Methods 3, Week 6:

Towards Bayesian Multi-Level Modelling

What did we talk about last week?

- Tuesday
  - Assignment 2 Research Outline
  - Assignment 2 Data Set
  - Step-by-step Regression Modelling on the Project Data
    * Linear Regression
- Thursday
  - Getting *brms* to work on your machine
  - Implementing formulas
  - Setting priors
  - Fitting models

What will we talk about today?

- Step-by-step regression modelling on the Project Data
  - The Art of Multilevel Modelling (MLM)
  - The Art of Prior Elicitation

Mean Length of Utterance
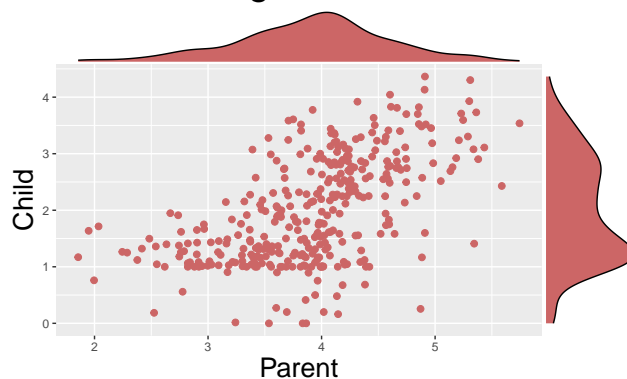
Multilevel Models (MLMs)

Why use MLMs?

- **Correct inferences**: No grouping underestimates standard errors of regression coefficients
  - Higher-level predictor coefficients most affected
- **Group effects**: Extent of grouping in individual outcomes and identification of 'outlying' groups correspond to upper-level residuals in MLM
- **Simulatenous group effects and group-level predictor estimation**
- **Inference to a population of groups**
  - In MLMs, sample groups treated as a random sample from a population of groups.
    - ∗ Inferences in fixed effects models cannot be made beyond sample groups

Randomness

- MLMs use randomness to account for the structure and variability in data that arise from nested or hierarchical relationships

RANDOMNESS
You never saw it coming.

DIY.DESPAIR.COM

Variables

- Random
  - Assumed to be measured with error (ex: mlu)
  - Values generalizable to a much larger population with a certain probability distribution
  - Number of values small compared to population
- Fixed
  - Measured without measurement error (ex: gender, diagnosis)
  - Desired generalization to population or other studies is to the same values
  - Variable contains all or most of population values

Effects

- Random
  - Assumes that an IV is random
  - Used if the IV levels thought to be subset of possible population values
  - Larger standard error (less powerful)
- Fixed
  - Assumes that an IV is fixed
  - Generalization of results apply to similar IV values in population
  - Smaller standard errors
- Intercept only models in MLR are equivalent to random effects ANOVA

- Inclusion of constant effects level-1 predictors in MLR models equivalent to a random effects ANCOVA.

Coefficients

- Random
  - Only applies to MLR analysis in which intercepts, slopes, and variances can assume to be random
  - Variances of the slopes and intercepts (if allowed to vary across groups) are called varying (random) coefficients.
- Fixed
  - Invariant across groups (between-group variance set to zero) -The average intercept or slope is referred to as a "constant (fixed) effect."

Random Seeding

- Reproducibility.
  - Anyone who re-runs your code will get the exact same outputs.
- Essential in many tasks
  1. Splitting data into training/validation/test sets
  - Ensure that the data is divided the same way every time the script is ran
  2. Model training
  - Non-deterministic algorithms (different outputs given the same input, e.g. random forest, gradient boosting)
  3. Benchmarking, Model Comparison, Parametrization
  - If you are testing and comparing multiple algorithms or comparing models, it's important that all versions have same input

Hierachical Linear Modelling with BRMS

- The *brm* function: default arguments
  - **chains**: Number of Markov Chains to use (default: 4)
    * Using more chains allows us to be more confident in fitting the posterior distributions, as each chain has a different starting point
    * Tip: #chains = #computer cores
  - **iter**: Total number of iterations per chain (default: 2000)
  - **inits**: Specify initial values for chains (default: 'Random')
  - **warmup** ("burn-in"): number of iterations thrown away at the beginning of an MCMC run (default: **floor(iter/2)**)
  - **cores**: Number of CPU cores used for chain building
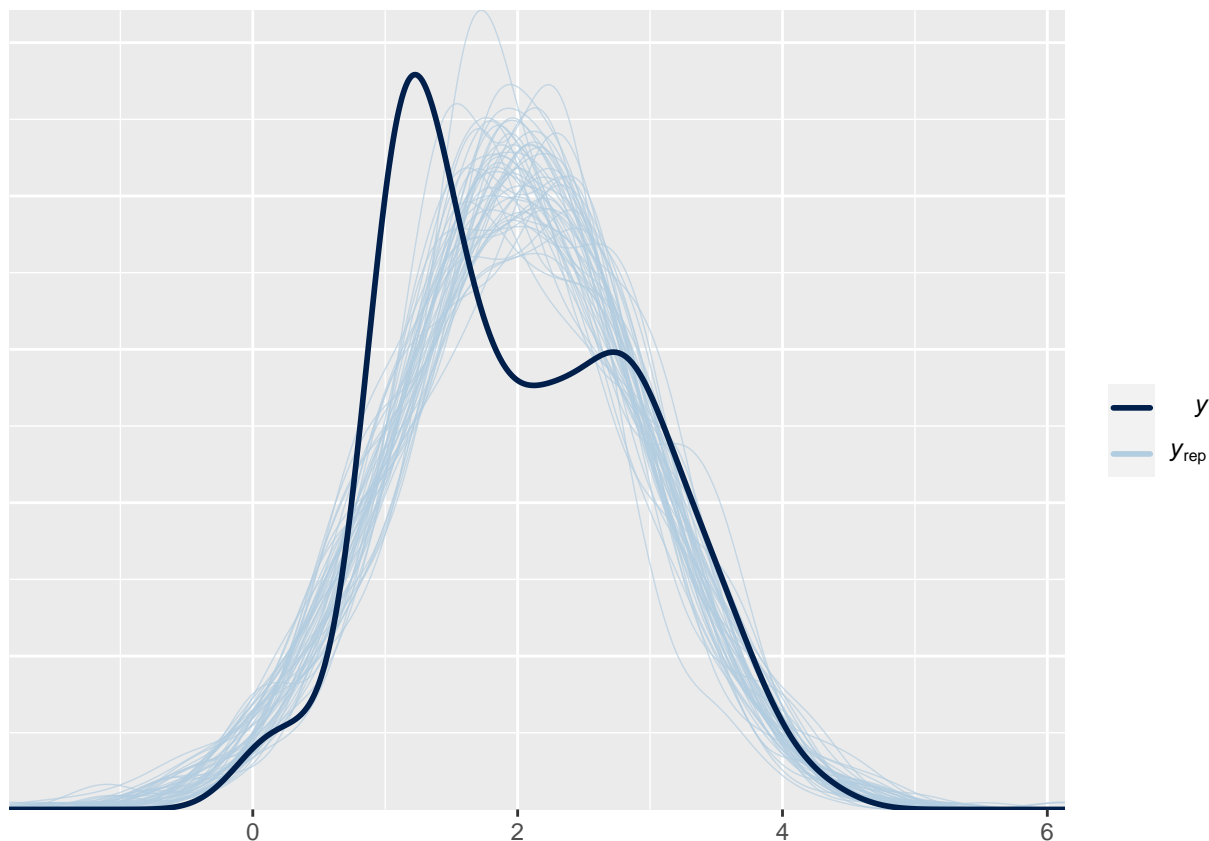 - **family**: Distribution type for the likelihood function (default = **gaussian**)

