

Complete this during the 2nd slide show!

Hierarchical linear regression in brms

We will again use the PDM data set, but with some different variables. You can load it using the following code in R:

```
library(curl)

# See https://github.com/mdnunez/encodingN200 for more information about the data
# See https://github.com/mdnunez/encodingN200
pdm_dat <- curl("https://tinyurl.com/PDMdataESCOP2022")
pdm <- read.csv(pdm_dat)

colnames(pdm) <- c('N200_latencies', 'N200_amplitudes',
  'RT', 'accuracy', 'condition', 'EEG_session',
  'experiment', 'session', 'subject')

pdm <- pdm[pdm$experiment == 1, ]

pdm$N200_latencies <- pdm$N200_latencies/1000

pdm$RT <- pdm$RT/1000

head(pdm)
```

1. What is the brms code to estimate a linear regression with *RT* as the dependent variable, *N200_latencies* and *N200_amplitudes* as the independent variables, and *an interaction term*?

The `summary()` should output something like this:

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: RT ~ N200_latencies * N200_amplitudes
## Data: pdm (Number of observations: 5532)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Population-Level Effects:
##
```

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat
## Intercept	0.62	0.03	0.56	0.69	1.00
## N200_latencies	0.83	0.15	0.54	1.12	1.00
## N200_amplitudes	-0.01	0.02	-0.04	0.02	1.00
## N200_latencies:N200_amplitudes	0.01	0.08	-0.14	0.16	1.00

```
## Bulk_ESS Tail_ESS
## Intercept      899    1805
## N200_latencies  893    1823
## N200_amplitudes 777    1571
## N200_latencies:N200_amplitudes 754    1647
```

```
##
## Family Specific Parameters:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.24      0.00   0.23   0.24 1.00    2337    2210
##
## 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).
```

2. What effects are significant in this model?

```
bayes_anova <- brm(RT ~ factor(condition)*factor(accuracy), data=pdm)
summary(bayes_anova)
```

```
summary(bayes_anova)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: RT ~ factor(condition) * factor(accuracy)
## Data: pdm (Number of observations: 5532)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##        total post-warmup draws = 4000
##
## Population-Level Effects:
##              Estimate Est.Error 1-95% CI u-95% CI Rhat
## Intercept          0.84      0.01   0.83   0.86 1.00
## factorcondition1    -0.05      0.01  -0.07  -0.02 1.00
## factorcondition2    -0.02      0.01  -0.04   0.01 1.00
## factoraccuracy1     -0.03      0.01  -0.06  -0.01 1.00
## factorcondition1:factoraccuracy1 -0.03      0.02  -0.06   0.00 1.00
## factorcondition2:factoraccuracy1 -0.06      0.02  -0.09  -0.02 1.00
##
##              Bulk_ESS Tail_ESS
## Intercept        1949    2431
## factorcondition1  1788    2443
## factorcondition2  1983    2563
## factoraccuracy1   1823    2202
## factorcondition1:factoraccuracy1 1727    2388
## factorcondition2:factoraccuracy1 1792    2122
##
## Family Specific Parameters:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.24      0.00   0.23   0.24 1.00    3297    1910
##
## 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).
```

3. What is the brms code to estimate a linear regression with *RT* as the dependent variable, *N200_latencies* and *N200_amplitudes* as the independent variables, an *interaction term*, and a random intercept for each *subject*?

The `summary()` should output something like this:

```

## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: RT ~ (1 | subject) + N200_latencies * N200_amplitudes
## Data: pdm (Number of observations: 5532)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Group-Level Effects:
## ~subject (Number of levels: 12)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)      0.13      0.03      0.09      0.21 1.01      541      1220
##
## Population-Level Effects:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat
## Intercept              0.61      0.05      0.52      0.71 1.01
## N200_latencies          0.86      0.14      0.59      1.12 1.00
## N200_amplitudes         0.00      0.02     -0.03      0.03 1.00
## N200_latencies:N200_amplitudes -0.02      0.07     -0.15      0.12 1.00
##      Bulk_ESS Tail_ESS
## Intercept              748      1142
## N200_latencies          1566      2060
## N200_amplitudes          1289      1762
## N200_latencies:N200_amplitudes 1320      1723
##
## Family Specific Parameters:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.21      0.00      0.21      0.22 1.00      2220      2041
##
## 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).

```

