

E3 alignment (Bayes version)

R. Cassano-Coleman

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This notebook analyzes alignment values using a Bayesian approach.

```
set.seed(15000)
```

Load the data.

```
data <- read_csv('../data/alignment_original.csv', show_col_types = FALSE)
```

Check number of subjects per group.

```
length(unique(filter(data, Musician == 'Yes')$sub))
```

```
## [1] 49
```

```
length(unique(filter(data, Musician == 'No')$sub))
```

```
## [1] 46
```

Make sure non-musicians and musicians are labelled with different numbers.

```
data %>% mutate(sub = ifelse(Musician == 'Yes', sub, sub + 49))
```

Pivot the data longer.

```
data %>% pivot_longer(cols = -c(Musician, sub, scramble),
                        names_to = 'level', values_to = 'value')
```

For comparisons across levels, look at nested structure only (levels 2, 4, 8, 16).

```
data_nested <- data %>%
  filter(!level %in% c(1,3,5))
```

Make group, scramble, and level into factors and set contrasts.

```
data %>% mutate(
  Musician = factor(Musician, levels = c('Yes', 'No')),
  scramble = factor(scramble, levels = c('Intact', '8B', '2B', '1B')),
  level = factor(level, levels = c(1,2,3,4,5,8,16), ordered = TRUE)
)

contrasts(data$scramble) <- contr.treatment(4) # Intact as reference
contrasts(data$level) <- contr.treatment(7, base = 6) # 8-bar as reference

data_nested %>% mutate(
  Musician = factor(Musician, levels = c('Yes', 'No')),
  scramble = factor(scramble, levels = c('Intact', '8B', '2B', '1B')),
  level = factor(level, levels = c(2,4,8,16), ordered = TRUE)
)
```

```
contrasts(data_nested$scramble) <- contr.treatment(4) # Intact as reference
contrasts(data_nested$level) <- contr.treatment(4, base = 3) # 8-bar as reference
```

Check normality of the data.

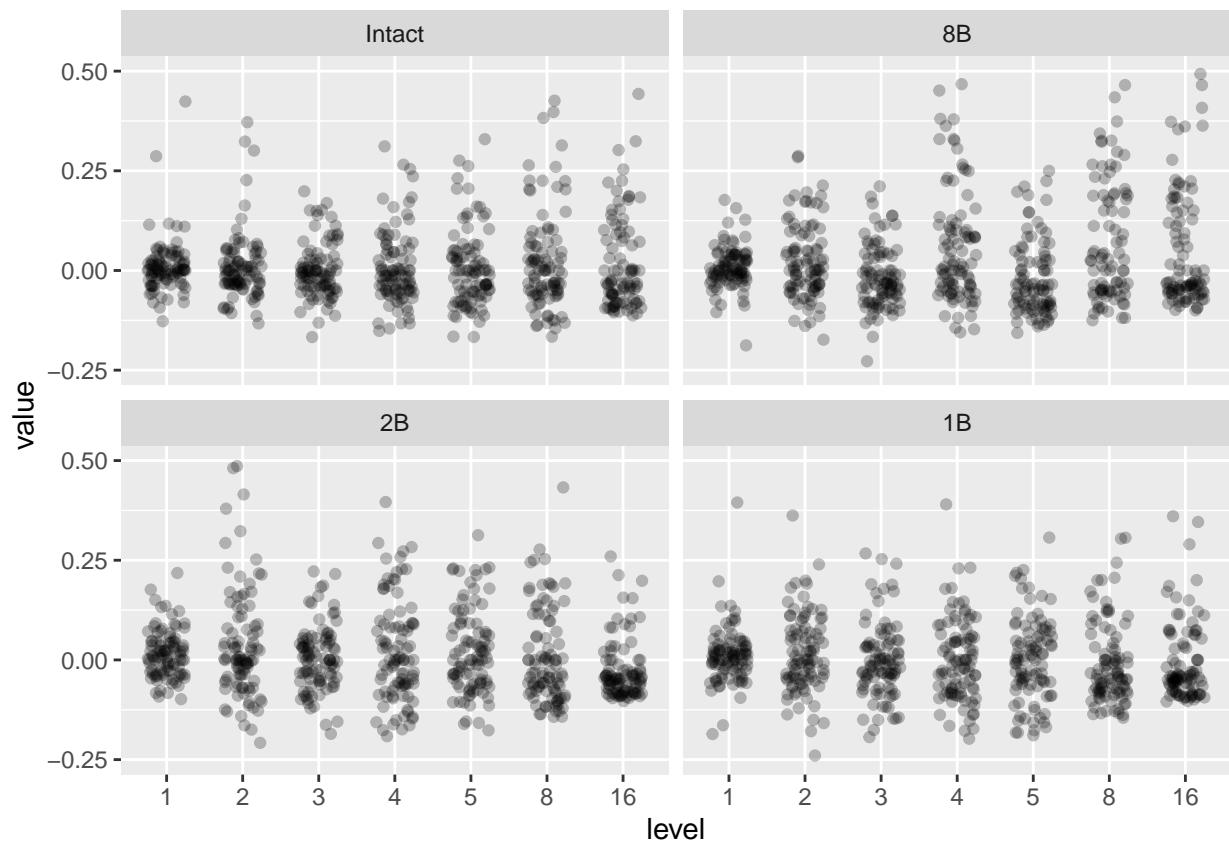
```
data %>%
  group_by(scramble, level) %>%
  shapiro_test(value)
```

```
## # A tibble: 28 x 5
##   scramble level variable statistic      p
##   <fct>    <ord>  <chr>     <dbl>    <dbl>
## 1 Intact    1     value     0.737 9.32e-12
## 2 Intact    2     value     0.812 1.15e- 9
## 3 Intact    3     value     0.952 1.48e- 3
## 4 Intact    4     value     0.922 2.96e- 5
## 5 Intact    5     value     0.930 7.38e- 5
## 6 Intact    8     value     0.898 1.99e- 6
## 7 Intact   16    value     0.852 2.69e- 8
## 8 8B        1     value     0.946 6.98e- 4
## 9 8B        2     value     0.964 9.62e- 3
## 10 8B       3     value     0.962 8.07e- 3
## # i 18 more rows
```

Visualize.

```
data %>%
  ggplot(aes(x = level, y = value)) +
  geom_jitter(width = 0.25, alpha = 0.25) +
  facet_wrap(vars(scramble)) +
  ylim(-0.25, 0.5)
```

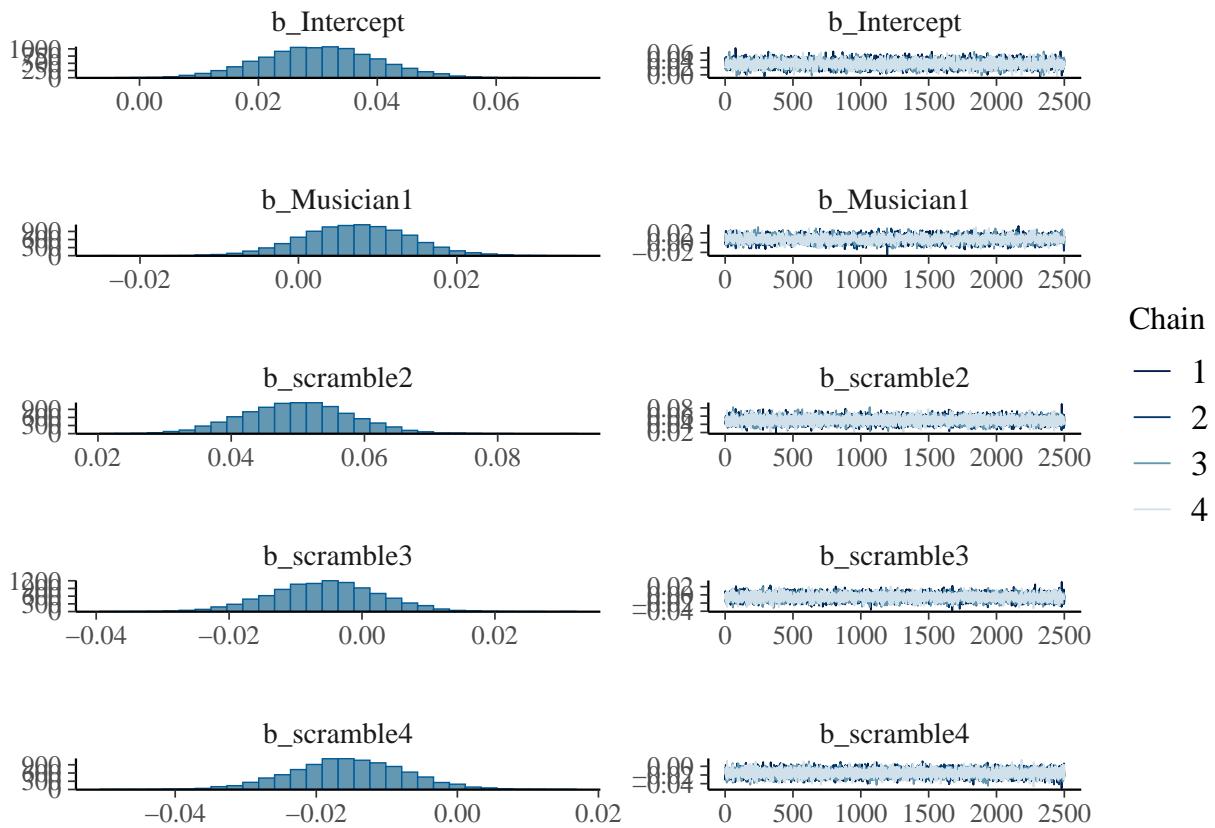
```
## Warning: Removed 17 rows containing missing values or values outside the scale range
## (~geom_point()`).
```

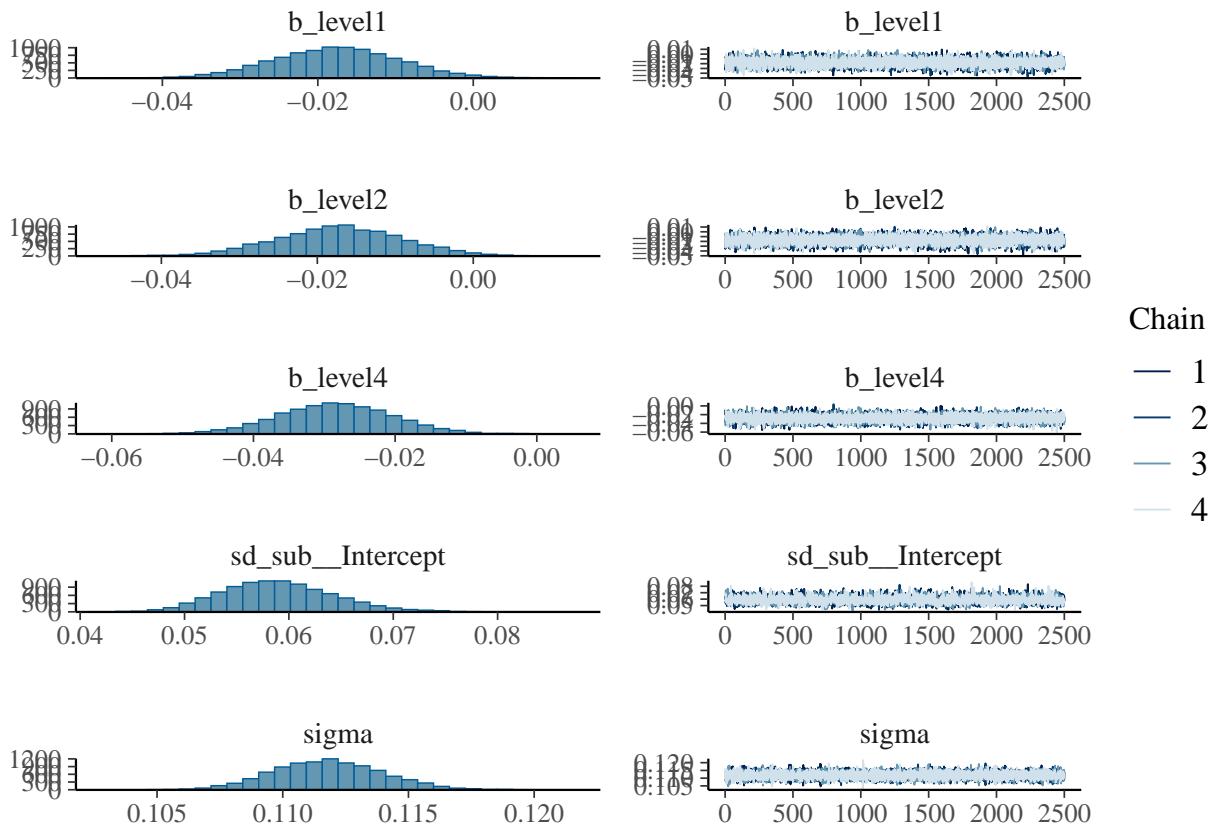


Main analysis

```
nested_3way <- brm(value ~ Musician + scramble + level + (1|sub), data = data_nested,
                     prior = c(
                       set_prior('normal(-0.1, 0.1)', coef = 'Musician1'),
                       set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                       set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                       set_prior('normal(-0.1, 0.1)', coef = 'scramble4'),
                       set_prior('normal(-0.2, 0.1)', coef = 'level1'),
                       set_prior('normal(-0.1, 0.1)', coef = c('level2', 'level4'))
                     ),
                     save_pars = save_pars(all = TRUE), iter = 5000,
                     file = '../models/E3_alignment_3way_noInt')
```

plot(nested_3way)





```
print(summary(nested_3way), digits = 4)
```

```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ Musician + scramble + level + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0590    0.0054   0.0493   0.0705 1.0002     3748    5461
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0302    0.0097   0.0114   0.0495 1.0002     5912    7214
## Musician1    0.0073    0.0068  -0.0059   0.0207 1.0012     3685    5649
## scramble2    0.0499    0.0081   0.0343   0.0656 1.0001    13862    8853
## scramble3   -0.0056    0.0081  -0.0215   0.0100 1.0008    12393    8571
## scramble4   -0.0155    0.0080  -0.0315   0.0001 0.9998    14035    8472
## level1     -0.0176    0.0081  -0.0332  -0.0017 0.9999    14104    7889
## level2     -0.0171    0.0081  -0.0330  -0.0016 1.0004    13102    8532
## level4     -0.0284    0.0081  -0.0443  -0.0127 1.0000    14450    8874
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.1118    0.0022   0.1077   0.1160 1.0004    18228    7569
```

```
##  
## Draws were sampled using sampling(NUTS). 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).
```

```

nested_noMus <- brm(value ~ scramble + level + (1|sub), data = data_nested,
                     prior = c(
                       set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                       set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                       set_prior('normal(-0.1, 0.1)', coef = 'scramble4'),
                       set_prior('normal(-0.2, 0.1)', coef = 'level1'),
                       set_prior('normal(-0.1, 0.1)', coef = c('level2', 'level4'))
                     ),
                     save_pars = save_pars(all = TRUE), iter = 5000,
                     file = '../models/E3_alignment_2way_noMus')

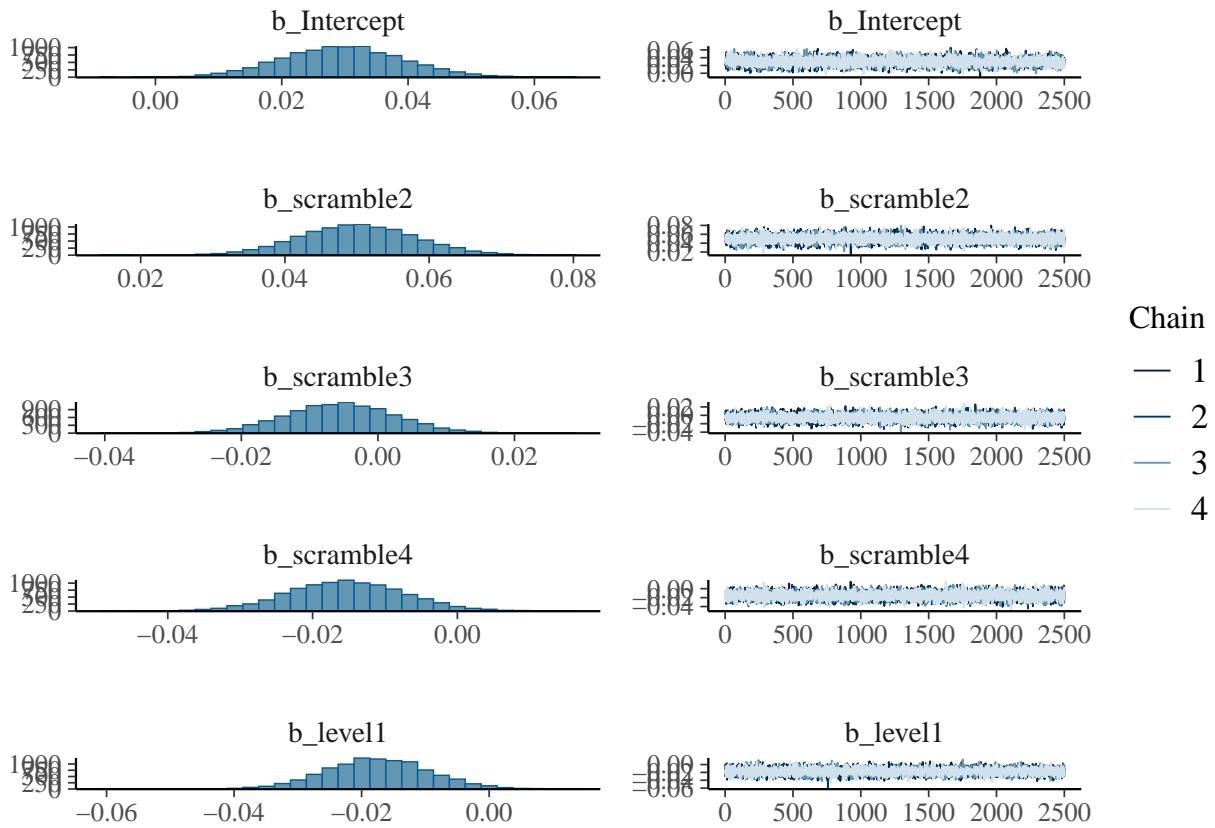
nested_noScram <- brm(value ~ Musician + level + (1|sub), data = data_nested,
                        prior = c(
                          set_prior('normal(-0.1, 0.1)', coef = 'Musician1'),
                          set_prior('normal(-0.2, 0.1)', coef = 'level1'),
                          set_prior('normal(-0.1, 0.1)', coef = c('level2', 'level4'))
                        ),
                        save_pars = save_pars(all = TRUE), iter = 5000,
                        file = '../models/E3_alignment_2way_noScram')

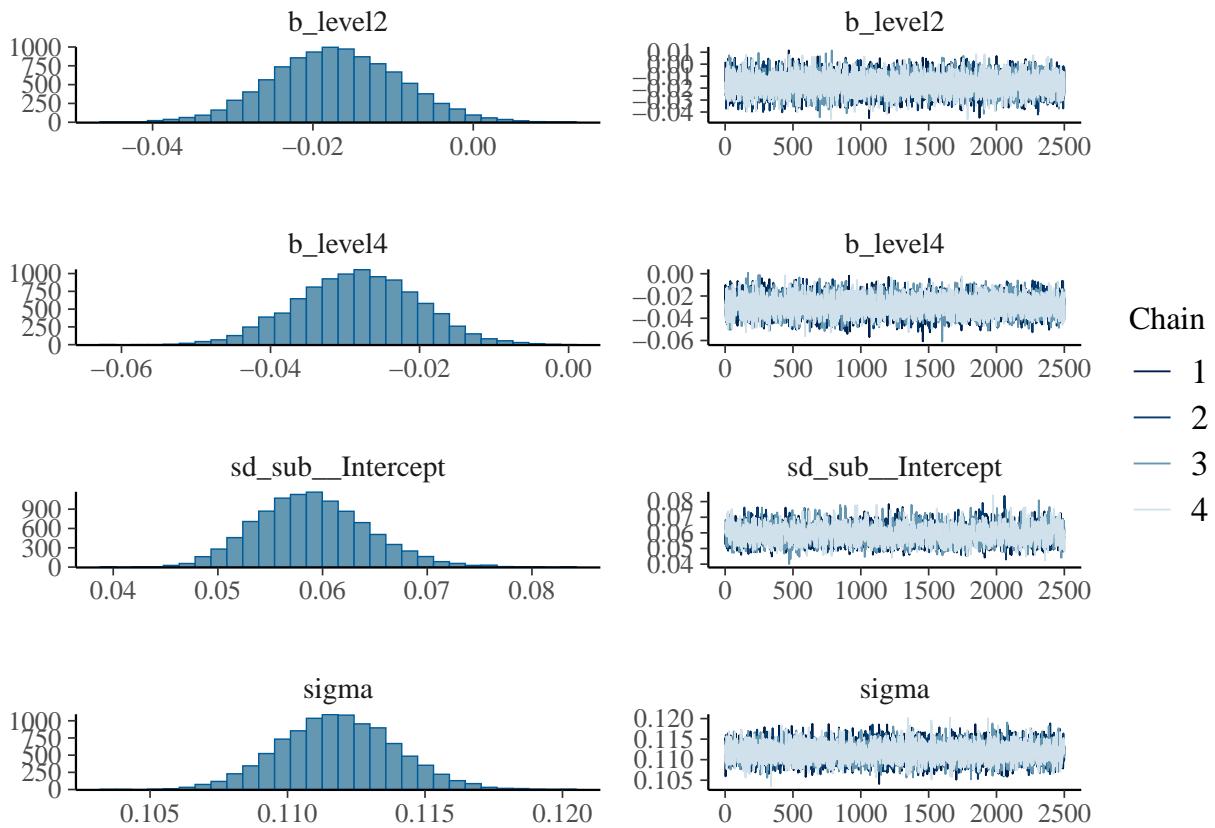
nested_noLevel <- brm(value ~ Musician + scramble + (1|sub), data = data_nested,
                        prior = c(
                          set_prior('normal(-0.1, 0.1)', coef = 'Musician1'),
                          set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                          set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                          set_prior('normal(-0.1, 0.1)', coef = 'scramble4')
                        ),
                        save_pars = save_pars(all = TRUE), iter = 5000,
                        file = '../models/E3_alignment_2way_noLevel')