Formulas

- Left-hand outcome, right-hand predictors
- Constant effects added first, followed by varying ones between brackets.
  - Variables right of "|" are grouping variables.
- Intercepts ("1") are assumed by default in R, otherwise ("0").
- All correlations between each pair of random effects are estimated
  - Use || between two random effects that are not correlated
- Interactions between two predictors can be created by the : sign or by multiplying them instead of simply adding them
- Even if you only care about overall effects, you still need to specify the hierarchical structure of your data
  - Dependencies in the data will affect overall estimates by increasing overall uncertainty

Simple regression model

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ 1 + MOT_MLU
##    Data: data (Number of observations: 352)
##   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 Bulk_ESS Tail_ESS
## Intercept    -1.06      0.24    -1.53    -0.60 1.00     3854     2714
## MOT_MLU       0.78      0.06     0.66     0.90 1.00     3918     2639
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.77      0.03     0.72     0.83 1.00     4005     2880
##
## 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).

##     Estimate Est.Error      Q2.5     Q97.5
## R2 0.3186164 0.0334731 0.2497849 0.3804363
```

Simple Regression Model Results

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ 1 + MOT_MLU
##    Data: data (Number of observations: 352)
##   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 Bulk_ESS Tail_ESS
## Intercept    -1.06      0.24    -1.53    -0.60 1.00     3854     2714
## MOT_MLU       0.78      0.06     0.66     0.90 1.00     3918     2639
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.77      0.03     0.72     0.83 1.00     4005     2880
##
## 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).

##     Estimate Est.Error      Q2.5     Q97.5
## R2 0.3186164 0.0334731 0.2497849 0.3804363
```
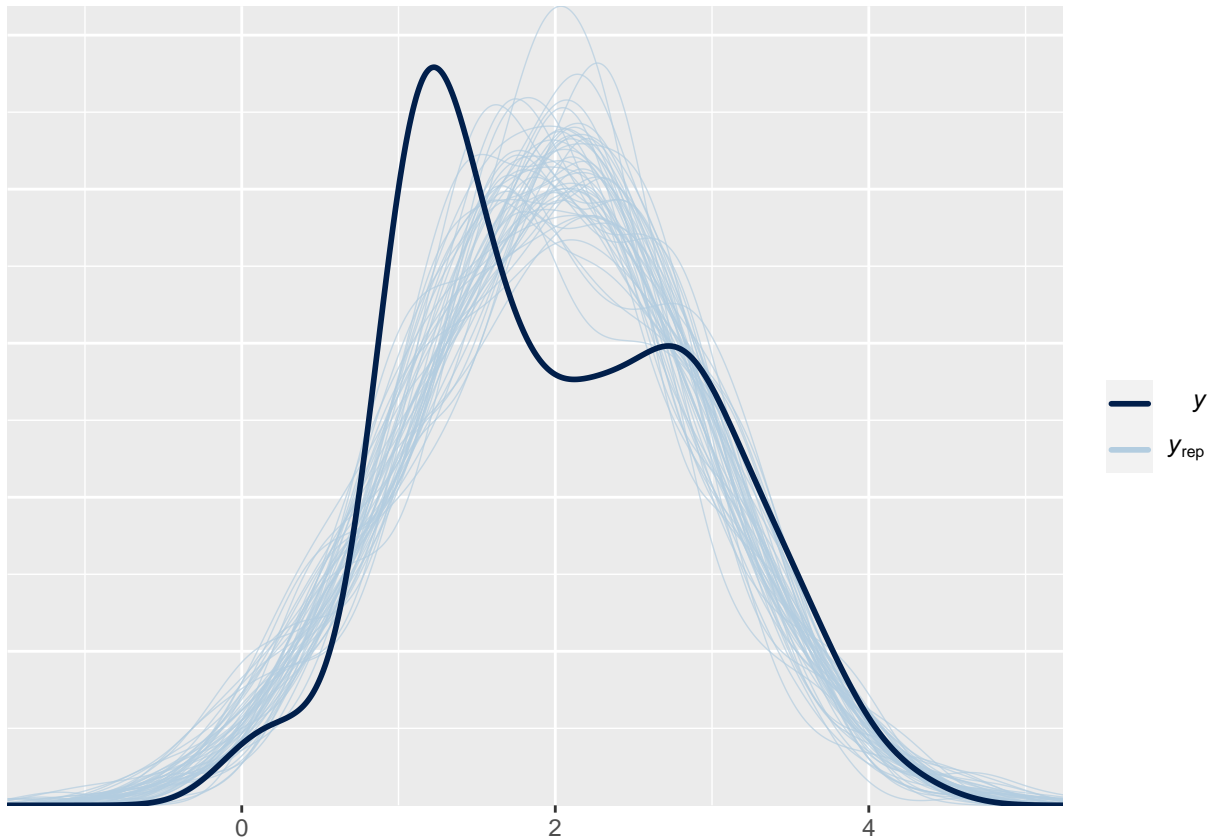
Multiple predictors

```r
multiple_predictors_model <- brms::brm(
  brms::bf(CHI_MLU ~ MOT_MLU + Diagnosis + Visit + Child.ID),
  data = data,
  file = 'data/w6/multiple_predictors',
  chains = 2,
  cores = 2,
  seed = 112
)
```

Multiple Predictors Results

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ MOT_MLU + Diagnosis + Visit + Child.ID
##    Data: data (Number of observations: 352)
##   Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 2000
##
## Population-Level Effects:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      -0.80      0.25    -1.31    -0.34 1.00     2607     1722
## MOT_MLU         0.54      0.06     0.41     0.67 1.00     2159     1728
## DiagnosisTD     0.40      0.08     0.24     0.57 1.00     2176     1424
## Visit           0.17      0.02     0.12     0.21 1.00     2161     1398
```

```
## Child.ID       -0.00      0.00     -0.01      0.00 1.00      2622      1613
##
## Family Specific Parameters:
##        Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma       0.71      0.03     0.66     0.76 1.00      2293      1354
##
## 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).

