final_report

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Final Report: Application of the integrated gateway model on child nutrition behaviors in Niger

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Introduction

Application of the integrated gateway model on child nutrition behaviors in Niger: An exploratory analysis by Leanne Dougherty and Chaibou Dadi uses the Integrated Gateway Model (adapted from Schwandt et. al., 2015) to identify potential factors and behaviors that are associated with the World Health Organization's infant and young child feeding (IYCF) practices ("Global strategy for infant and young child feeding", 2003) in the Maradi and Zinder regions of Niger. This framework aims to support positive behaviors in reproductive, maternal, and child health, which supports more comprehensive nutritional communication strategies.

Summary of the Data

The data was collected via survey from 2021 to February 2023. The survey data consists of responses from 2,727 married women of reproductive age (MWRA) including details on child feeding practices for their 2,551 children between the ages of 0 to 23 months. Our cleaned data selected 30 of the 900 + variables to the best of our ability (see critiques section for details). These variables are organized under the following structure:

- Gateway behaviors:
  - antenatal care (received_antenatal care): percentage of MRWA who have given birth in the last 5 years and received antenatal care for their last pregnancy; 1 = received antenatal care, 0 = otherwise
  - facility delivery (fac_delivery): percentage of MWRA who have given birth in the years preceding the survey who delivered in a facility for their last birth
  - communication in nutrition practices (nutrition): percentage of MWRA who spoke with 1) husband/partner, 2) family member, 3) health provider, 4) nobody about child's nutrition
- Gateway Factors
  - Behavioral determinants on 4 IYCF practices (early initiation of breastfeeding, exclusive breastfeeding, minimum meal frequency, and minimum dietary diversity)

- Knowledge:
  - know_1: percentage of MRWA who state it is healthy for a woman to give only breast milk for the first 6 months; 1 = those who agree it is healthy for a woman to give a child only breastmilk for the first 6 months, 0 otherwise
  - know_2: percentage of MWRA who reported a child 6-23 months should eat 4 or more meals each day; 1 = those who agree a child 6-23 months should receive 4 or meals a day, 0 otherwise
  - know 3: percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more; 1 = those who agree a child 6-23 months should receive 4 or more different types of food, 0 = otherwise
- Attitude
  - att_1: percentage of MWRA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick; 1 = those who agree that if a baby is exclusively breastfed for 6 months, they are less likely to get sick, 0 = otherwise
  - att_2: percentage of MWRA who agree providing meals 4 times a day ensures them to have adequate strength; 1 = those who agree providing 4 meals a day ensures strength, 0 = otherwise
  - att_3: percentage of MWRA who agree children who eat a variety of foods are less likely to get sick; 1 = those who agree children who eat a variety of foods are less likely to get sick, 0 = otherwise
- Self-efficacy
  - se_1: percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all; 1 = those who agree only giving breast milk to the baby for the first 6 months is not difficult at all, 0 = otherwise
  - se_2: percentage of MRWA who agree giving a child a meal 4 times a day is not difficult at all; 1 = those who agree giving a child a meal 4 times a day is not difficult at all, 0 = otherwise
  - se_3: percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all; 1 = those who agree that giving a child a minimum of 4 or more different types of food a day is not difficult at all, 0 = otherwise
- Perceived norms
  - pn_1 : percentage of MRWA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months; 1 = those who agree people in the community think it is healthy for a woman to give her baby only breast milk for first 6 months, 0 = otherwise
  - pn_2: percentage of MRWA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more; 1 = those who believe the number of meals people in the community think a child 6-23 months should eat each day is 4 or more, 0 = otherwise
  - pn_3: percentage of MRWA who believes number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more; 1 = those who believe the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more, 0 = otherwise

– decision-making agency (decision_combined): Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives; 1 = responded either decides herself or jointly with her partner on all three decision categories, 0 = otherwise

– exposure to information (exp): percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition; 1 = has been exposed, 0 = otherwise

– woman's group participation (wg): Percentage of MRWA who belong to a women's community group; 1 belonged to a womens group, 0 otherwise

- Control variables:
  - age: age: percentage of MWRA who reported their current age and grouped (15-24 years, 25-39 years, 35 - 49 years)
  - parity: Percentage of MRWA who reported living children and grouped (0 children, 1-2 children, 3-4 children, 5-6 children, and 7+ children)
  - educational attainment (any_edu): percentage of MWRA who reported to have ever gone to school; 0 - no, 1 - yes
  - household wealth (wealth): percentage of MWRA who reported household assets constructed in wealth terciles (1 = poorest, 3 = richest)

Models and Methods

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(broom)
library(ggplot2)
library(stats)
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```r
library(glmtoolbox)
niger <- read_csv("./CLEANNigerData.csv")
```

```
## Rows: 2183 Columns: 30
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (3): age, wealth, parity
## dbl (27): any_edu, fac_delivery, nutrition, know_1, pn_1, att_1, se_1, exp, ...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
# Recode the numeric values into descriptive categories
niger$nutrition <- factor(niger$nutrition,
                          levels = c(1, 2, 3, 4, 5, 96, 99),
                          labels = c("husband/partner", "family member", "health provider", "mother in

# Convert the factor into a new factor with 4 levels
niger$nutrition <- cut(as.numeric(niger$nutrition), breaks = c(0, 1, 2, 3, 99), labels = c(1, 2, 3, 4))
```

Our models were constructed based on the variables identified in Table 1 , Table 3, and Table 4 within the article. The variables chosen are based on our best approximation of these identified variables (see critiques section for further details).

Our models below do not contain control variables i in order to prevent overfitting.

Early Initiation of Breastfeeding

Model 1:

```r
glm_eib_1 <- glm( se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
             family = binomial(link = "logit"),
             data = niger)

tidy(glm_eib_1, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term                   estimate std.error statistic  p.value conf.low conf.high
##   <chr>                     <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)             -0.999      0.307    -3.25  1.15e- 3  -1.60      -0.398
## 2 know_1                   1.46       0.201     7.28  3.26e-13   1.07       1.86
## 3 att_1                   -0.0353     0.205    -0.172 8.63e- 1  -0.436      0.369
## 4 pn_1                    -1.20       0.194    -6.19  6.11e-10  -1.59      -0.826
## 5 exp                      1.87       0.102    18.3   8.79e-75   1.67       2.07
## 6 decision_combined        0.101      0.129     0.783 4.34e- 1  -0.152      0.355
## 7 wg                       0.233      0.100     2.33  2.01e- 2   0.0365     0.429
## 8 received_antenatal_c~    0.0129     0.124     0.104 9.17e- 1  -0.230      0.256
```

```r
# Odds Ratio
odds_ratios_eib1 <- exp(coef(glm_eib_1))
odds_ratios_eib1
```

```
##             (Intercept)                  know_1                   att_1
##               0.3683014               4.3171946               0.9653218
##                    pn_1                     exp       decision_combined
##               0.3015861               6.4598706               1.1064596
##                      wg received_antenatal_care
##               1.2619724               1.0130297
```

Model 2:

```r
glm_eib_2 <- glm(se_1 ~ know_1 + att_1 + pn_1  + exp + decision_combined + wg + fac_delivery,
              family = binomial(link = "logit"),
              data = niger)

tidy(glm_eib_2, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)         -2.10      0.299    -7.04  1.91e-12   -2.69     -1.52
## 2 know_1               1.51      0.209     7.25  4.32e-13    1.11      1.93
## 3 att_1                0.173     0.209     0.829 4.07e- 1   -0.236     0.585
## 4 pn_1                -1.07      0.200    -5.33  9.60e- 8   -1.46     -0.680
## 5 exp                  1.68      0.106    15.8   2.27e-56    1.47      1.89
## 6 decision_combined    0.114     0.132     0.860 3.90e- 1   -0.145     0.375
## 7 wg                   0.380     0.106     3.60  3.22e- 4    0.173     0.588
## 8 fac_delivery         1.40      0.104    13.5   8.98e-42    1.20      1.61
```

```r
# Odds Ratio
odds_ratios_eib2 <- exp(coef(glm_eib_2))
odds_ratios_eib2
```

```
##       (Intercept)            know_1             att_1              pn_1
##         0.1219080         4.5375404         1.1891670         0.3446008
##               exp decision_combined                wg      fac_delivery
##         5.3702306         1.1207180         1.4626410         4.0685091
```

Model 3:

```r
glm_eib_3 <- glm(se_1 ~ know_1 + att_1  + pn_1 + exp + decision_combined + wg + nutrition,
              family = binomial(link = "logit"),
              data = niger)
tidy(glm_eib_3, conf.int = TRUE)
```

```
## # A tibble: 10 x 7
##    term              estimate std.error statistic  p.value conf.low conf.high
##    <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
##  1 (Intercept)         -0.976     0.283    -3.44  5.75e- 4  -1.53      -0.422
##  2 know_1               1.39      0.203     6.84  7.69e-12   0.997      1.79
##  3 att_1               -0.0970    0.205    -0.473 6.36e- 1  -0.498      0.308
##  4 pn_1                -1.24      0.194    -6.38  1.76e-10  -1.62      -0.863
##  5 exp                  1.73      0.106    16.3   1.08e-59   1.52       1.94
##  6 decision_combined    0.209     0.133     1.57  1.15e- 1  -0.0509     0.470
##  7 wg                   0.152     0.103     1.48  1.39e- 1  -0.0496     0.353
##  8 nutrition2           0.558     0.248     2.25  2.47e- 2   0.0806     1.06
##  9 nutrition3           1.65      0.198     8.36  6.41e-17   1.28       2.05
## 10 nutrition4           0.177     0.137     1.29  1.97e- 1  -0.0924     0.447
```

```r
# Odds Ratio
odds_ratios_eib3 <- exp(coef(glm_eib_3))
odds_ratios_eib3
```

```
##       (Intercept)            know_1             att_1              pn_1
##         0.3768707         4.0184247         0.9075226         0.2904637
##               exp decision_combined                wg        nutrition2
##         5.6443377         1.2325096         1.1637014         1.7472837
##        nutrition3        nutrition4
##         5.2219346         1.1941272
```

Exclusive Initiation of Breastfeeding

Model 1:

```r
glm_exib_1 <- glm(se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenata
              data = niger,
              family = binomial)

tidy(glm_exib_1, conf.int = TRUE)
```

```
## # A tibble: 9 x 7
##   term                  estimate std.error statistic  p.value conf.low conf.high
##   <chr>                    <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)            -1.62       0.330    -4.89  1.01e- 6  -2.27      -0.971
## 2 know_1                  1.44       0.211     6.82  8.97e-12   1.03       1.86
## 3 att_1                   0.378      0.225     1.68  9.22e- 2  -0.0592     0.822
## 4 se_3                    2.06       0.157    13.1   4.55e-39   1.76       2.37
## 5 pn_1                   -1.23       0.192    -6.41  1.46e-10  -1.62      -0.862
## 6 exp                     1.68       0.107    15.7   2.69e-55   1.47       1.90
## 7 decision_combined       0.0621     0.137     0.454 6.50e- 1  -0.206      0.331
## 8 wg                      0.398      0.106     3.77  1.60e- 4   0.192      0.605
## 9 received_antenatal_c~  -0.0700     0.131    -0.535 5.93e- 1  -0.327      0.187
```

```r
# Odds Ratio
OR_glm_exib_1 <- exp(coef(glm_exib_1))
OR_glm_exib_1
```

```
##             (Intercept)                  know_1                   att_1
##               0.1987742               4.2193661               1.4593433
##                    se_3                    pn_1                     exp
##               7.8311099               0.2915572               5.3841378
##       decision_combined                      wg received_antenatal_care
##               1.0641144               1.4893880               0.9323556
```

Model 2:

```r
glm_exib_2 <- glm(se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery, # 
              data = niger,
              family = binomial)

tidy(glm_exib_2, conf.int = TRUE)
```

```
## # A tibble: 9 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -2.45       0.318    -7.71  1.31e-14  -3.08      -1.83
## 2 know_1              1.49       0.215     6.94  4.03e-12   1.07       1.92
## 3 att_1               0.473      0.227     2.08  3.77e- 2   0.0298     0.923
## 4 se_3                1.69       0.161    10.6   4.66e-26   1.39       2.02
## 5 pn_1               -1.11       0.197    -5.62  1.94e- 8  -1.50      -0.725
## 6 exp                 1.55       0.110    14.1   1.88e-45   1.34       1.77
## 7 decision_combined   0.0682     0.138     0.495 6.20e- 1  -0.201      0.339
## 8 wg                  0.492      0.109     4.51  6.59e- 6   0.279      0.707
## 9 fac_delivery        1.11       0.109    10.2   2.80e-24   0.893      1.32
```

```r
# Odds Ratio
OR_glm_exib_2 <- exp(coef(glm_exib_2))
OR_glm_exib_2
```

```
##       (Intercept)            know_1             att_1              se_3
##        0.08628303        4.43738542        1.60411072        5.44444997
##              pn_1               exp decision_combined                wg
##        0.33105028        4.73048902        1.07061553        1.63584326
##      fac_delivery
##        3.02070186
```

Model 3:

```r
glm_exib_3 <- glm(se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition, # + a
              data = niger,
              family = binomial)

tidy(glm_exib_3, conf.int = TRUE)
```

```
## # A tibble: 11 x 7
##    term              estimate std.error statistic  p.value conf.low conf.high
##    <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
##  1 (Intercept)         -1.70      0.305    -5.57  2.56e- 8  -2.30      -1.10
##  2 know_1               1.39      0.213     6.51  7.60e-11   0.976      1.81
##  3 att_1                0.343     0.223     1.54  1.24e- 1  -0.0909     0.784
##  4 se_3                 1.95      0.160    12.2   4.87e-34   1.64       2.27
##  5 pn_1                -1.25      0.193    -6.50  7.93e-11  -1.64      -0.880
##  6 exp                  1.56      0.112    14.0   1.13e-44   1.35       1.78
##  7 decision_combined    0.199     0.139     1.43  1.53e- 1  -0.0740     0.472
##  8 wg                   0.333     0.108     3.09  1.97e- 3   0.122      0.544
##  9 nutrition2           0.244     0.279     0.873 3.83e- 1  -0.297      0.800
```

```
## 10 nutrition3           1.35      0.202     6.69  2.27e-11   0.966      1.76
## 11 nutrition4           0.290     0.143     2.04  4.15e- 2   0.0108     0.570
```

```r
# Odds Ratio
OR_glm_exib_3 <- exp(coef(glm_exib_3))
OR_glm_exib_3
```

```
##       (Intercept)            know_1             att_1              se_3
##         0.1833846         4.0059820         1.4091060         7.0300022
##              pn_1               exp decision_combined                wg
##         0.2859612         4.7804179         1.2199903         1.3950819
##        nutrition2        nutrition3        nutrition4
##         1.2760058         3.8613531         1.3370810
```

Minimum Meal Frequency

Note: these are models fit according to the exact specifications of the article. The models we will interpret/evaluate may be different based on the evaluation of assumptions.

Model 1:

```r
glm_mmf_1 <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care,
                 data = niger,
                 family = binomial(link = "logit"))

tidy(glm_mmf_1, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term                    estimate std.error statistic  p.value conf.low conf.high
##   <chr>                      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)              -2.77       0.353    -7.86  3.98e-15   -3.47     -2.09
## 2 att_2                     1.75       0.260     6.71  1.90e-11    1.24      2.26
## 3 se_2                      0.996      0.149     6.67  2.61e-11    0.702     1.29
## 4 pn_2                      2.67       0.146    18.2   2.19e-74    2.39      2.96
## 5 exp                      -0.168      0.141    -1.19  2.34e- 1   -0.444     0.108
## 6 decision_combined         0.503      0.195     2.58  9.79e- 3    0.129     0.894
## 7 wg                        0.0616     0.145     0.425 6.71e- 1   -0.222     0.347
## 8 received_antenatal_c~     0.0634     0.194     0.326 7.44e- 1   -0.326     0.437
```

```r
# Odds ratio:
odds_ratios_mmf1 <- exp(coef(glm_mmf_1))
odds_ratios_mmf1
```

```
##             (Intercept)                   att_2                    se_2
##               0.0625421               5.7266853               2.7076558
##                    pn_2                     exp       decision_combined
##              14.4853727               0.8457457               1.6536627
##                      wg received_antenatal_care
##               1.0635267               1.0654750
```

Model 2:

```r
glm_mmf_2 <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg + fac_delivery,
                 data = niger,
                 family = binomial(link = "logit"))

tidy(glm_mmf_2, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -2.49       0.312    -7.98  1.47e-15   -3.11    -1.89
## 2 att_2               1.65       0.264     6.24  4.29e-10    1.14     2.18
## 3 se_2                1.01       0.149     6.78  1.18e-11    0.719    1.30
## 4 pn_2                2.66       0.144    18.4   6.29e-76    2.38     2.95
## 5 exp                -0.0972     0.145    -0.673 5.01e- 1   -0.381    0.186
## 6 decision_combined   0.496      0.194     2.56  1.05e- 2    0.124    0.885
## 7 wg                  0.0513     0.145     0.354 7.24e- 1   -0.233    0.337
## 8 fac_delivery       -0.289      0.150    -1.93  5.31e- 2   -0.585    0.00265
```

```r
# Odds ratio:
odds_ratios_mmf2 <- exp(coef(glm_mmf_2))
odds_ratios_mmf2
```

```
##       (Intercept)             att_2              se_2              pn_2
##        0.08279079        5.20647643        2.75267066       14.34800927
##               exp decision_combined                wg      fac_delivery
##        0.90733313        1.64240231        1.05264646        0.74864478
```

Model 3:

```r
glm_mmf_3 <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))

tidy(glm_mmf_3, conf.int = TRUE)
```

```
## # A tibble: 10 x 7
##    term              estimate std.error statistic  p.value conf.low conf.high
##    <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
##  1 (Intercept)        -2.68       0.296    -9.09  1.03e-19   -3.28    -2.12
##  2 att_2               1.68       0.266     6.31  2.83e-10    1.16     2.21
##  3 se_2                0.981      0.149     6.57  5.17e-11    0.687    1.27
##  4 pn_2                2.75       0.149    18.4   6.27e-76    2.46     3.04
##  5 exp                -0.288      0.148    -1.94  5.18e- 2   -0.580    0.00208
##  6 decision_combined   0.592      0.202     2.94  3.32e- 3    0.205    0.996
##  7 wg                  0.0201     0.146     0.138 8.90e- 1   -0.265    0.307
##  8 nutrition2         -0.0360     0.355    -0.102 9.19e- 1   -0.704    0.693
##  9 nutrition3          0.598      0.223     2.69  7.20e- 3    0.169    1.04
## 10 nutrition4         -0.162      0.203    -0.798 4.25e- 1   -0.554    0.243
```

```r
summary(glm_mmf_3)
```

```
##
## Call:
## glm(formula = know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined +
##     wg + nutrition, family = binomial(link = "logit"), data = niger)
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -2.68497    0.29552  -9.086  < 2e-16 ***
## att_2              1.67694    0.26586   6.308 2.83e-10 ***
## se_2               0.98101    0.14941   6.566 5.17e-11 ***
## pn_2               2.74563    0.14890  18.440  < 2e-16 ***
## exp               -0.28834    0.14829  -1.944  0.05184 .
## decision_combined  0.59192    0.20161   2.936  0.00332 **
## wg                 0.02012    0.14582   0.138  0.89025
## nutrition2        -0.03603    0.35478  -0.102  0.91910
## nutrition3         0.59815    0.22256   2.688  0.00720 **
## nutrition4        -0.16203    0.20305  -0.798  0.42488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2076.4  on 2182  degrees of freedom
## Residual deviance: 1421.5  on 2173  degrees of freedom
## AIC: 1441.5
##
## Number of Fisher Scoring iterations: 5
```

```r
# Odds ratio:
odds_ratios_mmf3 <- exp(coef(glm_mmf_3))
odds_ratios_mmf3
```

```
##       (Intercept)             att_2              se_2              pn_2
##        0.06822296        5.34914896        2.66716032       15.57443490
##               exp decision_combined                wg        nutrition2
##        0.74950904        1.80745201        1.02032559        0.96460742
##        nutrition3        nutrition4
##        1.81875817        0.85041635
```

Minimum Dietary Diversity

Model 1:

```r
glm_mdd_1 <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + received_antena
                 data = niger,
                 family = binomial)
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
# tidy(glm_mdd_1, conf.int = TRUE) idk why this gives me an error
tidy(glm_mdd_1,)
```

```
## # A tibble: 9 x 5
##   term                    estimate std.error statistic p.value
##   <chr>                      <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)             -2.66e+ 1    38113. -6.97e- 4   0.999
## 2 know_2                   3.57e-14    21143.  1.69e-18   1
## 3 att_3                   -3.47e-14    34234. -1.01e-18   1
## 4 se_3                    -6.31e-14    20400. -3.09e-18   1
## 5 pn_3                     9.14e-14    17945.  5.09e-18   1
## 6 wg                       4.27e-14    15989.  2.67e-18   1
## 7 decision_combined       -5.62e-14    20384. -2.76e-18   1
## 8 exp                      4.17e-14    16405.  2.54e-18   1
## 9 received_antenatal_care  2.60e-14    19608.  1.33e-18   1
```