```

Model without group:

```
plot(nested_noMus)
```





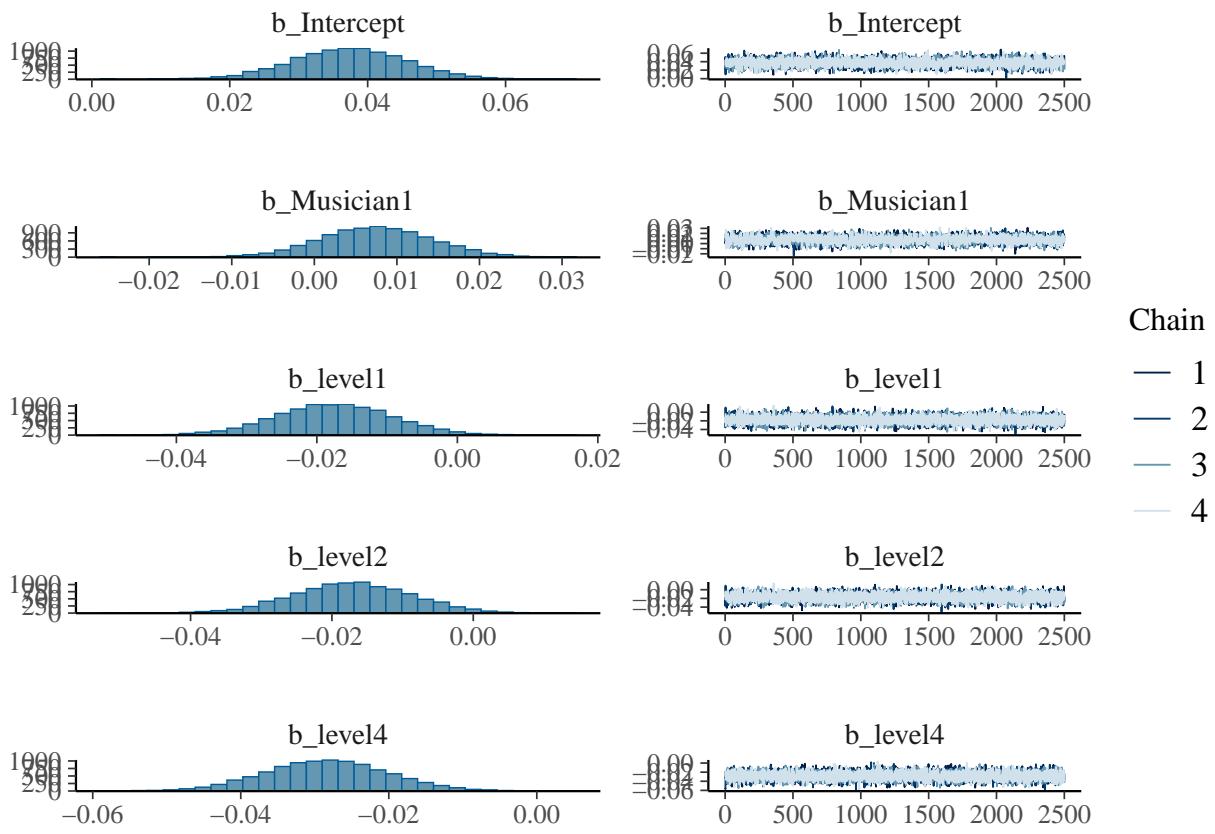
```
print(summary(nested_noMus), digits = 4)
```

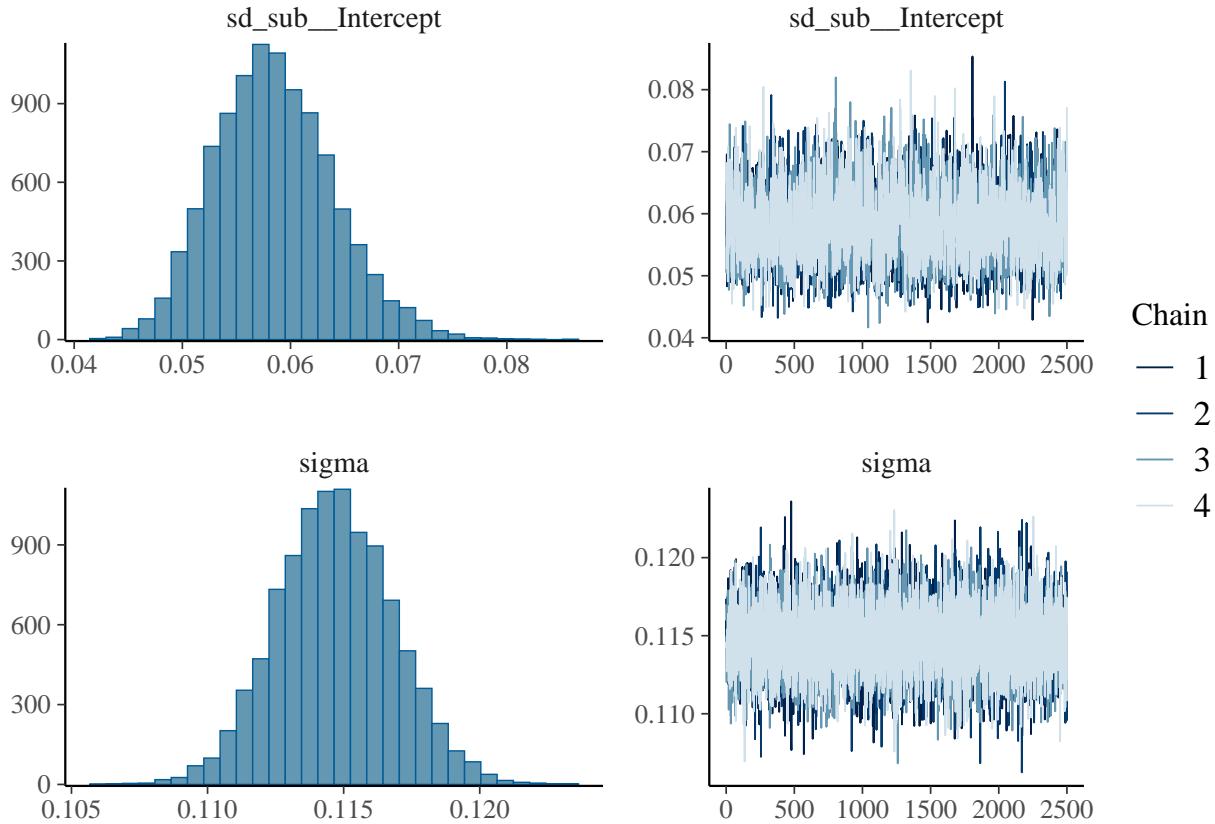
```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble + level + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0590    0.0053   0.0493   0.0703 1.0000     3427     4287
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0297    0.0096   0.0112   0.0488 1.0004     6075     7243
## scramble2    0.0501    0.0081   0.0345   0.0660 1.0001    13473     7960
## scramble3   -0.0055    0.0081  -0.0212   0.0105 0.9999    13031     8280
## scramble4   -0.0153    0.0081  -0.0312   0.0005 1.0002    13159     8358
## level1     -0.0175    0.0080  -0.0331  -0.0017 1.0009    13925     8452
## level2     -0.0171    0.0080  -0.0322  -0.0013 1.0008    13834     8810
## level4     -0.0283    0.0081  -0.0439  -0.0127 1.0002    13184     8629
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.1118    0.0021   0.1078   0.1161 1.0001    15818     7810
## 
```

```
## Draws were sampled using sampling(NUTS). 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).
```

Model without condition:

```
plot(nested_noScram)
```





```

print(summary(nested_noScram), digits = 4)

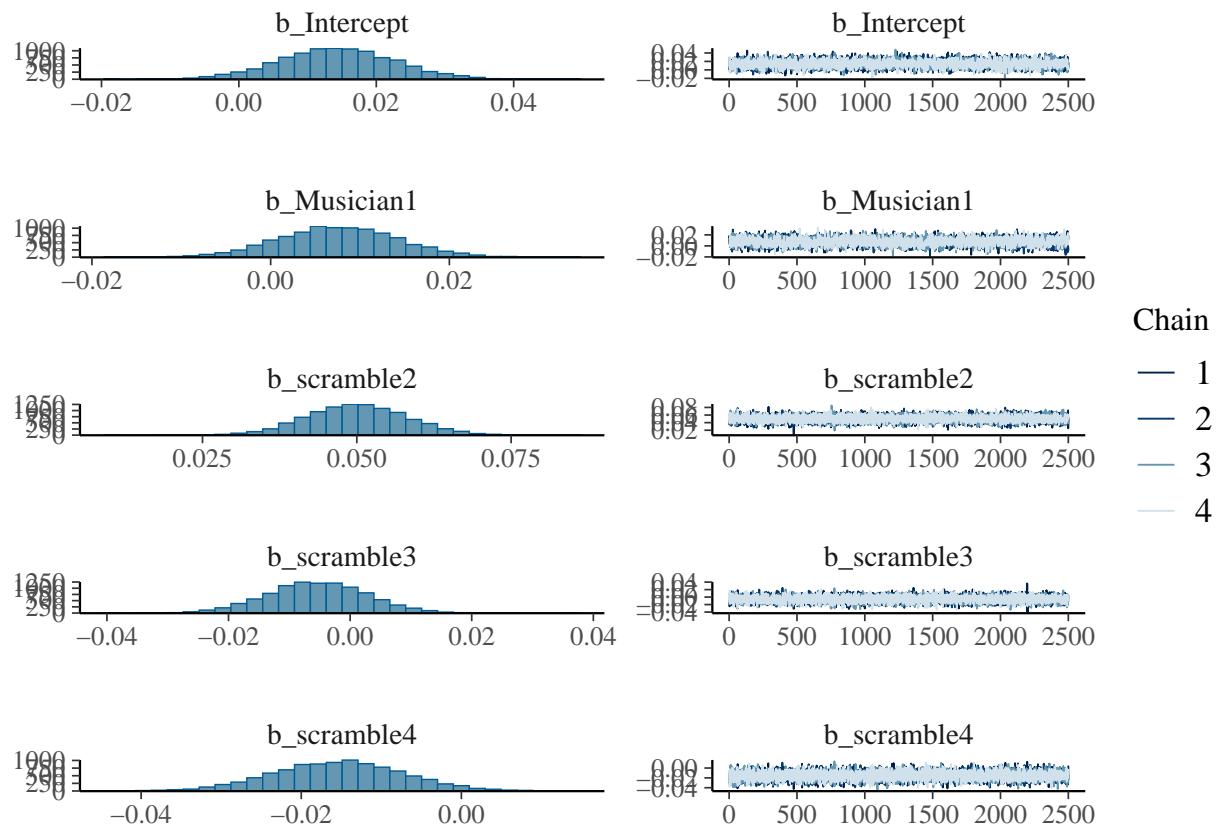
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ Musician + level + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0585     0.0055   0.0487   0.0702 1.0002      3468     5144
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0374     0.0083   0.0212   0.0537 1.0004      5328     6505
## Musician1    0.0075     0.0068  -0.0056   0.0209 1.0007      3893     5676
## level1      -0.0176     0.0084  -0.0342  -0.0013 1.0008     12706     7752
## level2      -0.0171     0.0083  -0.0335  -0.0009 1.0004     14323     8872
## level4      -0.0284     0.0083  -0.0446  -0.0121 1.0001     12930     8380
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1147     0.0022   0.1106   0.1190 1.0011     16605     6464
## 
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential

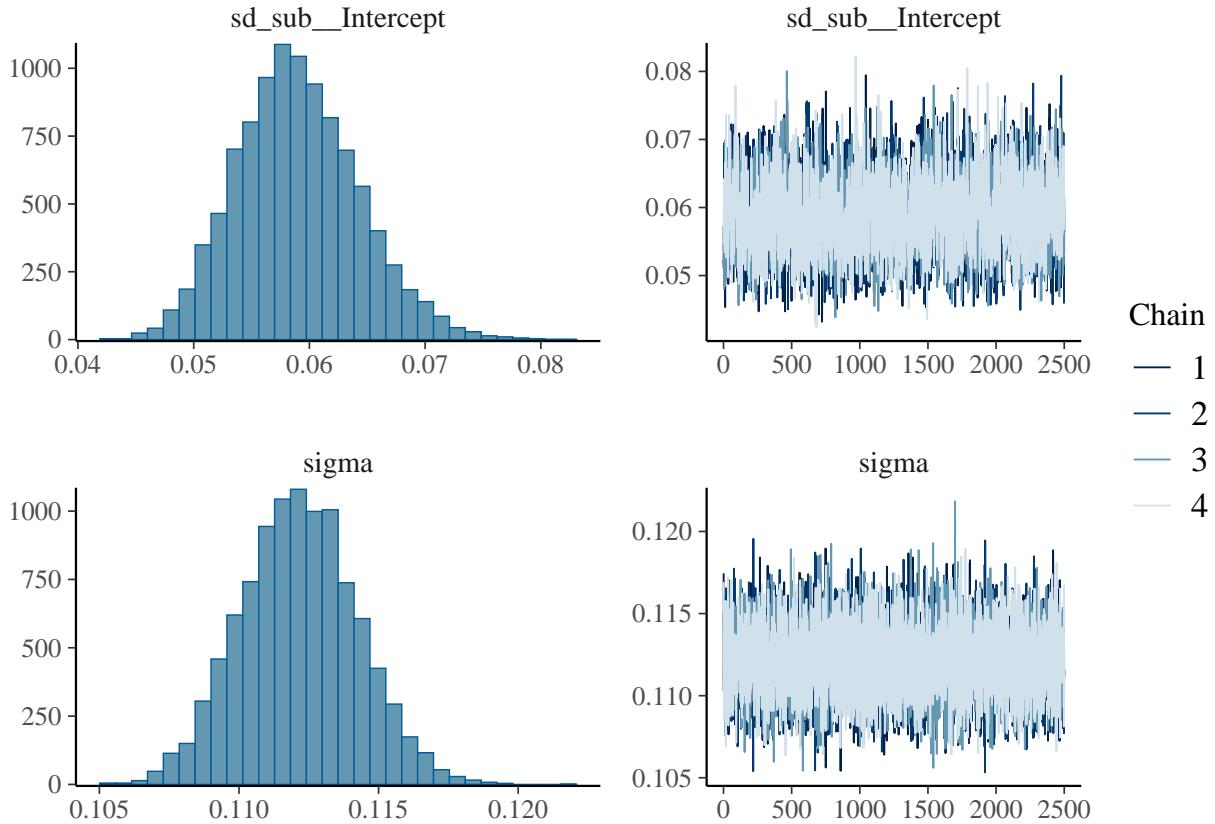
```

```
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Model without level:

```
plot(nested_noLevel)
```





```

print(summary(nested_noLevel), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ Musician + scramble + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0590     0.0053   0.0493   0.0702 1.0009      3772     6007
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0143     0.0084  -0.0021   0.0310 1.0001      5054     6342
## Musician1    0.0076     0.0067  -0.0056   0.0208 1.0003      4393     5702
## scramble2    0.0501     0.0080   0.0345   0.0658 1.0006     14093     8047
## scramble3   -0.0055     0.0082  -0.0216   0.0104 1.0004     13825     8272
## scramble4   -0.0154     0.0081  -0.0312   0.0004 1.0000     13445     8426
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1122     0.0021   0.1081   0.1163 1.0002     19492     7847
## 
## Draws were sampled using sampling(NUTS). 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).
```

Main effect of group

```
BF_nested_mus <- bayes_factor(nested_3way, nested_noMus)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6

print(BF_nested_mus)

## Estimated Bayes factor in favor of nested_3way over nested_noMus: 0.07838
```

Strong evidence against a main effect of group.

Main effect of condition

```
BF_nested_scram <- bayes_factor(nested_3way, nested_noScram)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6

print(BF_nested_scram)

## Estimated Bayes factor in favor of nested_3way over nested_noScram: 3059905290500.95850
```

Very strong evidence for a main effect of condition.

Main effect of level

```
BF_nested_level <- bayes_factor(nested_3way, nested_noLevel)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
```

```
## Iteration: 6
## Iteration: 7
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
print(BF_nested_level)

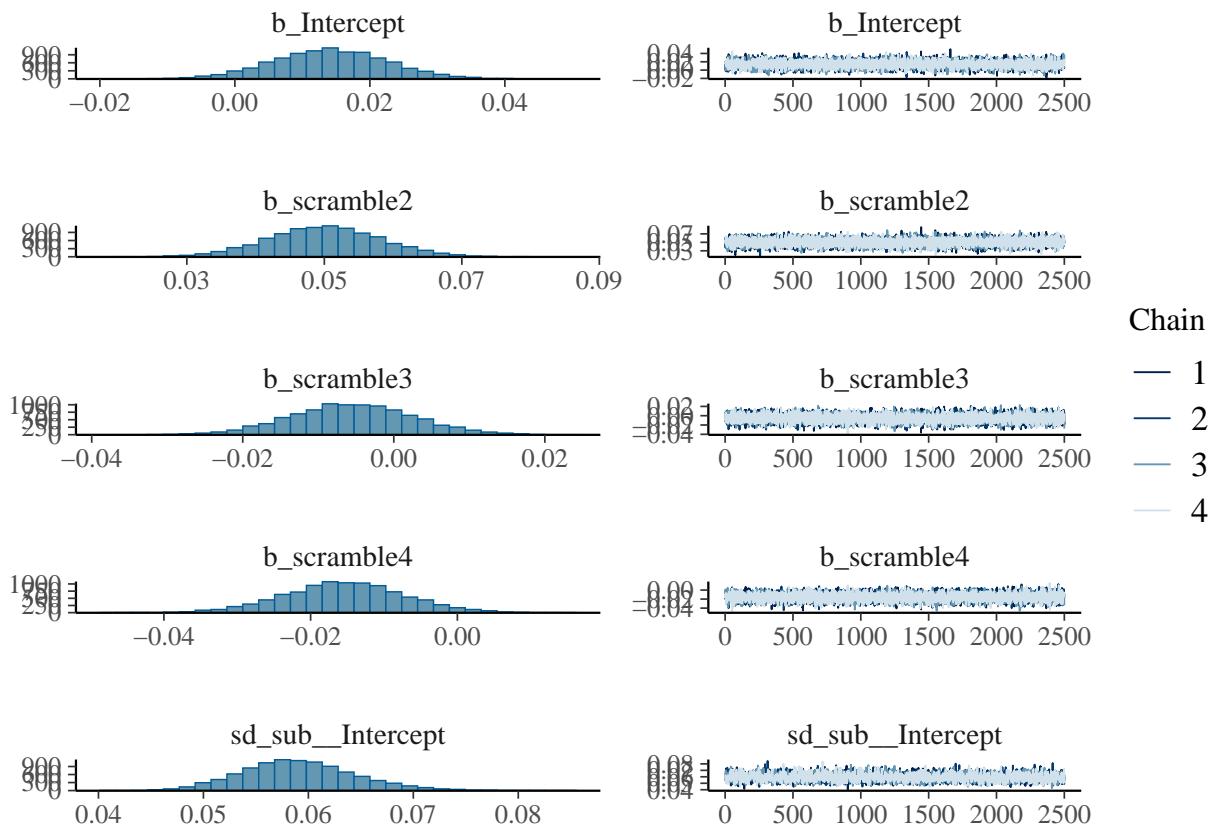
## Estimated Bayes factor in favor of nested_3way over nested_noLevel: 0.01005
Moderate evidence against a main effect of level.
```

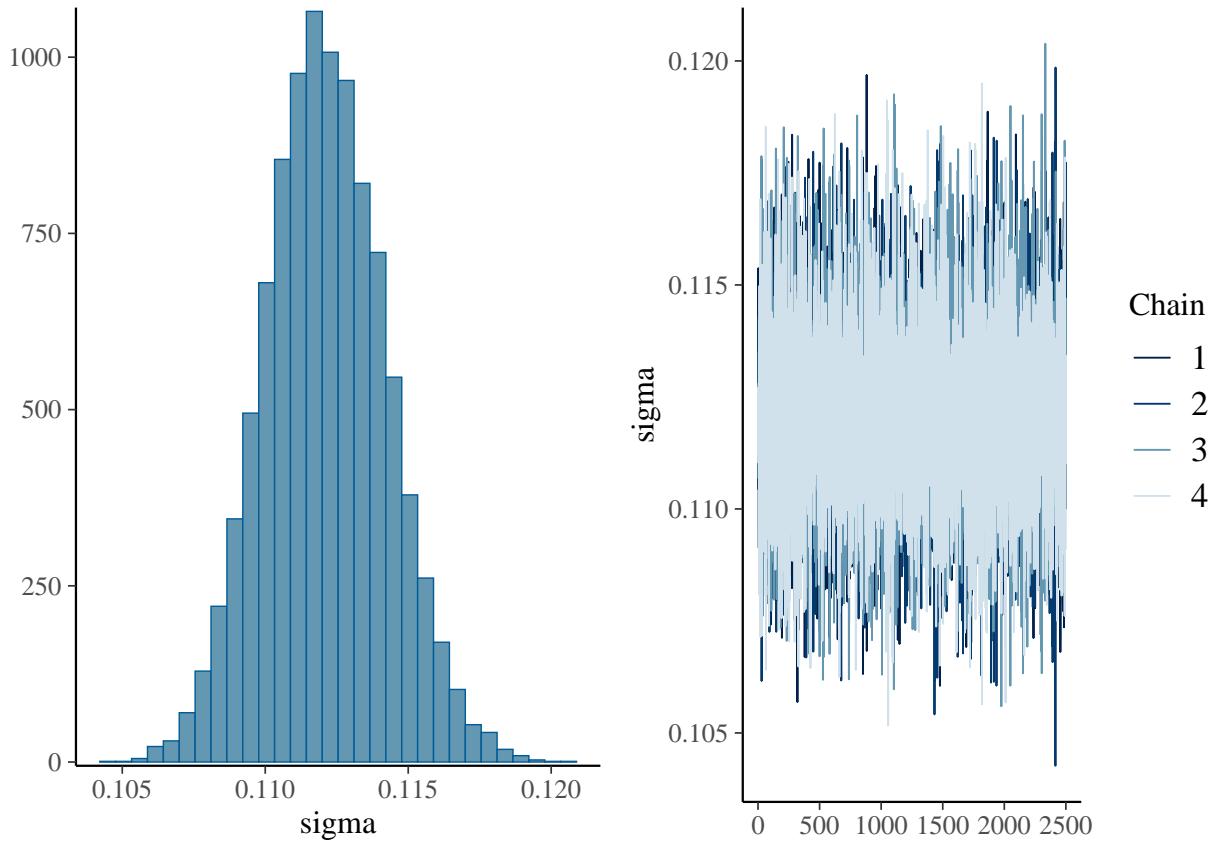
Interactions

Does adding an interaction between condition and level improve the model? (Without group)

```
nested_justScram <- brm(value ~ scramble + (1|sub), data = data_nested,
                         prior = c(
                           set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                           set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                           set_prior('normal(-0.1, 0.1)', coef = 'scramble4')
                         ),
                         save_pars = save_pars(all = TRUE), iter = 5000,
                         file = '../models/E3_alignment_justScram')
```

```
plot(nested_justScram)
```





```

print(summary(nested_justScram), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0591    0.0054   0.0493   0.0705 1.0013     3566    5783
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0141    0.0084  -0.0021   0.0307 1.0003     5250    6598
## scramble2    0.0500    0.0081   0.0341   0.0660 1.0003    14271    8059
## scramble3   -0.0055    0.0081  -0.0211   0.0105 1.0000    14606    8554
## scramble4   -0.0154    0.0082  -0.0315   0.0007 1.0000    13654    8488
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1121    0.0021   0.1081   0.1164 1.0006    19163     7000
## 
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential

```

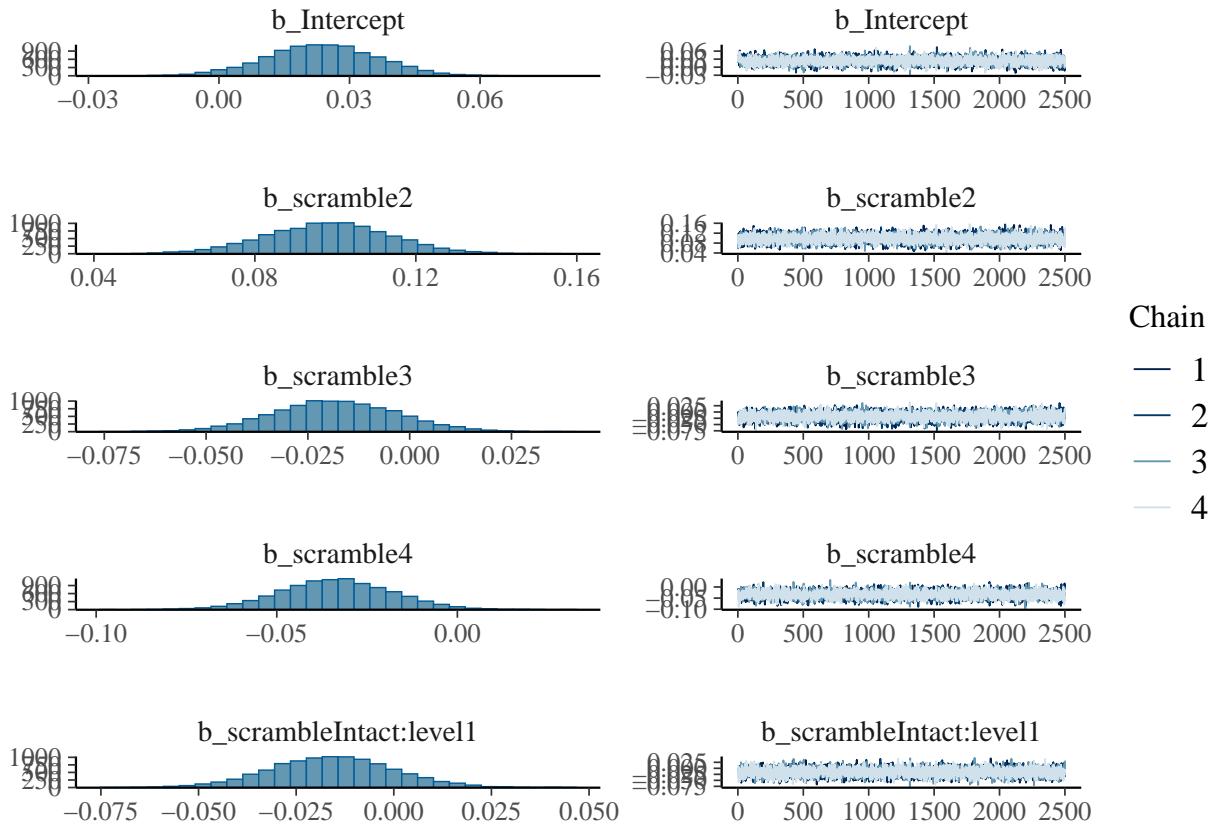
```
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

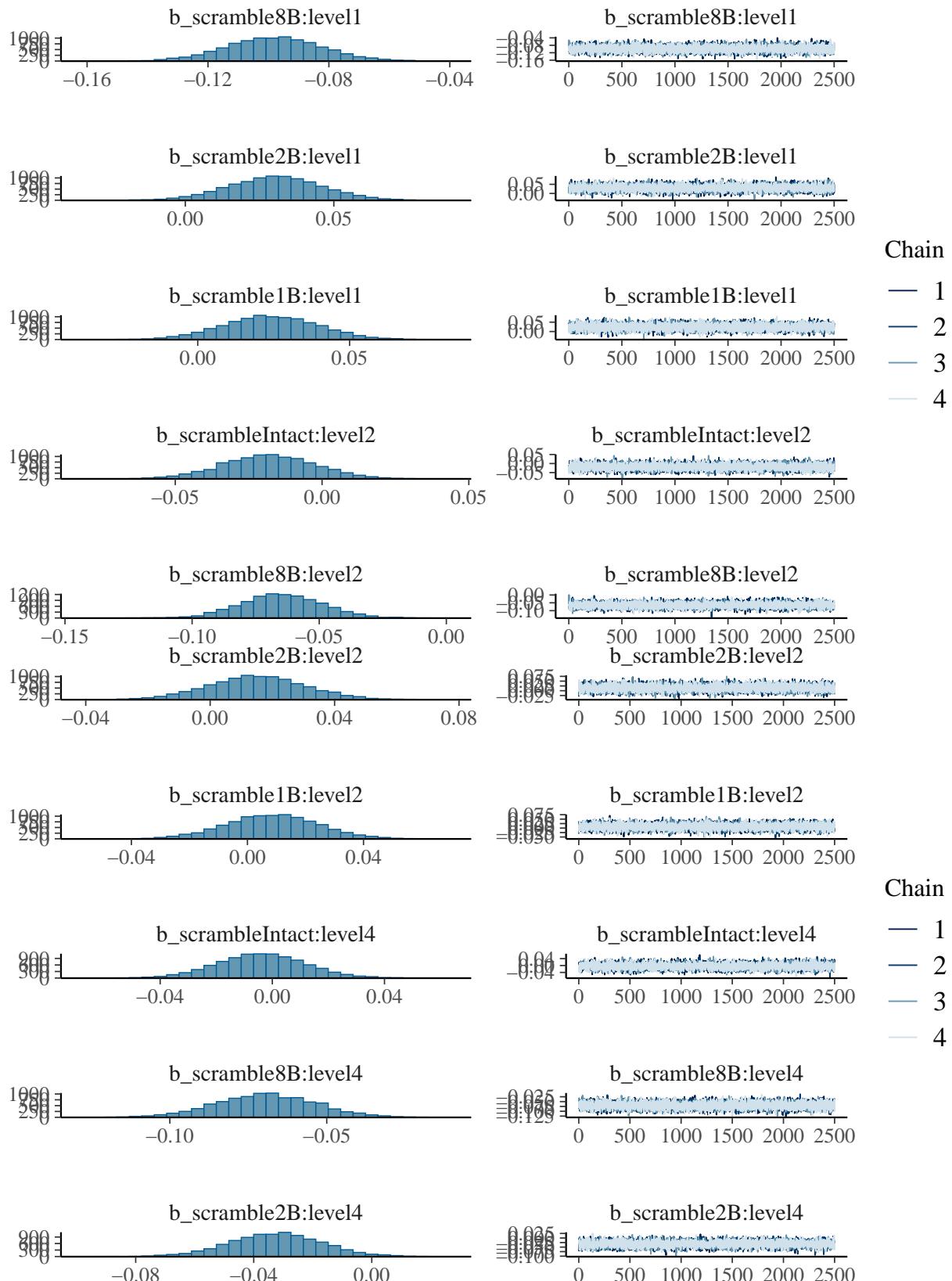
```

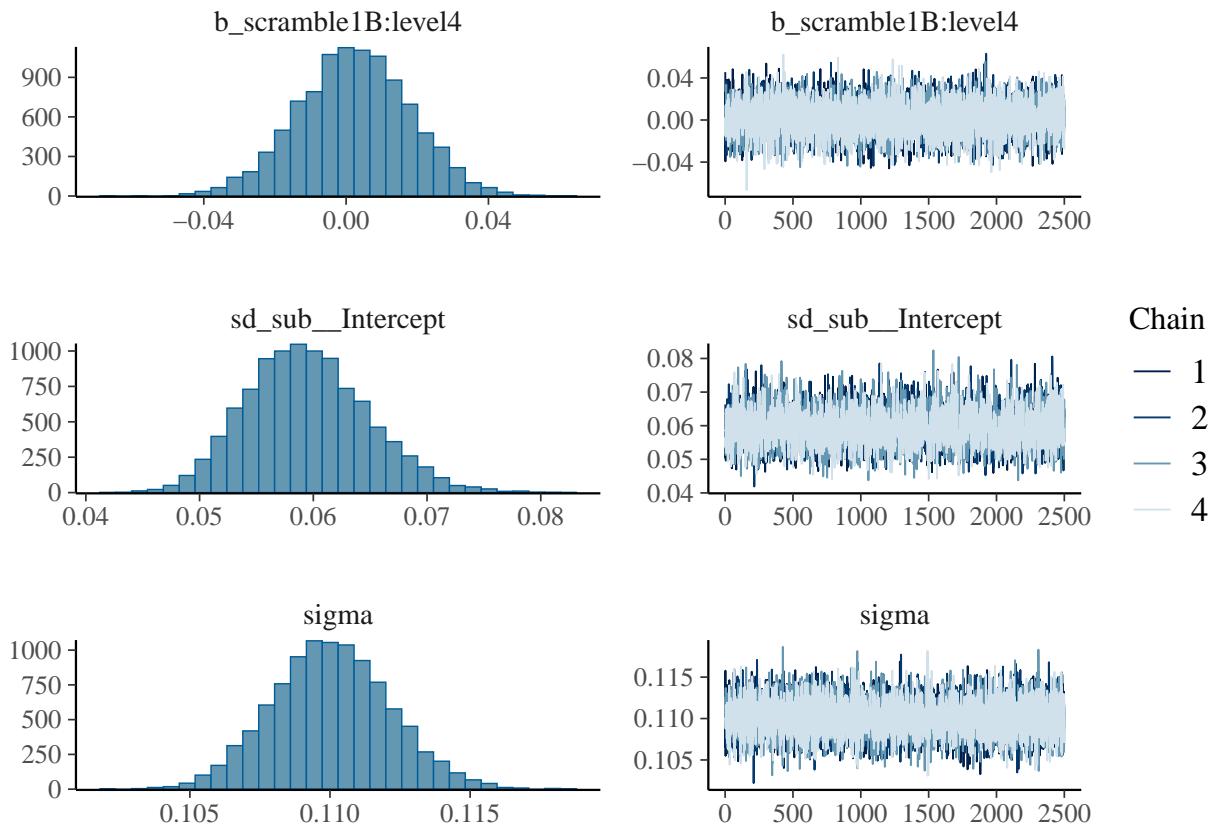
nested_2way_levelScram <- brm(value ~ scramble + scramble:level + (1|sub), data = data_nested,
                               prior = c(
                                 set_prior('normal(0, 0.1)', class = 'b'), # all interactions
                                 set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                                 set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                                 set_prior('normal(-0.1, 0.1)', coef = 'scramble4')
                               ),
                               save_pars = save_pars(all = TRUE), iter = 5000,
                               file = '../models/E3_alignment_2way_levelScramInt')