##      Estimate  Est.Error      Q2.5     Q97.5
## R2 0.4319807 0.03094327 0.3701946 0.4901642
```


Multiple Interacting Predictors

```r
multiple_interacting_predictors_model <- brms::brm(
  brms::bf(CHI_MLU ~ MOT_MLU*Diagnosis + Visit + MOT_MLU:Visit + Diagnosis:Visit),
  data = data,
  file = 'data/w6/multiple_interacting_predictors',
  chains = 2,
  cores = 2,
  seed = 112
)
```
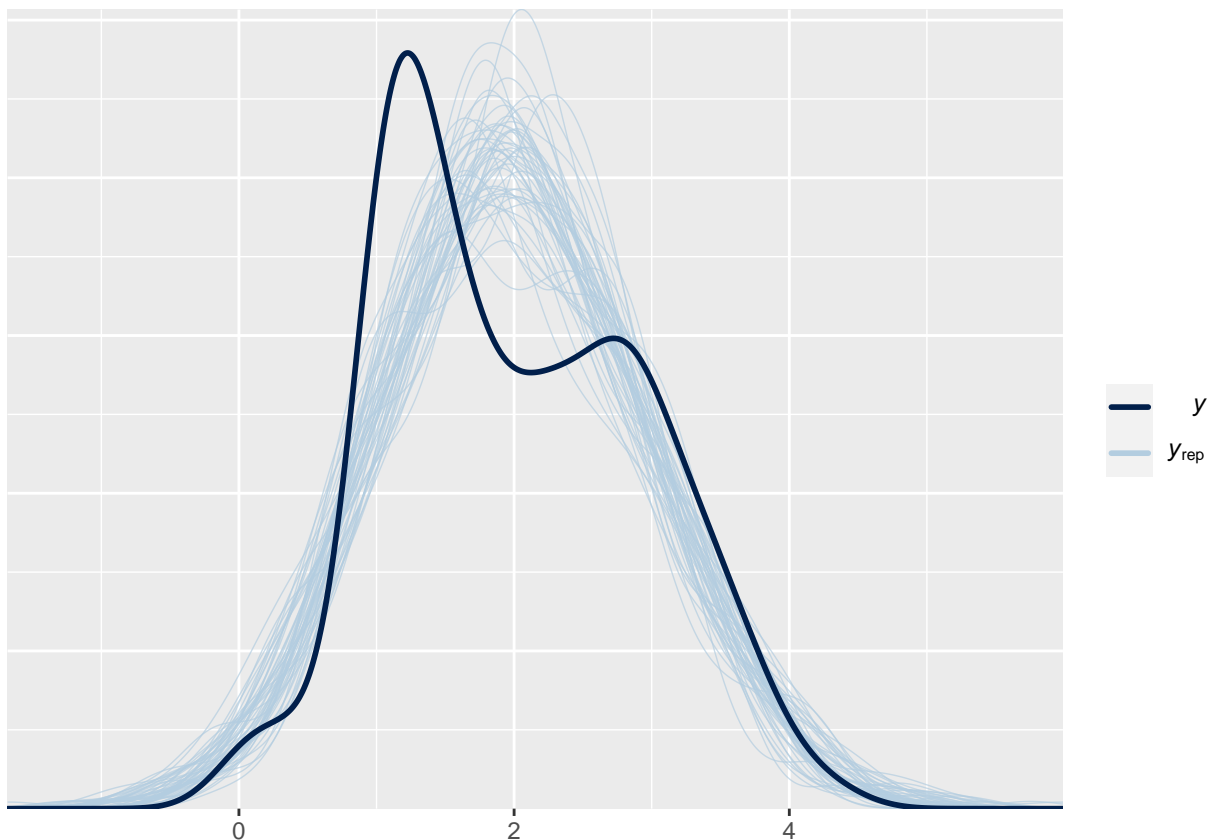
Multiple Interacting Predictors Results

```
##  Family: gaussian
```

```
##    Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ MOT_MLU * Diagnosis + Visit + MOT_MLU:Visit + Diagnosis:Visit
##     Data: data (Number of observations: 352)
##   Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 2000
##
## Population-Level Effects:
##                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept              -0.50      0.50    -1.48     0.50 1.00     1070     1155
## MOT_MLU                 0.54      0.14     0.25     0.83 1.00     1021     1167
## DiagnosisTD            -0.36      0.51    -1.34     0.66 1.00     1196     1073
## Visit                   0.06      0.13    -0.21     0.32 1.00     1035      975
## MOT_MLU:DiagnosisTD    -0.01      0.13    -0.28     0.25 1.00     1169     1036
## MOT_MLU:Visit          -0.00      0.04    -0.07     0.07 1.00      971      985
## DiagnosisTD:Visit       0.24      0.05     0.14     0.33 1.00     1721     1279
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.68      0.03     0.63     0.74 1.00     1786     1302
##
## 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).

##     Estimate  Est.Error     Q2.5     Q97.5
## R2 0.4732861 0.02745144 0.4171806 0.5217459
```
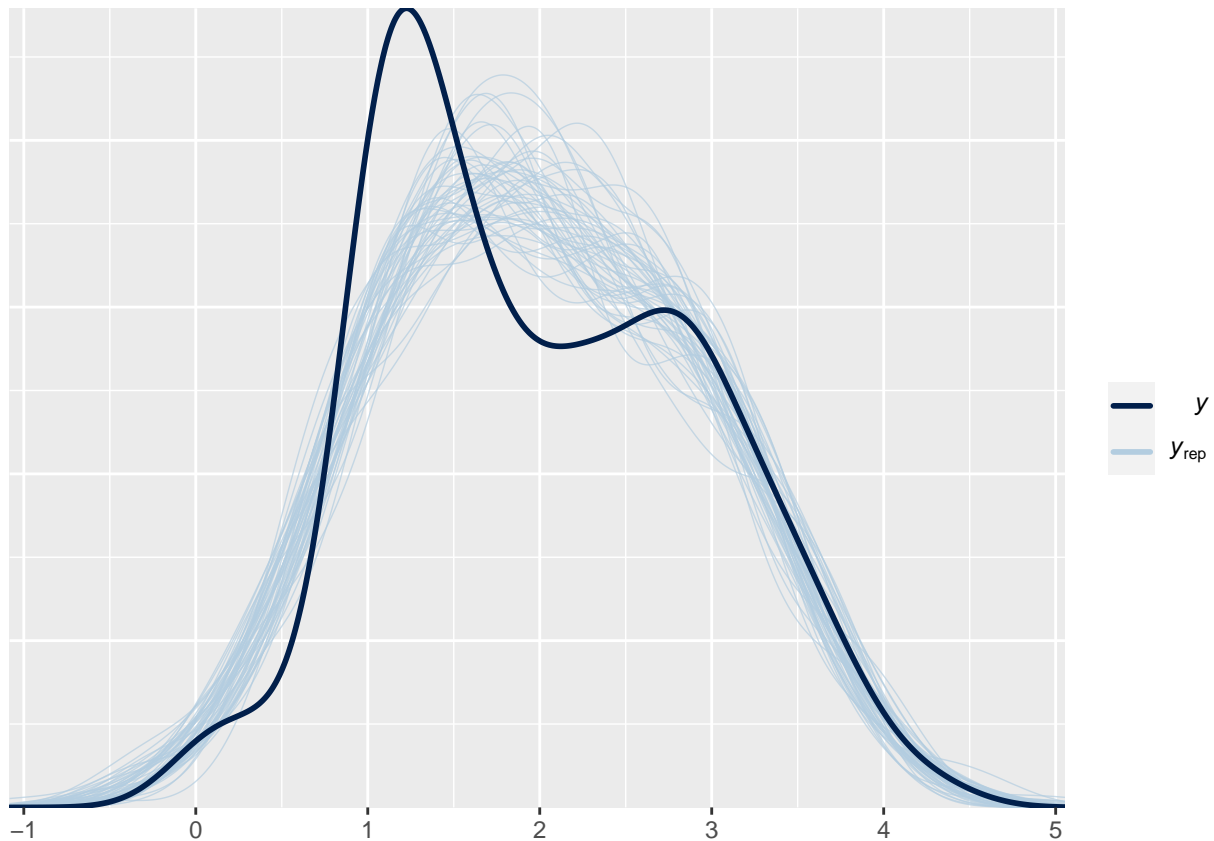
Random intercepts model

