Multilevel logistic mixed models

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1 Guatemalan Immunization Study

The objective of this study is to identify important family- and community-level factors that affect whether Guatemalan children are immunized. A nationally representative sample of 5160 mothers, between 15 and 44 years old were interviewed.

The Variables

Level 1 (children):

- immun: dummy variable for child being immunized, the response variable.
- kid2p: child at least 2 years old at the time of the interview.

Level 2 (mothers)

- mom: identifier for mother
- Ethnicity
 - indNoSpa: mother is indigenous, not Spanish speaking
 - indSpa: mother is indigenous, Spanish speaking
- Mother's education (dummy variables with 'no education' as reference category)
 - monEdPri: mother has primary education
 - monEdSec: mother has secondary education
- Husband's education (dummy variables with 'no education' as reference category)
 - husEdPri: husband has primary education
 - husEdSec: husband has secondary education
 - husEdDK: husband's education is not known

Level 3 (communities)

- cluster: identifier for communities
- rural: dummy variable for community being rural
- pcInd81: percentage of population that was indigenous in 1981

```
library(tidyverse)
library(haven)
library(lme4)
guatemala <- read_dta("guatemala.dta")
str(guatemala)</pre>
```

```
## tibble [2,159 x 19] (S3: tbl_df/tbl/data.frame)
## $ kid : num [1:2159] 2 269 272 273 274 275 276 277 278 280 ...
## ..- attr(*, "format.stata")= chr "%9.0g"
## $ mom : num [1:2159] 2 185 186 187 188 188 189 190 190 191 ...
## ..- attr(*, "format.stata")= chr "%9.0g"
## $ cluster : num [1:2159] 1 36 36 36 36 36 36 36 36 36 ...
## ..- attr(*, "format.stata")= chr "%9.0g"
## $ immun : num [1:2159] 1 0 0 0 0 1 1 1 1 1 ...
## ..- attr(*, "format.stata")= chr "%9.0g"
```

```
$ kid2p : num [1:2159] 1 1 1 1 1 1 1 0 1 1 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ mom25p : num [1:2159] 0 0 0 0 1 0 0 1 1 1 ...
     ..- attr(*, "format.stata")= chr "%9.0g"
##
##
   $ order23 : num [1:2159] 0 1 0 1 0 1 1 0 0 0 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ order46 : num [1:2159] 0 0 0 0 1 0 0 0 1 1 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
##
    $ order7p : num [1:2159] 0 0 0 0 0 0 1 0 0 ...
##
##
    ..- attr(*, "format.stata")= chr "%9.0g"
    $ indNoSpa: num [1:2159] 0 0 0 0 0 0 0 0 0 ...
     ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ indSpa : num [1:2159] 0 0 0 0 0 0 0 0 0 ...
##
    ..- attr(*, "format.stata")= chr "%9.0g"
##
##
   $ momEdPri: num [1:2159] 0 1 1 1 1 1 0 1 1 1 ...
##
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ momEdSec: num [1:2159] 1 0 0 0 0 1 0 0 0 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ husEdPri: num [1:2159] 0 1 0 1 0 0 1 1 1 0 ...
##
##
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ husEdSec: num [1:2159] 1 0 1 0 0 0 0 0 1 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
   $ husEdDK : num [1:2159] 0 0 0 0 1 1 0 0 0 0 ...
##
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ momWork : num [1:2159] 0 1 1 1 1 1 1 1 1 1 ...
##
    ..- attr(*, "format.stata")= chr "%9.0g"
##
            : num [1:2159] 0 0 0 0 0 0 0 0 0 0 ...
   $ rural
    ..- attr(*, "format.stata")= chr "%9.0g"
##
   $ pcInd81 : num [1:2159] 0.1075 0.0437 0.0437 0.0437 0.0437 ...
    ..- attr(*, "format.stata")= chr "%9.0g"
guatemala <- zap_formats(guatemala)</pre>
str(guatemala)
## tibble [2,159 x 19] (S3: tbl_df/tbl/data.frame)
              : num [1:2159] 2 269 272 273 274 275 276 277 278 280 ...
              : num [1:2159] 2 185 186 187 188 188 189 190 190 191 ...
##
   $ mom
   $ cluster : num [1:2159] 1 36 36 36 36 36 36 36 36 36 ...
   $ immun : num [1:2159] 1 0 0 0 0 1 1 1 1 1 ...
   $ kid2p : num [1:2159] 1 1 1 1 1 1 1 0 1 1 ...
##
   $ mom25p : num [1:2159] 0 0 0 0 1 0 0 1 1 1 ...
   $ order23 : num [1:2159] 0 1 0 1 0 1 1 0 0 0 ...
  $ order46 : num [1:2159] 0 0 0 0 1 0 0 0 1 1 ...
   $ order7p : num [1:2159] 0 0 0 0 0 0 0 1 0 0 ...
##
   $ indNoSpa: num [1:2159] 0 0 0 0 0 0 0 0 0 ...
   $ indSpa : num [1:2159] 0 0 0 0 0 0 0 0 0 ...
##
   $ momEdPri: num [1:2159] 0 1 1 1 1 1 0 1 1 1 ...
   $ momEdSec: num [1:2159] 1 0 0 0 0 1 0 0 0 ...
   $ husEdPri: num [1:2159] 0 1 0 1 0 0 1 1 1 0 ...
   $ husEdSec: num [1:2159] 1 0 1 0 0 0 0 0 1 ...
   $ husEdDK : num [1:2159] 0 0 0 0 1 1 0 0 0 0 ...
   $ momWork : num [1:2159] 0 1 1 1 1 1 1 1 1 1 ...
   $ rural : num [1:2159] 0 0 0 0 0 0 0 0 0 0 ...
   $ pcInd81 : num [1:2159] 0.1075 0.0437 0.0437 0.0437 0.0437 ...
```