```

```
plot(nested_2way_levelScram)
```







```
print(summary(nested_2way_levelScram), digits = 4)
```

```
## Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: value ~ scramble + scramble:level + (1 | sub)
##   Data: data_nested (Number of observations: 1520)
##   Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0595  0.0053  0.0499  0.0705 1.0009  2952    4596
##
## Regression Coefficients:
##                               Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS
## Intercept                  0.0236  0.0126 -0.0013  0.0480 1.0007  4334
## scramble2                   0.0983  0.0155  0.0675  0.1288 1.0004  5400
## scramble3                 -0.0182  0.0153 -0.0479  0.0121 1.0004  5206
## scramble4                 -0.0336  0.0156 -0.0643 -0.0033 1.0000  5738
## scrambleIntact:level1     -0.0158  0.0157 -0.0468  0.0154 1.0006  7217
## scramble8B:level1        -0.0980  0.0156 -0.1289 -0.0670 0.9999  8576
## scramble2B:level1         0.0304  0.0157 -0.0004  0.0610 1.0001  9549
## scramble1B:level1         0.0241  0.0155 -0.0062  0.0542 1.0006  9142
## scrambleIntact:level2     -0.0180  0.0156 -0.0486  0.0126 1.0002  7218
## scramble8B:level2        -0.0647  0.0158 -0.0947 -0.0339 1.0011  9295
## scramble2B:level2         0.0151  0.0155 -0.0151  0.0458 1.0000  9267
## scramble1B:level2         0.0085  0.0157 -0.0230  0.0391 1.0000  9387
```

```

## scrambleIntact:level4 -0.0039  0.0157 -0.0347  0.0269 1.0003    7070
## scramble8B:level4     -0.0694  0.0158 -0.1006 -0.0385 1.0007    9160
## scramble2B:level4     -0.0325  0.0155 -0.0636 -0.0021 1.0004    9107
## scramble1B:level4      0.0023  0.0157 -0.0293  0.0326 1.0002    9621
##
##                                     Tail_ESS
## Intercept                         5906
## scramble2                          6852
## scramble3                          6841
## scramble4                          6741
## scrambleIntact:level1             7505
## scramble8B:level1                7640
## scramble2B:level1                8256
## scramble1B:level1                7961
## scrambleIntact:level2             7683
## scramble8B:level2                8281
## scramble2B:level2                8017
## scramble1B:level2                7587
## scrambleIntact:level4             7747
## scramble8B:level4                8314
## scramble2B:level4                7694
## scramble1B:level4                7609
##
## Further Distributional Parameters:
##           Estimate   Est.Error  l-95% CI  u-95% CI   Rhat Bulk_ESS Tail_ESS
## sigma     0.1100    0.0021    0.1060    0.1143 0.9999    16014     7177
##
## Draws were sampled using sampling(NUTS). 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).
BF_nested_2way_levelScram <- bayes_factor(nested_2way_levelScram, nested_justScram)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6

print(BF_nested_2way_levelScram)

## Estimated Bayes factor in favor of nested_2way_levelScram over nested_justScram: 3116.78694
Strong evidence for an interaction between condition and level.

```

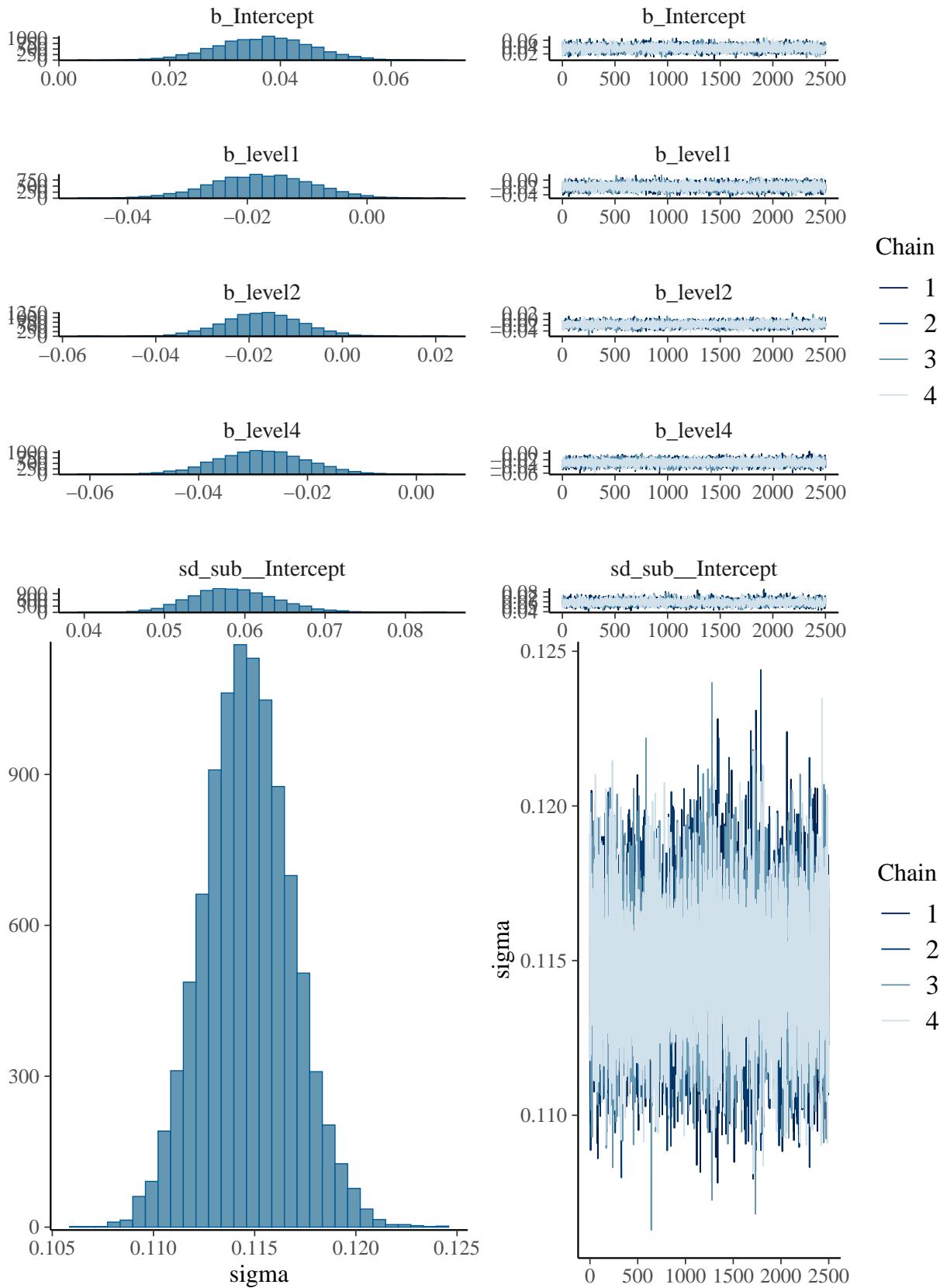
Check the other interactions.

```
nested_justLevel <- brm(value ~ level + (1|sub), data = data_nested,
                         prior = c(
                           set_prior('normal(-0.2, 0.1)', coef = 'level1'),
                           set_prior('normal(-0.1, 0.1)', coef = c('level2', 'level4'))
                         ),
                         save_pars = save_pars(all = TRUE), iter = 5000,
                         file = '../models/E3_alignment_justLevel')

nested_2way_musScram <- brm(value ~ scramble + scramble:Musician + (1|sub), data = data_nested,
                               prior = c(
                                 set_prior('normal(0, 0.1)', class = 'b'), # all interactions
                                 set_prior('normal(0.1, 0.1)', coef = 'scramble2'),
                                 set_prior('normal(-0.1, 0.1)', coef = 'scramble3'),
                                 set_prior('normal(-0.1, 0.1)', coef = 'scramble4')
                               ),
                               save_pars = save_pars(all = TRUE), iter = 5000,
                               file = '../models/E3_alignment_2way_musScramInt')

nested_2way_musLevel <- brm(value ~ level + level:Musician + (1|sub), data = data_nested,
                             prior = c(
                               set_prior('normal(0, 0.1)', class = 'b'), # all interactions
                               set_prior('normal(-0.2, 0.1)', coef = 'level1'),
                               set_prior('normal(-0.1, 0.1)', coef = c('level2', 'level4'))
                             ),
                             save_pars = save_pars(all = TRUE), iter = 5000,
                             file = '../models/E3_alignment_2way_musLevelInt')
```

```
plot(nested_justLevel)
```



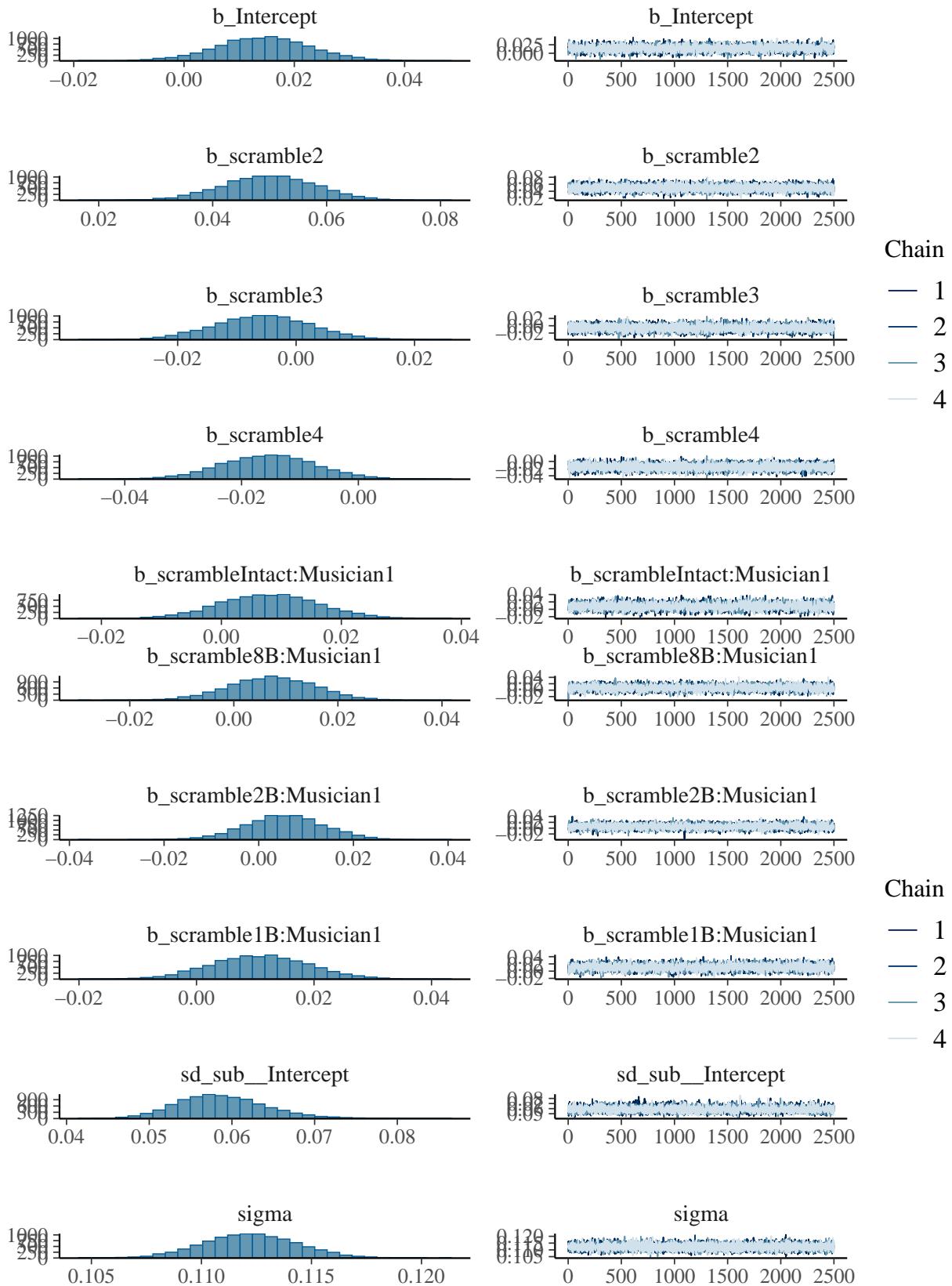
```

print(summary(nested_justLevel), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ level + (1 | sub)
##  Data: data_nested (Number of observations: 1520)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0587   0.0053   0.0490   0.0700 1.0005     3963     5422
##
## Regression Coefficients:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept   0.0371   0.0085   0.0206   0.0536 1.0003     5433     6849
## level1     -0.0176   0.0083  -0.0339  -0.0016 1.0001    13005     8604
## level2     -0.0171   0.0083  -0.0336  -0.0009 1.0001    13437     8302
## level4     -0.0284   0.0082  -0.0448  -0.0124 1.0003    13738     8414
##
## Further Distributional Parameters:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.1147   0.0022   0.1105   0.1190 1.0005    16404     7126
##
## Draws were sampled using sampling(NUTS). 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).

```

```
plot(nested_2way_musScram)
```



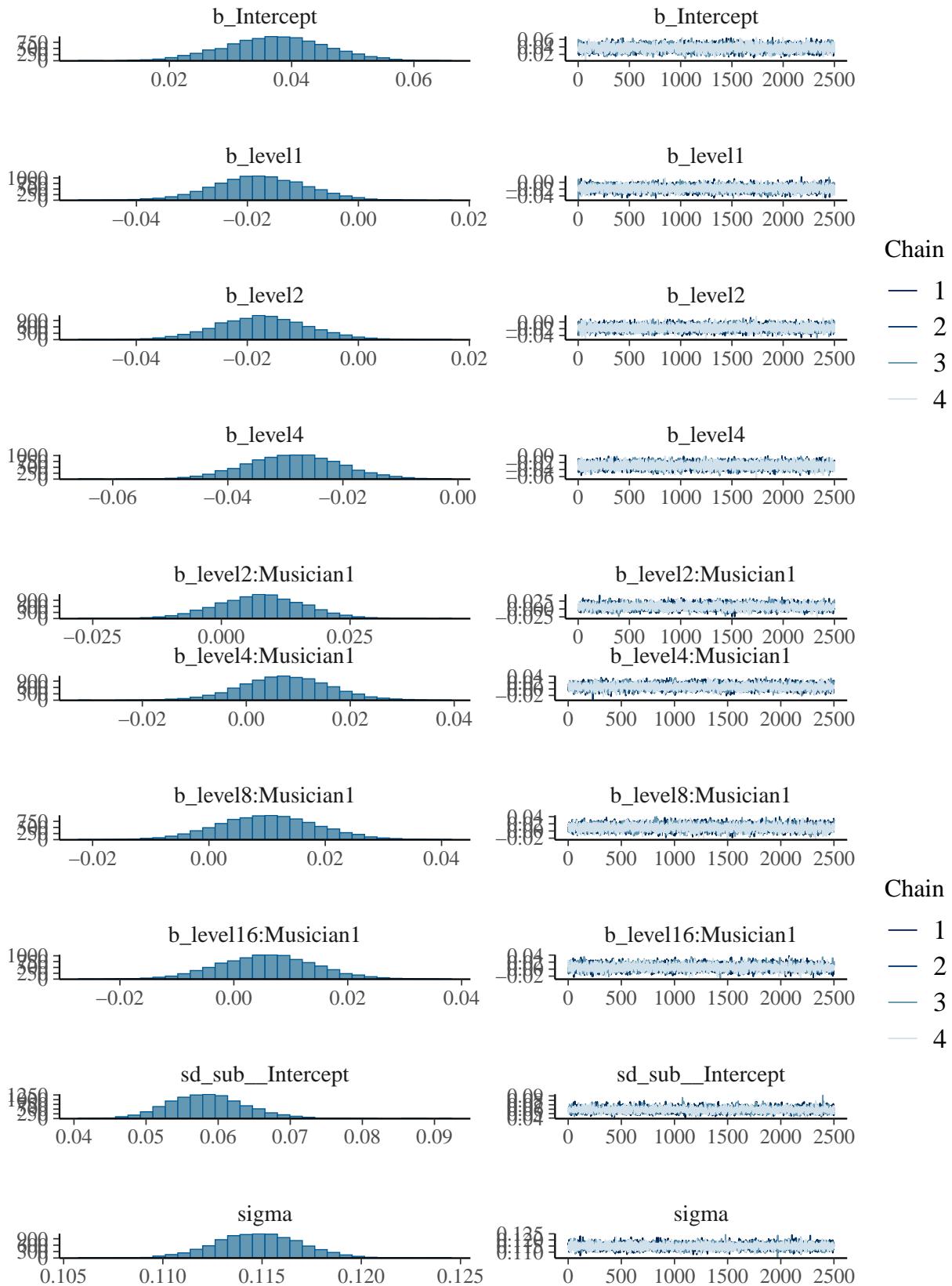
```

print(summary(nested_2way_musScram), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble + scramble:Musician + (1 | sub)
##   Data: data_nested (Number of observations: 1520)
##   Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0588   0.0054   0.0492   0.0703 1.0010      3748     5803
##
## Regression Coefficients:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS
## Intercept        0.0145   0.0085  -0.0024   0.0312 1.0004      5460
## scramble2         0.0499   0.0081   0.0342   0.0657 1.0002     13673
## scramble3        -0.0056   0.0081  -0.0214   0.0101 1.0001     14980
## scramble4        -0.0154   0.0081  -0.0312   0.0004 1.0000     14578
## scrambleIntact:Musician1  0.0080   0.0083  -0.0082   0.0242 1.0011     4416
## scramble8B:Musician1    0.0073   0.0082  -0.0090   0.0230 1.0009     4464
## scramble2B:Musician1    0.0055   0.0083  -0.0106   0.0217 1.0013     4549
## scramble1B:Musician1    0.0108   0.0082  -0.0051   0.0270 1.0003     4331
##
## Tail_ESS
## Intercept        7142
## scramble2        8222
## scramble3        8757
## scramble4        8592
## scrambleIntact:Musician1  7032
## scramble8B:Musician1    6617
## scramble2B:Musician1    6468
## scramble1B:Musician1    6517
##
## Further Distributional Parameters:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma     0.1122   0.0021   0.1081   0.1164 1.0006      18544     7191
##
## Draws were sampled using sampling(NUTS). 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).