```r
# Odds Ratio
odds_ratios_mdd1 <- exp(coef(glm_mdd_1))
odds_ratios_mdd1
```

```
##             (Intercept)                  know_2                   att_3
##            2.900701e-12            1.000000e+00            1.000000e+00
##                    se_3                    pn_3                      wg
##            1.000000e+00            1.000000e+00            1.000000e+00
##       decision_combined                     exp received_antenatal_care
##            1.000000e+00            1.000000e+00            1.000000e+00
```

Model 2:

```r
glm_mdd_2 <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + fac_delivery, #
                 data = niger,
                 family = binomial)
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
# tidy(glm_mdd_2, conf.int = TRUE)

tidy(glm_mdd_2)
```

```
## # A tibble: 9 x 5
##   term              estimate std.error statistic p.value
##   <chr>                <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)       -2.66e+ 1    34959. -7.60e- 4   0.999
## 2 know_2            -2.24e-14    21123. -1.06e-18   1
## 3 att_3              3.30e-14    34308.  9.63e-19   1
## 4 se_3               3.62e-14    20876.  1.73e-18   1
## 5 pn_3              -7.40e-14    18058. -4.10e-18   1
## 6 wg                -2.86e-14    15985. -1.79e-18   1
## 7 decision_combined  3.99e-14    20151.  1.98e-18   1
## 8 exp               -3.63e-14    16566. -2.19e-18   1
## 9 fac_delivery       4.94e-14    16737.  2.95e-18   1
```

```r
# Odds Ratio
odds_ratios_mdd2 <- exp(coef(glm_mdd_2))
odds_ratios_mdd2
```

```
##       (Intercept)            know_2             att_3              se_3
##      2.900701e-12      1.000000e+00      1.000000e+00      1.000000e+00
##              pn_3                wg decision_combined               exp
##      1.000000e+00      1.000000e+00      1.000000e+00      1.000000e+00
##      fac_delivery
##      1.000000e+00
```

Model 3:

```r
glm_mdd_3 <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + nutrition, # + 
                 data = niger,
                 family = binomial)
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
# tidy(glm_mdd_3, conf.int = TRUE)
tidy(glm_mdd_3)
```

```
## # A tibble: 11 x 5
##    term              estimate std.error statistic p.value
##    <chr>                <dbl>     <dbl>     <dbl>   <dbl>
##  1 (Intercept)       -2.66e+ 1    34169. -7.77e- 4   0.999
##  2 know_2            -8.39e-14    21108. -3.97e-18   1
##  3 att_3              1.42e-13    34550.  4.10e-18   1
##  4 se_3               2.12e-13    20788.  1.02e-17   1
##  5 pn_3              -1.80e-13    18128. -9.92e-18   1
##  6 wg                -6.77e-14    16048. -4.22e-18   1
##  7 decision_combined  4.95e-14    21244.  2.33e-18   1
##  8 exp               -4.50e-14    16901. -2.66e-18   1
##  9 nutrition2         3.44e-16    37460.  9.19e-21   1
## 10 nutrition3        -4.00e-13    24374. -1.64e-17   1
## 11 nutrition4         1.69e-15    22538.  7.48e-20   1
```

```r
# Odds Ratio
odds_ratios_mdd3 <- exp(coef(glm_mdd_3))
odds_ratios_mdd3
```

```
##       (Intercept)            know_2             att_3              se_3
##      2.900701e-12      1.000000e+00      1.000000e+00      1.000000e+00
##              pn_3                wg decision_combined               exp
##      1.000000e+00      1.000000e+00      1.000000e+00      1.000000e+00
##        nutrition2        nutrition3        nutrition4
##      1.000000e+00      1.000000e+00      1.000000e+00
```

Assumptions

Early Initiation of Breastfeeding

Model 1:

```
# fitting a more complicated model
niger1 <- mutate(niger, know_1_2 = (know_1^2))
eib_1_comp <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
                  data = niger1,
                  family = binomial(link = "logit"))

anova(glm_eib_1, eib_1_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care + know_1 * received_antenatal_care +
##     know_1_2 * received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     2525.5
## 2      2174     2524.0  1   1.4595    0.227
```

```
#fitting the model with cut explanatory variables; cut know_1

eib1_cut <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care,
                data = niger,
                family = binomial(link = "logit"))

anova(eib1_cut, glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2581.1
## 2      2175     2525.5  1   55.631 8.743e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

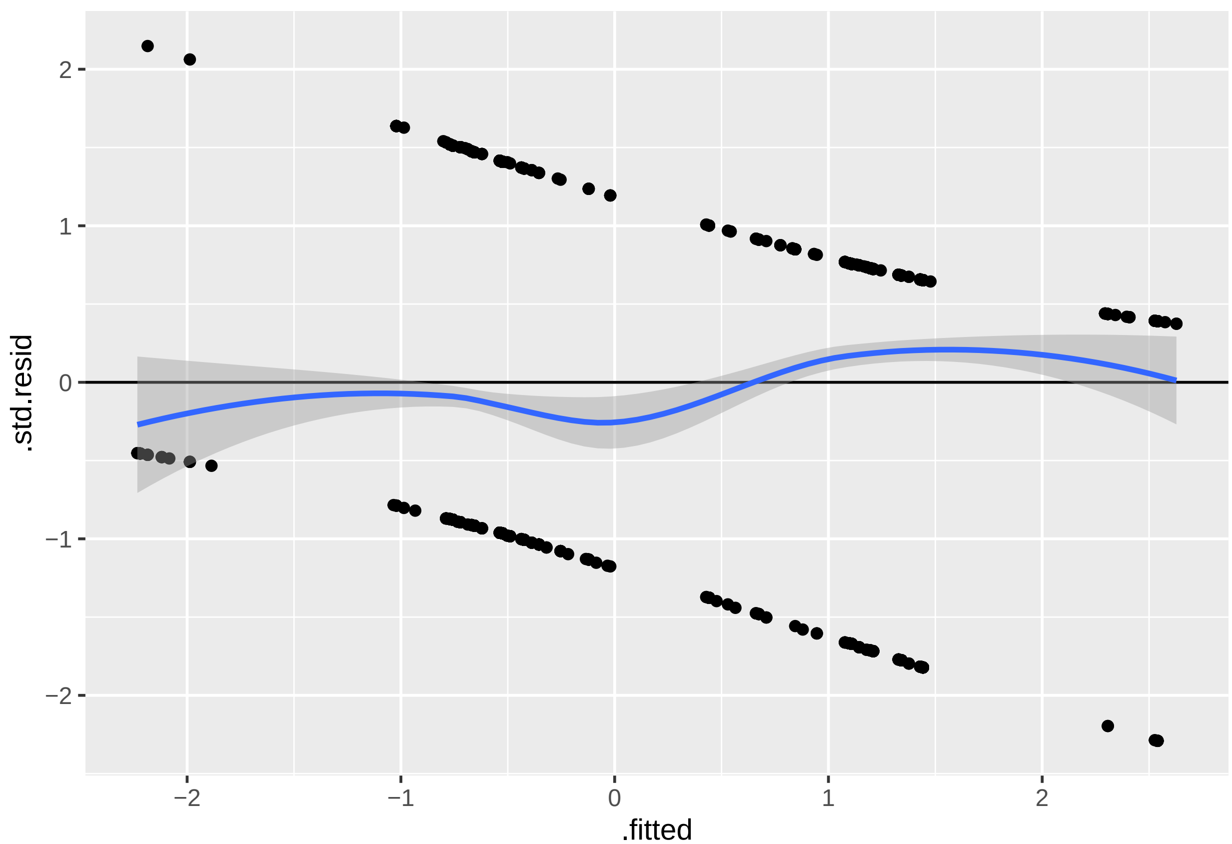
```
hltest(glm_eib_1)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##   Group Size Observed  Expected
```

```
##       1  168       51  46.61369
##       2  437      124 139.50509
##       3  197       80  68.78354
##       4  208       89  77.69062
##       5  228      114 133.06174
##       6  298      237 224.04073
##       7  198      152 152.89748
##       8  258      208 204.50436
##       9  191      155 162.90275
##
##          Statistic =  21.03646
## degrees of freedom =  7
##            p-value =  0.0037166
```

```r
aeib1 <- augment(glm_eib_1)

ggplot(data = aeib1, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



Model 2:

```r
# fitting a more complicated model
niger1 <- mutate(niger, know_1_2 = (know_1^2))
eib_2_comp <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg + fac_delivery + know_1 *
                  data = niger1,
                  family = binomial(link = "logit"))

anova(glm_eib_2, eib_2_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery + know_1 * fac_delivery + know_1_2 * fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     2333.2
## 2      2174     2333.2  1 0.010019   0.9203
```

```r
#fitting the model with cut explanatory variables; cut know_1

eib2_cut <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + fac_delivery,
                data = niger,
                family = binomial(link = "logit"))

anova(eib2_cut, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2389.0
## 2      2175     2333.2  1   55.788 8.073e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

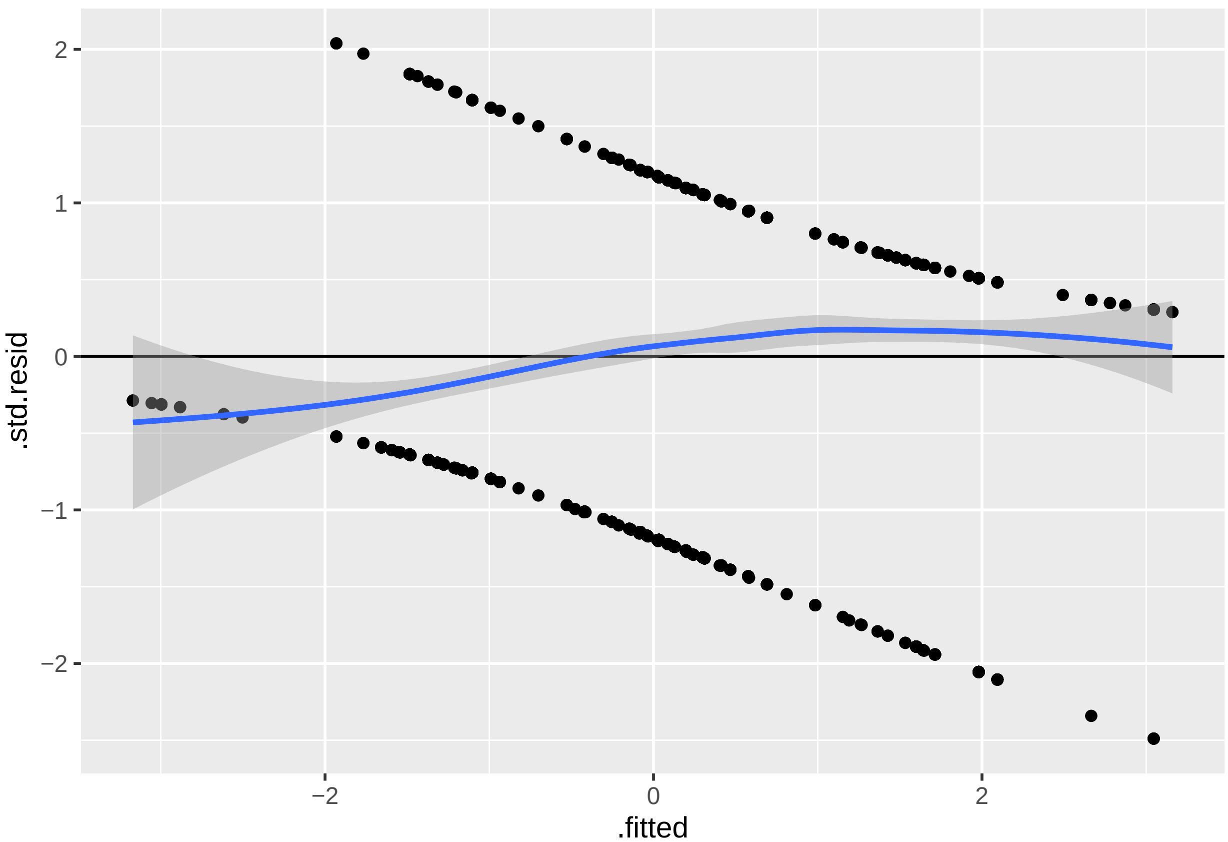
```r
hltest(glm_eib_2)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  364       49  64.61573
##      2  221       60  52.98262
##      3  114       51  43.37385
##      4  231      111 110.82815
##      5  264      146 144.23194
##      6  222      150 139.69688
##      7   94       74  73.54548
##      8  256      215 212.99416
```

```
##      9  296      247 256.75303
##     10  121      107 110.97816
##
##          Statistic =  14.71442
## degrees of freedom =  8
##             p-value =  0.064942
```

```r
aeib2 <- augment(glm_eib_2)

ggplot(data = aeib2, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



Model 3:

```r
# fitting a more complicated model
niger1 <- mutate(niger, know_1_2 = (know_1^2))
eib_3_comp <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg + nutrition + know_1 * nu
                  data = niger1,
                  family = binomial(link = "logit"))

anova(glm_eib_3, eib_3_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition + know_1 * nutrition + know_1_2 * nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173     2435.4
## 2      2170     2426.4  3   9.0031  0.02925 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#fitting the model with cut explanatory variables; cut know_1

eib3_cut <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + nutrition,
                data = niger,
                family = binomial(link = "logit"))

anova(eib3_cut, glm_eib_3, test = "LRT")
```

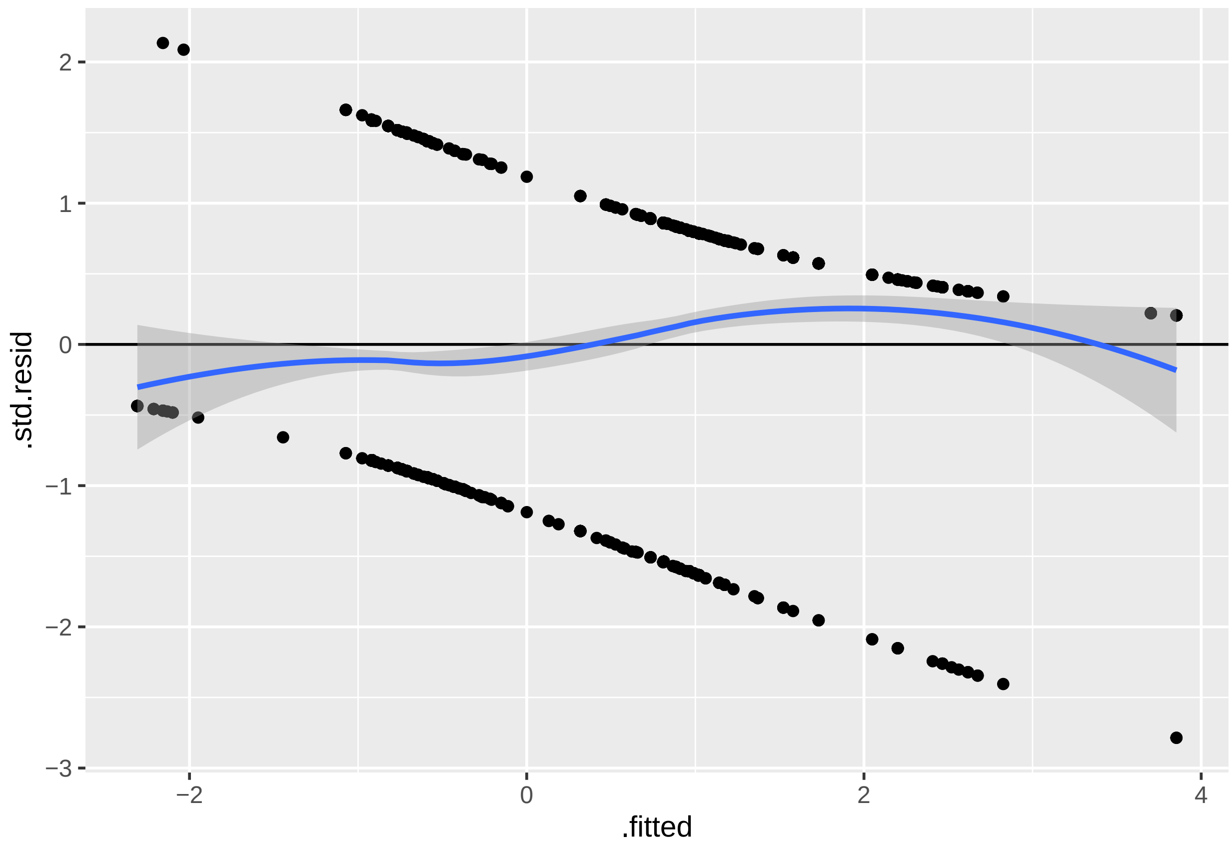
```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2485.0
## 2      2173     2435.4  1   49.594 1.891e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hltest(glm_eib_3)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##   Group Size Observed   Expected
##       1   50       15   9.138964
##       2  404       94 115.264900
##       3  189       72  59.462353
##       4  250      102  83.950192
##       5  214       78 101.615362
##       6  252      190 174.109435
##       7  234      172 168.449496
##       8  219      149 164.064362
##       9  242      219 212.907563
##      10  129      119 121.037370
##
##          Statistic =  42.71836
## degrees of freedom =  8
##            p-value =  9.9247e-07
```

```r
aeib3 <- augment(glm_eib_3)

ggplot(data = aeib3, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



Exclusive Initiation of Breastfeeding

Model 1:

```r
# fitting a more complicated model
niger_exib_1 <- mutate(niger, know_1_2 = (know_1^2))
exib1_comp <- glm(se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + recei
                  data = niger_exib_1,
                  family = binomial(link = "logit"))

anova(glm_exib_1, exib1_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + received_antenatal_care
```

```
## Model 2: se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + received_antenatal_care + know_1 * received_antenatal_care +
##     know_1_2 * received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174     2302.9
## 2      2173     2302.9  1 0.084787   0.7709
```

```
#fitting a model with cut explanatory variables; cut know_1

exib1_cut <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care,
                 data = niger,
                 family = binomial(link = "logit"))

anova(exib1_cut, glm_exib_1, test = "LRT")
```

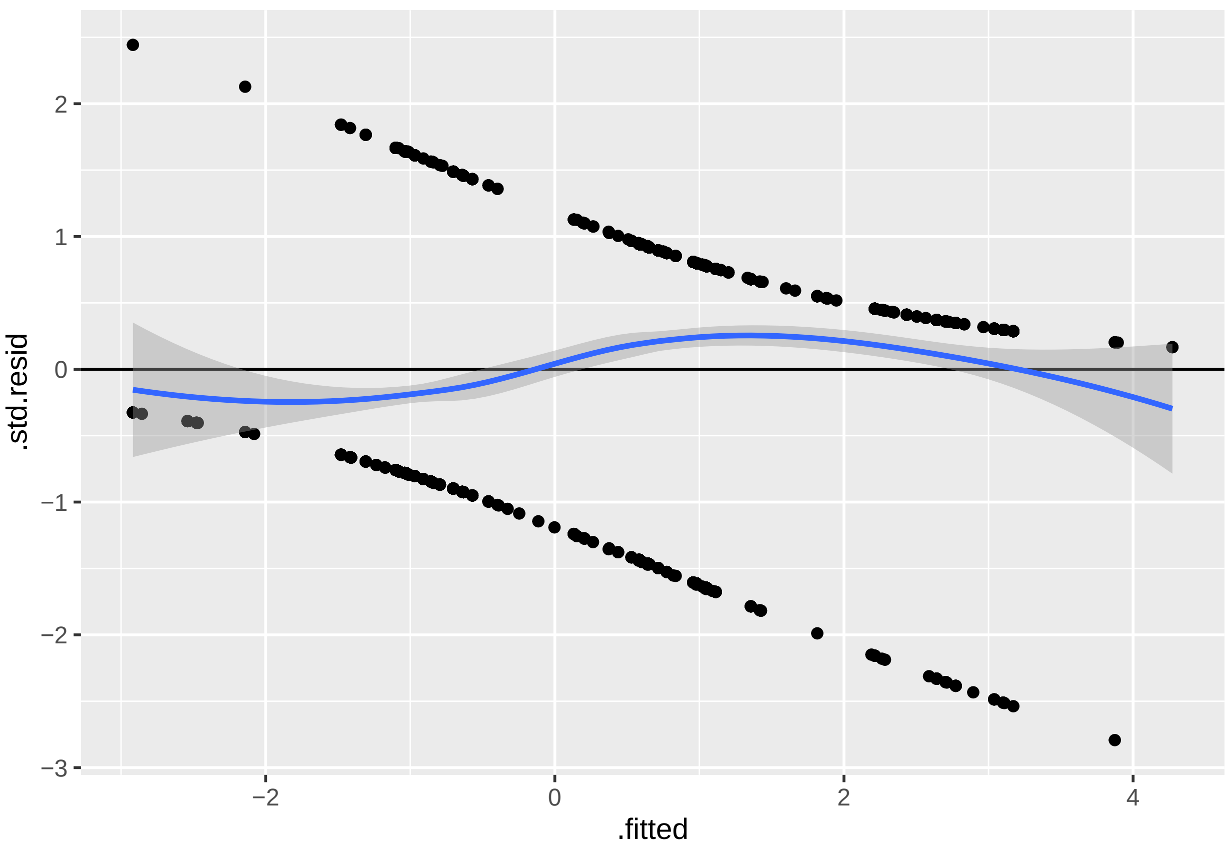
```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2175     2352.8
## 2      2174     2302.9  1   49.906 1.613e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
hltest(glm_exib_1)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1   71       11  10.86283
##      2  379       74  94.61773
##      3  220       63  59.50679
##      4  250       87  84.28917
##      5  292      184 173.58621
##      6  199      148 135.55859
##      7  205      156 149.22577
##      8  224      177 179.34536
##      9  221      199 206.24523
##     10  122      111 116.76232
##
##          Statistic =  23.24477
## degrees of freedom =  8
##            p-value =  0.0030638
```

```
aexib1 <- augment(glm_exib_1)

ggplot(data = aexib1, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



For the more complicated model, we have incredibly weak evidence of a model misspecification (p-value = 0.7709). However, for the model where know_1 is cut, we have strong evidence to suggest a model misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow goodness-of-fit test shows strong evidence of a lack of fit given the relatively small p-value (p-value = 0.0030638). Therefore, the cut model exib1_cut is probably the better fit and will be the model we are interpreting.

Model 2:

```
# fitting a more complicated model
niger_exib_1 <- mutate(niger, know_1_2 = (know_1^2))
exib2_comp <- glm(se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_de
                  data = niger_exib_1,
                  family = binomial(link = "logit"))

anova(glm_exib_2, exib2_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + fac_delivery
## Model 2: se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + fac_delivery + know_1 * fac_delivery + know_1_2 * fac_delivery
##   Resid. Df Resid. Dev Df  Deviance Pr(>Chi)
## 1      2174       2198
## 2      2173       2198  1 0.0040373   0.9493
```

```r
#fitting a model with cut explanatory variables; cut know_1

exib2_cut <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery,
                 data = niger,
                 family = binomial(link = "logit"))

anova(exib2_cut, glm_exib_2, test = "LRT")
```

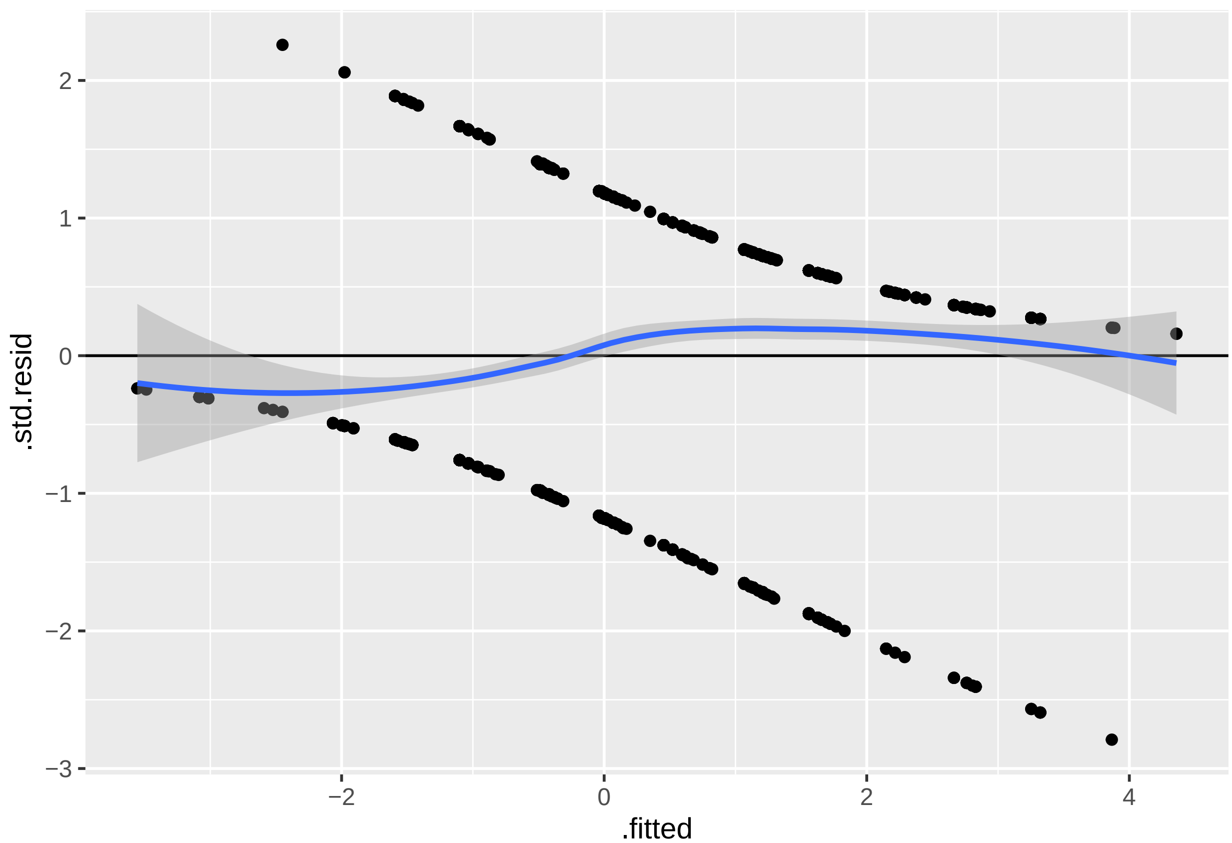
```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2175     2249.8
## 2      2174     2198.0  1   51.757 6.283e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hltest(glm_exib_2)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  355       47  56.61765
##      2  214       55  49.60078
##      3  246       75  87.56024
##      4  212      106  98.27474
##      5  224      141 131.31034
##      6  237      180 173.90327
##      7  231      190 185.73741
##      8  192      163 168.61499
##      9  241      226 228.34411
##     10   31       27  30.03647
##
##          Statistic =  21.53789
## degrees of freedom =  8
##            p-value =  0.0058478
```

```r
aexib2 <- augment(glm_exib_2)

ggplot(data = aexib2, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



For the more complicated model, we have incredibly weak evidence of a model misspecification (p-value = 0.9493). However, for the model where know_1 is cut, we have strong evidence to suggest a model misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow goodness-of-fit test shows strong evidence of a lack of fit given the relatively small p-value (p-value = 0.0058478). Therefore, the cut model exib2_cut is probably the better fit and will be the model we are interpreting.

Model 3:

```
# fitting a more complicated model
niger_exib_1 <- mutate(niger, know_1_2 = (know_1^2))
exib3_comp <- glm(se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutri
                  data = niger_exib_1,
                  family = binomial(link = "logit"))

anova(glm_exib_3, exib3_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + nutrition
## Model 2: se_1 ~ know_1 + know_1_2 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + nutrition + know_1 * nutrition + know_1_2 * nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2172     2248.9
## 2      2169     2243.6  3   5.2743   0.1528
```

```r
#fitting a model with cut explanatory variables; cut know_1

exib3_cut <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))

anova(exib3_cut, glm_exib_3, test = "LRT")
```

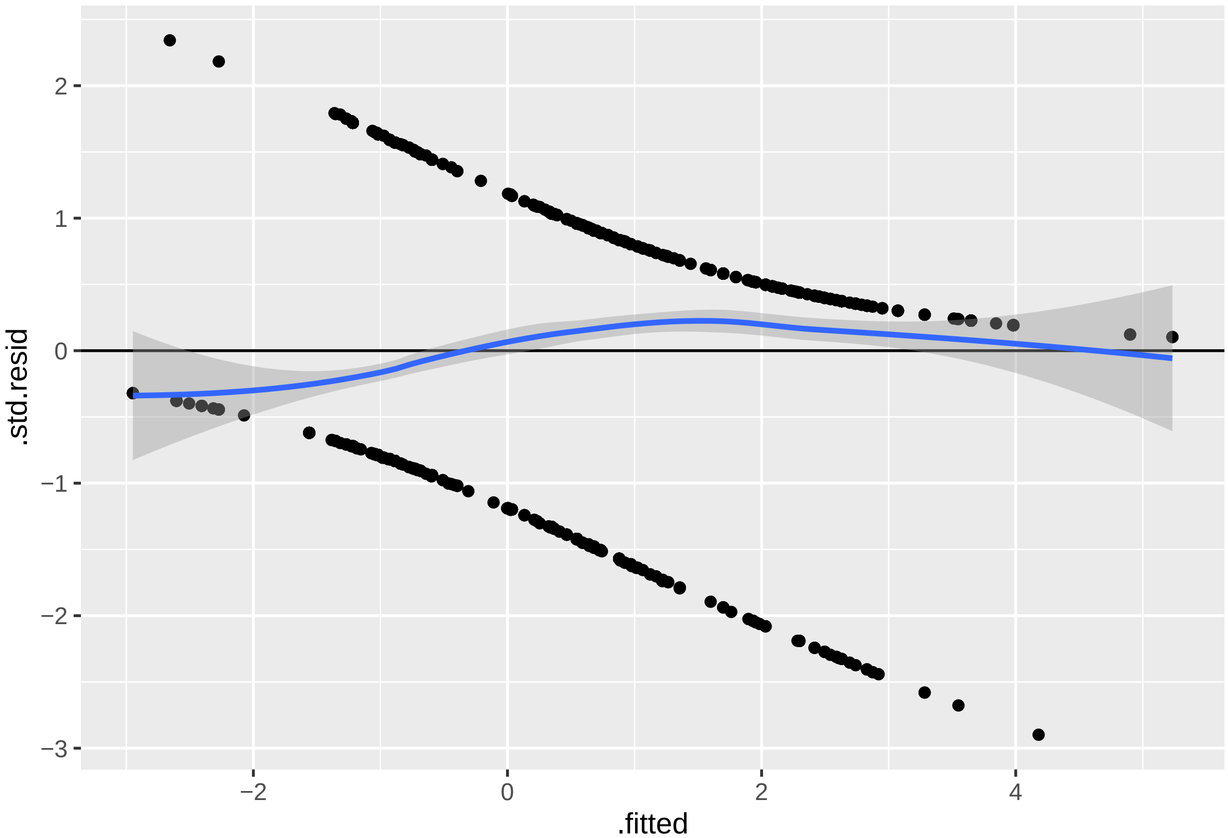
```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ know_1 + att_1 + se_3 + pn_1 + exp + decision_combined +
##     wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173     2294.6
## 2      2172     2248.9  1    45.67  1.4e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hltest(glm_exib_3)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##   Group Size Observed   Expected
##       1   66       11   9.897452
##       2  366       61  83.597209
##       3  194       62  53.305167
##       4  212       69  64.220693
##       5  270      137 135.912157
##       6  158      103  99.450310
##       7  199      149 133.153648
##       8  207      155 159.360181
##       9  240      220 214.151389
##      10  235      208 221.562733
##      11   36       35  35.389060
##
##          Statistic =  33.35862
## degrees of freedom =  9
##            p-value =  0.00011565
```

```r
aexib3 <- augment(glm_exib_3)

ggplot(data = aexib3, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



For the more complicated model, we have very weak evidence of a model misspecification (p-value = 0.1528). However, for the model where know_1 is cut, we have strong evidence to suggest a model misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow goodness-of-fit test shows strong evidence of a lack of fit given the small p-value (p-value = 0.00011565). Therefore, the cut model exib3_cut is probably the better fit and will be the model we are interpreting.

Minimum Meal Frequency

Model 1:

```
# fitting a more complicated model
niger1 <- mutate(niger, att_2_2 = (att_2^2))
mmf1_comp <- glm(know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined + wg + received_antena
                 data = niger1,
                 family = binomial(link = "logit"))

anova(glm_mmf_1, mmf1_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     received_antenatal_care
## Model 2: know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined +
##     wg + received_antenatal_care + att_2 * received_antenatal_care +
```

```
##     att_2_2 * received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     1430.4
## 2      2174     1429.6  1  0.78932   0.3743
```

```r
#fitting a model with cut explanatory variables; cut att_2

mmf1_cut <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care,
                 data = niger,
                 family = binomial(link = "logit"))

anova(mmf1_cut, glm_mmf_1, test = "LRT")
```

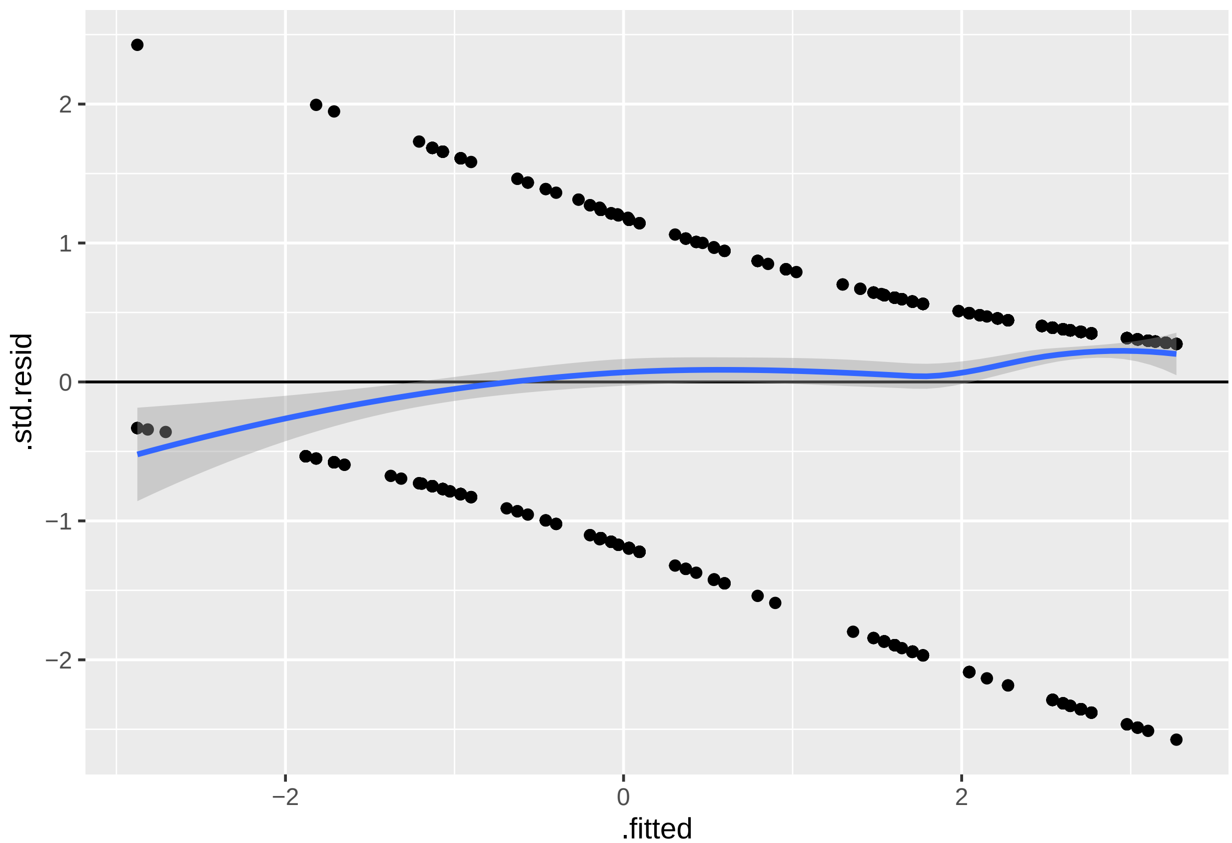
```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     1478.7
## 2      2175     1430.4  1    48.32 3.62e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hltest(glm_mmf_1)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  219       58  50.37243
##      2  215      117 118.33552
##      3  232      181 194.48185
##      4  320      288 294.57601
##      5  210      197 195.47983
##      6  177      166 165.53117
##      7  360      343 337.45386
##      8  213      203 200.93295
##      9  237      231 226.83638
##
##          Statistic =  12.96478
## degrees of freedom =  7
##            p-value =  0.072971
```

```r
ammf1 <- augment(glm_mmf_1)

ggplot(data = ammf1, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



For the more complicated model, we have very weak evidence of a model misspecification (p-value = 0.3743). However, for the model where att_2 is cut, we have strong evidence to suggest a model misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow goodness-of-fit test shows moderate to weak evidence of a lack of fit (p-value = 0.0729). Therefore, mmf_cut is probably a better fit and will be the model we are interpreting.

Model 2:

```
# fitting a more complicated model
niger1 <- mutate(niger, att_2_2 = (att_2^2))
mmf2_comp <- glm(know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined + wg + fac_delivery +
                 data = niger1,
                 family = binomial(link = "logit"))

anova(glm_mmf_2, mmf2_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
## Model 2: know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined +
##     wg + fac_delivery + att_2 * fac_delivery + att_2_2 * fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     1426.7
## 2      2174     1424.8  1   1.9143   0.1665
```

```r
#fitting a model with cut explanatory variables; cut att_2

mmf2_cut <- glm(know_2 ~ + se_2 + pn_2 + exp + decision_combined + wg + fac_delivery,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf2_cut, glm_mmf_2, test = "LRT")
```

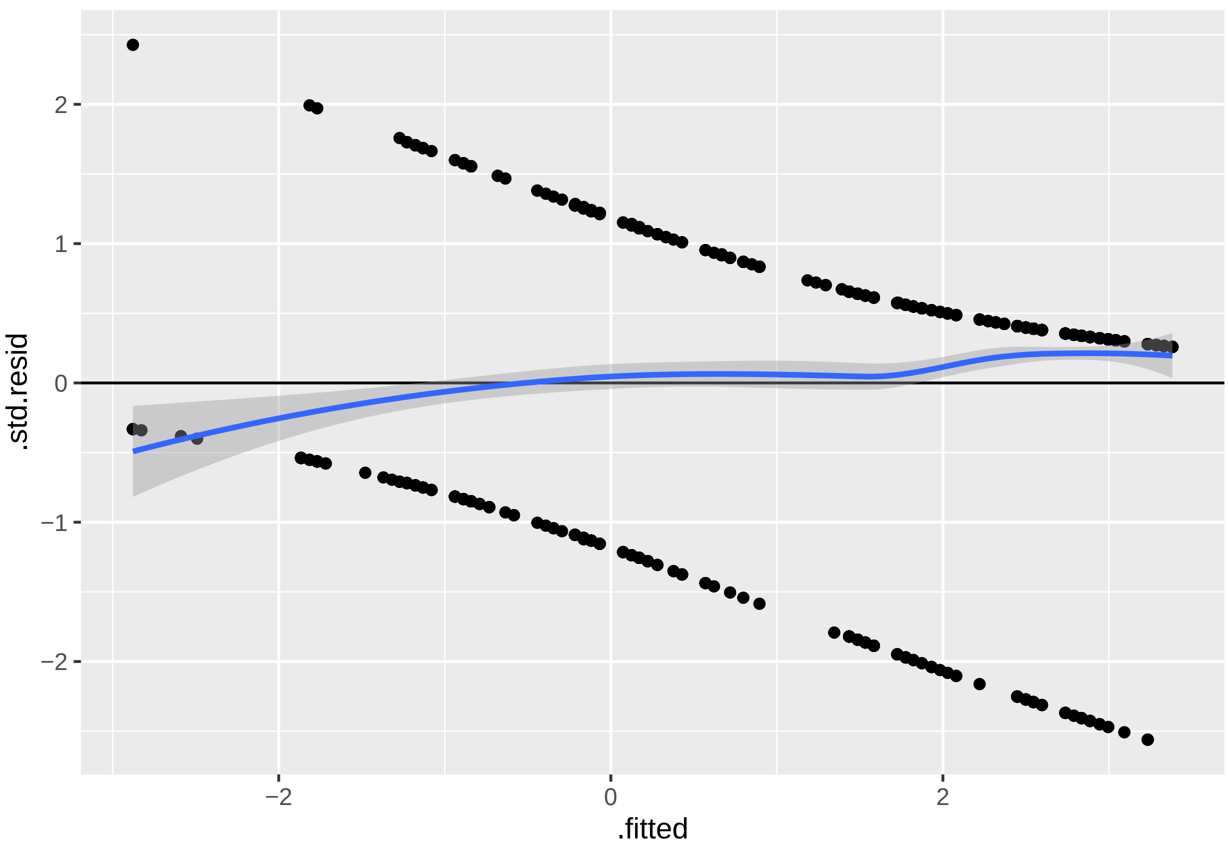
```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ +se_2 + pn_2 + exp + decision_combined + wg + fac_delivery
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     1468.0
## 2      2175     1426.7  1   41.323 1.291e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
hltest(glm_mmf_2)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  212       53  47.63302
##      2  211      114 112.25003
##      3  225      173 187.41549
##      4  247      221 224.59435
##      5  159      146 146.92984
##      6  196      183 181.74051
##      7  231      220 216.44460
##      8  262      253 247.46415
##      9  226      213 214.25950
##     10  214      208 205.26852
##
##          Statistic =  12.50007
## degrees of freedom =  8
##            p-value =  0.13025
```

```r
ammf2 <- augment(glm_mmf_2)

ggplot(data = ammf2, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



When compared to the more complicated model, there is moderate to weak evidence of model misspecification (p-value= 0.1665). The model where att_2 is cut shows strong evidence of misspecification (p-value < 0.001). The Hosmer-Lemeshow test shows moderate to weak evidence of a lack of fit (p-value 0.13025). Given the only moderate evidence of overall lack of fit, we should be fine sticking with the original model glm_mmf_2.

Model 3:

```
# fitting a more complicated model
niger1 <- mutate(niger, att_2_2 = (att_2^2))
mmf3_comp <- glm(know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined + wg + nutrition + at
                 data = niger1,
                 family = binomial(link = "logit"))

anova(glm_mmf_3, mmf3_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     nutrition
## Model 2: know_2 ~ att_2 + att_2_2 + se_2 + pn_2 + exp + decision_combined +
##     wg + nutrition + att_2 * nutrition + att_2_2 * nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173     1421.5
## 2      2170     1414.7  3      6.8  0.07855 .
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#fitting a model with cut explanatory variables; cut att_2
mmf3_cut <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition,
                data = niger,
                family = binomial(link = "logit"))
anova(mmf3_cut, glm_mmf_3, test = "LRT")
```

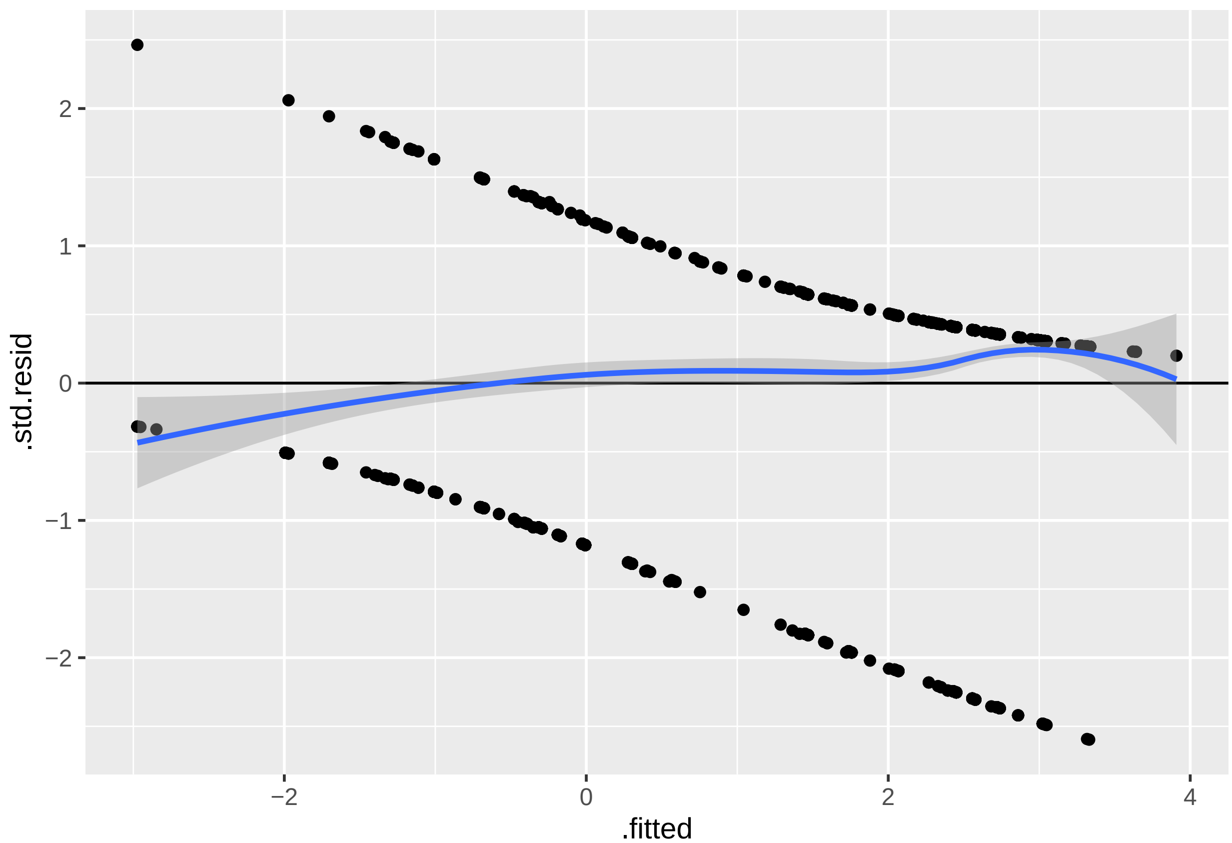
```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     1463.4
## 2      2173     1421.5  1   41.933 9.444e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
hltest(glm_mmf_3)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  218       57  49.80229
##      2  216      119 118.86645
##      3  219      174 182.36312
##      4  257      223 234.17911
##      5  255      232 235.52261
##      6   84       76  78.12469
##      7  324      313 303.94952
##      8  211      202 199.07805
##      9  195      187 186.02739
##     10  204      201 196.08679
##
##          Statistic =  19.56492
## degrees of freedom =  8
##            p-value =  0.012114
```

```
ammf3 <- augment(glm_mmf_3)

ggplot(data = ammf3, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



When compared to the more complicated model, there is weak/moderate evidence of a misspecification (p-value = 0.07855). However, there is strong evidence to suggest misspecification when comparing the original model to the one where att_2 is cut (p-value < 0.001). Moreover, the Hosmer-Lemeshow test has a small p-value (p-value = 0.01211), which indicates that there is relatively strong evidence of a lack of fit. Therefore, the model that will be evaluated/intrepreted will be mmf3_cut.

Minimum Dietary Diversity

Model 1:

```
# fitting a more complicated model
niger2 <- mutate(niger, know_2_2 = (know_2^2))
mdd1_comp <- glm(know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined + wg + rece
                 data = niger2,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(glm_mdd_1, mdd1_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
```

```
##     exp + received_antenatal_care
## Model 2: know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined +
##     wg + received_antenatal_care + know_2 * received_antenatal_care +
##     know_2_2 * received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174 1.2665e-08
## 2      2173 1.2665e-08  1        0        1
```

```
#fitting a model with cut explanatory variables; cut know_2

mdd1_cut <- glm(know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg + received_antenatal_care,
                 data = niger,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd1_cut, glm_mdd_1, test = "LRT")
```

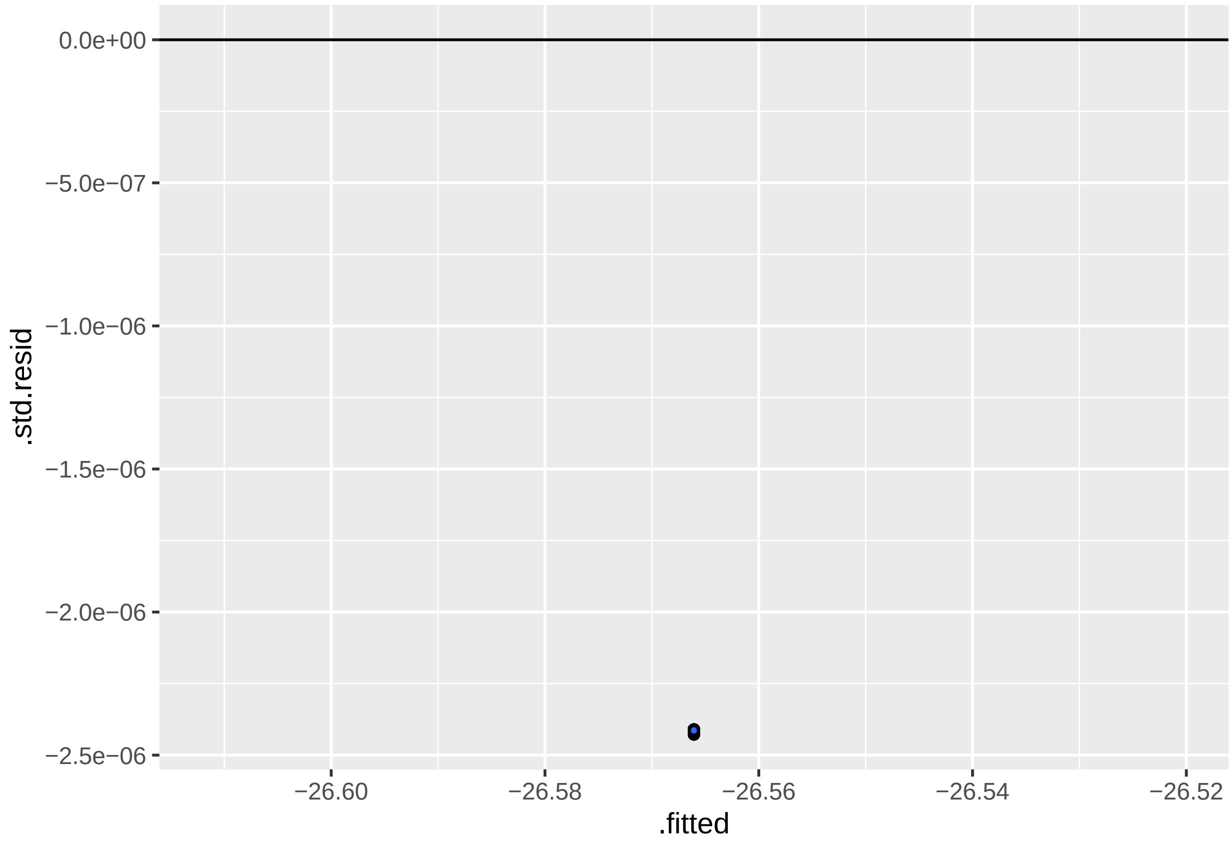
```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```
hltest(glm_mdd_1)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed     Expected
##      1  238        0 6.903669e-10
##      2  195        0 5.656368e-10
##      3   92        0 2.668645e-10
##      4  342        0 9.920399e-10
##      5  244        0 7.077712e-10
##      6  314        0 9.108203e-10
##      7  224        0 6.497571e-10
##      8  223        0 6.468564e-10
##      9  208        0 6.033459e-10
##     10  103        0 2.987723e-10
##
##          Statistic =  0
## degrees of freedom =  8
##            p-value =  1
```

```
amdd1 <- augment(glm_mdd_1)
```

```r
ggplot(data = amdd1, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



When compared to the more complicated model, there is weak evidence of a misspecification (p-value = 0.7165). However, there is strong evidence to suggest misspecification when comparing the original model to the one where know_2 is cut (p-value $<$ 0.001). Moreover, the Hosmer-Lemeshow test has an extremely small p-value (p-value $<$ 0.001), which indicates that there is relatively strong evidence of a lack of fit. Therefore, the model that will be evaluated/intrepreted will be mdd1_cut.

Model 2:

```r
# fitting a more complicated model
niger2 <- mutate(niger, know_2_2 = (know_2^2))
mdd2_comp <- glm(know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined + wg + fac_c
                 data = niger2,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(glm_mdd_2, mdd2_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
## Model 2: know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined +
##     wg + fac_delivery + know_2 * fac_delivery + know_2_2 * fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174 1.2665e-08
## 2      2173 1.2665e-08  1        0        1
```

```r
#fitting a model with cut explanatory variables; cut know_2

mdd2_cut <- glm(know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg + fac_delivery,
                 data = niger,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_cut, glm_mdd_2, test = "LRT")
```

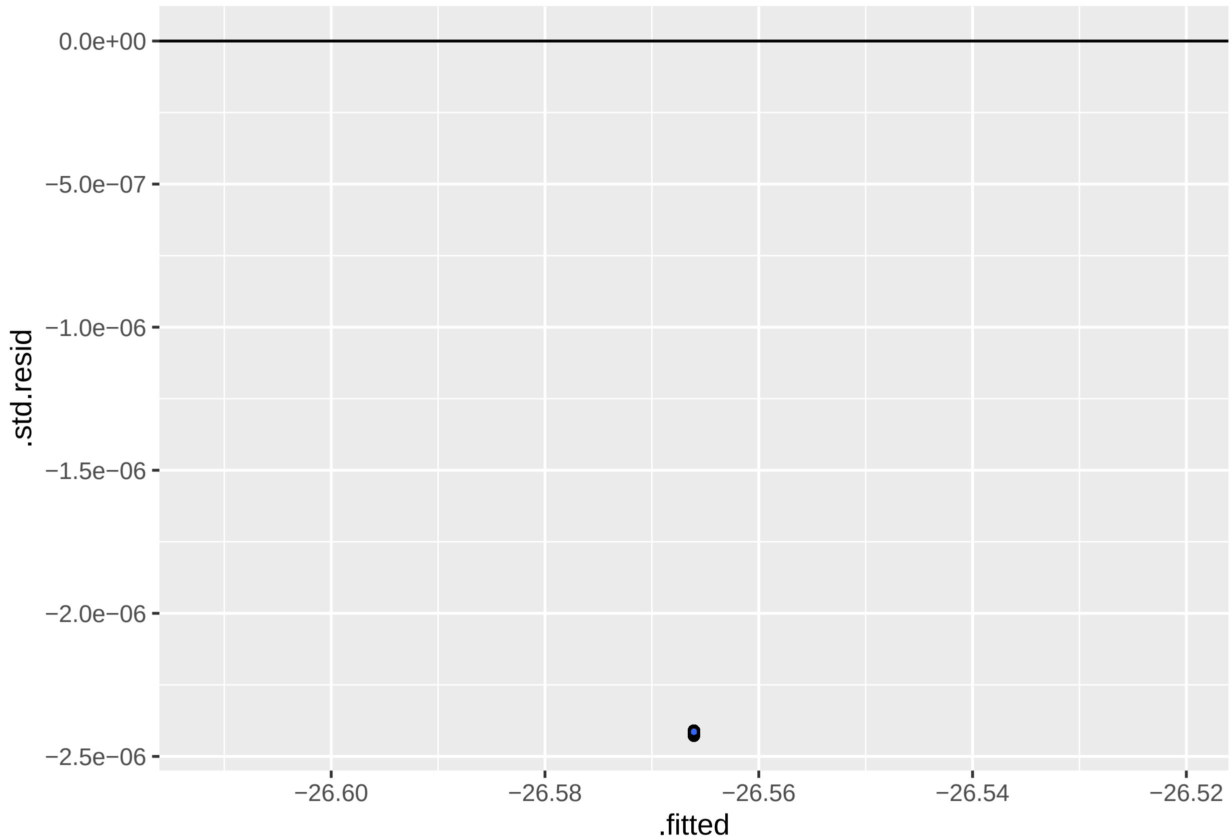
```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
hltest(glm_mdd_2)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed     Expected
##      1  222        0 6.439557e-10
##      2  214        0 6.207501e-10
##      3  150        0 4.351052e-10
##      4  245        0 7.106719e-10
##      5  208        0 6.033459e-10
##      6  288        0 8.354020e-10
##      7  239        0 6.932677e-10
##      8  226        0 6.555585e-10
##      9  211        0 6.120480e-10
##     10  180        0 5.221263e-10
##
##          Statistic =  0
## degrees of freedom =  8
##            p-value =  1
```

```r
amdd2 <- augment(glm_mdd_2)

ggplot(data = amdd2, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



When compared to the more complicated model, there is very strong evidence of a misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow test has an extremely small p-value (p-value < 0.001), which indicates that there is relatively strong evidence of a lack of fit. Therefore, the model that will be evaluated/intrepreted will be mdd2_cut.

Model 3:

```r
# fitting a more complicated model
niger2 <- mutate(niger, know_2_2 = (know_2^2))
mdd3_comp <- glm(know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined + wg + nutri
                 data = niger2,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(glm_mdd_3, mdd3_comp, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
## Model 2: know_3 ~ know_2 + know_2_2 + att_3 + se_3 + pn_3 + exp + decision_combined +
##     wg + nutrition + know_2 * nutrition + know_2_2 * nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2172 1.2665e-08
## 2      2169 1.2665e-08  3        0        1
```

```r
#fitting a model with cut explanatory variables; cut know_2

mdd3_cut <- glm(know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_cut, glm_mdd_3, test = "LRT")
```

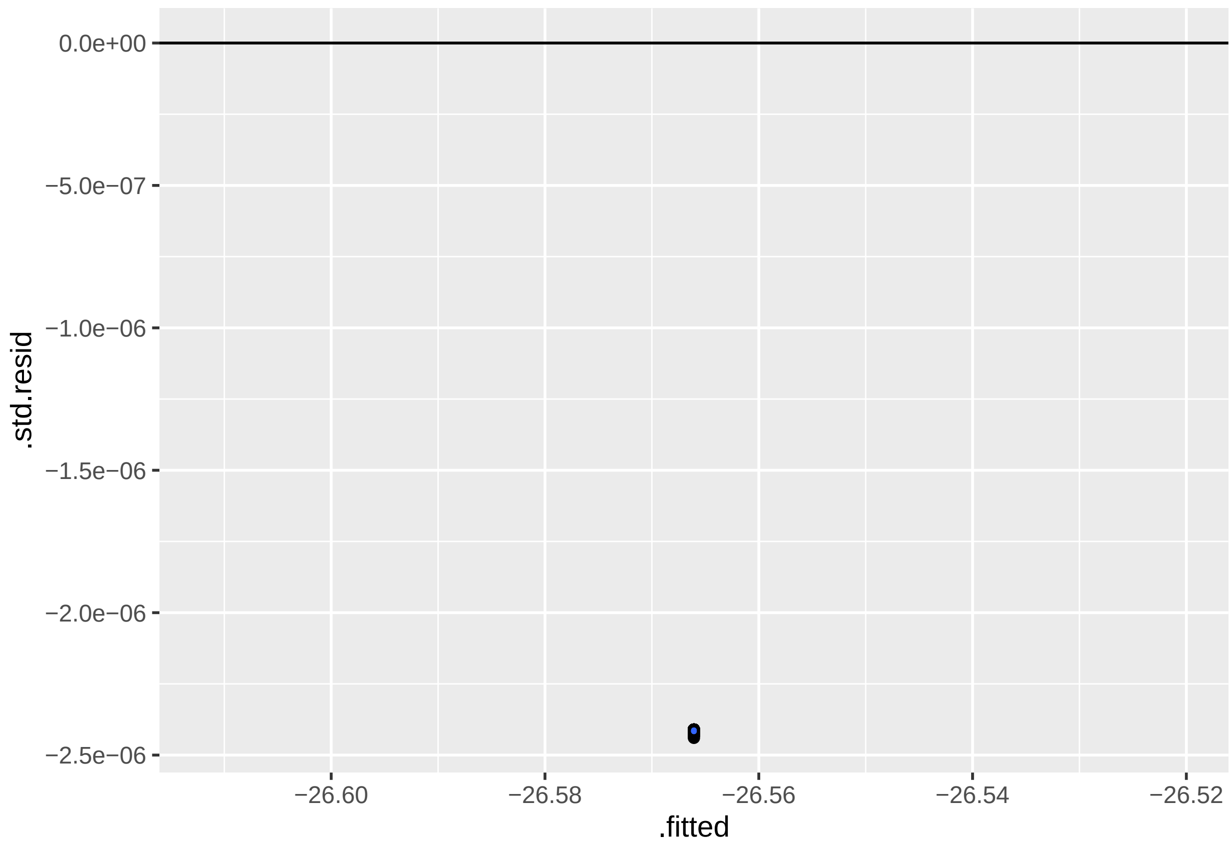
```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```r
hltest(glm_mdd_3)
```

```
##
##   The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed     Expected
##      1  233        0 6.758634e-10
##      2  216        0 6.265515e-10
##      3  202        0 5.859417e-10
##      4  183        0 5.308284e-10
##      5  221        0 6.410550e-10
##      6  220        0 6.381543e-10
##      7  426        0 1.235699e-09
##      8  213        0 6.178494e-10
##      9  216        0 6.265515e-10
##     10   53        0 1.537372e-10
##
##          Statistic =  0
## degrees of freedom =  8
##            p-value =  1
```

```r
amdd3 <- augment(glm_mdd_3)

ggplot(data = amdd3, mapping = aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(method = "loess", formula = y ~x)
```



When compared to the more complicated model, there is very strong evidence of a misspecification (p-value < 0.001). Moreover, the Hosmer-Lemeshow test has an extremely small p-value (p-value < 0.001), which indicates that there is relatively strong evidence of a lack of fit. Therefore, the model that will be evaluated/intrepreted will be mdd3_cut.