```
random_intercepts_model <- brms::brm(
  brms::bf(CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (1|Visit) + (1|Child.ID) + (1|Diagnosis)),
  data = data,
  file = 'data/w6/random_intercepts',
  chains = 2,
  cores = 2,
  seed = 112)
```

Random Intercepts Results

```
## Warning: There were 160 divergent transitions after warmup. Increasing
## adapt_delta above 0.8 may help. See
## http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup

##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (1 | Visit) + (1 | Child.ID) + (1 | Diagno
##    Data: data (Number of observations: 352)
##   Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 2000
##
## Group-Level Effects:
## ~Child.ID (Number of levels: 61)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.56      0.06     0.46     0.68 1.01      329      632
##
## ~Diagnosis (Number of levels: 2)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.44      1.10     0.07     4.02 1.01      902      795
##
## ~Visit (Number of levels: 6)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.17      0.11     0.06     0.43 1.01      474      658
##
## Population-Level Effects:
##                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept            0.03      1.33    -2.90     2.86 1.00      777      799
## MOT_MLU              0.37      0.05     0.27     0.48 1.00      946     1313
## DiagnosisTD         -0.28      1.85    -4.18     3.63 1.01      819      842
## DiagnosisASD:Visit   0.06      0.05    -0.03     0.17 1.00      463      472
## DiagnosisTD:Visit    0.30      0.05     0.20     0.40 1.01      458      459
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.41      0.02     0.38     0.45 1.00     1146     1117
##
## 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).

##     Estimate  Est.Error      Q2.5     Q97.5
## R2 0.8066044 0.01062774 0.7840735 0.8253711
```

Random Slopes Model

```r
random_slopes_model <- brms::brm(
  brms::bf(CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU|Diagnosis) + (MOT_MLU + Diagnosis
  data = data,
  file = 'data/w6/random_slopes',
  chains = 2,
  cores = 2,
  seed = 112)
```

Random Slopes Results

```
## Warning: There were 327 divergent transitions after warmup. Increasing
## adapt_delta above 0.8 may help. See
## http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup

##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU + Diagnosis | Visit) + (MOT_MLU
##    Data: data (Number of observations: 352)
##   Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 2000
##
## Group-Level Effects:
## ~Child.ID (Number of levels: 61)
##                            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                  0.50      0.24     0.05     0.98 1.00      220
```

```
## sd(MOT_MLU)                            0.21      0.06     0.11       0.35 1.01        144
## sd(DiagnosisTD)                        0.54      0.16     0.23       0.87 1.01        213
## sd(Visit)                              0.09      0.02     0.06       0.13 1.01        135
## cor(Intercept,MOT_MLU)               -0.62      0.33    -0.96       0.28 1.02        112
## cor(Intercept,DiagnosisTD)            0.26      0.37    -0.52       0.86 1.03        139
## cor(MOT_MLU,DiagnosisTD)             -0.68      0.18    -0.94      -0.25 1.01        452
## cor(Intercept,Visit)                 -0.49      0.32    -0.93       0.26 1.03         88
## cor(MOT_MLU,Visit)                    0.37      0.27    -0.16       0.83 1.02        307
## cor(DiagnosisTD,Visit)               -0.52      0.24    -0.92       0.00 1.01        371
##                              Tail_ESS
## sd(Intercept)                     388
## sd(MOT_MLU)                       442
## sd(DiagnosisTD)                   573
## sd(Visit)                         241
## cor(Intercept,MOT_MLU)            230
## cor(Intercept,DiagnosisTD)        393
## cor(MOT_MLU,DiagnosisTD)          839
## cor(Intercept,Visit)              270
## cor(MOT_MLU,Visit)                734
## cor(DiagnosisTD,Visit)            801
##
## ~Diagnosis (Number of levels: 2)
##                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)        1.88      1.65     0.08       6.16 1.01     1007
## sd(MOT_MLU)          0.56      0.49     0.03       1.80 1.01      333
## cor(Intercept,MOT_MLU)  -0.04   0.57    -0.96       0.96 1.01     1402
##                  Tail_ESS
## sd(Intercept)        1028
## sd(MOT_MLU)           863
## cor(Intercept,MOT_MLU)  1020
##
## ~Visit (Number of levels: 6)
##                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)        0.20      0.22     0.01       0.72 1.01      608
## sd(MOT_MLU)          0.08      0.06     0.01       0.22 1.01      366
## sd(DiagnosisTD)      0.35      0.25     0.09       0.97 1.00      668
## cor(Intercept,MOT_MLU)  -0.34   0.49    -0.97       0.78 1.01      712
## cor(Intercept,DiagnosisTD)  0.02  0.49   -0.88       0.88 1.00      569
## cor(MOT_MLU,DiagnosisTD)  -0.17  0.42    -0.87       0.72 1.01     1199
##                  Tail_ESS
## sd(Intercept)        770
## sd(MOT_MLU)          549
## sd(DiagnosisTD)      908
## cor(Intercept,MOT_MLU)  1082
## cor(Intercept,DiagnosisTD)  976
## cor(MOT_MLU,DiagnosisTD)  943
##
## Population-Level Effects:
##                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept            0.61      1.86    -3.67       4.39 1.01      423      883
## MOT_MLU              0.34      0.36    -0.45       1.01 1.01      162      123
## DiagnosisTD         -0.97      2.63    -6.67       5.12 1.01      465      866
## DiagnosisASD:Visit   0.06      0.07    -0.09       0.19 1.00      602      525
## DiagnosisTD:Visit    0.29      0.12     0.06       0.52 1.01      723      518
```

```
## 
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.34      0.02     0.31     0.38 1.00      362     1096
## 
## 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).