```

```
plot(nested_2way_musLevel)
```



```

print(summary(nested_2way_musLevel), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ level + level:Musician + (1 | sub)
##   Data: data_nested (Number of observations: 1520)
##   Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0586    0.0054   0.0486   0.0700 1.0004      3506     5134
##
## Regression Coefficients:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept       0.0374    0.0083   0.0213   0.0536 0.9999      6507     6965
## level1        -0.0177    0.0082  -0.0338  -0.0015 1.0000     13964     8190
## level2        -0.0172    0.0082  -0.0330  -0.0010 1.0002     13626     7944
## level4        -0.0285    0.0082  -0.0445  -0.0124 1.0004     13921     8351
## level2:Musician1  0.0076    0.0084  -0.0088   0.0241 1.0008      4710     6688
## level4:Musician1  0.0076    0.0084  -0.0090   0.0244 1.0008      4986     7103
## level8:Musician1  0.0102    0.0085  -0.0064   0.0269 1.0011      4872     6281
## level16:Musician1 0.0059    0.0084  -0.0104   0.0225 1.0009      4800     6367
##
## Further Distributional Parameters:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma     0.1148    0.0021   0.1106   0.1190 1.0002     19386     7490
##
## Draws were sampled using sampling(NUTS). 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).

```

```

BF_nested_2way_musScram <- bayes_factor(nested_2way_musScram, nested_justScram)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6

print(BF_nested_2way_musScram)

## Estimated Bayes factor in favor of nested_2way_musScram over nested_justScram: 0.00006
BF_nested_2way_musLevel <- bayes_factor(nested_2way_musLevel, nested_justLevel)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7

print(BF_nested_2way_musLevel)

## Estimated Bayes factor in favor of nested_2way_musLevel over nested_justLevel: 0.00006

```

Very strong evidence against interactions between group and condition and group and level.

1B

```

data1B <- filter(data, scramble == '1B')

levels1B_null <- brm(value ~ 1 + (1|sub), data = data1B,
                      save_pars = save_pars(all = TRUE), iter = 5000,
                      file = '../models/E3_alignment_1B_null')

plot(levels1B_null)

```

The figure consists of four subplots arranged in a 2x2 grid. The top row shows histograms of the posterior distributions for `b_Intercept` (left) and `sd_sub_Intercept` (right). The bottom row shows trace plots for `sd_sub_Intercept` (left) and `sigma` (right), with a legend indicating four chains (Chain 1: solid black, Chain 2: dashed black, Chain 3: solid blue, Chain 4: dashed blue).

```

print(summary(levels1B_null), digits = 4)

## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: value ~ 1 + (1 | sub)
## Data: data1B (Number of observations: 665)
## Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##        total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0556     0.0053   0.0459    0.0670 1.0013      4063     6024
##
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0003     0.0065 -0.0123    0.0131 1.0004      5275     7011
##

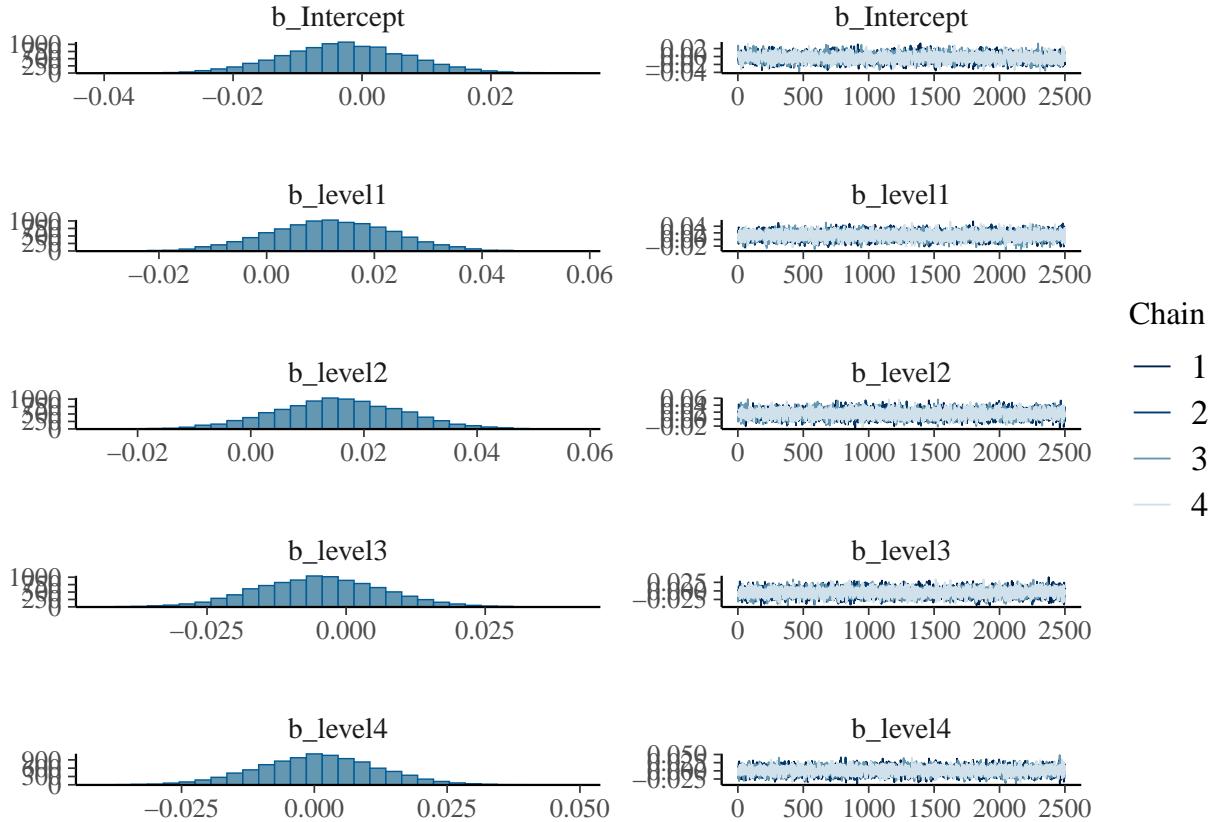
```

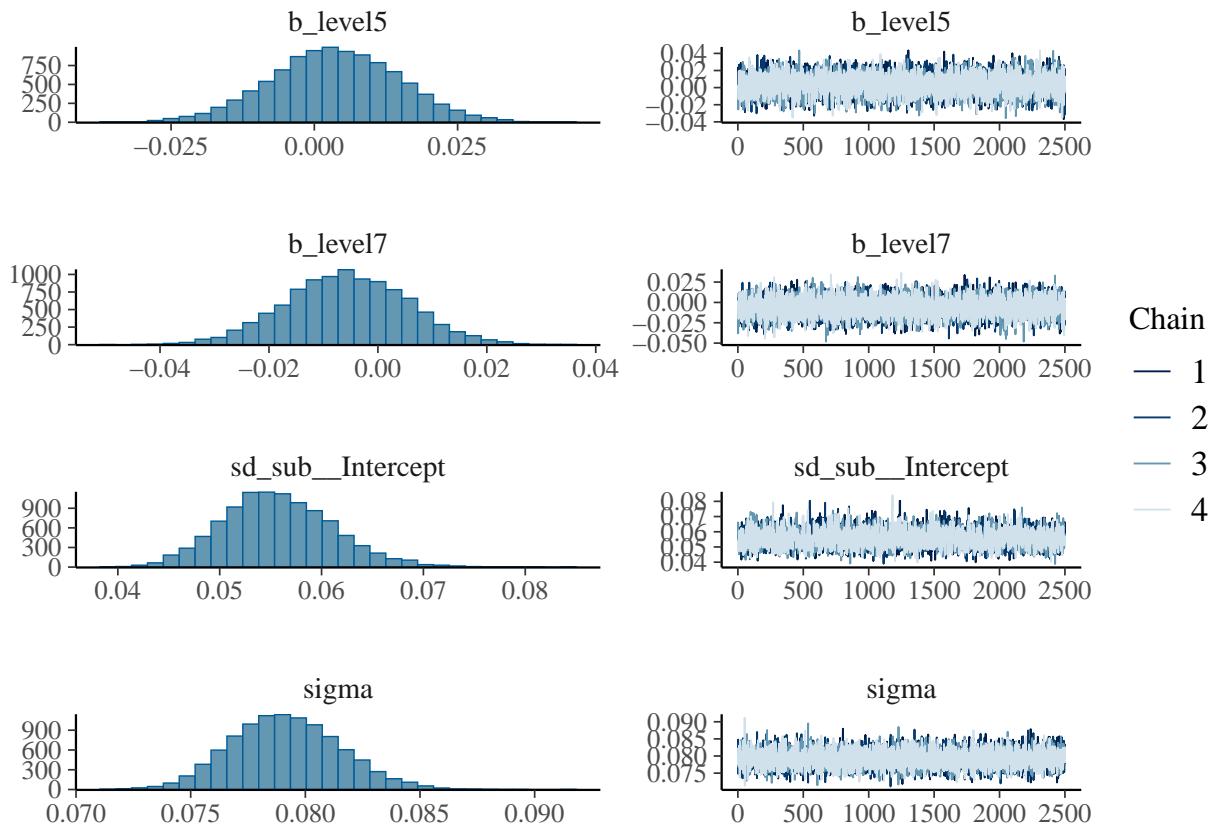
```

## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.0793   0.0024   0.0747   0.0840 1.0002     13916     7245
## 
## Draws were sampled using sampling(NUTS). 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).
levels1B <- brm(value ~ level + (1|sub), data = data1B,
                  prior = c(
                    set_prior('normal(-0.2, 0.1)', coef = c('level1', 'level2', 'level3', 'level5')),
                    set_prior('normal(-0.1, 0.1)', coef = c('level4', 'level7')))
                  ),
                  save_pars = save_pars(all = TRUE), iter = 5000,
                  file = '../models/E3_alignment_1B')

```

```
plot(levels1B)
```





```
print(summary(levels1B), digits = 4)
```

```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ level + (1 | sub)
##  Data: data1B (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0557    0.0054   0.0458   0.0671 1.0004     4224     5209
##
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept -0.0026    0.0097  -0.0216   0.0166 1.0009     6258     6415
## level1    0.0120    0.0114  -0.0105   0.0343 1.0001     9051     8223
## level2    0.0155    0.0112  -0.0065   0.0376 1.0002     8787     8131
## level3   -0.0047    0.0113  -0.0265   0.0173 1.0001     8414     7808
## level4    0.0007    0.0113  -0.0217   0.0225 1.0000     9150     8473
## level5    0.0036    0.0112  -0.0186   0.0256 0.9999     9024     8090
## level7   -0.0058    0.0112  -0.0276   0.0163 0.9998     9171     8121
##
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma     0.0792    0.0024   0.0748   0.0839 1.0001    13943     8310
##
```

```
## Draws were sampled using sampling(NUTS). 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).
```

```
BF_1B_level <- bayes_factor(levels1B, levels1B_null)
```

```
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6
```

```
print(BF_1B_level)
```

```
## Estimated Bayes factor in favor of levels1B over levels1B_null: 0.00000
```

There is very strong evidence against a main effect of level.

```
emm_1B <- emmeans(levels1B, specs = "level")  
summary(emm_1B)
```

```
##   level    emmean lower.HPD upper.HPD  
## 1      0.00927 -0.00958   0.0300  
## 2      0.01292 -0.00642   0.0327  
## 3     -0.00747 -0.02564   0.0131  
## 4     -0.00198 -0.02143   0.0174  
## 5      0.00115 -0.01797   0.0210  
## 8     -0.00271 -0.02171   0.0164  
## 16    -0.00844 -0.02826   0.0107  
##
```

```
## Point estimate displayed: median  
## HPD interval probability: 0.95
```

All levels at chance.

```
contrast(emm_1B, method = "pairwise")
```

```
##   contrast      estimate lower.HPD upper.HPD  
## 1 level1 - level2 -0.003504 -0.02617   0.0195  
## 2 level1 - level3  0.016705 -0.00460   0.0399  
## 3 level1 - level4  0.011409 -0.01038   0.0345  
## 4 level1 - level5  0.008379 -0.01424   0.0316  
## 5 level1 - level8  0.011872 -0.01137   0.0331  
## 6 level1 - level16 0.017710 -0.00625   0.0390  
## 7 level2 - level3  0.020238 -0.00212   0.0426  
## 8 level2 - level4  0.014941 -0.00795   0.0367  
## 9 level2 - level5  0.011933 -0.01171   0.0336  
## 10 level2 - level8 0.015440 -0.00760   0.0365  
## 11 level2 - level16 0.021204 -0.00109   0.0427  
## 12 level3 - level4 -0.005433 -0.02752   0.0170  
## 13 level3 - level5 -0.008274 -0.03026   0.0137
```

```
##  level3 - level8  -0.004791  -0.02616   0.0177
##  level3 - level16  0.001046  -0.02058   0.0238
##  level4 - level5  -0.002798  -0.02472   0.0196
##  level4 - level8   0.000721  -0.02189   0.0223
##  level4 - level16  0.006454  -0.01607   0.0283
##  level5 - level8   0.003521  -0.01727   0.0268
##  level5 - level16  0.009302  -0.01347   0.0314
##  level8 - level16  0.005786  -0.01630   0.0276
##
## Point estimate displayed: median
## HPD interval probability: 0.95
```

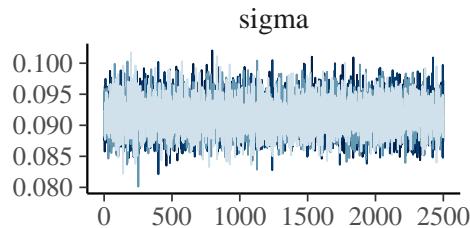
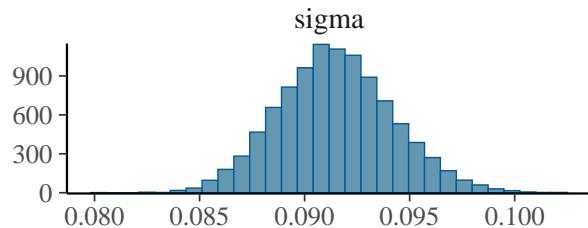
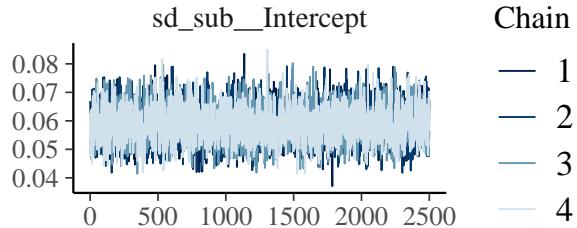
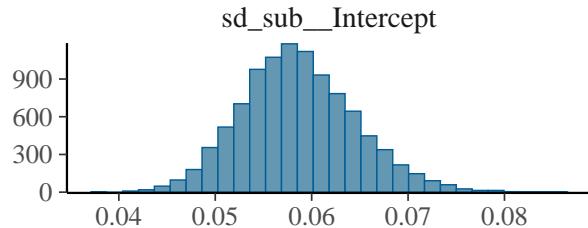
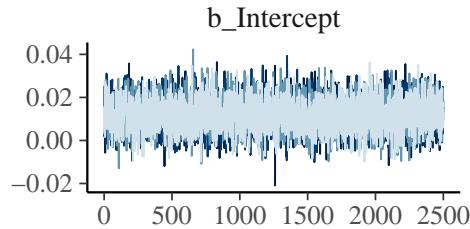
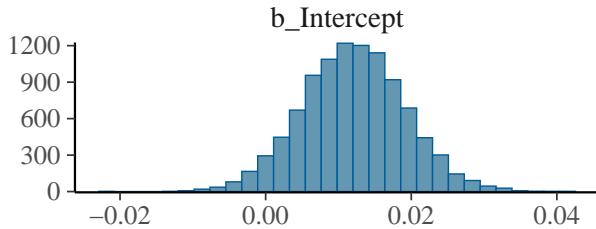
No differences between any levels.