head(guatemala)

| kid momclusterimmukrid 2 pmom 25 poler 28 rder 46 rder 7 pnd No. Sprad Spranom Erbler i Erbler E | | | | | | | | | | | | | | | | | | |
|---|-----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----------|
| 2 | 2 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0.1075042 |
| 269 | 185 | 36 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 0.0437295 |
| 272 | 186 | 36 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0.0437295 |
| 273 | 187 | 36 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 0.0437295 |
| 274 | 188 | 36 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0.0437295 |
| 275 | 188 | 36 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0.0437295 |

${\it \# Frequency of dhild-level observations}$

table(table(guatemala\$kid))

 $\frac{1}{2159}$

Frequency of mother-level observations

table(table(guatemala\$mom))

Frequency of cluster-level observations

data.frame(table(table(guatemala\$cluster)))

| Var1 | Freq |
|------|------|
| 1 | 2 |
| 2 | 7 |
| 3 | 7 |
| 4 | 6 |
| 5 | 6 |
| 6 | 7 |
| 7 | 6 |
| 8 | 8 |
| 9 | 11 |
| 10 | 13 |
| 11 | 13 |
| 12 | 5 |
| 13 | 2 |
| 14 | 5 |
| 15 | 6 |
| 16 | 7 |
| 17 | 6 |
| 18 | 4 |
| 19 | 2 |
| 20 | 3 |
| 21 | 6 |
| 22 | 3 |

| Var1 | Freq |
|------|------|
| 23 | 5 |
| 24 | 5 |
| 25 | 5 |
| 26 | 2 |
| 27 | 2 |
| 29 | 1 |
| 30 | 2 |
| 32 | 1 |
| 34 | 1 |
| 50 | 1 |
| 55 | 1 |
| | |

1.1 Unconditional two- and three-level Model

```
form <- immun ~ (1|mom)
(mod1 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
  Family: binomial (logit)
## Formula: immun ~ (1 | mom)
      Data: guatemala
##
##
         AIC
                   BIC
                          logLik deviance df.resid
  2925.317 2936.672 -1460.659 2921.317
                                                 2157
##
## Random effects:
## Groups Name
                       Std.Dev.
## mom
           (Intercept) 1.114
## Number of obs: 2159, groups: mom, 1595
## Fixed Effects:
## (Intercept)
       -0.2778
##
form <- immun ~ (1|cluster)</pre>
(mod2 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ (1 | cluster)
##
      Data: guatemala
                          logLik deviance df.resid
##
         AIC
                   BIC
## 2880.986 2892.341 -1438.493 2876.986
                                                 2157
## Random effects:
## Groups Name
                        Std.Dev.
## cluster (Intercept) 0.7573
## Number of obs: 2159, groups: cluster, 161
## Fixed Effects:
## (Intercept)
##
       -0.2339
form <- immun ~ (1|mom) + (1|cluster)</pre>
(mod3 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
##
  Family: binomial (logit)
## Formula: immun ~ (1 | mom) + (1 | cluster)
##
      Data: guatemala
        AIC
##
                  BIC
                         logLik deviance df.resid
  2860.950 2877.982 -1427.475 2854.950
## Random effects:
## Groups Name
                       Std.Dev.
## mom
            (Intercept) 0.9081
## cluster (Intercept) 0.8339
## Number of obs: 2159, groups: mom, 1595; cluster, 161
## Fixed Effects:
## (Intercept)
##
       -0.2754
anova(mod1, mod2, mod3)
```