##     Estimate  Est.Error      Q2.5     Q97.5
## R2 0.8683146 0.01016479 0.8467115 0.8852524
```
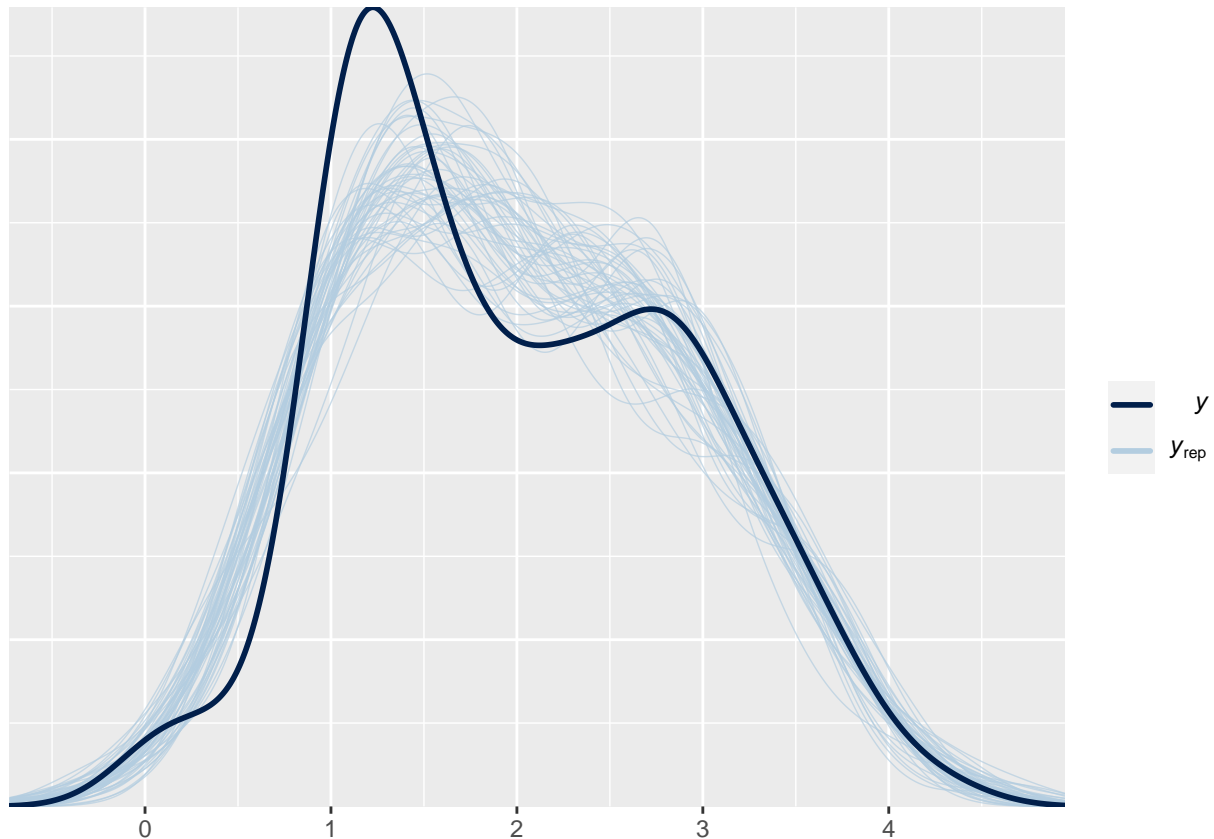

Nested Grouping Model

```
nested_grouping_model <- brms::brm(
  brms::bf(CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU|Diagnosis) + (MOT_MLU + Diagnosis
  data = data,
  file = 'data/w6/nested_grouping',
  chains = 2,
  cores = 2,
  seed = 112)
```

Nested Grouping Results

```
## Warning: There were 254 divergent transitions after warmup. Increasing
## adapt_delta above 0.8 may help. See
## http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU | Diagnosis) + (MOT_MLU + Diagnos
##     Data: data (Number of observations: 352)
##   Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 2000
##
## Group-Level Effects:
## ~Child.ID (Number of levels: 61)
##                             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                   0.65      0.26     0.15     1.14 1.00      379
## sd(MOT_MLU)                     0.30      0.07     0.18     0.44 1.00      289
## sd(DiagnosisTD)                 0.54      0.15     0.26     0.86 1.00      443
## cor(Intercept,MOT_MLU)         -0.82      0.21    -0.99    -0.20 1.01      167
## cor(Intercept,DiagnosisTD)      0.41      0.36    -0.38     0.95 1.00      189
## cor(MOT_MLU,DiagnosisTD)       -0.77      0.17    -0.98    -0.35 1.01      311
##                             Tail_ESS
## sd(Intercept)                    326
## sd(MOT_MLU)                      347
## sd(DiagnosisTD)                  730
## cor(Intercept,MOT_MLU)           259
## cor(Intercept,DiagnosisTD)       357
## cor(MOT_MLU,DiagnosisTD)         734
##
## ~Diagnosis (Number of levels: 2)
##                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)               1.80      1.51     0.07     5.81 1.00      996
## sd(MOT_MLU)                 0.50      0.45     0.03     1.65 1.01      714
## cor(Intercept,MOT_MLU)     -0.05      0.60    -0.96     0.97 1.00     1182
##                         Tail_ESS
## sd(Intercept)                868
## sd(MOT_MLU)                  967
## cor(Intercept,MOT_MLU)       584
##
## Population-Level Effects:
##                   Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept             0.36      1.66    -3.18     3.94 1.00     1086      849
## MOT_MLU               0.36      0.27    -0.31     0.93 1.01      738      846
## DiagnosisTD          -1.09      2.47    -7.04     3.93 1.00      931      618
## DiagnosisASD:Visit    0.07      0.02     0.03     0.11 1.00     1808     1252
## DiagnosisTD:Visit     0.29      0.02     0.25     0.33 1.00     2153     1335
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.39      0.02     0.36     0.43 1.01     1238     1089
##
## 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).