2B

```
data2B <- filter(data, scramble == '2B')

levels2B_null <- brm(value ~ 1 + (1|sub), data = data2B,
                      save_pars = save_pars(all = TRUE), iter = 5000,
                      file = '../models/E3_alignment_2B_null')

plot(levels2B_null)
```



```
print(summary(levels2B_null), digits = 4)
```

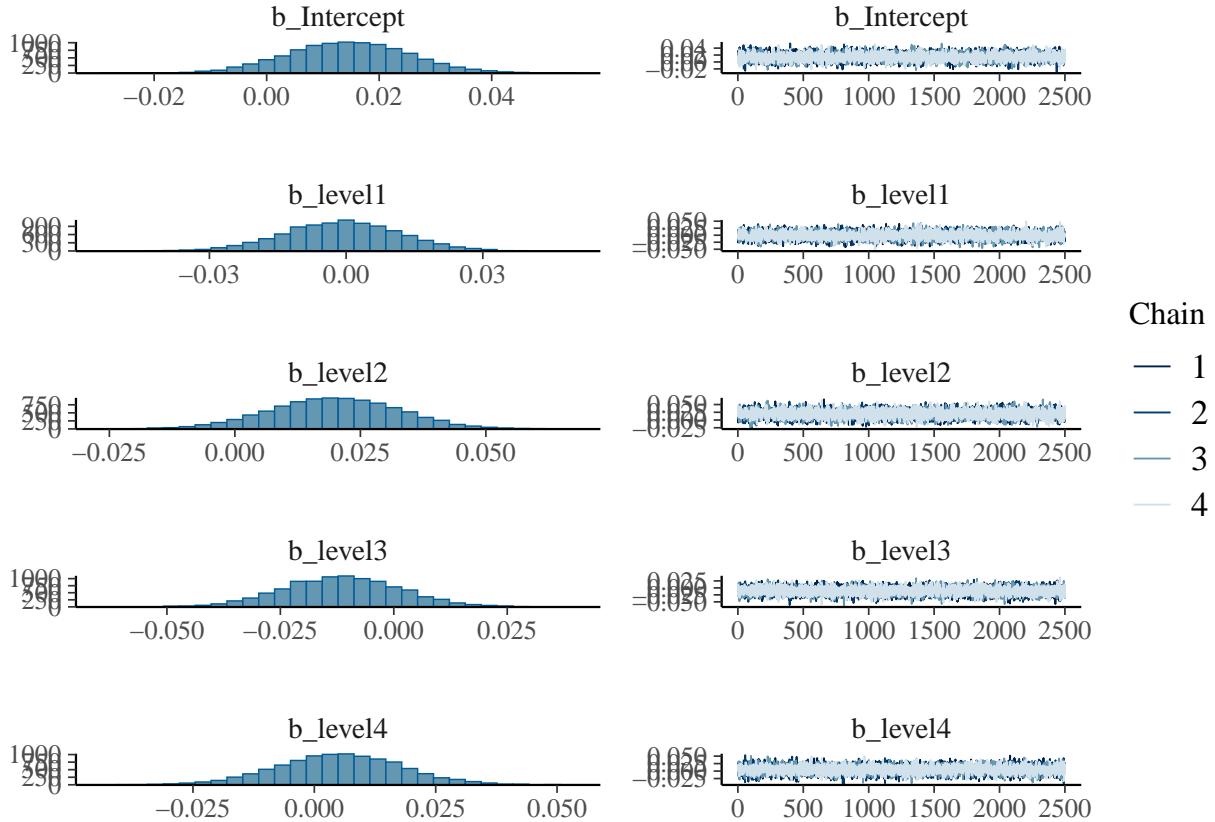
```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ 1 + (1 | sub)
##  Data: data2B (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##        total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0586     0.0059   0.0478    0.0711 1.0009      4125     5625
##
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0120     0.0071  -0.0018    0.0260 1.0000      6880     7618
## 
```

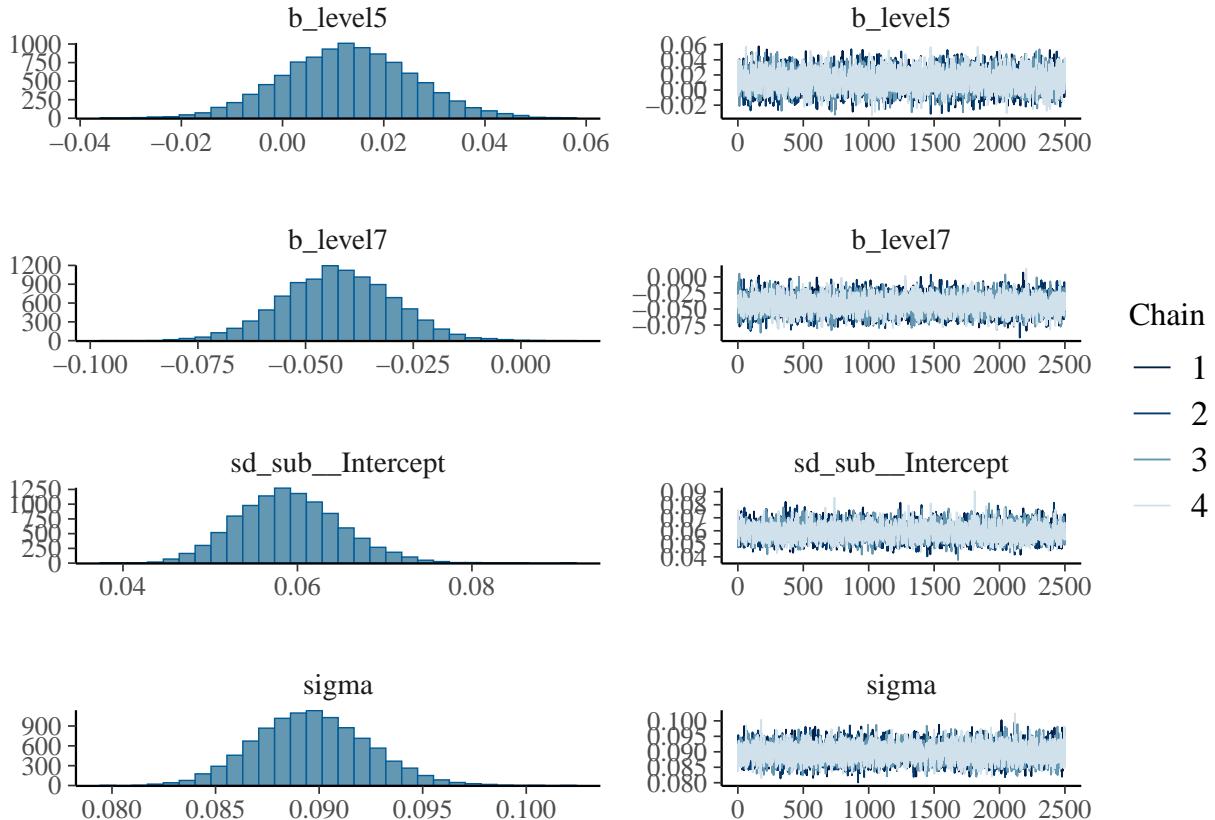
```

## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.0915   0.0027   0.0863   0.0970 1.0002     13984     7742
## 
## Draws were sampled using sampling(NUTS). 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).
levels2B <- brm(value ~ level + (1|sub), data = data2B,
  prior = c(
    set_prior('normal(-0.2, 0.1)', coef = c('level1', 'level2', 'level3', 'level5')),
    set_prior('normal(-0.1, 0.1)', coef = c('level4', 'level7')))
  ),
  save_pars = save_pars(all = TRUE), iter = 5000,
  file = '../models/E3_alignment_2B')

```

```
plot(levels2B)
```





```
print(summary(levels2B), digits = 4)
```

```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ level + (1 | sub)
##  Data: data2B (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0591     0.0059   0.0481   0.0715 1.0010      4068     5833
##
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0145     0.0108  -0.0061   0.0358 1.0001      6762     6713
## level1     -0.0008     0.0128  -0.0259   0.0244 1.0006      9463     8580
## level2      0.0198     0.0128  -0.0054   0.0442 1.0003      9465     8374
## level3     -0.0115     0.0129  -0.0363   0.0140 1.0000     10156     8448
## level4      0.0052     0.0128  -0.0201   0.0304 1.0010      9868     8308
## level5      0.0129     0.0129  -0.0121   0.0384 1.0009      9346     8260
## level7     -0.0425     0.0129  -0.0679  -0.0176 1.0000     9430     8494
##
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.0896     0.0027   0.0845   0.0951 1.0005     12185     7788
##
```

```
## Draws were sampled using sampling(NUTS). 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).
```

```
BF_2B_level <- bayes_factor(levels2B, levels2B_null)
```

```
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6
```

```
print(BF_2B_level)
```

```
## Estimated Bayes factor in favor of levels2B over levels2B_null: 0.00043
```

There is strong evidence against an effect of level.

```
emm_2B <- emmeans(levels2B, specs = "level")  
summary(emm_2B)
```

```
##   level    emmean lower.HPD upper.HPD  
## 1     0.01380 -0.00776  0.03597  
## 2     0.03437  0.01198  0.05490  
## 3     0.00318 -0.01833  0.02496  
## 4     0.01965 -0.00234  0.04109  
## 5     0.02756  0.00606  0.04965  
## 8     0.01442 -0.00681  0.03501  
## 16    -0.02788 -0.05023 -0.00669  
##  
## Point estimate displayed: median  
## HPD interval probability: 0.95
```

Above chance: 2, 5 Below chance: 16 All others at chance

```
contrast(emm_2B, method = "pairwise")
```

```
##   contrast      estimate lower.HPD upper.HPD  
## 1 level1 - level2 -0.020412 -0.04686  0.00454  
## 2 level1 - level3  0.010721 -0.01526  0.03449  
## 3 level1 - level4 -0.006027 -0.03050  0.02036  
## 4 level1 - level5 -0.013740 -0.03948  0.01195  
## 5 level1 - level8 -0.000761 -0.02640  0.02369  
## 6 level1 - level16  0.041821  0.01539  0.06703  
## 7 level2 - level3  0.031210  0.00705  0.05818  
## 8 level2 - level4  0.014685 -0.01060  0.04040  
## 9 level2 - level5  0.006683 -0.01941  0.03188  
## 10 level2 - level8  0.019879 -0.00573  0.04373  
## 11 level2 - level16  0.062305  0.03670  0.08812  
## 12 level3 - level4 -0.016544 -0.04289  0.00921  
## 13 level3 - level5 -0.024460 -0.04991  0.00204  
## 14 level3 - level8 -0.011503 -0.03779  0.01224
```

```
##  level3 - level16  0.031046  0.00491  0.05669
##  level4 - level5  -0.007902 -0.03299  0.01779
##  level4 - level8   0.005247 -0.01882  0.03161
##  level4 - level16  0.047719  0.02201  0.07316
##  level5 - level8   0.012899 -0.01241  0.03802
##  level5 - level16  0.055429  0.02896  0.08095
##  level8 - level16  0.042603  0.01749  0.06774
##
## Point estimate displayed: median
## HPD interval probability: 0.95
```

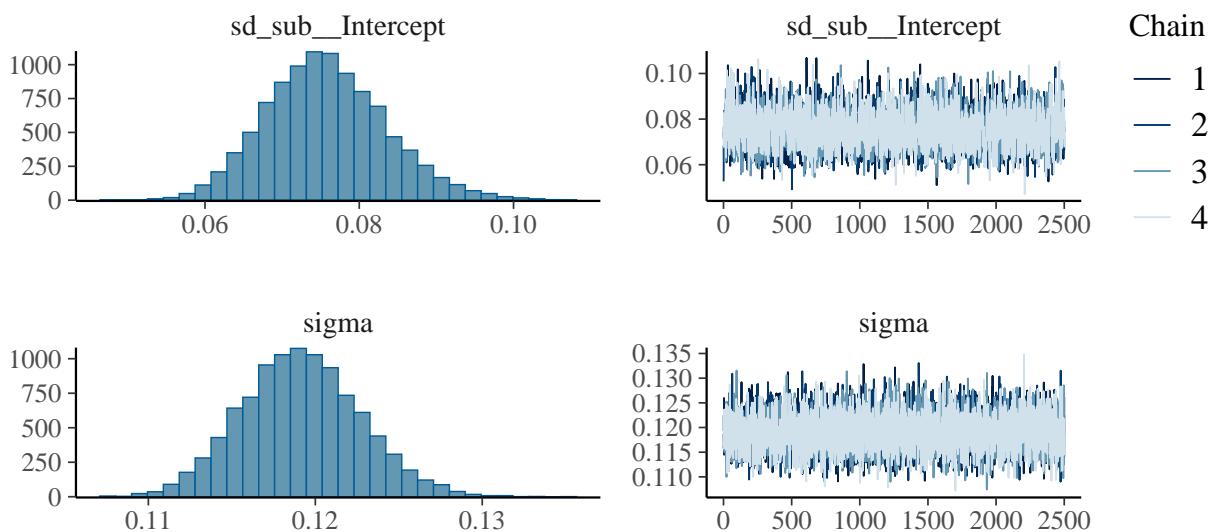
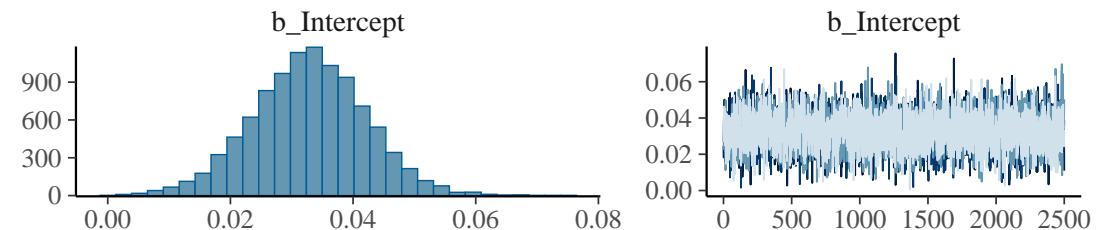
1 > 16, 2 > 16, 3 > 16, 4 > 16, 5 > 16, 8 > 16
2 > 3

8B

```
data8B <- filter(data, scramble == '8B')

levels8B_null <- brm(value ~ 1 + (1|sub), data = data8B,
                      save_pars = save_pars(all = TRUE), iter = 5000,
                      file = '../models/E3_alignment_8B_null')

plot(levels8B_null)
```



```
print(summary(levels8B_null), digits = 4)

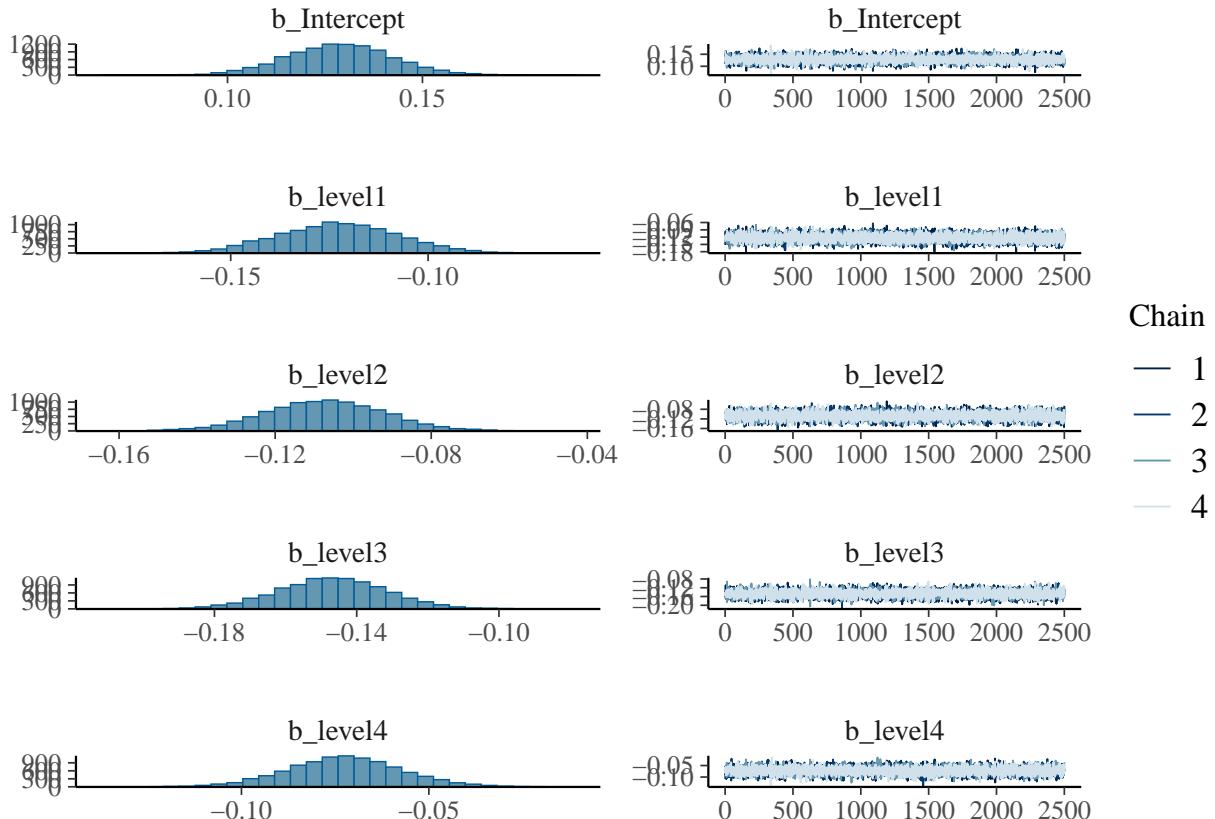
##  Family: gaussian
##  Links: mu = identity; sigma = identity
##  Formula: value ~ 1 + (1 | sub)
##  Data: data8B (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##         total post-warmup draws = 10000
##
##  Multilevel Hyperparameters:
##  ~sub (Number of levels: 95)
##                Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
##  sd(Intercept)   0.0757     0.0078    0.0614    0.0923 1.0019      3437     4643
##
##  Regression Coefficients:
##                Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
##  Intercept      0.0328     0.0093    0.0143    0.0508 1.0000      5892     6034
##
```

