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:

```r
library(curl)
```

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

1. (10min) 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 provide something like the output on the next page.

```
##  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 l-95% CI u-95% CI Rhat
## Intercept                          0.62      0.03     0.57     0.69 1.00
## N200_latencies                     0.83      0.15     0.54     1.13 1.00
## N200_amplitudes                   -0.01      0.02    -0.04     0.02 1.00
## N200_latencies:N200_amplitudes     0.01      0.08    -0.14     0.17 1.00
##                                Bulk_ESS Tail_ESS
## Intercept                          1374     2057
## N200_latencies                     1405     2162
## N200_amplitudes                    1224     1640
## N200_latencies:N200_amplitudes     1203     1697
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.24      0.00     0.23     0.24 1.00     2171     1785
##
## 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. (5min) 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 l-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                           2121     2877
## factorcondition1                    1964     2348
## factorcondition2                    2143     2362
## factoraccuracy1                     1851     2336
## factorcondition1:factoraccuracy1    1692     2190
## factorcondition2:factoraccuracy1    1901     2536
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.24      0.00     0.23     0.24 1.00     3681     2750
##
## 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. (10min) 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 l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.13      0.03     0.09     0.21 1.00      739     1349
##
## Population-Level Effects:
##                              Estimate Est.Error l-95% CI u-95% CI Rhat
## Intercept                        0.61      0.05     0.52     0.71 1.00
## N200_latencies                   0.86      0.14     0.58     1.13 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                         820     1127
## N200_latencies                   1443     1436
## N200_amplitudes                  1267     1279
## N200_latencies:N200_amplitudes   1207     1312
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.21      0.00     0.21     0.22 1.00     2268     2032
##
## 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).
```