Interpretation of Results

Interpretation of coefficients, measures of uncertainty, etc,

Early Initiation of Breastfeeding

Model 1:

```r
tidy(eib1_cut, conf.int = TRUE)
```

```
## # A tibble: 7 x 7
##   term                   estimate std.error statistic  p.value conf.low conf.high
##   <chr>                     <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)            -1.23e-1    0.278  -0.444    6.57e- 1  -0.668      0.421
## 2 att_1                   1.03e-4    0.202   0.000511 1.00e+ 0  -0.394      0.398
## 3 pn_1                   -6.15e-1    0.166  -3.70     2.19e- 4  -0.945     -0.292
## 4 exp                     1.77e+0    0.0988 17.9      1.71e-71   1.57       1.96
## 5 decision_combined       6.53e-2    0.127   0.513    6.08e- 1  -0.184      0.316
## 6 wg                      2.53e-1    0.0987  2.57     1.03e- 2   0.0598     0.447
## 7 received_antenatal_c~ -5.59e-2    0.122  -0.459    6.46e- 1  -0.295      0.183
```

```r
odds_ratios_eib1_cut <- exp(coef(eib1_cut))
odds_ratios_eib1_cut
```

```
##            (Intercept)                  att_1                   pn_1
##              0.8840075              1.0001031              0.5408950
##                    exp      decision_combined                     wg
##              5.8506516              1.0674459              1.2883277
## received_antenatal_care
##              0.9456105
```

Fitted regression surface:

logit(p_i) = -0.196 + 0.0532X_1 - 0.633X_2 + 1.76X_3 + 0.0209X_4 + 0.356X_5 - 0.186X_6 where p_i is the estimated likelihood of an MWRA reporting that they agree giving only breast milk to the baby for the first 6 months is not difficult at all, X_1 is an indicator for MRWA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick, X_2 is an indicator for MWRA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months, X_3 is an indicator for MWRA who had heard or seen a message related to breastfeeding or young child nutrition, X_4 is an indicator for MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_5 is an indicator for MRWA who belong to a women's community group, and X_6 is an indicator for MWRA MRWA who have given birth in the last 5 years and received antenatal care for their last pregnancy

Interpretation of regression coefficients/odds:

- Intercept: When all other variables are set to zero, the odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all initiating breastfeeding early is -0.196.
- β_1 : The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.0532 times higher for those that agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick adjusting for the other predictors in the model.However, with a p-value of 0.836, this increase is not statistically significant, meaning we cannot confidently state that attitudes significantly influence the early initiation of breastfeeding in this context.
- β_2: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.633 times higher for those that agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months adjusting for the other predictors in the model. The p-value of 0.004 indicates that this effect is statistically significant, suggesting that more negative community norms substantially decrease the likelihood of early initiation of breastfeeding.
- β_3: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.76 times higher for those that have exposure to nutrition messages adjusting for the other predictors in the model.The very low p-value (< 0.001) makes this a highly statistically

significant predictor, indicating that exposure to nutrition messages greatly increases the likelihood of early initiation.

- β_4: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.0209 times higher for those that have combined decision-making scores (pertaining to decisions made jointly with partners on purchases, visits, and health seeking) adjusting for the other predictors in the model. With a p-value of 0.896, this influence is not statistically significant, indicating that decision-making, as measured, does not significantly affect early initiation of breastfeeding.

- β_5: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.356 times higher for those that have women's groups adjusting for the other predictors in the model.The p-value of 0.005 indicates this effect is statistically significant, demonstrating that involvement in women's groups positively influences early initiation.

- β_6: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.186 times less for those that have received antenatal care adjusting for the other predictors in the model. The p-value of 0.332 suggests that this decrease is not statistically significant, implying that receiving antenatal care, in this study, does not have a significant impact on early initiation of breastfeeding.

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6}$

```
# testing for an association between se_1 and know_1
eib1_redk <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care,data = ni
anova(eib1_redk, glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2581.1
## 2      2175     2525.5  1   55.631 8.743e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between se_1 and att_1
eib1_reda <- glm(se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care,data = n
anova(eib1_reda, glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2525.5
## 2      2175     2525.5  1 0.029594   0.8634
```

```r
# testing for an association between se_1 and pn_1
eib1_redp <- glm(se_1 ~ know_1 + att_1 + exp + decision_combined + wg + received_antenatal_care,data = n
anova(eib1_redp, glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2567.7
## 2      2175     2525.5  1   42.282  7.9e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and exp
eib1_rede <- glm(se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + received_antenatal_care,data =
anova(eib1_rede,glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2902.1
## 2      2175     2525.5  1   376.59 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and decision_combined
eib1_redd <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + received_antenatal_care,data = niger, family
anova(eib1_redd, glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2526.1
## 2      2175     2525.5  1   0.6135   0.4335
```

```r
# testing for an association between received_antenatal_care and se_1
eib1_redr <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined,data = niger, family = bin
anova(eib1_redr,glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
```

```
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2525.5
## 2      2175     2525.5  1 0.010908   0.9168
```

```
# testing for an association between wg and se_1
eib1_redw <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + received_antenatal_care + decision_combined,data =
anova(eib1_redw,glm_eib_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + received_antenatal_care +
##     decision_combined
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2530.9
## 2      2175     2525.5  1   5.4023  0.02011 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Based on the analysis of deviance, att_1, received_antenatal_care, and possibly decision_combined and wg, emerge as significant predictors with strong associations to the outcome. These variables not only improve model fit but also highlight key areas (like attitudes and healthcare engagement) that are crucial in influencing the studied behavior or condition.

Model 2:

```
tidy(eib2_cut, conf.int = TRUE)
```

```
## # A tibble: 7 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -1.26       0.271    -4.64  3.57e- 6   -1.79     -0.726
## 2 att_1               0.215      0.206     1.04  2.97e- 1   -0.188     0.621
## 3 pn_1               -0.458      0.173    -2.65  8.12e- 3   -0.801    -0.122
## 4 exp                 1.58       0.103    15.3   6.47e-53    1.38      1.78
## 5 decision_combined   0.0916     0.130     0.703 4.82e- 1   -0.163     0.348
## 6 wg                  0.399      0.104     3.82  1.32e- 4    0.195     0.603
## 7 fac_delivery        1.38       0.102    13.6   6.28e-42    1.18      1.58
```

```
odds_ratios_eib2_cut <- exp(coef(eib2_cut))
odds_ratios_eib2_cut
```

```
##       (Intercept)             att_1              pn_1               exp
##         0.2848313         1.2399910         0.6325793         4.8394236
## decision_combined                wg      fac_delivery
##         1.0959139         1.4896211         3.9866085
```

logit(p_i) = -1.26 + 0.200X_1 - 0.585X_2 + 1.61X_3 + 0.0416X_4 + 0.527X_5 + 1.33X_6 where p_i is the estimated likelihood of an MWRA reporting that they agree giving only breast milk to the baby for the first 6 months is not difficult at all, X_1 is an indicator for MRWA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick, X_2 is an indicator for MWRA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months, X_3 is an indicator for MWRA who had heard or seen a message related to breastfeeding or young child nutrition, X_4 is an indicator for MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_5 is an indicator for MRWA who belong to a women's community group, and X_6 is an indicator for MWRA who have given birth in the years preceding the survey who delivered in a facility for their last birth

Interpretation of regression coefficients/odds:

- Intercept: When all other variables are set to zero, the odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all initiating breastfeeding early is -1.26.
- β_1 : The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.200 times higher for those that agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick adjusting for the other predictors in the model. A p-value of 0.443 indicates that this effect is not statistically significant, indicating that while there is a positive association, it is not strong enough to confirm a definitive impact on the outcome.
- β_2: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.585 times less for those that agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months adjusting for the other predictors in the model.The p-value of 0.0115 indicates that this effect is statistically significant, suggesting that more negative community norms substantially decrease the likelihood of the outcome.
- β_3: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.61 times higher for those that have exposure to nutrition messages adjusting for the other predictors in the model.The very low p-value (< 0.001) suggests this is a highly statistically significant predictor, indicating that exposure to nutrition messages greatly increases the likelihood of the outcome.
- β_4: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.0416 times higher for those that have combined decision-making scores (pertaining to decisions made jointly with partners on purchases, visits, and health seeking) adjusting for the other predictors in the model. With a p-value of 0.797, this influence is not statistically significant, indicating that decision-making, as measured, does not significantly affect early initiation of breastfeeding.
- β_5: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.527 times higher for those that have participation in women's groups adjusting for the other predictors in the model. The p-value of 8.72e-5 indicates this effect is statistically significant, demonstrating that involvement in women's groups positively influences early initiation.
- β_6: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.33 times higher for those that have delivered in a facility adjusting for the other predictors in the model. The p-value of 2.39e-24 suggests that this increase is highly statistically significant, indicating that facility deliveries are a strong predictor of the outcome.

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: logit(p_i) = β_0 H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: logit(p_i) = $\beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6}$

```r
# testing for an association between se_1 and know_1
eib2_redk <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + fac_delivery,data = niger, family
anova(eib2_redk, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2389.0
## 2      2175     2333.2  1   55.788 8.073e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and att_1
eib2_reda <- glm(se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + fac_delivery,data = niger, famil
anova(eib1_reda, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2525.5
## 2      2175     2333.2  1   192.29 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and pn_1
eib2_redp <- glm(se_1 ~ know_1 + att_1 + exp + decision_combined + wg + fac_delivery,data = niger, famil
anova(eib1_redp, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2567.7
## 2      2175     2333.2  1   234.54 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and exp
eib2_rede <- glm(se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + fac_delivery,data = niger, fam
anova(eib1_rede, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
```

```
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2902.1
## 2      2175     2333.2  1   568.86 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between wg and se_1
eib2_redw <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + fac_delivery ,data = niger, fa
anova(eib2_redw, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + fac_delivery
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2346.2
## 2      2173     2435.4  3  -89.201
```

```
# testing for an association between se_1 and decision_combined
eib2_redd <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + fac_delivery,data = niger, family = binomial
anova(eib1_redd, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2526.1
## 2      2175     2333.2  1   192.88 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between fac_delivery and se_1
eib2_redr <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined,data = niger, family = bin
anova(eib2_redr, glm_eib_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2525.5
## 2      2175     2333.2  1   192.27 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Facility delivery and exposure to information are strong and significant in predicting the outcome.

Model 3:

```r
tidy(eib3_cut, conf.int = TRUE)
```

```
## # A tibble: 9 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -0.196      0.254    -0.770 4.41e- 1  -0.696      0.303
## 2 att_1              -0.0552     0.202    -0.273 7.85e- 1  -0.449      0.343
## 3 pn_1               -0.700      0.169    -4.15  3.31e- 5  -1.03      -0.373
## 4 exp                 1.63       0.103    15.8   4.04e-56   1.43       1.83
## 5 decision_combined   0.184      0.131     1.40  1.61e- 1  -0.0728     0.441
## 6 wg                  0.176      0.101     1.74  8.24e- 2  -0.0228     0.374
## 7 nutrition2          0.612      0.245     2.50  1.26e- 2   0.141      1.10
## 8 nutrition3          1.68       0.197     8.56  1.16e-17   1.31       2.08
## 9 nutrition4          0.210      0.137     1.54  1.24e- 1  -0.0583     0.478
```

```r
odds_ratios_eib3_cut <- exp(coef(eib3_cut))
odds_ratios_eib3_cut
```

```
##       (Intercept)             att_1              pn_1               exp
##         0.8220954         0.9463321         0.4965895         5.0915830
## decision_combined                wg        nutrition2        nutrition3
##         1.2015304         1.1922765         1.8432017         5.3740266
##        nutrition4
##         1.2337627
```

logit(p_i) = -0.374 + 0.0625X_1 - 0.625X_2 + 1.75X_3 + 0.0488X_4 + 0.359X_5 - 0.000408X_6

Interpretation of regression coefficients/odds:

- Intercept: When all other variables are set to zero, the odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all initiating breastfeeding early is -0.374.
- β_1 : The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.0625 times higher for those that agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick adjusting for the other predictors in the model. A p-value of 8.08e- 1 indicates that this effect is not statistically significant, indicating that while there is a positive association, it is not strong enough to confirm a definitive impact on the outcome.
- β_2: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.625 times less for those that agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months adjusting for the other predictors in the model.The p-value of 0.00449, which is less than 0.05, indicating that this effect is statistically significant and a strong predictor in the model.
- β_3: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.75 times higher for those that have exposure to nutrition messages adjusting for the other predictors in the model. The very low p-value (< 0.001) suggests this is a highly statistically significant predictor, indicating that exposure to nutrition messages greatly increases the likelihood of the outcome.

- β_4: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.0488 times higher for those that have combined decision-making scores (pertaining to decisions made jointly with partners on purchases, visits, and health seeking) adjusting for the other predictors in the model. With a p-value of 0.755, indicating that the influence of combined decision-making is not statistically significant.
- β_5: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.359 times higher for those that have participation in women's groups adjusting for the other predictors in the model. The p-value of 0.00482, which is statistically significant, pointing to a meaningful impact of this predictor.
- β_6: The odds of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.000408 times less for those that have delivered in a facility adjusting for the other predictors in the model. The p-value of 0.863, suggesting that this variable's impact is not statistically significant.

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6}$

```
# testing for an association between se_1 and know_1
eib3_redk <- glm(se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + nutrition,data = niger, family = b
anova(eib3_redk, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2485.0
## 2      2173     2435.4  1   49.594 1.891e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between se_1 and att_1
eib3_reda <- glm(se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + nutrition,data = niger, family =
anova(eib1_reda, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2525.5
## 2      2173     2435.4  3   90.094 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and pn_1
eib3_redp <- glm(se_1 ~ know_1 + att_1 + exp + decision_combined + wg + nutrition,data = niger, family =
anova(eib3_redp, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2480.1
## 2      2173     2435.4  1   44.678 2.323e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and exp
eib3_rede <- glm(se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + nutrition,data = niger, family
anova(eib1_rede, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2902.1
## 2      2173     2435.4  3   466.66 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_1 and decision_combined
eib3_redd <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + nutrition,data = niger, family = binomial(li
anova(eib3_redd, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174     2437.9
## 2      2173     2435.4  1   2.4838    0.115
```

```r
# testing for an association between wg and se_1
eib3_redw <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + nutrition ,data = niger, famil
anova(eib3_redw, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + nutrition
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
```

```
##     nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174     2437.6
## 2      2173     2435.4  1   2.1822   0.1396
```

```r
# testing for an association between nutrition and se_1
eib3_redr <- glm(se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined,data = niger, family = bino
anova(eib3_redr, glm_eib_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ know_1 + att_1 + pn_1 + exp + wg + decision_combined
## Model 2: se_1 ~ know_1 + att_1 + pn_1 + exp + decision_combined + wg +
##     nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2525.5
## 2      2173     2435.4  3   90.075 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We have very strong evidence to suggest an association between se_1 and exp (p-value < 0.001), se_1 and wg (p-value 0.006149), se_1 and pn_1(p-value 8.325e-08), se_1 and know_1(p-value 6.832e-12)

Exclusive Initiation of Breastfeeding

Model 1:

```r
tidy(exib1_cut, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term                    estimate std.error statistic  p.value conf.low conf.high
##   <chr>                      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)              -0.676      0.297    -2.28  2.27e- 2  -1.26     -0.0957
## 2 att_1                     0.407      0.221     1.84  6.54e- 2  -0.0230    0.845
## 3 se_3                      2.07       0.157    13.2   9.91e-40   1.77      2.38
## 4 pn_1                     -0.723      0.170    -4.25  2.12e- 5  -1.06     -0.393
## 5 exp                       1.58       0.104    15.2   5.34e-52   1.38      1.79
## 6 decision_combined         0.0200     0.134     0.149 8.81e- 1  -0.243     0.284
## 7 wg                        0.415      0.104     3.99  6.68e- 5   0.211     0.620
## 8 received_antenatal_c~    -0.147      0.129    -1.14  2.56e- 1  -0.400     0.106
```

```r
odds_ratios_exib1_cut <- exp(coef(exib1_cut))
odds_ratios_exib1_cut
```

```
##             (Intercept)                  att_1                   se_3
##               0.5084309              1.5028565              7.9044688
##                    pn_1                    exp      decision_combined
##               0.4852465              4.8631843              1.0202489
##                      wg received_antenatal_care
##               1.5146628              0.8636952
```

Fitted regression surface:

logit(p_i) = -0.676 + 0.407X_1 + 2.067X_2 - 0.723X_3 + 1.582X_4 + 0.020X_5 + 0.415X_6 - 0.147X_7 where pi_i is the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all, X_1 is the percentage of MWRA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick, X_2 is the percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months X_4 is the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition from the radio, health worker, or community event in the past 3 months, X_5 is the Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 is the percentage of MRWA who have given birth in the last 5 years and received antenatal care for their last pregnancy.

```
# for intercept
exp(-1.26)
```

```
## [1] 0.283654
```

```
exp(-0.09)
```

```
## [1] 0.9139312
```

```
# for att_1
exp(-0.02)
```

```
## [1] 0.9801987
```

```
exp(0.85)
```

```
## [1] 2.339647
```

```
# for se_3
exp(1.76)
```

```
## [1] 5.812437
```

```
exp(2.38)
```

```
## [1] 10.8049
```

```
# for pn_1
exp(-1.06)
```

```
## [1] 0.3464558
```

```r
exp(-0.39)
```

```
## [1] 0.6770569
```

```r
# exp
exp(1.37)
```

```
## [1] 3.935351
```

```r
exp(1.78)
```

```
## [1] 5.929856
```

```r
# decision_combined
exp(-0.24)
```

```
## [1] 0.7866279
```

```r
exp(0.28)
```

```
## [1] 1.32313
```

```r
# wg
exp(0.211)
```

```
## [1] 1.234912
```

```r
exp(0.619)
```

```
## [1] 1.85707
```

```r
 #received_antenatal_care
 exp(-0.39)
```

```
## [1] 0.6770569
```

```r
 exp(0.10)
```

```
## [1] 1.105171
```

Intercept: When all predictors are at their reference level, the odds of a MWRA agreeing to give only breast milk to the baby for the first 6 months being not difficult at all is approximately 0.508 times (between 0.28 and 0.91 times in 95% of repeated samples) more than when all predictors are at their alternative levels. β_1: The odds of a MWRA agreeing that if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick is about 1.50 times more (between 0.98 and 2.34 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model. β_2: The odds of a MWRA agreeing that giving a child a minimum of 4 or more different types of food a day is not difficult at all is about 7.90 times more (between 5.81 and 10.80 times more in 95% of repeated samples) for MWRA who say it is not difficult compared to MWRA who find it difficult, adjusting for the other predictors in the model. β_3: The odds of a MWRA agreeing that people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months is about 0.48 times (between 0.54 and 0.67 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model. β_4: The odds of a MWRA agreeing that giving only breast milk to the baby for the first 6 months is not difficult at all is about 4.86 times more (between 2.03 and 11.20 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition from the radio, health worker, or community event in the past 3 months compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model. β_5: The odds of a MWRA agreeing that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives is about 1.02 times (between 0.79 and 1.32 times more in 95% of repeated samples) for MWRA who responded in the affirmative compared to MWRA who do not, adjusting for the other predictors in the model. β_6: The odds of a MWRA agreeing that belonging to a women's community group is not difficult at all is about 1.51 times more (between 1.23 and 1.86 times more in 95% of repeated samples) for MWRA who belong to such a group compared to MWRA who do not, adjusting for the other predictors in the model. β_7: The odds of a MWRA agreeing that giving only breast milk to the baby for the first 6 months is not difficult at all is about 0.86 times (between 0.67 and 1.11 times more in 95% of repeated samples) for MWRA who have given birth in the last 5 years and received antenatal care for their last pregnancy compared to MWRA who have not received antenatal care, adjusting for the other predictors in the model. Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7}$ We have very strong evidence to suggest an association between se_3 and exib1 (p-value < 0.001), pn_1 and exib1 (p-value < 0.001), exp and exib1 (p-value < 0.001), moderately strong evidence to suggest an association between att_1 and exib1 (p-value $= 0.085$), weak evidence to suggest an association between decision_combined and exib1 (p-value $= 0.144$), wg and exib1 (p-value $= 0.048$), and received_antenatal_care and exib1 (p-value $= 0.107$).