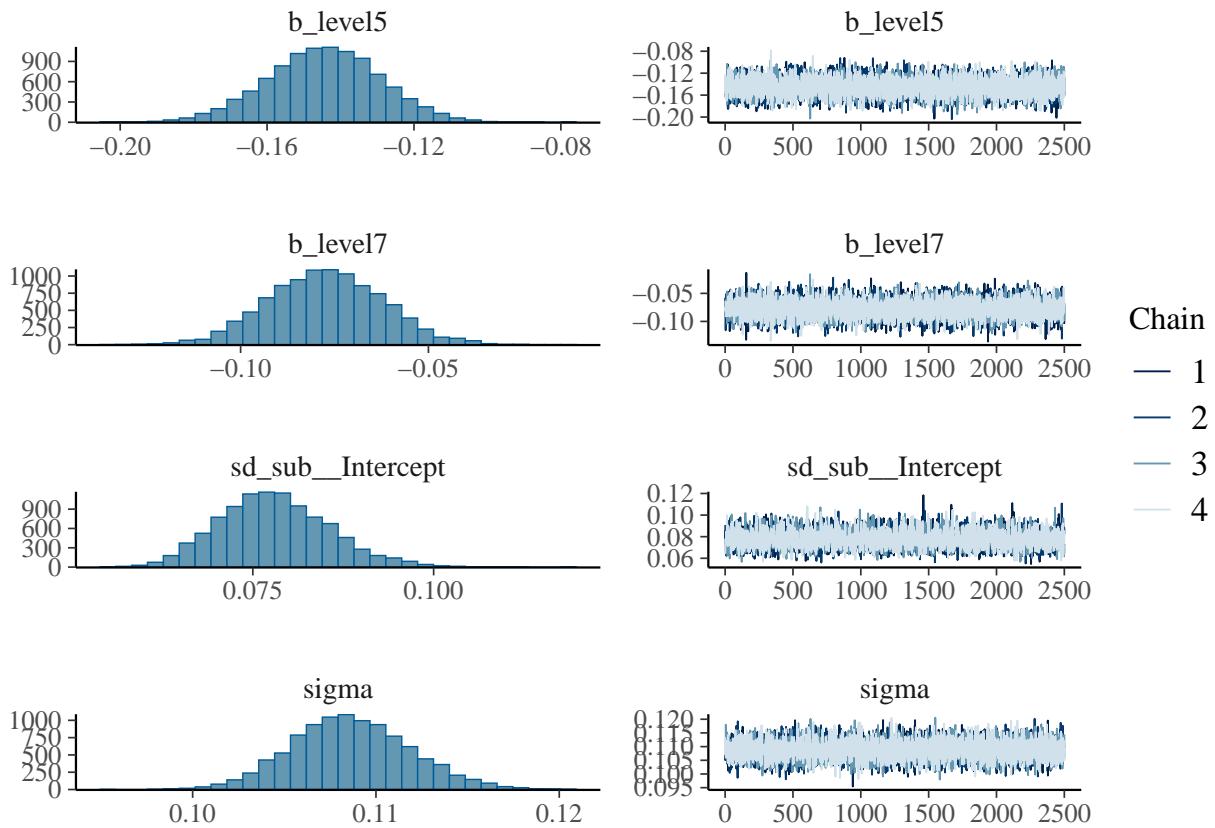
```

## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.1191   0.0036   0.1124   0.1263 1.0004     12203     7470
## 
## Draws were sampled using sampling(NUTS). 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).
levels8B <- brm(value ~ level + (1|sub), data = data8B,
  prior = c(
    set_prior('normal(-0.2, 0.1)', coef = c('level1', 'level2', 'level3', 'level5')),
    set_prior('normal(-0.1, 0.1)', coef = c('level4', 'level7')))
  ),
  save_pars = save_pars(all = TRUE), iter = 5000,
  file = '../models/E3_alignment_8B')

```

```
plot(levels8B)
```





```
print(summary(levels8B), digits = 4)
```

```
## Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: value ~ level + (1 | sub)
##   Data: data8B (Number of observations: 665)
##   Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0780    0.0076   0.0644   0.0943 1.0004     3636    5163
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.1287    0.0134   0.1025   0.1553 1.0004     7026    7246
## level1      -0.1228    0.0151  -0.1520  -0.0935 1.0009     9644    8680
## level2      -0.1072    0.0152  -0.1370  -0.0775 1.0006    10127    8498
## level3      -0.1469    0.0153  -0.1773  -0.1169 1.0003    9369    7962
## level4      -0.0724    0.0152  -0.1024  -0.0424 1.0001    10127    8407
## level5      -0.1445    0.0154  -0.1752  -0.1147 0.9998    10038    8903
## level7      -0.0774    0.0153  -0.1065  -0.0473 1.0004    10135    8515
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1087    0.0032   0.1026   0.1153 1.0001    14132    7739
## 
```

```

## Draws were sampled using sampling(NUTS). 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).

BF_8B_level <- bayes_factor(levels8B, levels8B_null)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5

print(BF_8B_level)

## Estimated Bayes factor in favor of levels8B over levels8B_null: 1478346635495802112.00000

There is very strong evidence for an effect of level.

emm_8B <- emmeans(levels8B, specs = "level")
summary(emm_8B)

##   level    emmean lower.HPD upper.HPD
## 1      0.00602 -0.02022   0.0328
## 2      0.02145 -0.00584   0.0476
## 3     -0.01811 -0.04395   0.0105
## 4      0.05624  0.02846   0.0819
## 5     -0.01576 -0.04236   0.0111
## 8      0.12878  0.10225   0.1547
## 16     0.05131  0.02468   0.0783
##
## Point estimate displayed: median
## HPD interval probability: 0.95

Above chance: 4, 8, 16 At chance: 1, 2, 3, 5

contrast(emm_8B, method = "pairwise")

##   contrast      estimate lower.HPD upper.HPD
## 1 level1 - level2 -0.01579 -0.04625  0.013196
## 2 level1 - level3  0.02410 -0.00781  0.053100
## 3 level1 - level4 -0.05024 -0.08016 -0.019680
## 4 level1 - level5  0.02187 -0.00897  0.052148
## 5 level1 - level8 -0.12276 -0.15247 -0.094190
## 6 level1 - level16 -0.04531 -0.07494 -0.014681
## 7 level2 - level3  0.03959  0.00887  0.071153
## 8 level2 - level4 -0.03466 -0.06476 -0.004805
## 9 level2 - level5  0.03739  0.00733  0.068266
## 10 level2 - level8 -0.10721 -0.13721 -0.077878
## 11 level2 - level16 -0.02964 -0.05976  0.000623
## 12 level3 - level4 -0.07428 -0.10559 -0.044766
## 13 level3 - level5 -0.00244 -0.03556  0.026698
## 14 level3 - level8 -0.14689 -0.17592 -0.115852

```

```

##  level3 - level16 -0.06949 -0.09993 -0.038679
##  level4 - level5   0.07205   0.04277  0.104769
##  level4 - level8  -0.07247  -0.10216 -0.042200
##  level4 - level16  0.00489  -0.02626  0.035176
##  level5 - level8  -0.14442  -0.17406 -0.113918
##  level5 - level16 -0.06726  -0.09757 -0.036412
##  level8 - level16  0.07740   0.04886  0.107633
##
## Point estimate displayed: median
## HPD interval probability: 0.95

2 > 3, 2 > 5
4 > 1, 4 > 2, 4 > 3, 4 > 5
8 > 1, 8 > 2, 8 > 3, 8 > 4, 8 > 5, 8 > 16
16 > 1, 16 > 3, 16 > 5

```

Phrase level greater than all others. Structurally relevant levels (2,4,8,16) are consistently greater than structurally irrelevant levels (3,5), BUT participants align to longer SRL (4,8) more than 2 - consistent with lower rate of response

Intact

```

dataI <- filter(data, scramble == 'Intact')

levelsI_null <- brm(value ~ 1 + (1|sub), data = dataI,
                     save_pars = save_pars(all = TRUE), iter = 5000,
                     file = '../models/E3_alignment_Intact_null')

plot(levelsI_null)

```

The figure consists of four subplots arranged in a 2x2 grid. The top row shows histograms of the posterior distributions for `b_Intercept` (left) and `sd_sub_Intercept` (right). The bottom row shows trace plots for `sd_sub_Intercept` (left) and `sigma` (right) across four chains (Chain 1, Chain 2, Chain 3, Chain 4).

```

print(summary(levelsI_null), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
##  Formula: value ~ 1 + (1 | sub)
##  Data: dataI (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
##  Multilevel Hyperparameters:
##  ~sub (Number of levels: 95)
##              Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
##  sd(Intercept)  0.0579     0.0057   0.0477   0.0698 1.0008      3436     4740
##
##  Regression Coefficients:
##              Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
##  Intercept    0.0096     0.0067  -0.0033   0.0226 1.0004      4952     6845
##

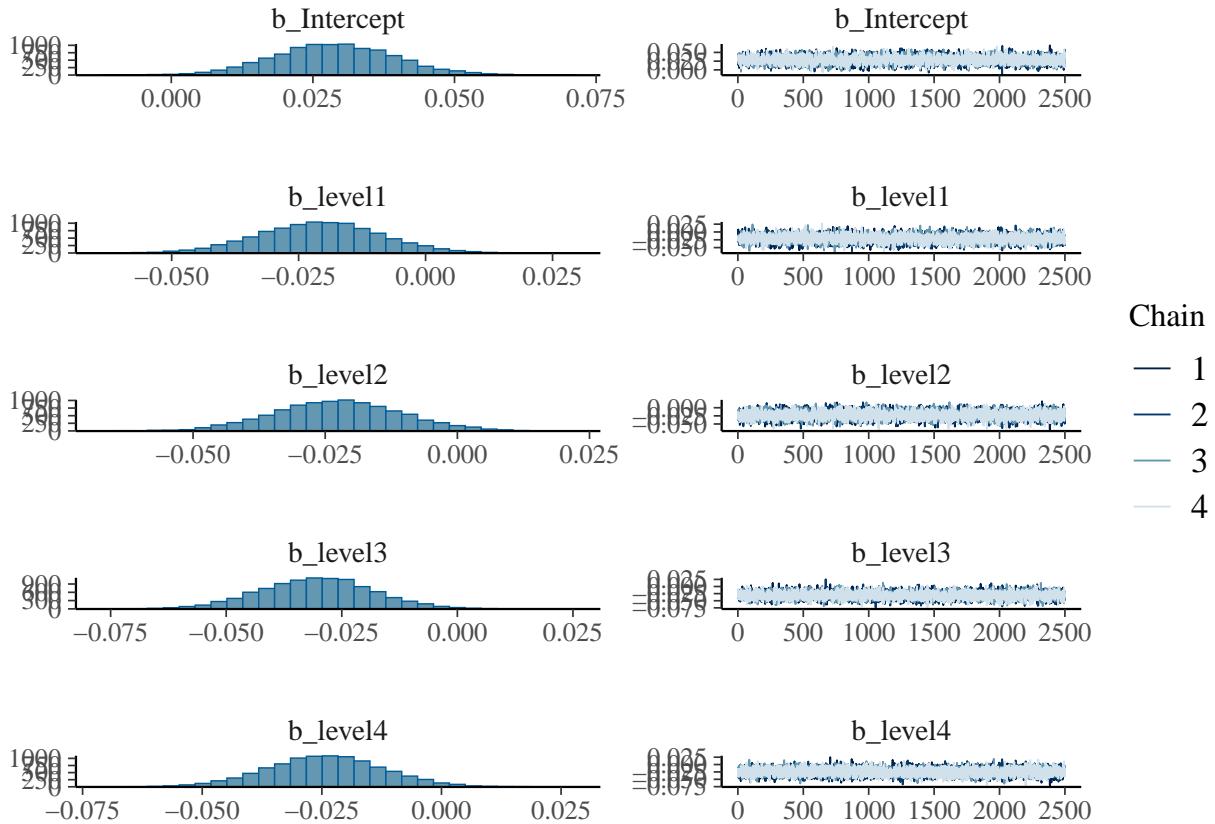
```

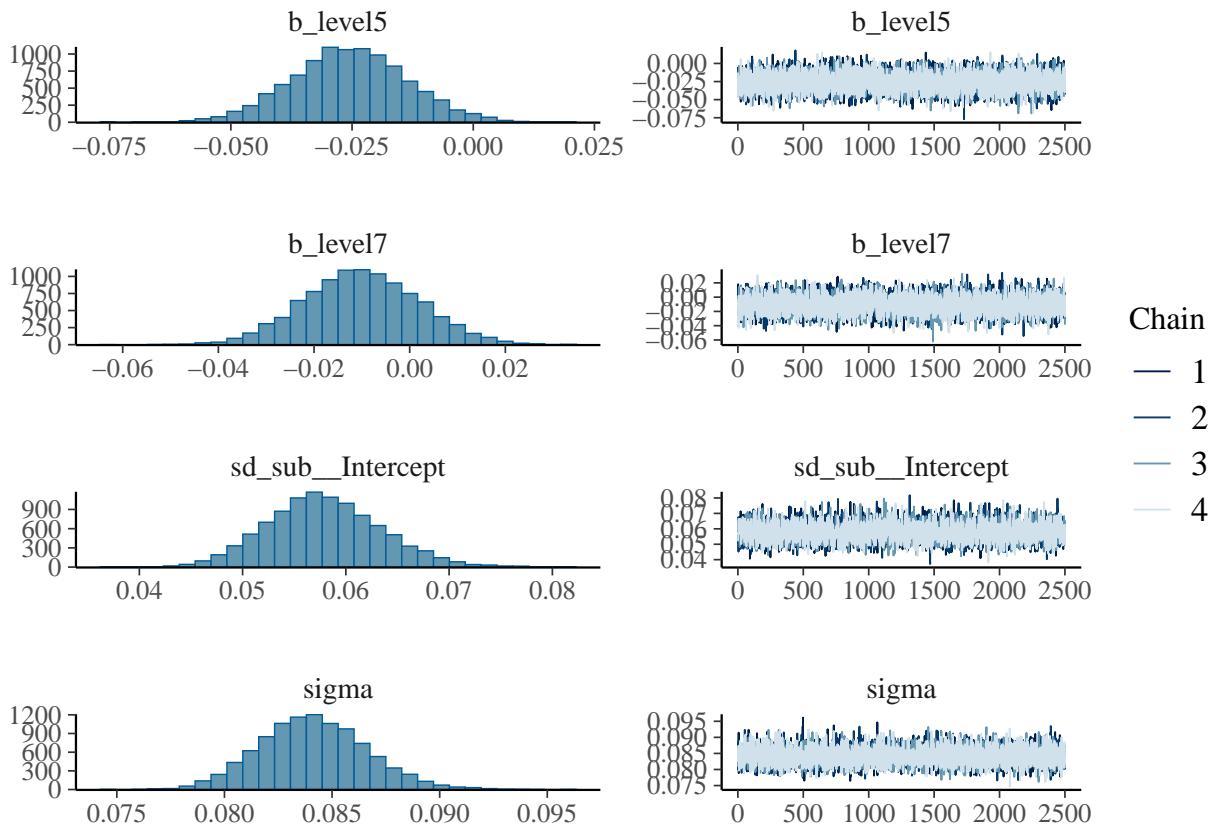
```

## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma     0.0841   0.0025   0.0792   0.0892 1.0007    11091     7216
## 
## Draws were sampled using sampling(NUTS). 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).
levelsI <- brm(value ~ level + (1|sub), data = dataI,
                 prior = c(
                   set_prior('normal(-0.2, 0.1)', coef = c('level1', 'level2', 'level3', 'level5')),
                   set_prior('normal(-0.1, 0.1)', coef = c('level4', 'level7')))
                 ),
                 save_pars = save_pars(all = TRUE), iter = 5000,
                 file = '../models/E3_alignment_Intact')

```

```
plot(levelsI)
```





```
print(summary(levelsI), digits = 4)
```

```
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ level + (1 | sub)
##  Data: dataI (Number of observations: 665)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 95)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.0579     0.0055   0.0477   0.0693 1.0004      4051     6347
##
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0288     0.0106   0.0084   0.0500 1.0000      6387     6897
## level1     -0.0208     0.0120  -0.0443   0.0025 0.9999      9439     8633
## level2     -0.0226     0.0120  -0.0457   0.0013 0.9998      9751     8366
## level3     -0.0304     0.0121  -0.0542  -0.0069 1.0001      9463     8352
## level4     -0.0243     0.0120  -0.0480  -0.0010 1.0001      9580     8817
## level5     -0.0255     0.0120  -0.0490  -0.0017 1.0005      9674     8658
## level7     -0.0100     0.0120  -0.0332   0.0136 1.0011      9626     8605
##
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.0841     0.0025   0.0795   0.0892 1.0009     14469     7597
##
```

```
## Draws were sampled using sampling(NUTS). 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).
BF_I_level <- bayes_factor(levelsI, levelsI_null)

## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 3
## Iteration: 4

print(BF_I_level)
```

```
## Estimated Bayes factor in favor of levelsI over levelsI_null: 0.00000
```

There is strong evidence against an effect of level.

```
emm_I <- emmeans(levelsI, specs = "level")
summary(emm_I)
```

```

##   level    emmean lower.HPD upper.HPD
## 1      0.00806 -0.01239  0.0279
## 2      0.00613 -0.01428  0.0263
## 3     -0.00157 -0.02247  0.0184
## 4      0.00466 -0.01591  0.0245
## 5      0.00326 -0.01695  0.0239
## 8      0.02870  0.00793  0.0494
## 16     0.01884 -0.00234  0.0382
##
## Point estimate displayed: median
## HPD interval probability: 0.95

```

Only level above chance is 8-bar level.

```
contrast(emm_I, method = "pairwise")
```

##	contrast	estimate	lower.HPD	upper.HPD
##	level1 - level2	0.00170	-0.0225	0.024499
##	level1 - level3	0.00967	-0.0142	0.033186
##	level1 - level4	0.00345	-0.0200	0.026666
##	level1 - level5	0.00462	-0.0179	0.028233
##	level1 - level8	-0.02073	-0.0441	0.002612
##	level1 - level16	-0.01075	-0.0346	0.013070
##	level2 - level3	0.00786	-0.0163	0.031905
##	level2 - level4	0.00177	-0.0213	0.025682
##	level2 - level5	0.00291	-0.0202	0.027166
##	level2 - level8	-0.02258	-0.0458	0.001147
##	level2 - level16	-0.01247	-0.0355	0.011224
##	level3 - level4	-0.00626	-0.0299	0.016806
##	level3 - level5	-0.00495	-0.0285	0.018805
##	level3 - level8	-0.03030	-0.0536	-0.006368
##	level3 - level16	-0.02050	-0.0437	0.004825

```
##  level4 - level5  0.00117  -0.0235  0.024230
##  level4 - level8  -0.02433  -0.0473 -0.000473
##  level4 - level16 -0.01439  -0.0381  0.009413
##  level5 - level8  -0.02554  -0.0494 -0.002706
##  level5 - level16 -0.01553  -0.0388  0.007871
##  level8 - level16  0.01018  -0.0126  0.034128
##
## Point estimate displayed: median
## HPD interval probability: 0.95
8 > 3, 8 > 4, 8 > 5
```

8B vs Intact, 8 vs 16

```

data_longTS <- data %>%
  filter(scramble %in% c('Intact', '8B')) %>%
  filter(level %in% c('8', '16')) %>%
  mutate(scramble = factor(scramble, levels = c('Intact', '8B')),
         level = factor(level, levels = c('8', '16')))

contrasts(data_longTS$level) <- contr.treatment(2)

data_longTS_M <- filter(data_longTS, Musician == 'Yes')
data_longTS_NM <- filter(data_longTS, Musician == 'No')

longTS_M <- brm(value ~ scramble + level + (1|sub),
                  prior = set_prior('normal(0, 0.1)', class = 'b'),
                  save_pars = save_pars(all = TRUE), iter = 5000,
                  file = '../models/E3_alignment_longTimescales_mus')

plot(longTS_M)