| | npar | AIC | BIC | logLik | deviance | Chisq | Df | Pr(>Chisq) |
|------|------|----------|----------|-----------|----------|----------|----|------------|
| mod1 | 2 | 2925.317 | 2936.672 | -1460.659 | 2921.317 | NA | NA | NA |
| mod2 | 2 | 2880.987 | 2892.341 | -1438.493 | 2876.987 | 44.33067 | 0 | NA |
| mod3 | 3 | 2860.950 | 2877.982 | -1427.475 | 2854.950 | 22.03636 | 1 | 2.7e-06 |

1.2 Unconditional three-level Model with nested RE's

```
form <- immun ~ (1|cluster/mom)</pre>
(mod4 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
  Family: binomial (logit)
## Formula: immun ~ (1 | cluster/mom)
##
     Data: guatemala
##
         AIC
                   BIC
                          logLik deviance df.resid
## 2860.950 2877.982 -1427.475 2854.950
                                                2156
## Random effects:
## Groups
                Name
                            Std.Dev.
## mom:cluster (Intercept) 0.9081
               (Intercept) 0.8339
## Number of obs: 2159, groups: mom:cluster, 1595; cluster, 161
## Fixed Effects:
## (Intercept)
##
       -0.2754
```

1.3 Three-level random intercept model

```
form <- immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 + (1|mom)
(mod5 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +</pre>
```

```
##
       (1 | mom)
##
      Data: guatemala
                          logLik deviance
##
         AIC
                   BIC
  2770.280 2815.699 -1377.140 2754.280
                                                 2151
##
## Random effects:
  Groups Name
                       Std.Dev.
           (Intercept) 1.286
## mom
## Number of obs: 2159, groups:
                                 mom, 1595
## Fixed Effects:
  (Intercept)
                      kid2p
                                momEdPri
                                              husEdPri
                                                            momWork
                                                                            rural
##
       -0.7544
                     1.2758
                                   0.2845
                                                0.2776
                                                              0.3272
                                                                          -0.7623
##
       pcInd81
       -0.8296
##
mod1
## Generalized linear mixed model fit by maximum likelihood (Laplace
##
     Approximation) [glmerMod]
  Family: binomial (logit)
## Formula: immun ~ (1 | mom)
##
      Data: guatemala
##
         AIC
                   BIC
                          logLik deviance
                                            df.resid
  2925.317 2936.672 -1460.659
                                   2921.317
                                                 2157
## Random effects:
                       Std.Dev.
## Groups Name
## mom
           (Intercept) 1.114
## Number of obs: 2159, groups:
                                 mom, 1595
## Fixed Effects:
  (Intercept)
##
       -0.2778
##
In a linear model having the random effect variance increase in this scenario is not possible.
form <- immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 + (1|cluster)
(mod6 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
    Family: binomial (logit)
## Formula: immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +
##
       (1 | cluster)
##
      Data: guatemala
##
         AIC
                   BIC
                          logLik deviance
                                             df.resid
## 2768.005 2813.425 -1376.003 2752.005
                                                 2151
## Random effects:
                        Std.Dev.
## Groups Name
## cluster (Intercept) 0.6256
## Number of obs: 2159, groups: cluster, 161
## Fixed Effects:
## (Intercept)
                      kid2p
                                 momEdPri
                                              husEdPri
                                                            momWork
                                                                            rural
       -0.5105
                     1.0027
                                                              0.2041
                                                                          -0.6074
##
                                   0.1720
                                                0.2196
##
       pcInd81
       -0.8043
##
```