##     Estimate  Est.Error      Q2.5      Q97.5
## R2 0.8234624 0.01069002 0.7998395 0.8431738
```
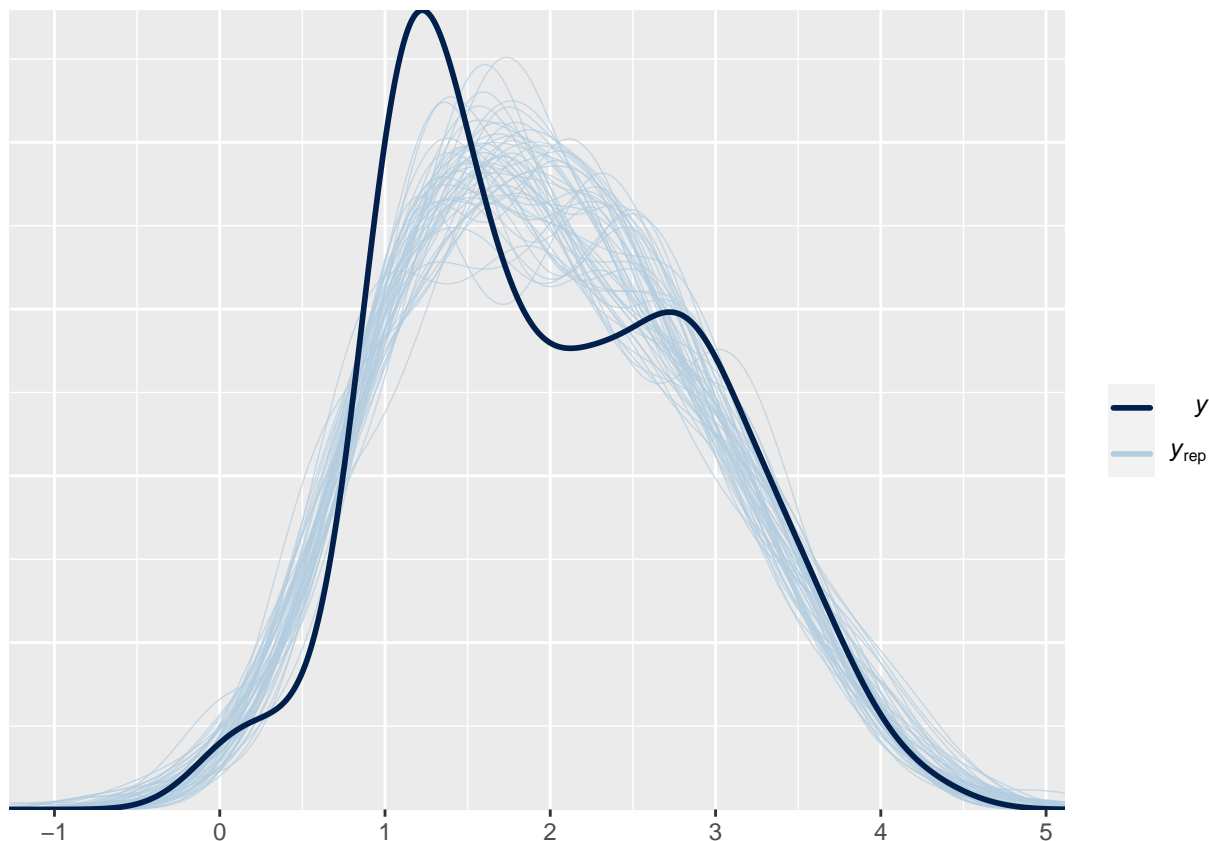
Estimation of multiple parameters

- The first formula implicitly corresponds to the μ parameter
  - Required by all brms families
  - Must have the desired outcome variable as DV
- Each subsequent formula can correspond to any of the other (non-μ) distributional parameters in the family
  - Since our family is gaussian, the second formula will have sigma as DV

