, was -2.071, 95% CI [-6.738, 2.446] in the “food” condition; the difference in the posterior estimates of the a parameter for the two

groups, $\alpha_{\text{comorbidity present}}^- - \alpha_{\text{comorbidity absent}}^-$, was 0.195, 95% CI [-4.514, 4.900] in the “neutral” condition.

For bulimic patients, the difference in the posterior estimates of the α^- parameter for the two groups, $\alpha_{\text{comorbidity present}}^- - \alpha_{\text{comorbidity absent}}^-$, was 1.357, 95% CI [-5.061, 7.299] in the “food” condition; the difference in the posterior estimates of the a parameter for the two groups, $\alpha_{\text{comorbidity present}}^- - \alpha_{\text{comorbidity absent}}^-$, was 1.457, 95% CI [-4.393, 7.366] in the “neutral” condition.

Parameter α^+

For anorexic patients, the difference in the posterior estimates of the α^+ parameter for the two groups, $\alpha_{\text{comorbidity present}}^+ - \alpha_{\text{comorbidity absent}}^+$, was 0.429, 95% CI [-3.261, 4.326] in the “food” condition; the difference in the posterior estimates of the a parameter for the two groups, $\alpha_{\text{comorbidity present}}^+ - \alpha_{\text{comorbidity absent}}^+$, was 0.823, 95% CI [-3.273, 5.345] in the “neutral” condition.

For bulimic patients, the difference in the posterior estimates of the α^+ parameter for the two groups, $\alpha_{\text{comorbidity present}}^+ - \alpha_{\text{comorbidity absent}}^+$, was 1.674, 95% CI [-3.723, 7.396] in the “food” condition; the difference in the posterior estimates of the a parameter for the two groups, $\alpha_{\text{comorbidity present}}^+ - \alpha_{\text{comorbidity absent}}^+$, was 1.080, 95% CI [-4.487, 6.337] in the “neutral” condition.

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