```
exib1_red <- glm(se_1 ~ 1, data = niger, family = binomial(link = "logit"))
anova(exib1_red, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ 1
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     3000.5
## 2      2175     2352.8  7   647.65 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

there is statistically significant evidence that at least one of the predictors is associated with the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all.

```
# testing for an association between att_1 and se_1
exib1_reds <- glm(se_1 ~  se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care, data = n
anova(exib1_reds, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
```

```
## Model 1: se_1 ~ se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2356.3
## 2      2175     2352.8  1   3.4393  0.06366 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_3 and se_1
exib1_redp <- glm(se_1 ~  att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care, data =
anova(exib1_redp, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2581.1
## 2      2175     2352.8  1   228.24 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between exp and se_1
exib1_rede <- glm(se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + received_antenatal_care, data =
anova(exib1_rede, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2598.1
## 2      2175     2352.8  1   245.28 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between pn_1 and se_1
exib1_redd <- glm(se_1 ~ att_1 + se_3 + exp + decision_combined + wg + received_antenatal_care, data = r
anova(exib1_redd, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + exp + decision_combined + wg + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2371.7
## 2      2175     2352.8  1   18.833 1.427e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between wg and se_1

exib1_redw <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + received_antenatal_care, data =
anova(exib1_redw, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2368.8
## 2      2175     2352.8  1   15.924 6.594e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between received_antenatal_care and se_1
exib1_reda <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg, data = niger, family = bin
anova(exib1_reda, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2354.1
## 2      2175     2352.8  1   1.2919   0.2557
```

```r
# testing for an association between decision_combined and se_1
exib1_redq <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + wg + received_antenatal_care, data = niger, family
anova(exib1_redq, exib1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + wg + received_antenatal_care
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2352.9
## 2      2175     2352.8  1  0.02224   0.8815
```

we have very strong evidence that indicates that se_1 is associated with se_3, exp, pn_1, and wg–all with (p-value < 0.001). There is moderate evidence of association between se_1 and att_1 with a p-value of 0.06366. There is moderate to weak evidence of association between se_1 and recieved_antenetal_care with a p-value of 0.2557. There is weak evidence of association between se_1 and decision_combined with a p-value of 0.8815.

Model 2:

```r
tidy(exib2_cut, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term             estimate std.error statistic  p.value conf.low conf.high
##   <chr>               <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -1.55      0.287    -5.41  6.43e- 8  -2.11      -0.990
## 2 att_1               0.518     0.224     2.31  2.09e- 2   0.0814     0.961
## 3 se_3                1.71      0.160    10.7   1.22e-26   1.40       2.03
## 4 pn_1               -0.574     0.175    -3.28  1.03e- 3  -0.921     -0.235
## 5 exp                 1.44      0.106    13.6   5.53e-42   1.24       1.65
## 6 decision_combined   0.0357    0.135     0.263 7.92e- 1  -0.229      0.302
## 7 wg                  0.508     0.108     4.72  2.41e- 6   0.297      0.719
## 8 fac_delivery        1.08      0.107    10.1   3.79e-24   0.875      1.29
```

```r
odds_ratios_exib2_cut <- exp(coef(exib2_cut))
odds_ratios_exib2_cut
```

```
##       (Intercept)             att_1              se_3              pn_1
##         0.2124397         1.6783185         5.5055495         0.5632640
##               exp decision_combined                wg      fac_delivery
##         4.2412557         1.0363188         1.6614037         2.9568083
```

$\text{logit}(p_i)$ = -1.549 + $0.518X_1$ + $1.706X_2$ - $0.574X_3$ + $1.445X_4$ + $0.036X_5$ + $0.508X_6$ + $1.084X_7$ where pi_i is the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all, X_1 is the percentage of MWRA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick, X_2 is the percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months X_4 is the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition from the radio, health worker, or community event in the past 3 months, X_5 is the Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 is the percentage of MRWA who have given birth in the years preceding the survey who delivered in a facility for their last birth.

```r
# for intercept
exp(-2.11)
```

```
## [1] 0.121238
```

```r
exp(-0.99)
```

```
## [1] 0.3715767
```

```r
# for att_1
exp(0.08)
```

```
## [1] 1.083287
```

```r
exp(0.96)
```

```
## [1] 2.611696
```

```r
# for se_3
exp(1.39)
```

```
## [1] 4.01485
```

```r
exp(2.02)
```

```
## [1] 7.538325
```

```r
# for pn_1
exp(-0.92)
```

```
## [1] 0.398519
```

```r
exp(-0.23)
```

```
## [1] 0.7945336
```

```r
# exp
exp(1.23)
```

```
## [1] 3.42123
```

```r
exp(1.65)
```

```
## [1] 5.20698
```

```r
# decision_combined
exp(-0.23)
```

```
## [1] 0.7945336
```

```r
exp(0.30)
```

```
## [1] 1.349859
```

```r
# wg
exp(0.29)
```

```
## [1] 1.336427
```

```r
exp(0.72)
```

```
## [1] 2.054433
```

```r
#fac_delivery
exp(0.87)
```

```
## [1] 2.386911
```

```r
exp(1.29)
```

```
## [1] 3.632787
```

intercept: When all predictors are at their reference level, the odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is approximately 0.508 times (between 0.21 and 0.37 times in 95% of repeated samples) more than when all predictors are at their alternative levels. β_1: The odds of a MWRA reporting that if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick is about 1.5 times more (between 1.08 and 2.61 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model. β_2: The odds of a MWRA reporting that giving a child a minimum of 4 or more different types of food a day is not difficult at all is about 7.9 times more (between 4.01 and 7.53 times more in 95% of repeated samples) for MWRA who say it is not difficult compared to MWRA who find it difficult, adjusting for the other predictors in the model. β_3: The odds of a MWRA reporting that people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months is about 0.48 times (between 0.39 and 0.79 times in 95% of repeated samples) more for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model. β_4: The odds of a MWRA reporting that giving only breast milk to the baby for the first 6 months is not difficult at all is about 4.86 times more (between 2.39 and 3.64 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model. β_5: The odds of a MWRA reporting that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives is about 1.02 times more (between 0.79 and 1.34 times more in 95% of repeated samples) for MWRA who responded in the affirmative compared to MWRA who do not, adjusting for the other predictors in the model. β_6: The odds of a MWRA reporting that belonging to a women's community group is not difficult at all is about 1.5 times more (between 1.33 and 2.05 times more in 95% of repeated samples) for MWRA who belong to such a group compared to MWRA who do not, adjusting for the other predictors in the model. β_7: The odds of a MWRA reporting that having a facility delivery for their last birth is not difficult at all is about 0.86 times (between 2.39 and 3.63 times more in 95% of repeated samples) for MWRA who delivered in a facility compared to MWRA who did not, adjusting for the other predictors in the model.

```r
exib2_red <- glm(se_1 ~ 1, data = niger, family = binomial(link = "logit"))
anova(exib2_red, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ 1
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     3000.5
## 2      2175     2249.8  7   750.75 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

there is statistically significant evidence that at least one of the predictors is associated with the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all.

```r
# testing for an association between att_1 and se_1
exib2_reds <- glm(se_1 ~  se_3 + pn_1 + exp + decision_combined + wg + fac_delivery, data = niger, famil
anova(exib2_reds, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2255.2
## 2      2175     2249.8  1   5.4184  0.01993 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_3 and se_1
exib2_redp <- glm(se_1 ~  att_1 + pn_1 + exp + decision_combined + wg + fac_delivery, data = niger, fam
anova(exib2_redp, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2389.0
## 2      2175     2249.8  1   139.23 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between exp and se_1
exib2_rede <- glm(se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + fac_delivery, data = niger, fam
anova(exib2_rede, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2441.6
## 2      2175     2249.8  1   191.86 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between pn_1 and se_1
exib2_redd <- glm(se_1 ~ att_1 + se_3 + exp + decision_combined + wg + fac_delivery, data = niger, famil
anova(exib2_redd, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + exp + decision_combined + wg + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
```

```
## 1      2176     2260.9
## 2      2175     2249.8  1   11.107 0.0008599 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between wg and se_1

exib2_redw <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + fac_delivery, data = niger, fam
anova(exib2_redw, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2272.2
## 2      2175     2249.8  1   22.394 2.22e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between fac_delivery and se_1
exib2_reda <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg, data = niger, family = bino
anova(exib2_reda, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2354.1
## 2      2175     2249.8  1   104.39 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between decision_combined and se_1
exib2_redq <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + wg + fac_delivery, data = niger, family = binomial
anova(exib2_redq, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + wg + fac_delivery
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     2249.8
## 2      2175     2249.8  1 0.069448   0.7921
```

there is very strong evidence that indicates that se_1 is associated with se_3, exp, pn_1, wg, and fac_delivery with extremely low p-values close to 0. There is relatively strong evidence of an association between se_1 and att_1 with a p-value of 0.01993. There is weak evidence that se_1 and decision_combined are associated with a p-value of 0.7921.

Model 3:

```r
tidy(exib3_cut, conf.int = TRUE)
```

```
## # A tibble: 10 x 7
##    term               estimate std.error statistic  p.value conf.low conf.high
##    <chr>                 <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
##  1 (Intercept)          -0.855     0.272     -3.14 1.69e- 3  -1.39      -0.323
##  2 att_1                 0.377     0.219      1.72 8.55e- 2  -0.0497     0.810
##  3 se_3                  1.96      0.160     12.3  1.66e-34   1.65       2.28
##  4 pn_1                 -0.773     0.172     -4.50 6.75e- 6  -1.11      -0.440
##  5 exp                   1.46      0.108     13.5  2.25e-41   1.25       1.68
##  6 decision_combined     0.171     0.137      1.24 2.13e- 1  -0.0980     0.440
##  7 wg                    0.353     0.106      3.32 9.05e- 4   0.144      0.561
##  8 nutrition2            0.279     0.274      1.02 3.07e- 1  -0.251      0.825
##  9 nutrition3            1.39      0.201      6.93 4.17e-12   1.01       1.80
## 10 nutrition4            0.328     0.142      2.32 2.06e- 2   0.0500     0.606
```

```r
odds_ratios_exib3_cut <- exp(coef(exib3_cut))
odds_ratios_exib3_cut
```

```
##       (Intercept)             att_1              se_3              pn_1
##         0.4252746         1.4575142         7.0699526         0.4615037
##               exp decision_combined                wg        nutrition2
##         4.3116239         1.1860343         1.4226214         1.3224270
##        nutrition3        nutrition4
##         4.0175457         1.3886139
```

logit(p_i) = -0.855 + 0.376X_1 + 1.956X_2 - 0.773X_3 + 1.461X_4 + 0.170X_5 + 0.363X_6 + 0.279X_7 + 1.391X_8 + 0.328X_9

where pi_i is the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all, X_1 is the percentage of MWRA who agree if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick, X_2 is the percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who agree people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months X_4 is the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition from the radio, health worker, or community event in the past 3 months, X_5 is the Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 is an indicator for MWRA who spoke with a family member about their child's nutrition, X_8 is an indicator for MWRA who spoke with a healthcare worker about their child's nutrition, X_9 is an indicator for MWRA who spoke to nobody about their child's nutrition (speaking to husband is the base class)

```r
# for intercept
exp(-1.39)
```

```
## [1] 0.2490753
```

```r
exp(-0.32)
```

```
## [1] 0.726149
```

```r
# for att_1
exp(-0.04)
```

```
## [1] 0.9607894
```

```r
exp(0.81)
```

```
## [1] 2.247908
```

```r
# for se_3
exp(1.65)
```

```
## [1] 5.20698
```

```r
exp(2.27)
```

```
## [1] 9.679401
```

```r
# for pn_1
exp(-1.11)
```

```
## [1] 0.329559
```

```r
exp(-0.44)
```

```
## [1] 0.6440364
```

```r
# exp
exp(1.25)
```

```
## [1] 3.490343
```

```r
exp(1.67)
```

```
## [1] 5.312168
```

```r
# decision_combined
exp(-0.09)
```

```
## [1] 0.9139312
```

```r
exp(0.44)
```

```
## [1] 1.552707
```

```r
# wg
exp(0.14)
```

```
## [1] 1.150274
```

```r
exp(0.56)
```

```
## [1] 1.750673
```

Interpretation:

Intercept: When all predictors are at their reference level, the odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is approximately 0.425 times (between 0.25 and 0.73 times in 95% of repeated samples) more than when all predictors are at their alternative levels. β_1: The odds of a MWRA reporting that if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick is about 1.46 times more (between 0.96 and 2.25 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model.

β_2: The odds of a MWRA reporting that giving a child a minimum of 4 or more different types of food a day is not difficult at all is about 7.07 times more (between 5.2 and 9.6 times more in 95% of repeated samples) for MWRA who say it is not difficult compared to MWRA who find it difficult, adjusting for the other predictors in the model.

β_3: The odds of a MWRA reporting that people in the community think it is healthy for a woman to give her baby only breast milk for the first 6 months is about 0.46 times (between 0.32 and 0.64 times in 95% of repeated samples) more for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model.

β_4: The odds of a MWRA reporting that giving only breast milk to the baby for the first 6 months is not difficult at all is about 4.31 times more (between 3.5 and 5.3 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model. β_5: The odds of a MWRA reporting that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives is about 1.18 times more (between 0.91 and 1.55 times more in 95% of repeated samples) for MWRA who responded in the affirmative compared to MWRA who do not, adjusting for the other predictors in the model.

β_6: The odds of a MWRA reporting that belonging to a women's community group is not difficult at all is about 1.44 times more (between 1.44 and 1.75 times more in 95% of repeated samples) for MWRA who belong to such a group compared to MWRA who do not, adjusting for the other predictors in the model.

```r
exib3_red <- glm(se_1 ~ 1, data = niger, family = binomial(link = "logit"))
anova(exib3_red, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ 1
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
```

```
## 1      2182     3000.5
## 2      2173     2294.6  9   705.94 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

there is statistically significant evidence that at least one of the predictors is associated with the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all.

```
exib3_red <- glm(se_1 ~ 1, data = niger, family = binomial(link = "logit"))
anova(exib3_red, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ 1
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     3000.5
## 2      2173     2294.6  9   705.94 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

there is statistically significant evidence that at least one of the predictors is associated with the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all.

```
exib2_red <- glm(se_1 ~ 1, data = niger, family = binomial(link = "logit"))
anova(exib2_red, exib2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ 1
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     3000.5
## 2      2175     2249.8  7   750.75 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

there is statistically significant evidence that at least one of the predictors is associated with the percentage of MWRA who agree giving only breast milk to the baby for the first 6 months is not difficult at all.

```
# testing for an association between att_1 and se_1
exib3_reds <- glm(se_1 ~  se_3 + pn_1 + exp + decision_combined + wg + nutrition, data = niger, family =
anova(exib3_reds, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ se_3 + pn_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174     2297.6
## 2      2173     2294.6  1   2.9942  0.08356 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_3 and se_1
exib3_redp <- glm(se_1 ~  att_1 + pn_1 + exp + decision_combined + wg + nutrition, data = niger, family
anova(exib3_redp, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + pn_1 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2485.0
## 2      2173     2294.6  1   190.43 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between exp and se_1
exib3_rede <- glm(se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + nutrition, data = niger, family
anova(exib3_rede, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + decision_combined + wg + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2484.2
## 2      2173     2294.6  1   189.61 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between pn_1 and se_1
exib3_redd <- glm(se_1 ~ att_1 + se_3 + exp + decision_combined + wg + nutrition, data = niger, family =
anova(exib3_redd, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + exp + decision_combined + wg + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2315.7
## 2      2173     2294.6  1   21.085 4.394e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between wg and se_1

exib3_redw <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + nutrition, data = niger, famil
anova(exib3_redw, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
```

```
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2174     2305.6
## 2      2173     2294.6  1   11.006 0.0009083 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between nutrition and se_1
exib3_reda <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg, data = niger, family = bino
anova(exib3_reda, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     2354.1
## 2      2173     2294.6  3   59.583 7.217e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# testing for an association between decision_combined and se_1
exib3_redq <- glm(se_1 ~ att_1 + se_3 + pn_1 + exp + wg + nutrition, data = niger, family = binomial(lin
anova(exib3_redq, exib3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: se_1 ~ att_1 + se_3 + pn_1 + exp + wg + nutrition
## Model 2: se_1 ~ att_1 + se_3 + pn_1 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174     2296.1
## 2      2173     2294.6  1   1.5494   0.2132
```

there is very strong evidence that indicates that se_1 is associated with se_3, exp, pn_1, wg, and nutrition with extremely low p-values close to 0. There is moderate to weak evidence of association between se_1 and decision_combined with a p-value of 0.2132. There is moderate to strong evidence of association between se_1 and att_1 with a p-value of 0.08356.

Minimum Meal Frequency

Model 1:

```
tidy(mmf1_cut, conf.int = TRUE)
```

```
## # A tibble: 7 x 7
##   term                estimate std.error statistic  p.value conf.low conf.high
##   <chr>                  <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)           -1.23      0.258     -4.75 2.03e- 6   -1.73     -0.720
## 2 se_2                   0.874     0.150      5.85 5.06e- 9    0.580     1.17
## 3 pn_2                   2.89      0.142     20.3  6.45e-92    2.62      3.18
## 4 exp                   -0.161     0.138     -1.17 2.44e- 1   -0.432     0.110
```

```
## 5 decision_combined       0.547      0.194     2.82  4.87e- 3   0.174       0.937
## 6 wg                      0.196      0.143     1.38  1.68e- 1  -0.0822      0.478
## 7 received_antenatal_c~  -0.0207     0.195    -0.106 9.16e- 1  -0.412       0.354
```

```
odds_ratios_mmf1_cut <- exp(coef(mmf1_cut))
odds_ratios_mmf1_cut
```

```
##             (Intercept)                     se_2                     pn_2
##               0.2932043                2.3961992               18.0713952
##                     exp        decision_combined                       wg
##               0.8513331                1.7285163                1.2171282
## received_antenatal_care
##               0.9795498
```

Fitted regression surface:

logit(p_i) = -1.227 + 0.874X_1 + 2.894X_2 - 0.161X_3 + 0.547X_4 + 0.197X_5 - 0.021X_6

where p_i is the estimated likelihood of an MWRA reporting a child 6-23 months should eat 4 or more meals each day, X_1 is an indicator for MRWA who agree giving a child a meal 4 times a day is not difficult at all, X_2 is an indicator for MRWA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more, X_3 is an indicator of MWRA who had heard or seen a message related to breastfeeding or young child nutrition in the past 3 months, X_4 is an indicator for MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_5 is an indicator for MRWA who belong to a women's community group, and X_6 is an indicator for MRWA who have given birth in the last 5 years and received antenatal care for their last pregnancy.

```
# for intercept
exp(-1.73319285)
```

```
## [1] 0.1767193
```

```
exp(-0.7195699)
```

```
## [1] 0.4869617
```

```
# for se_2
exp(0.57969582)
```

```
## [1] 1.785495
```

```
exp(1.1662174)
```

```
## [1] 3.209828
```

```
# for pn_2
exp(2.61821379)
```

```
## [1] 13.71121
```

```r
exp(3.1764922)
```

```
## [1] 23.96255
```

```r
# for exp
exp(-0.43181458)
```

```
## [1] 0.6493298
```

```r
exp(0.1099389)
```

```
## [1] 1.11621
```

```r
# for decision_combined
exp(0.17399200)
```

```
## [1] 1.190046
```

```r
exp(0.9369635)
```

```
## [1] 2.55222
```

```r
# for wg
exp(-0.08219711)
```

```
## [1] 0.9210904
```

```r
exp(0.4775840)
```

```
## [1] 1.612175
```

```r
# for received_antenatal_care
exp(-0.41223123)
```

```
## [1] 0.6621711
```

```r
exp(0.3544562)
```

```
## [1] 1.425405
```

Interpretation of regression coefficients/odds:

- Intercept: when all the predictors = 0 (MWRA did not agree that giving a child a meal 4 times a day is not difficult at all, did not agree that the community thinks a child 6-23 months should eat 4 meals a day or more, have not heard a message related to breastfeeding or nutrition in the past 3 months, does not jointly or individually make decisions across all decision categories, does not belong to a community group, and has not received antenatal care for their last pregnancy within the last 5 years), the odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 0.29 more /0.71 times less (between 0.18 times and 0.49 times more in 95% of repeated samples) than an individuals who do the opposite, on average.

- β_1 : The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 2.40 times higher (between 1.76 and 3.21 times higher in 95% of repeated samples) for MWRA who agree that giving a child a meal 4 times a day is not difficult at all compared to women who do not agree that it is not difficult at all, adjusting for the other predictors in the model.
- β_2: The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 18 times higher (between 13.71 and 23.96 times higher in 95% of repeated samples) for MWRA who believe the number of meals people in community think a child 6-23 months should eat each day is 4 or more compared to women who do not believe this, adjusting for all other predictors in the model.
- β_3: The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 0.85 times more (between 0.65 and 1.12 times more in 95% of repeated samples) when the MWRA has been exposed to nutrition/breastfeeding communications compared to those who are not exposed to such communication, adjusting for other predictors in the model.
- β_4: The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 1.73 times higher (between 1.19 and 2.55 times higher for 95% of repeated samples) for MWRA who make decisions regarding their health, financial decisions, AND visting family jointly or themselves compared to MWRA whose husbands exclusively make those decisions for them, adjusting for other predictors in the model.
- β_5: The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 1.22 times higher (between 0.92 and 1.61 times higher in 95% of repeated samples) for MWRA who are a part of a woman's group compared to MWRA that are not a part of a woman's group, adjusting for other predictors in the model.
- β_6: The odds of reporting that a child 6-23 months should eat 4 or more meals a day are about 0.98 times more (between 0.66 and 1.43 times more in 95% of repeated samples) for MWRA who received antenatal care for their last birth compared to MWRA who did not receive antenatal care, adjusting for other predictors.

Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$

H_A: at least one of the regression coefficients is non zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6}$

```
mmf1_red <- glm(know_2 ~ 1, data = niger, family = binomial(link = "logit"))
anova(mmf1_red, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ 1
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     2076.4
## 2      2176     1478.7  6   597.67 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported a child 6-23 months should eat 4 or more meals each day (p-value $<$ 0.001).

```r
# testing for an association between se_2 and know_2
mmf1_reds <- glm(know_2 ~ pn_2 + exp + decision_combined + wg + received_antenatal_care, data = niger, f
anova(mmf1_reds, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ pn_2 + exp + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2177     1511.8
## 2      2176     1478.7  1    33.11 8.708e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between pn_2 and know_2
mmf1_redp <- glm(know_2 ~ se_2 + exp + decision_combined + wg + received_antenatal_care, data = niger, f
anova(mmf1_redp, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + exp + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2177     1942.8
## 2      2176     1478.7  1   464.11 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between exp and know_2
mmf1_rede <- glm(know_2 ~ se_2 + pn_2 + decision_combined + wg + received_antenatal_care, data = niger,
anova(mmf1_rede, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2177     1480.1
## 2      2176     1478.7  1   1.3576   0.2439
```

```r
# testing for an association between decision_combined and know_2
mmf1_redd <- glm(know_2 ~ se_2 + pn_2 + exp + wg + received_antenatal_care, data = niger, family = binom
anova(mmf1_redd, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + wg + received_antenatal_care
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2177     1487.1
## 2      2176     1478.7  1   8.4044 0.003743 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between wg and know_2
mmf1_redw <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + received_antenatal_care, data = niger
anova(mmf1_redw, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + received_antenatal_care
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2177     1480.6
## 2      2176     1478.7  1   1.9065   0.1673
```

```r
# testing for an association between received_antenatal_care and know_2
mmf1_reda <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + wg, data = niger, family = binomial(li
anova(mmf1_reda, mmf1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2177     1478.7
## 2      2176     1478.7  1 0.011229   0.9156
```

We have very strong evidence to suggest that se_2 is associated with know_2 (p-value < 0.001), pn_2 is associated with know_2 (p-value < 0.001), and strong evidence to suggest that decision_combined is associated with know_2. There is moderate to weak evidence of association between exp and know_2 (p-value $= 0.2439$) and between wg and know_2 (p-value $= 0.1673$). There is very weak evidence to suggest that received_antenatal_care is associated with know_2 (p-value $= 0.9156$).

Model 2:

```r
tidy(glm_mmf_2, conf.int = TRUE)
```

```
## # A tibble: 8 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -2.49       0.312    -7.98  1.47e-15   -3.11    -1.89
## 2 att_2               1.65       0.264     6.24  4.29e-10    1.14     2.18
## 3 se_2                1.01       0.149     6.78  1.18e-11    0.719    1.30
## 4 pn_2                2.66       0.144    18.4   6.29e-76    2.38     2.95
## 5 exp                -0.0972     0.145    -0.673 5.01e- 1   -0.381    0.186
## 6 decision_combined   0.496      0.194     2.56  1.05e- 2    0.124    0.885
## 7 wg                  0.0513     0.145     0.354 7.24e- 1   -0.233    0.337
## 8 fac_delivery       -0.289      0.150    -1.93  5.31e- 2   -0.585    0.00265
```

```r
odds_ratios_mmf2
```

```
##       (Intercept)             att_2              se_2              pn_2
##        0.08279079        5.20647643        2.75267066       14.34800927
##               exp decision_combined                wg      fac_delivery
##        0.90733313        1.64240231        1.05264646        0.74864478
```

Fitted Regression surface:

logit(p_i) = -2.491 + 1.650X_1 + 1.013X_2 + 2.664X_3 - 0.097X_4 + 0.496X_5 + 0.051X_6 - 0.289X_7

where: where p_i is the estimated likelihood of MWRA who reporting a child 6-23 months should eat 4 or more meals each day, X_1 is an indicator for MWRA who agree providing meals 4 times a day ensures them to have adequate strength, X_2 is an indicator for MRWA who agree giving a child a meal 4 times a day is not difficult at all, X_3 is an indicator for MRWA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more, X_4 is an indicator for MWRA who had heard or seen a message related to breastfeeding or young child nutrition in the past 3 months, X_5 is an indicator for MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_6 is an indicator for MRWA who belong to a women's community group, and X_7 is an indicator for MWRA who have given birth in the years preceding the survey who delivered in a facility for their last birth.

```
# for intercept:
exp(-3.1141427)
```

```
## [1] 0.04441657
```

```
exp(-1.888672748)
```

```
## [1] 0.1512725
```

```
# for att_2:
exp(1.1380240)
```

```
## [1] 3.120596
```

```
exp(2.175606712)
```

```
## [1] 8.807527
```

```
# for se_2:
exp(0.7190069)
```

```
## [1] 2.052394
```

```
exp(1.304701712)
```

```
## [1] 3.686589
```

```
# for pn_2:
exp(2.3825952)
```

```
## [1] 10.83298
```

```
exp(2.949148441)
```

```
## [1] 19.08969
```

```r
# for exp::
exp(-0.3808422)
```

```
## [1] 0.6832857
```

```r
exp(0.186266328)
```

```
## [1] 1.204743
```

```r
# for decision_combined:
exp(0.1243243)
```

```
## [1] 1.132383
```

```r
exp(0.885080746)
```

```
## [1] 2.42318
```

```r
# for wg:
exp(-0.2325765)
```

```
## [1] 0.7924891
```

```r
exp(0.336828859)
```

```
## [1] 1.400499
```

```r
# for fac_delivery:
exp(-0.5846032)
```

```
## [1] 0.557327
```

```r
exp(0.002647919)
```

```
## [1] 1.002651
```

Interpretation of coefficients:

- intercept: when all predictors = 0, the estimated likelihood of MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 0.08 times higher (between 0.04 and 0.15 times higher in 95% of repeated samples) compared to when all predictors = 1
- β_1: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 5.21 times more (between 3.12 and 8.81 times more in 95% of repeated samples) for MWRA who agree providing meals 4 times a day ensures them to have adequate strength compared to MWRA who disagree, adjusting for the other predictors.

- β_2: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 2.75 times more (between 2.05 and 3.69 times more in 95% of repeated samples) for MWRA who agree that giving a child a meal 4 times a day is not difficult at all compared to women who do not agree that it is not difficult at all, adjusting for the other predictors in the model.
- β_3: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 14.35 times more (between 10.83 and 19.09 times more in 95% of repeated samples) for MWRA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more compared to MWRA who do not believe this, adjusting for other predictors in the model.
- β_4: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 0.91 times more (between 0.68 and 1.20 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition in the past 3 months compared to MWRA who are not exposed to these messages, adjusting for other predictors in the model.
- β_5: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 1.64 times more (between 1.13 and 2.42 times more in 95% of repeated samples) for MWRA who responded that she OR her and her partner jointly make decisions for all three categories compared to MWRA whose husbands make those decisions exclusively, adjusting for other predictors in the model.
- β_6: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 1.05 times more (between 0.79 and 1.40 times more in 95% of repeated samples) for MWRA who belong to a woman's community group compared to MWRA who do not belong to a woman's group, adjusting for other predictors in the model.
- β_7: The odds of reporting that a child 6-23 months should eat 4 or more meals a day is about 0.75 times more (between 0.56 and 1.00 times more in 95% of repeated samples) for MWRA who delivered their last birth in a facility compared to MWRA who did not deliver their last birth in a facility, adjustinf for other predictors in the model.

Testing for association:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$

H_A: at least one of the regression coefficients is non zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7}$

```
mmf2_red <- glm(know_2 ~ 1, data = niger, family = binomial(link = "logit"))
anova(mmf2_red, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ 1
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     2076.4
## 2      2175     1426.7  7   649.65 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported a child 6-23 months should eat 4 or more meals each day (p-value $<$ 0.001).

```r
# testing for an association between att_2 and know_2
mmf2_reda <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + fac_delivery, data = niger, famil
anova(mmf2_reda, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + fac_delivery
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     1468.0
## 2      2175     1426.7  1   41.323 1.291e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between se_2 and know_2
mmf2_reds <- glm(know_2 ~ att_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care, data =
anova(mmf2_reds, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + pn_2 + exp + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     1473.4
## 2      2175     1426.7  1   46.657 8.457e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between pn_2 and know_2
mmf2_redp <- glm(know_2 ~ att_2 + se_2 + exp + decision_combined + wg + fac_delivery, data = niger, fami
anova(mmf2_redp, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + exp + decision_combined + wg + fac_delivery
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2176     1784.0
## 2      2175     1426.7  1   357.24 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between exp and know_2
mmf2_rede <- glm(know_2 ~ att_2 + se_2 + pn_2 + decision_combined + wg + fac_delivery, data = niger, fa
anova(mmf1_rede, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
```

```
## Model 1: know_2 ~ se_2 + pn_2 + decision_combined + wg + received_antenatal_care
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2177     1480.1
## 2      2175     1426.7  2   53.344 2.609e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between decision_combined and know_2
mmf2_redd <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + wg + fac_delivery, data = niger, family = binomia
anova(mmf2_redd, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + wg + fac_delivery
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     1433.7
## 2      2175     1426.7  1   6.9312  0.00847 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# testing for an association between wg and know_2
mmf2_redw <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + fac_delivery, data = niger, fa
anova(mmf2_redw, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + fac_delivery
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     1426.8
## 2      2175     1426.7  1  0.12511   0.7236
```

```r
# testing for an association between fac_delivery and know_2
mmf2_redf <- glm(know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg, data = niger, family = bi
anova(mmf2_redf, glm_mmf_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg
## Model 2: know_2 ~ att_2 + se_2 + pn_2 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2176     1430.5
## 2      2175     1426.7  1   3.7719  0.05212 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We have very strong evidence of an association between att_2 and know_2 (p-value < 0.001), se_2 and know_2 (p-value < 0.001), pn_2 and know_2 (p-value < 0.001), and exp and know_2 (p-value < 0.001). We have strong evidence of an association between decision_combined and know_2 (p-value = 0.00847). We have moderately strong evidence of an association between fac_delivery and know_2 (p-value = 0.05212). We have weak evidence of an association between wg and know_2 (p-value = 0.7236).

Model 3:

```r
tidy(mmf3_cut, conf.int = TRUE)
```

```
## # A tibble: 9 x 7
##   term              estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
## 1 (Intercept)        -1.33       0.186   -7.15   8.69e-13   -1.69    -0.966
## 2 se_2                0.865      0.149    5.79   6.84e- 9    0.571    1.16
## 3 pn_2                2.99       0.145   20.6    1.27e-94    2.71     3.28
## 4 exp                -0.301      0.145   -2.07   3.84e- 2   -0.586   -0.0163
## 5 decision_combined   0.660      0.202    3.27   1.08e- 3    0.272    1.06
## 6 wg                  0.131      0.144    0.912  3.62e- 1   -0.150    0.415
## 7 nutrition2          0.0493     0.362    0.136  8.92e- 1   -0.630    0.793
## 8 nutrition3          0.841      0.224    3.75   1.78e- 4    0.409    1.29
## 9 nutrition4         -0.0192     0.204   -0.0943 9.25e- 1   -0.412    0.388
```

```r
odds_ratios_mmf3_cut <- exp(coef(mmf3_cut))
odds_ratios_mmf3_cut
```

```
##       (Intercept)              se_2              pn_2               exp
##         0.2654368         2.3753891        19.8438634         0.7401413
## decision_combined                wg        nutrition2        nutrition3
##         1.9340893         1.1402067         1.0504982         2.3190913
##        nutrition4
##         0.9809350
```

Fitted regression surface:

logit(p_i) = -1.326 + 0.865X_1 + 2.988X_2 - 0.301X_3 + 0.660X_4 + 0.131X_5 + 0.049X_6 + 0.842X_7 - 0.018X_8

where: where p_i is the estimated likelihood of an MWRA reporting a child 6-23 months should eat 4 or more meals each day, X_1 is an indicator for MRWA who agree giving a child a meal 4 times a day is not difficult at all, X_2 is an indicator for MRWA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more, X_3 is an indicator for MWRA who had heard or seen a message related to breastfeeding or young child nutrition in the past 3 months, X_4 is an indicator for MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives, X_5 is an indicator for MRWA who belong to a women's community group, and X_6 is an indicator for MWRA who spoke with a family member about their child's nutrition, X_7 is an indicator for MWRA who spoke with a healthcare worker about their child's nutrition, X_8 is an indicator for MWRA who spoke to nobody about their child's nutrition (speaking to husband is the base class)

```r
# for intercept
exp(-1.6941556)
```

```
## [1] 0.1837543
```

```r
exp(-0.96644056)
```

```
## [1] 0.3804348
```

```r
# for se_2
exp(0.5713848)
```

```
## [1] 1.770717
```

```r
exp(1.15708475)
```

```
## [1] 3.180647
```

```r
# for pn_2
exp(2.7074383)
```

```
## [1] 14.99082
```

```r
exp(3.27533181)
```

```
## [1] 26.452
```

```r
# for exp
exp(-0.5863639)
```

```
## [1] 0.5563465
```

```r
exp(-0.01628325)
```

```
## [1] 0.9838486
```

```r
# for decision_combined
exp(0.2722374)
```

```
## [1] 1.312899
```

```r
exp(1.06397614)
```

```
## [1] 2.89787
```

```r
# for wg
exp(-0.1501488)
```

```
## [1] 0.8605799
```

```r
exp(0.41459717)
```

```
## [1] 1.513761
```

```r
# for nutrition2
exp(-0.6296524)
```

```
## [1] 0.532777
```

```r
exp(0.79344206)
```

```
## [1] 2.210994
```

```r
# for nutrition3
exp(0.4088797)
```

```
## [1] 1.505131
```

```r
exp(1.28913679)
```

```
## [1] 3.629652
```

```r
# for nutrition4
exp(-0.4124389)
```

```
## [1] 0.6620336
```

```r
exp(0.38845754)
```

```
## [1] 1.474704
```

Interpretation:

- intercept: when all predictors = 0, the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 0.27 times more (between 0.18 and 0.38 times more in 95% of repeated samples) than when all predictors = 1
- β_1:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 2.38 times more (between 1.77 and 3.18 times more in 95% of repeated samples) for MWRA who agree giving a child a meal 4 times a day is not difficult at all compared to MWRA who do not agree, adjusting for the other predictors in the model.
- β_2: the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 19.84 times more (between 14.99 and 26.45 times more in 95% of repeated samples) for MWRA who believes the number of meals people in community think a child 6-23 months should eat each day is 4 or more compared to MWRA who believe otherwise, adjusting for the other predictors in the model.

- β_3:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 0.74 times more (between 0.56 and 0.98 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition in the past 3 months compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model.
- β_4:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about1.93 times more (between 1.31 and 2.90 times more in 95% of repeated samples) for MWRA who responded that she OR her and her partner jointly make decisions for all three categories compared to MWRA whose husband exclusively makes such decisions, adjusting for the other predictors in the model.
- β_5:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 1.14 times more (between 0.86 and 1.51 times more in 95% of repeated samples) or MWRA who belong to a women's community group compared to MWRA who do not belong to a woman's group, adjusting for the other predictors in the model.
- β_6:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 1.05 times more (between 0.53 and 3.63 times more in 95% of repeated samples) for MWRA who talk to their family members about their child's nutrition compared to MWRA who talk to their husbands about their child's nutrition, adjusting for the other predictors in the model.
- β_7:the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 2.33 times more (between 1.51 and 2.32 times more in 95% of repeated samples) for MWRA who talk to a healthcare provider about their child's nutrition compared to MWRA who talk to their husbands about their child's nutrition, adjusting for the other predictors in the model.
- β_8: the odds of an MWRA reporting a child 6-23 months should eat 4 or more meals each day is about 0.98 times more (between 0.66 and 1.47 times more in 95% of repeated samples) for MWRA who do not talk to anybody about their child's nutrition compared to MWRA who talk to their husbands about their child's nutrition, adjusting for the other predictors in the model.

Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = \beta_8 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$

H_A: at least one of the regression coefficients is non zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7} + \beta_8 X_{i8}$

```
mmf3_red <- glm(know_2 ~ 1, data = niger, family = binomial(link = "logit"))
anova(mmf3_red, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ 1
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2182     2076.4
## 2      2174     1463.4  8   612.95 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported a child 6-23 months should eat 4 or more meals each day (p-value < 0.001).

```r
# for se_2
mmf3_reds <- glm(know_2 ~ + pn_2 + exp + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_reds, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ +pn_2 + exp + decision_combined + wg + nutrition
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2175     1496.0
## 2      2174     1463.4  1   32.551 1.161e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# for pn_2
mmf3_redp <- glm(know_2 ~ se_2 + exp + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_redp, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + exp + decision_combined + wg + nutrition
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2175     1951.5
## 2      2174     1463.4  1   488.12 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#for exp
mmf3_rede <- glm(know_2 ~ se_2 + pn_2 + decision_combined + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_rede, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + decision_combined + wg + nutrition
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     1467.7
## 2      2174     1463.4  1   4.2935  0.03826 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# for decision_combined
mmf3_redd <- glm(know_2 ~ se_2 + pn_2 + exp + wg + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_redd, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + wg + nutrition
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      2175     1474.9
## 2      2174     1463.4  1    11.44 0.0007189 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# for wg
mmf3_redw <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + nutrition,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_redw, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + nutrition
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175     1464.2
## 2      2174     1463.4  1  0.83342   0.3613
```

```
# for nutrition
mmf3_redn <- glm(know_2 ~ se_2 + pn_2 + exp + decision_combined + wg,
                 data = niger,
                 family = binomial(link = "logit"))
anova(mmf3_redn, mmf3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg
## Model 2: know_2 ~ se_2 + pn_2 + exp + decision_combined + wg + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2177     1478.7
## 2      2174     1463.4  3   15.295 0.001581 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We have very strong evidence to suggest an association between se_2 and know_2 (p-value < 0.001), pn_2 and know_2 (p-value < 0.001), decision_combined and know_2 (p-value $= 0.0007189$), strong evidence to suggest an association between nutrition and know_2 (p-value $= 0.001581$), moderately strong evidence to suggest an association between exp and know_2 (p-value $= 0.03826$) and weak evidence to suggest an association between wg and know_2 (p-vale $= 0.3613$).

Minimum Dietary Diversity

Model 1:

```r
tidy(mdd1_cut)
```

```
## # A tibble: 8 x 5
##   term                   estimate std.error statistic p.value
##   <chr>                     <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)            -2.66e+ 1    37257. -7.13e- 4   0.999
## 2 att_3                   1.54e-14    32422.  4.76e-19   1
## 3 se_3                    7.37e-14    20394.  3.61e-18   1
## 4 pn_3                   -1.05e-13    17940. -5.86e-18   1
## 5 exp                    -5.05e-14    16365. -3.09e-18   1
## 6 decision_combined       5.70e-14    20331.  2.81e-18   1
## 7 wg                     -5.06e-14    15977. -3.17e-18   1
## 8 received_antenatal_care -3.11e-14    19572. -1.59e-18   1
```

```r
odds_ratios_mdd1_cut <- exp(coef(mdd1_cut))
odds_ratios_mdd1_cut
```

```
##             (Intercept)                   att_3                    se_3
##            2.900701e-12            1.000000e+00            1.000000e+00
##                    pn_3                     exp       decision_combined
##            1.000000e+00            1.000000e+00            1.000000e+00
##                      wg received_antenatal_care
##            1.000000e+00            1.000000e+00
```

Fitted regression surface:

logit(p_i) = -3.77 + 1.35X_1 + 1.52X_2 + 2.431X_3 + 0.218X_4 + 0.440X_5 + 0.687X_6 - 0.368X_7

where p_i percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more, X_1 is the percentage of MWRA who agree children who eat a variety of foods are less likely to get sick, X_2 percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who believes number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more; 1 = those who believe the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more, 0 = otherwise , X_4 is an indicator for the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition, X_5 is an indicator for Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives; 1 = responded either decides herself or jointly with her partner on all three decision categories, 0 = otherwise, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 percentage of MRWA who have given birth in the last 5 years and received antenatal care for their last pregnancy.