Generalized linear mixed model fit by maximum likelihood (Laplace

```
Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ (1 | cluster)
##
      Data: guatemala
         AIC
                   BIC
                          logLik deviance df.resid
## 2880.986 2892.341 -1438.493 2876.986
                                                2157
## Random effects:
## Groups Name
                        Std.Dev.
## cluster (Intercept) 0.7573
## Number of obs: 2159, groups: cluster, 161
## Fixed Effects:
## (Intercept)
       -0.2339
##
form <- immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +</pre>
  (1|mom) + (1|cluster)
mod6 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial)
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0026005 (tol = 0.002, component 1)
summary(mod6)
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
  Family: binomial (logit)
## Formula: immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +
       (1 | mom) + (1 | cluster)
##
      Data: guatemala
##
##
        AIC
                 BIC
                       logLik deviance df.resid
##
     2737.7
              2788.8 -1359.9
                                2719.7
                                           2150
##
## Scaled residuals:
      Min
                1Q Median
                                3Q
                                       Max
## -1.6628 -0.6424 -0.3527 0.6927 2.5342
##
## Random effects:
## Groups Name
                        Variance Std.Dev.
            (Intercept) 1.2401
                                 1.1136
   cluster (Intercept) 0.4908
                                 0.7006
## Number of obs: 2159, groups: mom, 1595; cluster, 161
## Fixed effects:
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.6776
                            0.2605 -2.601 0.009299 **
## kid2p
                 1.2662
                            0.1577
                                    8.030 9.72e-16 ***
## momEdPri
                 0.2450
                            0.1378
                                     1.778 0.075472 .
## husEdPri
                 0.2822
                            0.1325
                                     2.130 0.033205 *
                            0.1357
                                     2.055 0.039832 *
## momWork
                 0.2789
## rural
                -0.7573
                            0.1952 -3.879 0.000105 ***
## pcInd81
                -1.0001
                            0.2461 -4.064 4.82e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation of Fixed Effects:
##
            (Intr) kid2p mmEdPr hsEdPr momWrk rural
## kid2p
            -0.455
## momEdPri -0.313 0.089
## husEdPri -0.230 0.082 -0.151
## momWork -0.377 0.036 0.030 0.026
           -0.471 -0.101 -0.042 -0.064 0.092
## pcInd81 -0.433 -0.121 0.174 -0.014 0.107 0.020
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0026005 (tol = 0.002, component 1)
form <- immun ~ kid2p + momEdPri + husEdPri + kid2p*momWork +</pre>
  (1|mom) + (1|cluster)
mod6b <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial)</pre>
summary (mod6b)
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ kid2p + momEdPri + husEdPri + kid2p * momWork + (1 |
      mom) + (1 | cluster)
##
##
     Data: guatemala
##
##
       ATC
                BIC
                      logLik deviance df.resid
##
     2765.5
             2810.9 -1374.7
                              2749.5
##
## Scaled residuals:
               1Q Median
                               ЗQ
      Min
## -1.7861 -0.6388 -0.3697 0.6910 2.1843
##
## Random effects:
                        Variance Std.Dev.
## Groups Name
            (Intercept) 1.1839
## cluster (Intercept) 0.6557
                                0.8097
## Number of obs: 2159, groups: mom, 1595; cluster, 161
##
## Fixed effects:
                Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                -1.57651
                            0.22213 -7.097 1.27e-12 ***
## kid2p
                 1.01289
                            0.19516 5.190 2.10e-07 ***
## momEdPri
                 0.35417
                            0.13658
                                      2.593 0.00951 **
## husEdPri
                 0.26821
                            0.13209
                                      2.031 0.04230 *
                            0.26256 -0.094 0.92492
## momWork
                -0.02474
## kid2p:momWork 0.54661
                            0.28624
                                      1.910 0.05619 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Correlation of Fixed Effects:
               (Intr) kid2p mmEdPr hsEdPr momWrk
## kid2p
              -0.756
## momEdPri
              -0.295 0.052
## husEdPri
              -0.315 0.058 -0.146
              -0.509 0.536 -0.032 0.014
## momWork
## kid2p:mmWrk 0.384 -0.602 0.058 0.006 -0.855
```