```
multiple_parameters_model <- brms::brm(
 brms::bf(
    CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU|Diagnosis) + (MOT_MLU + Diagnosis|Visit)
    sigma ~ MOT_MLU + Diagnosis + (Diagnosis|Visit)),
  data = data,
  file = 'data/w6/multiple_parameters',
  chains = 2,
  cores = 2,
  seed = 112)
```

Multiple Parameters Estimation Results

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: CHI_MLU ~ MOT_MLU + Diagnosis + Diagnosis:Visit + (MOT_MLU | Diagnosis) + (MOT_MLU + Diagnos
##          sigma ~ MOT_MLU + Diagnosis + (Diagnosis | Visit)
##     Data: data (Number of observations: 352)
##    Draws: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
```

```
##          total post-warmup draws = 2000
##
## Group-Level Effects:
## ~Child.ID (Number of levels: 61)
##                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)               0.50      0.21     0.11     0.94 1.03       83
## sd(MOT_MLU)                 0.20      0.06     0.10     0.33 1.10       18
## sd(DiagnosisTD)             0.48      0.16     0.21     0.79 1.01       58
## sd(Visit)                   0.09      0.02     0.06     0.13 1.01      161
## cor(Intercept,MOT_MLU)     -0.57      0.32    -0.95     0.22 1.09       19
## cor(Intercept,DiagnosisTD)  0.24      0.38    -0.54     0.85 1.04       44
## cor(MOT_MLU,DiagnosisTD)   -0.72      0.20    -0.97    -0.24 1.03       67
## cor(Intercept,Visit)       -0.50      0.29    -0.91     0.13 1.02       59
## cor(MOT_MLU,Visit)          0.41      0.26    -0.14     0.85 1.01       94
## cor(DiagnosisTD,Visit)     -0.51      0.25    -0.90     0.04 1.01      128
##                         Tail_ESS
## sd(Intercept)                203
## sd(MOT_MLU)                  106
## sd(DiagnosisTD)              195
## sd(Visit)                    339
## cor(Intercept,MOT_MLU)       135
## cor(Intercept,DiagnosisTD)   186
## cor(MOT_MLU,DiagnosisTD)     118
## cor(Intercept,Visit)         221
## cor(MOT_MLU,Visit)           220
## cor(DiagnosisTD,Visit)       336
##
## ~Diagnosis (Number of levels: 2)
##                        Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)              2.62      2.73     0.05     9.32 1.03       61
## sd(MOT_MLU)                0.55      0.59     0.03     2.06 1.01      208
## cor(Intercept,MOT_MLU)    -0.05      0.56    -0.95     0.93 1.02      329
##                        Tail_ESS
## sd(Intercept)               76
## sd(MOT_MLU)                370
## cor(Intercept,MOT_MLU)     686
##
## ~Visit (Number of levels: 6)
##                                        Estimate Est.Error l-95% CI u-95% CI
## sd(Intercept)                              0.24      0.22     0.01     0.75
## sd(MOT_MLU)                                0.08      0.06     0.01     0.23
## sd(DiagnosisTD)                            0.30      0.21     0.07     0.87
## sd(sigma_Intercept)                        0.14      0.13     0.01     0.48
## sd(sigma_DiagnosisTD)                      0.28      0.23     0.01     0.86
## cor(Intercept,MOT_MLU)                    -0.41      0.49    -0.99     0.69
## cor(Intercept,DiagnosisTD)                 0.11      0.49    -0.88     0.90
## cor(MOT_MLU,DiagnosisTD)                  -0.19      0.43    -0.89     0.74
## cor(sigma_Intercept,sigma_DiagnosisTD)    -0.01      0.58    -0.95     0.94
##                                        Rhat Bulk_ESS Tail_ESS
## sd(Intercept)                          1.02       89      355
## sd(MOT_MLU)                            1.02       96      404
## sd(DiagnosisTD)                        1.02      175      362
## sd(sigma_Intercept)                    1.01      145      468
## sd(sigma_DiagnosisTD)                  1.02      140       84
```

```
## cor(Intercept,MOT_MLU)                    1.04      58        28
## cor(Intercept,DiagnosisTD)                1.02     152       196
## cor(MOT_MLU,DiagnosisTD)                  1.02     397       622
## cor(sigma_Intercept,sigma_DiagnosisTD) 1.01     119       264
##
## Population-Level Effects:
##                   Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept            -0.34      3.05    -9.90     3.90 1.05       61       17
## sigma_Intercept      -1.87      0.35    -2.56    -1.17 1.01      411      746
## MOT_MLU               0.38      0.37    -0.25     1.40 1.01      126      148
## DiagnosisTD           0.53      5.47    -6.44    18.70 1.03       56       16
## DiagnosisASD:Visit    0.08      0.07    -0.05     0.21 1.01      174      250
## DiagnosisTD:Visit     0.29      0.10     0.09     0.49 1.01      273      323
## sigma_MOT_MLU         0.21      0.09     0.03     0.39 1.01      365      583
## sigma_DiagnosisTD    -0.16      0.18    -0.63     0.14 1.02      269      219
##
## 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).

##    Estimate  Est.Error     Q2.5      Q97.5
## R2 0.8621564 0.01224518 0.8348675 0.8826969
```
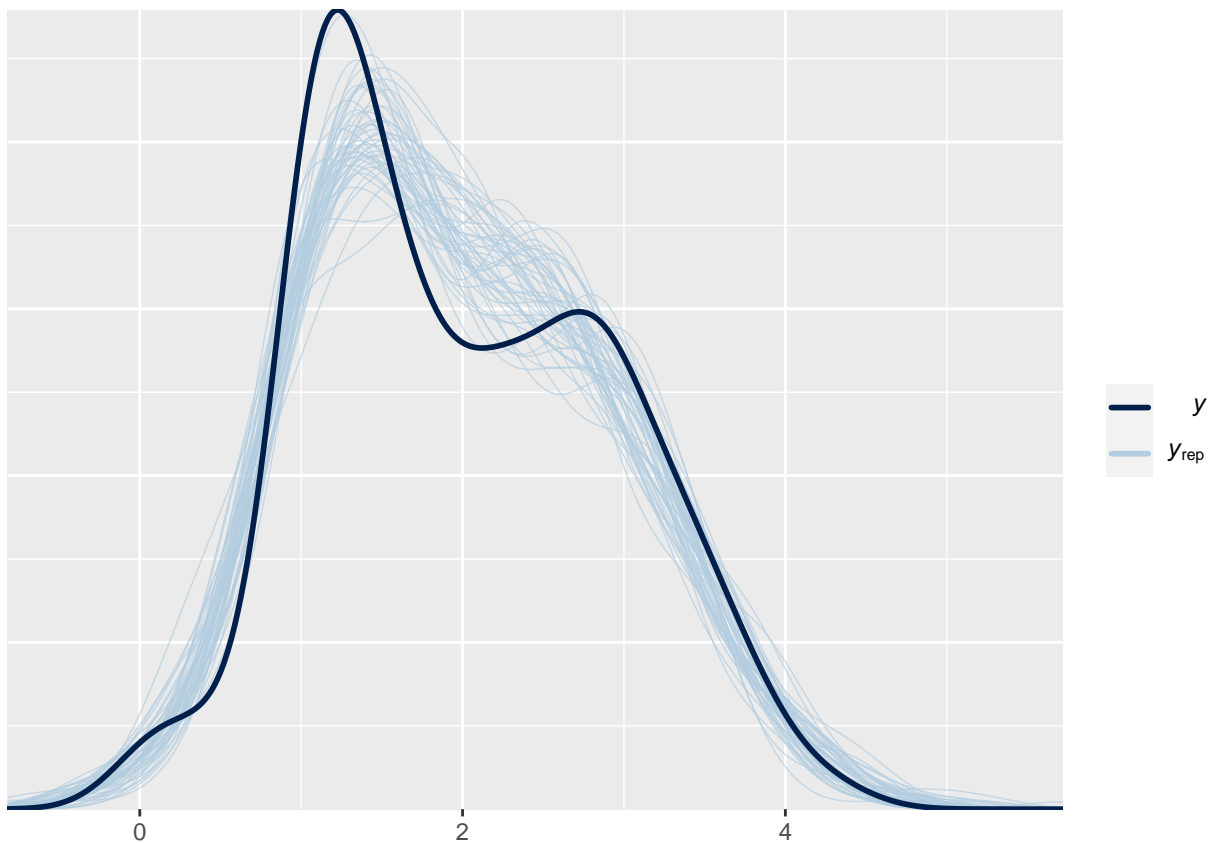
Prior Elicitation

Why Gaussian distributions?

- Most natural expression of our state of ignorance
    - If we only assume that a variable has finite variance, the Gaussian distribution is the shape that can be realized in the largest number of ways
    - Least surprising and least informative assumption to make.
    - "If you don't think the distribution should be Gaussian, then that implies that you know something else (. . .), something that would improve inference". (McIlreath, pp. 75–76)