```r
# for intercept
exp(-4.67)
```

```
## [1] 0.00937227
```

```r
exp(-2.95)
```

```
## [1] 0.05233971
```

```r
# for att_3
exp(0.661)
```

```
## [1] 1.936728
```

```r
exp(2.11)
```

```
## [1] 8.248241
```

```r
# for se_3
exp(1.13)
```

```
## [1] 3.095657
```

```r
exp(1.91)
```

```
## [1] 6.753089
```

```r
# for pn_3
exp(2.12)
```

```
## [1] 8.331137
```

```r
exp(2.75)
```

```
## [1] 15.64263
```

```r
# for decision_combined
exp(0.0660)
```

```
## [1] 1.068227
```

```r
exp(0.811)
```

```
## [1] 2.250157
```

```r
# for wg
exp(0.368)
```

```
## [1] 1.444842
```

```r
exp(1.01)
```

```
## [1] 2.745601
```

```r
# recieved_antenatal_care
exp(-0.837)
```

```
## [1] 0.4330076
```

```r
exp(0.111)
```

```
## [1] 1.117395
```

```r
# for exp
exp(-0.109)
```

```
## [1] 0.8967304
```

```r
exp(0.544)
```

```
## [1] 1.722885
```

Intercept: When all predictors are at their reference level, the odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is approximately 0.02 times (between 0.009 and 0.05 times more in 95% of repeated samples) more than when all predictors are at their alternative levels.

β_1: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 3.85 times more (between 1.9 and 8.2 times more in 95% of repeated samples) for MWRA who agree that children who eat a variety of foods are less likely to get sick compared to MWRA who do not agree, adjusting for the other predictors in the model.

β_2: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 4.55 times more (between 3.1 and 6.8 times more in 95% of repeated samples) for MWRA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all compared to MWRA who find it difficult, adjusting for the other predictors in the model.

β_3: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 11.36 times more (between 8.3 and 15.6 times more in 95% of repeated samples) for MWRA who believe the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more compared to MWRA who believe otherwise, adjusting for the other predictors in the model.

β_4: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 1.24 times more (between 0.889 and 1.72 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model.

β_5: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 1.55 times more (between 1.1 and 2.3 times more in 95% of repeated samples) for MWRA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives compared to MWRA whose husband exclusively makes such decisions, adjusting for the other predictors in the model.

β_6: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 1.98 times more (between 1.4 and 2.7 times more in 95% of repeated samples) for MWRA who belong to a women's community group compared to MWRA who do not belong to a women's group, adjusting for the other predictors in the model.

β_7: The odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is about 0.691 times (between 0.433 and 1.118 times more in 95% of repeated samples) for MWRA who have given birth in the last 5 years and received antenatal care for their last pregnancy compared to MWRA who have not received antenatal care, adjusting for the other predictors in the model.

Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7}$ We have very strong evidence to suggest an association between att_3 and mdd1 (p-value < 0.001), se_3 and mdd1 (p-value < 0.001), pn_3 and mdd1 (p-value $<$ 0.001), decision_combined and mdd1 (p-value < 0.001), moderately strong evidence to suggest an association between wg and mdd1 (p-value $= 0.049$) and weak evidence to suggest an association between exp and mdd1 (p-value $= 0.234$).

```
mdd1_red <- glm(know_3 ~ 1, data = niger, family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd1_red, mdd1_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ 1
## Model 2: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
##     received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2182 1.2665e-08
## 2      2175 1.2665e-08  7        0        1
```

there is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more(p-value < 0.001).

```
# testing for an association between know_2 and know_3
mdd1_reda <- glm(know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp + received_antenatal_care,
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd1_reda, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between att_3 and know_3
mdd1_reds <- glm(know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp + received_antenatal_care
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_reds, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between se_3 and know_3
mdd1_redw <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + received_antena
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_redw, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174 1.2665e-08
## 2      2174 1.2665e-08  0        0
```

```r
# testing for an association between pn_3 and know_3
mdd1_redd <- glm(know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp + received_antenatal_care
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_redd, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between wg and know_3
mdd1_rede <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp + received_antenatal_ca
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_rede, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between decision_combined and know_3
mdd1_redq <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg  + exp + received_antenatal_care, data = ni
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_redq, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + exp + received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between exp and know_3
mdd1_redr <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + received_antenatal_ca
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_redr, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     received_antenatal_care
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between recieved_antenatal_care and know_3
mdd1_redz <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp, data = niger, fa
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd1_redz, glm_mdd_1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + received_antenatal_care
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

there is very strong evidence that indicates know_3 is associated with know_2, se_3, pn_3, and wg with p-values close to or equal to 0. There is moderately strong evidence that know_3 is associated with att_3 and exp with p-values of 0.02877 and 0.04736 respectively. There is moderate evidence that know_3 is associated with decision_combined and recieved_antenatal_care with p-values of 0.1503 and 0.3225 respectively.

Model 2:

```r
tidy(mdd2_cut)
```

```
## # A tibble: 8 x 5
##   term              estimate std.error statistic p.value
##   <chr>                <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)      -2.66e+ 1    34176. -7.77e- 4   0.999
## 2 att_3             4.20e-14    32506.  1.29e-18   1
## 3 se_3              6.28e-14    20866.  3.01e-18   1
## 4 pn_3             -1.48e-13    18056. -8.17e-18   1
## 5 exp              -8.35e-14    16528. -5.05e-18   1
## 6 decision_combined  8.10e-14   20084.  4.03e-18   1
## 7 wg               -5.73e-14    15973. -3.59e-18   1
## 8 fac_delivery      9.89e-14    16722.  5.91e-18   1
```

```r
odds_ratios_mdd2_cut <- exp(coef(mdd2_cut))
odds_ratios_mdd2_cut
```

```
##       (Intercept)             att_3              se_3              pn_3
##      2.900701e-12      1.000000e+00      1.000000e+00      1.000000e+00
##               exp decision_combined                wg      fac_delivery
##      1.000000e+00      1.000000e+00      1.000000e+00      1.000000e+00
```

Fitted regression surface:

$\text{logit}(p_i)$ = -4.19 + $1.36X_1$ + $1.47X_2$ + $2.41X_3$ + $0.200X_4$ + $0.492X_5$ + $0.694X_6$ + $0.156X_7$

where p_i percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more, X_1 is the percentage of MWRA who agree children who eat a variety of foods are less likely to get sick, X_2 percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who believes number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more; 1 = those who believe the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more, 0 = otherwise , X_4 is an indicator for the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition, X_5 is an indicator for Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives; 1 = responded either decides herself or jointly with her partner on all three decision categories, 0 = otherwise, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 percentage of MWRA who have given birth in the years preceding the survey who delivered in a facility for their last birth.

```
# for intercept
exp(-5.0)
```

```
## [1] 0.006737947
```

```
exp(-3.44)
```

```
## [1] 0.03206469
```

```
# for att_3
exp(0.676)
```

```
## [1] 1.965998
```

```
exp(2.12)
```

```
## [1] 8.331137
```

```
# for se_3
exp(1.07)
```

```
## [1] 2.915379
```

```
exp(1.88)
```

```
## [1] 6.553505
```

```
# for pn_3
exp(2.1)
```

```
## [1] 8.16617
```

```
exp(2.73)
```

```
## [1] 15.33289
```

```r
# for decision_combined
exp(0.124)
```

```
## [1] 1.132016
```

```r
exp(0.857)
```

```
## [1] 2.356082
```

```r
# for wg
exp(0.375)
```

```
## [1] 1.454991
```

```r
exp(1.02)
```

```
## [1] 2.773195
```

```r
# fac_delivery
exp(-0.176)
```

```
## [1] 0.838618
```

```r
exp(0.487)
```

```
## [1] 1.627427
```

```r
# for exp
exp(-0.129)
```

```
## [1] 0.878974
```

```r
exp(0.528)
```

```
## [1] 1.695538
```

Interpretation:

Intercept: When all predictors are at their reference level, the odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is approximately 0.015 times (between 0.006 and 0.03 times in 95% of repeated samples) more than when all predictors are at their alternative levels. β_1: The odds of a MWRA reporting that if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick is about 3.9 times more (between 1.96 and 8.32 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model.

β_2: The odds of a MWRA reporting that giving a child a minimum of 4 or more different types of food a day is not difficult at all is about 4.36 times more (between 2.9 and 6.5 times more in 95% of repeated samples) for MWRA who say it is not difficult compared to MWRA who find it difficult, adjusting for the other predictors in the model.

β_3: The odds of a MWRA reporting that the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more is about 11.14 times more (between 8.2 and 15.33 times more in 95% of repeated samples) for MWRA who believe this compared to MWRA who do not believe so, adjusting for the other predictors in the model.

β_4: The odds of a MWRA reporting that giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.22 times more (between 0.87 and 1.69 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model.

β_5: The odds of a MWRA reporting that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives is about 1.64 times more (between 1.13 and 2.35 times more in 95% of repeated samples) for MWRA who responded in the affirmative compared to MWRA who do not, adjusting for the other predictors in the model.

β_6: The odds of a MWRA reporting that belonging to a women's community group is not difficult at all is about 2 times more (between 1.45 and 2.77 times more in 95% of repeated samples) for MWRA who belong to such a group compared to MWRA who do not, adjusting for the other predictors in the model.

β_7: The odds of a MWRA reporting that giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.17 times more (between 0.84 and 1.63 times more in 95% of repeated samples) for MWRA who have given birth in the years preceding the survey and delivered in a facility for their last birth compared to MWRA who have not delivered in a facility, adjusting for the other predictors in the model. Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7}$

```
mdd2_red <- glm(know_3 ~ 1, data = niger, family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd2_red, mdd2_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ 1
## Model 2: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
##     fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2182 1.2665e-08
## 2      2175 1.2665e-08  7        0        1
```

there is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more(p-value < 0.001).

```
# testing for an association between know_2 and know_3
mdd2_reda <- glm(know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp + fac_delivery, data = nig
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_reda, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between att_3 and know_3
mdd2_reds <- glm(know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp + fac_delivery, data = ni
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_reds, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between se_3 and know_3
mdd2_redw <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + fac_delivery, da
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_redw, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2174 1.2665e-08
## 2      2174 1.2665e-08  0        0
```

```r
# testing for an association between pn_3 and know_3
mdd2_redd <- glm(know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp + fac_delivery, data = ni
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_redd, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between wg and know_3
mdd2_rede <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp + fac_delivery, data =
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_rede, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between decision_combined and know_3
mdd2_redq <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg  + exp + fac_delivery, data = niger, family
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_redq, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + exp + fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between exp and know_3
mdd2_redr <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + fac_delivery, data =
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_redr, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     fac_delivery
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

```r
# testing for an association between fac_delivery and know_3
mdd2_redz <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp, data = niger, fa
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd2_redz, glm_mdd_2, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + fac_delivery
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2174 1.2665e-08  1        0        1
```

there's moderately strong evidence that indicates know_3 is associated with att_3 , decision_combined, exp, and fac_delivery with a p-value of 0.02602, 0.1015, 0.0735, and 0.1307 respectively. There is very strong evidence that indicates know_3 is associated with know_2, pn_3, and wg with a p-value of almost 0. There is extremely strong evidence that indicates know_3 is associated with se_3 with a p-value of 0.

Model 3:

```r
tidy(mdd3_cut)
```

```
## # A tibble: 10 x 5
##    term              estimate std.error statistic p.value
##    <chr>                <dbl>     <dbl>     <dbl>   <dbl>
##  1 (Intercept)       -2.66e+ 1    33462. -7.94e- 4   0.999
##  2 att_3             -6.68e-14    32737. -2.04e-18   1
##  3 se_3              -1.30e-13    20784. -6.24e-18   1
##  4 pn_3               1.17e-13    18123.  6.47e-18   1
##  5 exp                2.66e-14    16857.  1.58e-18   1
##  6 decision_combined -3.03e-14    21178. -1.43e-18   1
##  7 wg                 4.27e-14    16035.  2.67e-18   1
##  8 nutrition2         9.33e-15    37459.  2.49e-19   1
##  9 nutrition3         2.63e-13    24373.  1.08e-17   1
## 10 nutrition4        -1.23e-15    22536. -5.46e-20   1
```

```r
odds_ratios_mdd3_cut <- exp(coef(mdd3_cut))
odds_ratios_mdd3_cut
```

```
##       (Intercept)             att_3              se_3              pn_3 
##      2.900701e-12      1.000000e+00      1.000000e+00      1.000000e+00 
##               exp decision_combined                wg        nutrition2 
##      1.000000e+00      1.000000e+00      1.000000e+00      1.000000e+00 
##        nutrition3        nutrition4 
##      1.000000e+00      1.000000e+00
```

Fitted regression surface:

logit(p_i) = -3.93 + 1.31X_1 + 1.50X_2 + 2.50X_3 + 0.122X_4 + 0.478X_5 + 0.714X_6 - 0.0182X_7

where p_i percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more, X_1 is the percentage of MWRA who agree children who eat a variety of foods are less likely to get sick, X_2 percentage of MRWA who say giving a child a minimum of 4 or more different types of food a day is not difficult at all, X_3 is the percentage of MRWA who believes number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more; 1 = those who believe the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more, 0 = otherwise , X_4 is an indicator for the percentage of MWRA who had heard or seen a message related to breastfeeding or young child nutrition, X_5 is an indicator for Percentage of MRWA who responded that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives; 1 = responded either decides herself or jointly with her partner on all three decision categories, 0 = otherwise, X_6 is the Percentage of MRWA who belong to a women's community group, and X_7 percentage of MWRA who spoke with 1) husband/partner, 2) family member, 3) health provider, 4) nobody about child's nutrition.

```r
# for intercept
exp(-4.73)
```

```
## [1] 0.008826471
```

```r
exp(-3.19)
```

```
## [1] 0.04117187
```

```r
# for att_3
exp(0.608)
```

```
## [1] 1.836754
```

```r
exp(2.08)
```

```
## [1] 8.004469
```

```r
# for se_3
exp(1.10)
```

```
## [1] 3.004166
```

```r
exp(1.90)
```

```
## [1] 6.685894
```

```r
# for pn_3
exp(2.18)
```

```
## [1] 8.846306
```

```r
exp(2.82)
```

```
## [1] 16.77685
```

```r
# for decision_combined
exp(0.105)
```

```
## [1] 1.110711
```

```r
exp(0.849)
```

```
## [1] 2.337308
```

```r
# for wg
exp(0.390)
```

```
## [1] 1.476981
```

```r
exp(1.04)
```

```
## [1] 2.829217
```

```r
# nutrition
exp(-0.0274)
```

```
## [1] 0.972972
```

```r
exp(-0.0102)
```

```
## [1] 0.9898518
```

```r
# for exp
exp(-0.212)
```

```
## [1] 0.8089647
```

```r
exp(0.454)
```

```
## [1] 1.574598
```

Intercept: When all predictors are at their reference level, the odds of a MWRA reporting that a child 6-23 months should eat 4 or more different types of food a day is approximately 0.019 times (between 0.008 and 0.04 times in 95% of repeated samples) more than when all predictors are at their alternative levels. β_1: The odds of a MWRA reporting that if a baby is exclusively breastfed for 6 months, he/she is less likely to be sick is about 3.69 times more (between 1.84 and 8 times more in 95% of repeated samples) for MWRA who agree compared to MWRA who do not agree, adjusting for the other predictors in the model. β_2: The odds of a MWRA reporting that giving a child a minimum of 4 or more different types of food a day is not difficult at all is about 4.48 times more (between 3 and 6.68 times more in 95% of repeated samples) for MWRA who say it is not difficult compared to MWRA who find it difficult, adjusting for the other predictors in the model.

β_3: The odds of a MWRA reporting that the number of different types of food people in the community think a child 6-23 months should eat a day is 4 or more is about 12.19 times more (between 8.88 and 16.77 times more in 95% of repeated samples) for MWRA who believe this compared to MWRA who do not believe so, adjusting for the other predictors in the model.

β_4: The odds of a MWRA reporting that giving only breast milk to the baby for the first 6 months is not difficult at all is about 1.13 times more (between 0.80 and 1.57 times more in 95% of repeated samples) for MWRA who had heard or seen a message related to breastfeeding or young child nutrition compared to MWRA who were not exposed to these messages, adjusting for the other predictors in the model.

β_5: The odds of a MWRA reporting that she OR her and her partner jointly make decisions for all three categories: household purchases, healthcare, and visiting relatives is about 1.61 times more (between 1.48 and 2.83 times more in 95% of repeated samples) for MWRA who responded in the affirmative compared to MWRA who do not, adjusting for the other predictors in the model.

β_6: The odds of a MWRA reporting that belonging to a women's community group is not difficult at all is about 2.04 times more (between 1.4 and 2.8 times more in 95% of repeated samples) for MWRA who belong to such a group compared to MWRA who do not, adjusting for the other predictors in the model. β_7: The odds of a MWRA reporting that speaking with nobody about their child's nutrition is not difficult at all is about 0.98 times (between 0.80 and 0.98 times more in 95% of repeated samples) for MWRA who have spoken with nobody compared to MWRA who have spoken to their husbands, family members, or healthcare providers about their child's nutrition, adjusting for the other predictors in the model. Testing for associations:

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (the predictors are not associated with the outcome variable) $\rightarrow$ reduced model: $\text{logit}(p_i) = \beta_0$ H_A: at least one of the regression coefficients is non-zero (at least one of the predictors is associated with the outcome variable) $\rightarrow$ full model: $\text{logit}(p_i) = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \beta_5 X_{i5} + \beta_6 X_{i6} + \beta_7 X_{i7}$

```r
mdd3_red <- glm(know_3 ~ 1, data = niger, family = binomial(link = "logit"))
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_red, mdd3_cut, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ 1
## Model 2: know_3 ~ att_3 + se_3 + pn_3 + exp + decision_combined + wg +
```

```
##     nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2182 1.2665e-08
## 2      2173 1.2665e-08  9        0        1
```

there is statistically significant evidence to suggest that at least one of the predictors is associated with the percentage of MWRA who reported that the number of different types of food a child 6-23 months should eat a day is 4 or more(p-value < 0.001).

```
# testing for an association between know_2 and know_3
mdd3_reda <- glm(know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp + nutrition, data = niger,
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd3_reda, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ att_3 + se_3 + pn_3 + wg + decision_combined + exp +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```
# testing for an association between att_3 and know_3
mdd3_reds <- glm(know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp + nutrition, data = niger
```

```
## Warning: glm.fit: algorithm did not converge
```

```
anova(mdd3_reds, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + se_3 + pn_3 + wg + decision_combined + exp +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```
# testing for an association between se_3 and know_3
mdd3_redw <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp + nutrition, data
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_redw, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2172 1.2665e-08
## 2      2172 1.2665e-08  0        0
```

```r
# testing for an association between pn_3 and know_3
mdd3_redd <- glm(know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp + nutrition, data = niger
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_redd, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + wg + decision_combined + exp +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```r
# testing for an association between wg and know_3
mdd3_rede <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp + nutrition, data = nig
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_rede, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + decision_combined + exp +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```r
# testing for an association between decision_combined and know_3
mdd3_redq <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg  + exp + nutrition, data = niger, family = b
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_redq, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + exp + nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```r
# testing for an association between exp and know_3
mdd3_redr <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + nutrition, data = nig
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_redr, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     nutrition
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2173 1.2665e-08
## 2      2172 1.2665e-08  1        0        1
```

```r
# testing for an association between nutrition and know_3
mdd3_redz <- glm(know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined + exp, data = niger, fa
```

```
## Warning: glm.fit: algorithm did not converge
```

```r
anova(mdd3_redz, glm_mdd_3, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp
## Model 2: know_3 ~ know_2 + att_3 + se_3 + pn_3 + wg + decision_combined +
##     exp + nutrition
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      2175 1.2665e-08
## 2      2172 1.2665e-08  3        0        1
```

there is very strong evidence that indicates know_3 is associated with know_2, se_3, pn_3, nutrition, and wg with p-values close to or equal to 0. There is relatively strong evidence that know_3 is associated with att_3 with a p-value of 0.05317. There is moderately strong evidence that know_3 is associated with decision_combined and exp with p-values of 0.1356 and 0.1775 respectively.

Critiques/Expansion of Analysis

A fundamental component of any empirical research is the clear definition and accessible documentation of variables used in the analysis. This critique highlights transparency and measurement concerns in a Niger study.Firstly, the lack of a clear variable key linking survey responses to the analysis creates a barrier to understanding how data was translated into quantifiable variables. This omission significantly undermines the ability to understand how survey responses were translated into quantifiable data. Peer reviews and fellow researchers are unable to trace how data inputs are derived from the survey questions, complicating the interpretation of the results. Secondly, the study's reliance on self-reported data introduces potential biases. Participants might answer based on social desirability or be influenced by a spouse's presence, leading to skewed results. Finally, the critique identifies the missing information on how missing data was handled. Depending on the approach used, missing data can introduce further biases or mask underlying patterns. To improve the study, researchers should provide a detailed variable key, acknowledge and address potential biases, and explain their approach to handling missing data. These steps would enhance transparency, strengthen the analysis, and allow for more reliable interpretation of the study's findings.

Findings and Conclusion

The shortcomings identified in the survey clarity, variable documentation, and data collection approach raise substantial concerns about the study's reliability and validity. To enhance the credibility of future research, it is imperative to address these issues by providing comprehensive variable keys and metadata. As expected, our findings do not match those of the study as we used different dependent variables.

note: 4 pages double spaced, 12 pt font MAX (not including graphics/tables/code)

References

Global strategy for infant and young child feeding. Geneva: WHO; 2003. Available: https://www.who.int/publications/i/item/9241562218.

Schwandt HM, Skinner J, Takruri A, Storey D. The Integrated Gateway Model: A catalytic approach to behavior change. International Journal of Gynecology & Obstetrics. 2015;130: E62–E68. pmid:26003817