1.4 Two-level random intercept slope model

```
form <- immun ~ kid2p + (1 + kid2p|cluster)</pre>
(mod7 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ kid2p + (1 + kid2p | cluster)
##
      Data: guatemala
##
         AIC
                   BIC
                          logLik deviance df.resid
## 2807.202 2835.589 -1398.601 2797.202
                                                 2154
## Random effects:
## Groups Name
                        Std.Dev. Corr
## cluster (Intercept) 1.0629
            kid2p
                        0.7258
                                  -0.68
## Number of obs: 2159, groups: cluster, 161
## Fixed Effects:
## (Intercept)
                      kid2p
##
        -1.131
                      1.110
anova(mod2, mod7)
```

| | npar | AIC | BIC | logLik | deviance | Chisq | Df | Pr(>Chisq) |
|----------|------|----------|----------|-----------|----------|----------|----|------------|
| mod2 | 2 | 2880.987 | 2892.341 | -1438.493 | 2876.987 | NA | NA | NA |
| $\mod 7$ | 5 | 2807.202 | 2835.589 | -1398.601 | 2797.202 | 79.78422 | 3 | 0 |

```
form <- immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +
  (1 + kid2p|cluster)
(mod8 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.416888 (tol = 0.002, component 1)
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +
##
       (1 + kid2p | cluster)
##
      Data: guatemala
##
         AIC
                   BIC
                          logLik deviance df.resid
## 2766.472 2823.246 -1373.236 2746.472
                                                2149
## Random effects:
                        Std.Dev. Corr
## Groups Name
## cluster (Intercept) 0.8640
##
           kid2p
                        0.7291
                                 -0.69
## Number of obs: 2159, groups: cluster, 161
## Fixed Effects:
## (Intercept)
                      kid2p
                                momEdPri
                                             husEdPri
                                                           momWork
                                                                           rural
##
      -0.5822
                     1.0855
                                  0.1715
                                               0.2210
                                                            0.2081
                                                                         -0.6199
##
      pcInd81
      -0.8189
##
## optimizer (Nelder_Mead) convergence code: 0 (OK); 0 optimizer warnings; 1 lme4 warnings
```

1.5 Three-level random intercept slope model

```
form <- immun ~ kid2p + (1 + kid2p|cluster) + (1|mom)</pre>
(mod10 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial))</pre>
## Generalized linear mixed model fit by maximum likelihood (Laplace
    Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: immun ~ kid2p + (1 + kid2p | cluster) + (1 | mom)
      Data: guatemala
##
##
         AIC
                   BIC
                          logLik deviance df.resid
## 2783.255 2817.320 -1385.628 2771.255
                                                2153
## Random effects:
## Groups Name
                        Std.Dev. Corr
            (Intercept) 1.0287
## mom
## cluster (Intercept) 1.1646
                        0.7329
           kid2p
##
                                 -0.66
## Number of obs: 2159, groups: mom, 1595; cluster, 161
## Fixed Effects:
## (Intercept)
                      kid2p
        -1.359
                      1.333
anova(mod7,mod10)
```

| | npar | AIC | BIC | logLik | deviance | Chisq | Df | Pr(>Chisq) |
|-------|------|----------|----------|-----------|----------|----------|----|------------|
| mod7 | 5 | 2807.202 | 2835.589 | -1398.601 | 2797.202 | NA | NA | NA |
| mod10 | 6 | 2783.255 | 2817.320 | -1385.628 | 2771.255 | 25.94698 | 1 | 4e-07 |

```
form <- immun ~ kid2p + momEdPri + husEdPri + momWork + rural + pcInd81 +
    (1 + kid2p|cluster) + (1|mom)
mod11 <- glmer(formula = form, data = guatemala, nAGQ = 1, family = binomial)
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.481706 (tol = 0.002, component 1)
anova(mod6,mod11)</pre>
```

| | npar | AIC | BIC | logLik | deviance | Chisq | Df | Pr(>Chisq) |
|-------|------|----------|----------|-----------|----------|----------|----|------------|
| mod6 | 9 | 2737.709 | 2788.806 | -1359.855 | 2719.709 | NA | NA | NA |
| mod11 | 11 | 2738.381 | 2800.832 | -1358.190 | 2716.381 | 3.328456 | 2 | 0.1893367 |