```

Chain

- 1
- 2
- 3
- 4

```

print(summary(longTS_M), digits = 4)

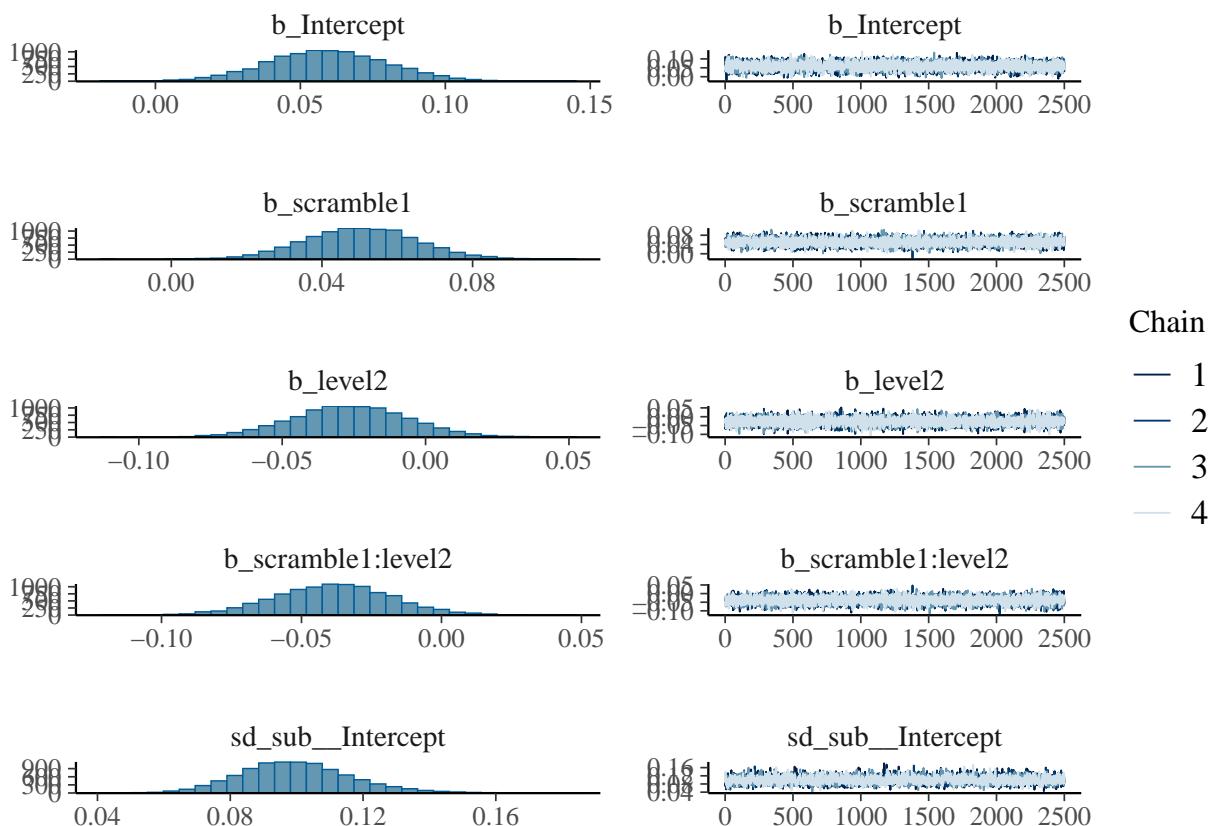
##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble + level + (1 | sub)
##   Data: data_longTS_M (Number of observations: 196)
##   Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
## 
```

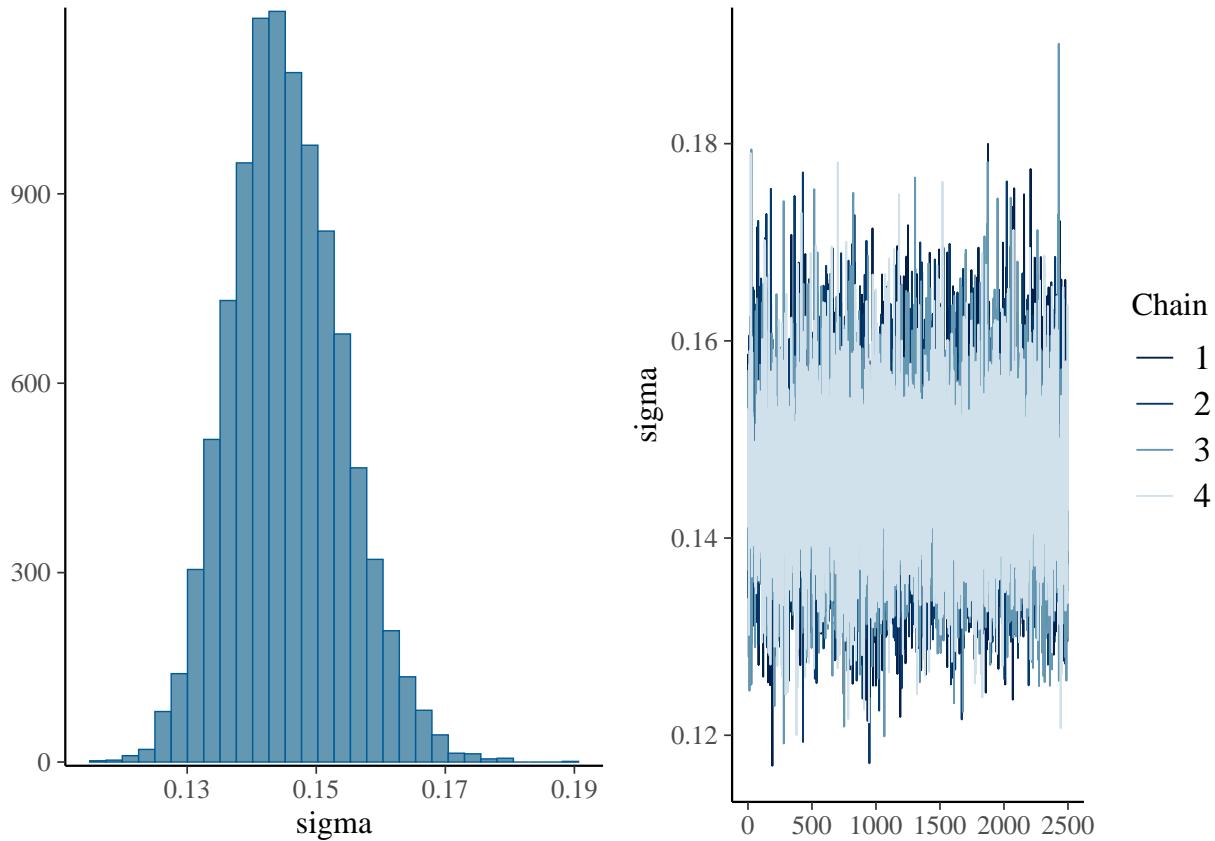
```

## Multilevel Hyperparameters:
## ~sub (Number of levels: 49)
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0994   0.0169   0.0682   0.1343 1.0003     3024     5112
##
## Regression Coefficients:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0595   0.0205   0.0191   0.0993 1.0005     6658     7010
## scramble1    0.0311   0.0104   0.0110   0.0514 1.0004     13510    7181
## level2      -0.0260   0.0202  -0.0653   0.0136 1.0005     13221    7377
##
## Further Distributional Parameters:
##           Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1472   0.0088   0.1312   0.1660 1.0005     7096    7452
##
## Draws were sampled using sampling(NUTS). 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).
longTS_M_int <- brm(value ~ scramble*level + (1|sub), data = data_longTS_M,
                      prior = set_prior('normal(0, 0.1)', class = 'b'),
                      save_pars = save_pars(all = TRUE), iter = 5000,
                      file = './models/E3_alignment_longTimescales_musInt')

```

```
plot(longTS_M_int)
```





```

print(summary(longTS_M_int), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble * level + (1 | sub)
##  Data: data_longTS_M (Number of observations: 196)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 49)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0999   0.0168   0.0693   0.1359 1.0003     3424     4712
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept      0.0593   0.0206   0.0191   0.0995 1.0000     7401     7340
## scramble1      0.0504   0.0147   0.0219   0.0798 1.0003    10771     6203
## level2       -0.0264   0.0204  -0.0663   0.0129 1.0007    16330     7066
## scramble1:level2 -0.0387   0.0207  -0.0802   0.0019 1.0002    11345     6822
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma      0.1455   0.0086   0.1300   0.1638 1.0002     7459     7479
## 
## Draws were sampled using sampling(NUTS). 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).  
BF_longM <- bayes_factor(longTS_M_int, longTS_M)  
  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6  
print(BF_longM)  
  
## Estimated Bayes factor in favor of longTS_M_int over longTS_M: 1.22068
```

There is weak evidence for an interaction for musicians.

```

longTS_NM <- brm(value ~ scramble + level + (1|sub), data = data_longTS_NM,
  prior = set_prior('normal(0, 0.1)', class = 'b'),
  save_pars = save_pars(all = TRUE), iter = 5000,
  file = '../models/E3_alignment_longTimescales_nonmus')

plot(longTS_NM)

  b_Intercept
  b_scramble1
  b_level2
  sd_sub_Intercept
  sigma

  b_Intercept
  b_scramble1
  b_level2
  sd_sub_Intercept
  sigma

Chain
  1
  2
  3
  4

print(summary(longTS_NM), digits = 4)

##  Family: gaussian
##  Links: mu = identity; sigma = identity
## Formula: value ~ scramble + level + (1 | sub)
##  Data: data_longTS_NM (Number of observations: 184)
##  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##          total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 46)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0882    0.0160   0.0585   0.1208 1.0003     3492     5566
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept    0.0875    0.0197   0.0490   0.1268 1.0004     7215     6563
## scramble1    0.0356    0.0101   0.0156   0.0553 0.9999     15025     7475
## level2      -0.0473    0.0203  -0.0878  -0.0065 1.0007     14946     6771
## 
## Further Distributional Parameters:

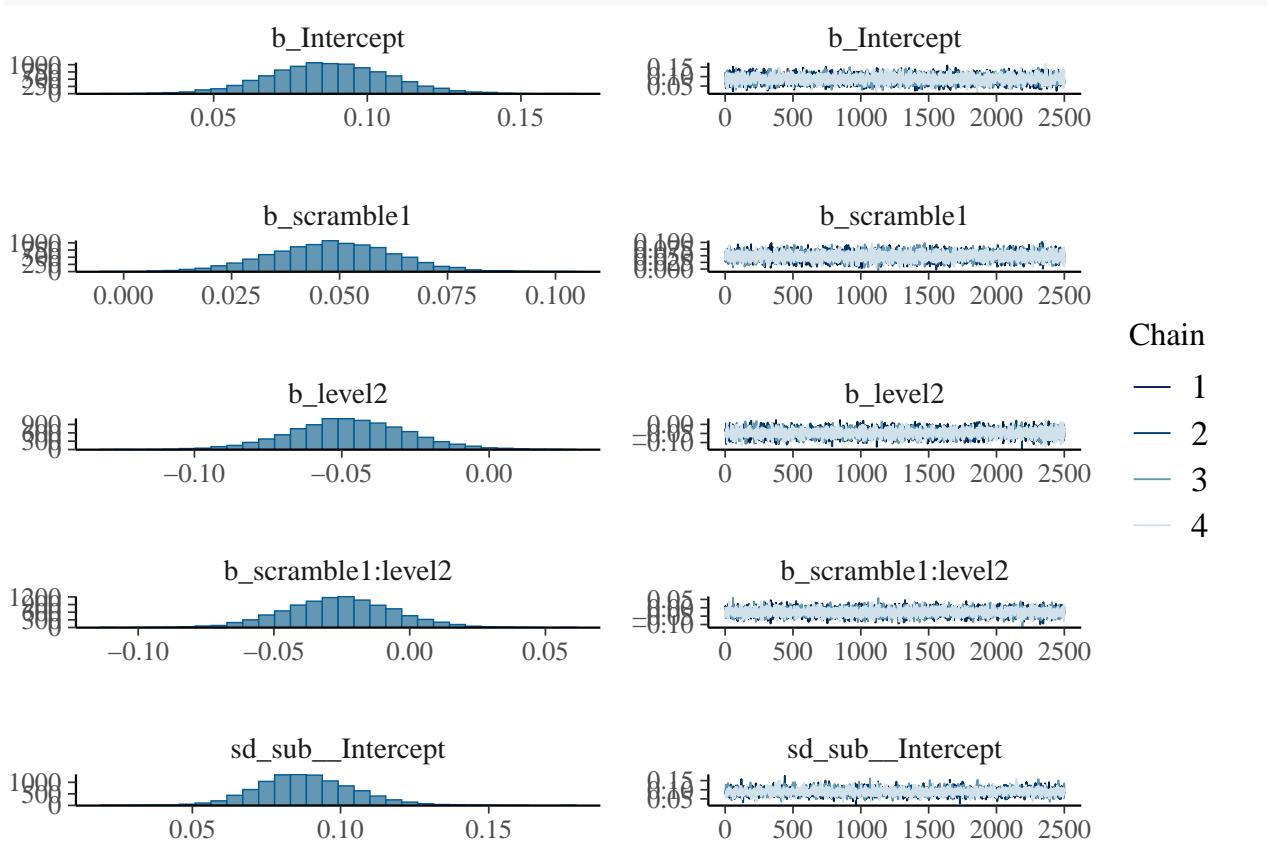
```

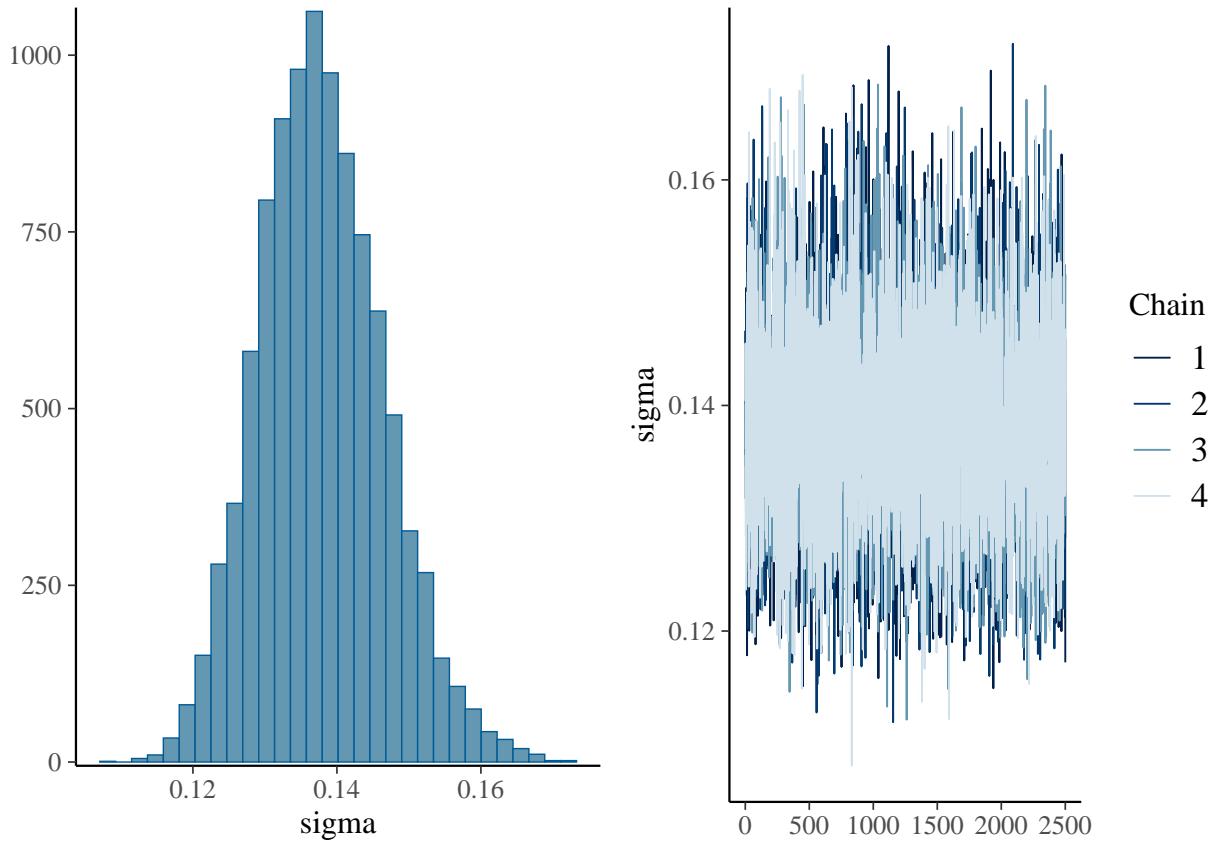
```

##      Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma    0.1381    0.0084   0.1228   0.1558 0.9998     7514     7219
##
## Draws were sampled using sampling(NUTS). 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).
longTS_NM_int <- brm(value ~ scramble*level + (1|sub), data = data_longTS_NM,
                      prior = set_prior('normal(0, 0.1)', class = 'b'),
                      save_pars = save_pars(all = TRUE), iter = 5000,
                      file = '../models/E3_alignment_longTimescales_nonmusInt')

plot(longTS_NM_int)

```





```
print(summary(longTS_NM_int), digits = 4)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: value ~ scramble * level + (1 | sub)
## Data: data_longTS_NM (Number of observations: 184)
## Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##         total post-warmup draws = 10000
##
## Multilevel Hyperparameters:
## ~sub (Number of levels: 46)
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sd(Intercept)  0.0884     0.0162   0.0587   0.1221 1.0005      3321     3993
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## Intercept       0.0875     0.0193   0.0491   0.1257 1.0002      7101     6262
## scramble1       0.0483     0.0143   0.0199   0.0761 1.0002     11700     6884
## level2        -0.0475     0.0200  -0.0871  -0.0077 1.0005     14952     6796
## scramble1:level2 -0.0260     0.0200  -0.0645   0.0134 0.9999     11265     7320
## 
## Further Distributional Parameters:
##             Estimate Est.Error l-95% CI u-95% CI    Rhat Bulk_ESS Tail_ESS
## sigma       0.1379     0.0087   0.1222   0.1563 1.0000      6915     7296
## 
## Draws were sampled using sampling(NUTS). 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).  
BF_longNM <- bayes_factor(longTS_NM_int, longTS_NM)  
  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6  
## Iteration: 1  
## Iteration: 2  
## Iteration: 3  
## Iteration: 4  
## Iteration: 5  
## Iteration: 6  
print(BF_longNM)  
  
## Estimated Bayes factor in favor of longTS_NM_int over longTS_NM: 0.47411
```

There is weak evidence against an interaction for musicians.