Simple bayesian regression

```
## CHI_MLU ~ 1 + MOT_MLU
```

```
brms::prior_summary(simple_model)
```

```
##                   prior     class    coef group resp dpar nlpar lb ub
##                  (flat)         b
##                  (flat)         b MOT_MLU
##   student_t(3, 1.9, 2.5) Intercept
##     student_t(3, 0, 2.5)     sigma                                   0
##       source
##      default
##  (vectorized)
##      default
##      default
```
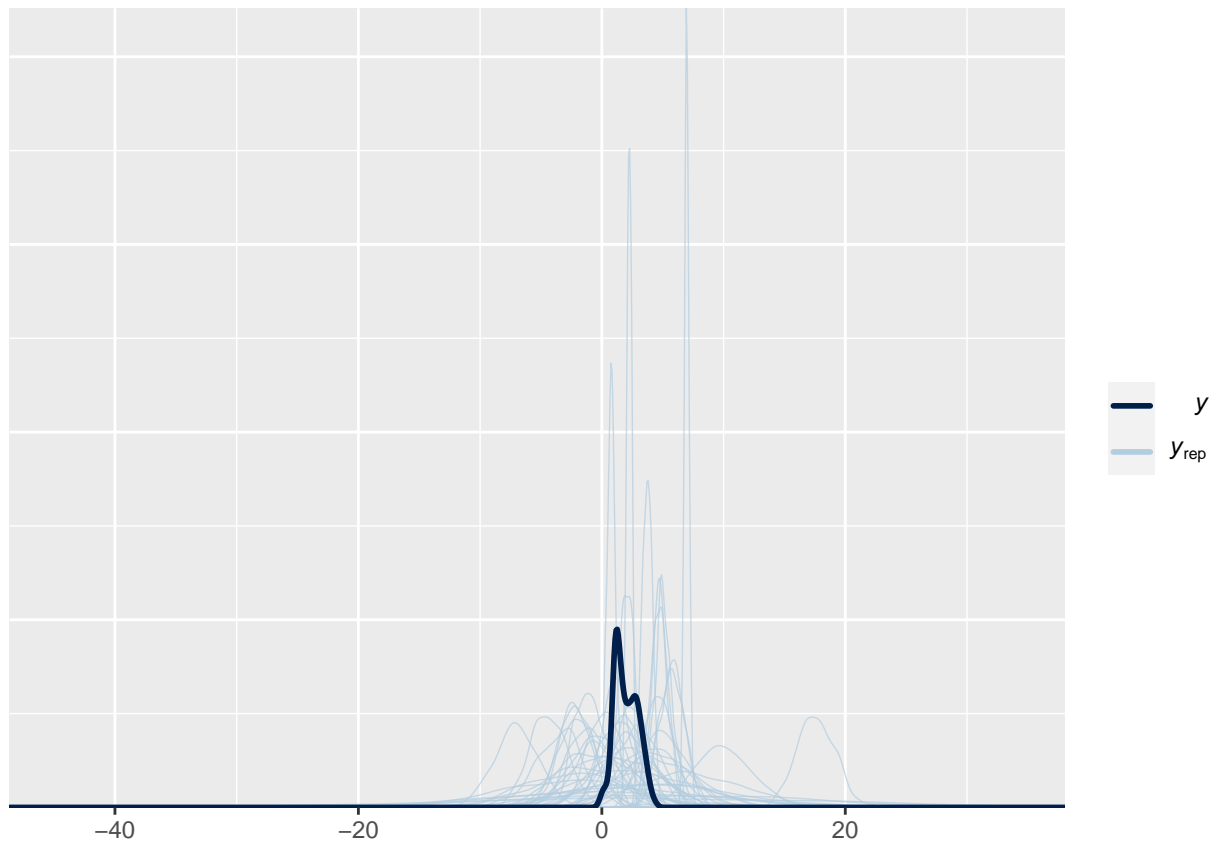
Setting Simple Model Priors

```
simple_model_priors <- c(prior(normal(0, .5), class = b),
                         prior(normal(0, 1), class = sd))
simple_model_with_priors <-
  update(simple_model,
         prior = simple_model_priors,
         file = 'data/w6/simple_model_with_priors',
         sample_prior = 'only',
         chains = 2)
```

Simple Model Prior Effect
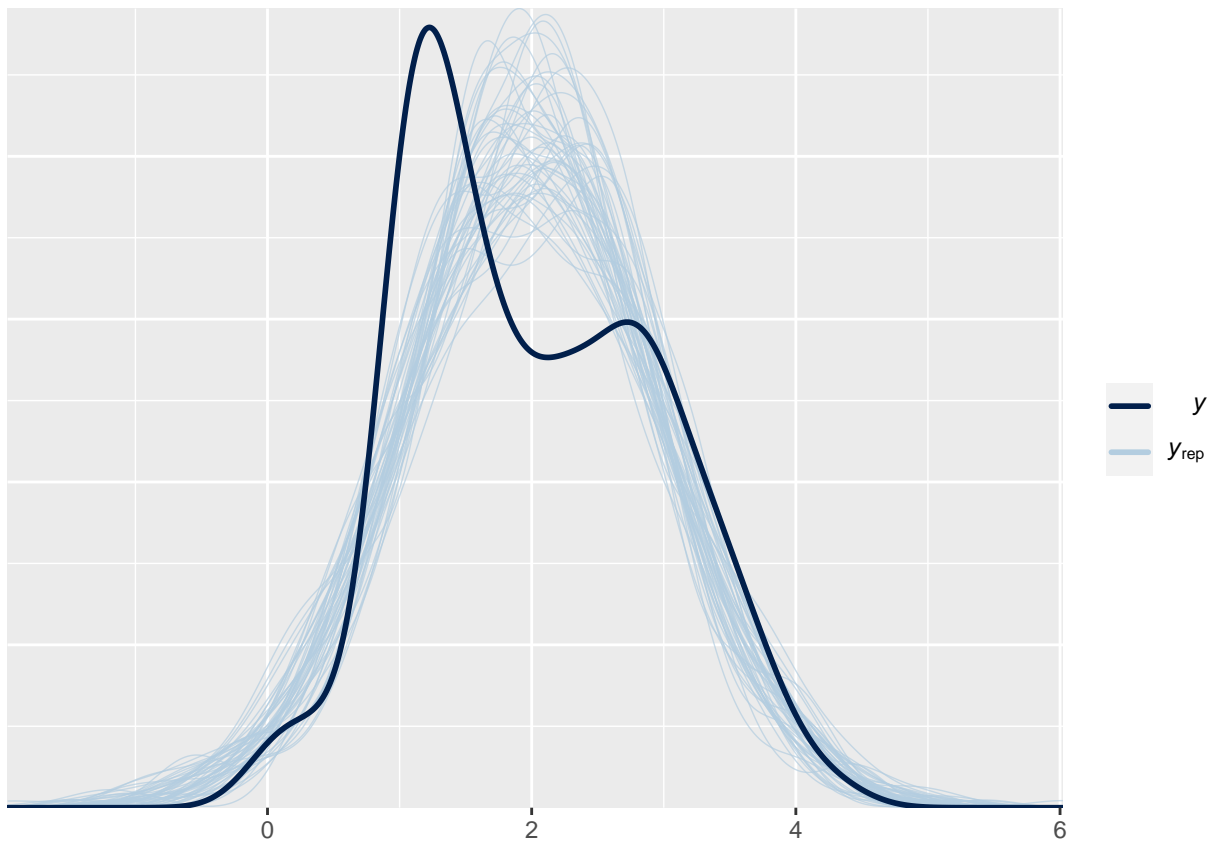
Simple Model with Lognormal Priors

```r
simple_model_lognormal_prior <-
  c(prior(lognormal(0, 1), class = b))
simple_model_with_lognormal_prior <-
  update(simple_model,
         prior = simple_model_lognormal_prior,
         file = 'data/w6/simple_model_with_lognormal_prior',
         sample_prior = 'only',
         chains = 2)
```

Simple Model Lognormal Prior Effect