Supplement 5

Risk factors

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Contents

This script generates models for potential predictors for having pain.

Both univariate analyses and multi-variable model selection are presented.

Import data

```
# Import data
pain <- read_rds('data-cleaned/wbpq.rds') %>%
    select(PID,
           pain_in_last_month,
           pain_worst) %>%
    mutate(pain = ifelse(pain_in_last_month == 'yes' & pain_worst > 0,
                         yes = 'yes',
                         no = 'no')) %>%
    select(PID, pain)

general <- read_rds('data-cleaned/general_info.rds') %>%
    select(PID, age, sex, educational_level, employment) %>%
    mutate(employment = fct_collapse(employment,
                                     employed = c('employed', 'employed (part time)'),
                                     unemployed = c('unemployed'),
                                     grant = c('disability grant', 'pension grant')))

mental_health <- read_rds('data-cleaned/hscl.rds') %>%
    select(PID, total_score)

# Join to core_info
data <- read_rds('data-cleaned/hiv_test.rds') %>%
    select(PID, test_result) %>%
    left_join(pain) %>%
    left_join(general) %>%
    left_join(mental_health)
```

Clean data

```
# Remove participants without test results
data %<>%
    filter(!is.na(test_result))

# Remove participants with missing pain data
data %<>%
    filter(!is.na(pain))

# Convert character classes to factors
data %<>%
    mutate_if(is.character, factor)
```

Quick look

```
# Dataframe dimensions
dim(data)
```

```
## [1] 535   8
```

```
# Column names
names(data)
```

```
## [1] "PID"              "test_result"      "pain"
## [4] "age"              "sex"              "educational_level"
## [7] "employment"       "total_score"
```

```
# Glimpse data
glimpse(data)
```

```
## Observations: 535
## Variables: 8
## $ PID               <fct> 001, 003, 004, 005, 006, 007, 008, 009, 010,...
## $ test_result       <fct> HIV negative, HIV negative, HIV negative, HI...
## $ pain              <fct> no, yes, yes, yes, yes, no, yes, yes, yes, y...
## $ age               <dbl> 35, 50, 38, 37, 30, 25, 39, 27, 23, 32, 36, ...
## $ sex               <fct> male, female, male, male, male, male, male, ...
## $ educational_level <ord> secondary school, no/primary school, seconda...
## $ employment        <fct> unemployed, grant, employed, employed, emplo...
## $ total_score       <dbl> 3.40, 1.28, 1.92, 1.04, 2.72, 1.64, 1.76, 2....
```

Check missingness

Full cohort

```
data %>%
    profile_missing() %>%
    mutate(pct_missing = round(100 * pct_missing)) %>%
    arrange(pct_missing)
```

```
## # A tibble: 8 x 3
##   feature           num_missing pct_missing
##   <fct>                   <int>       <dbl>
## 1 PID                         0           0
## 2 test_result                 0           0
## 3 pain                        0           0
## 4 sex                         2           0
## 5 age                         3           1
## 6 employment                  3           1
## 7 total_score                 5           1
## 8 educational_level          14           3
```

HIV-

```
data %>%
    filter(test_result == 'HIV negative') %>%
```

```r
    profile_missing() %>%
    mutate(pct_missing = round(100 * pct_missing)) %>%
    arrange(pct_missing)
```

```
## # A tibble: 8 x 3
##   feature           num_missing pct_missing
##   <fct>                   <int>       <dbl>
## 1 PID                         0           0
## 2 test_result                 0           0
## 3 pain                        0           0
## 4 age                         2           0
## 5 sex                         1           0
## 6 employment                  3           1
## 7 total_score                 5           1
## 8 educational_level          14           3
```

HIV+

```r
data %>%
    filter(test_result == 'HIV positive') %>%
    profile_missing() %>%
    mutate(pct_missing = round(100 * pct_missing)) %>%
    arrange(pct_missing)
```

```
## # A tibble: 8 x 3
##   feature           num_missing pct_missing
##   <fct>                   <int>       <dbl>
## 1 PID                         0           0
## 2 test_result                 0           0
## 3 pain                        0           0
## 4 educational_level           0           0
## 5 employment                  0           0
## 6 total_score                 0           0
## 7 age                         1           1
## 8 sex                         1           1
```

HIV status

Build model

```r
mod_hiv <- glm(pain ~ test_result,
               data = data,
               family = binomial(link = 'logit'))
```

Beta coefficients

```r
# Coefficients
coef(mod_hiv)
```

```
##             (Intercept) test_resultHIV positive
##               0.4234189             -0.4234189
```

```r
# 95% CI of the coefficients
confint(mod_hiv)
```

```
##                              2.5 %     97.5 %
## (Intercept)              0.2386153 0.61063071
## test_resultHIV positive -0.9293655 0.08220701
```

Odds ratio

```r
# OR
exp(coef(mod_hiv))
```

```
##             (Intercept) test_resultHIV positive
##               1.5271739              0.6548043
```

```r
# 95% CI of the OR
exp(confint(mod_hiv))
```

```
##                             2.5 %   97.5 %
## (Intercept)             1.2694900 1.841593
## test_resultHIV positive 0.3948041 1.085681
```

Overall model

```r
# likelihood ratio test
Anova(mod_hiv,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##             LR Chisq Df Pr(>Chisq)
## test_result   2.6992  1     0.1004
```

Model terms

```r
# Summary
summary(mod_hiv)
```

```
##
## Call:
## glm(formula = pain ~ test_result, family = binomial(link = "logit"),
##     data = data)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.362  -1.362   1.004   1.004   1.177
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)              0.42342    0.09483   4.465 8.01e-06 ***
## test_resultHIV positive -0.42342    0.25717  -1.646   0.0997 .
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 723.98  on 534  degrees of freedom
## Residual deviance: 721.28  on 533  degrees of freedom
## AIC: 725.28
##
## Number of Fisher Scoring iterations: 4
```

```
# Wald test
Anova(mod_hiv,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##             Df  Chisq Pr(>Chisq)
## test_result  1 2.7108    0.09967 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model fit

Pseudo-R^2

```
nagelkerke(mod_hiv)
```

```
## $Models
##
## Model: "glm, pain ~ test_result, binomial(link = \"logit\"), data"
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                           0.00372828
## Cox and Snell (ML)                 0.00503255
## Nagelkerke (Cragg and Uhler)       0.00678609
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff  Chisq p.value
##       -1     -1.3496 2.6992  0.1004
##
## $Number.of.observations
##
## Model: 535
## Null:  535
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

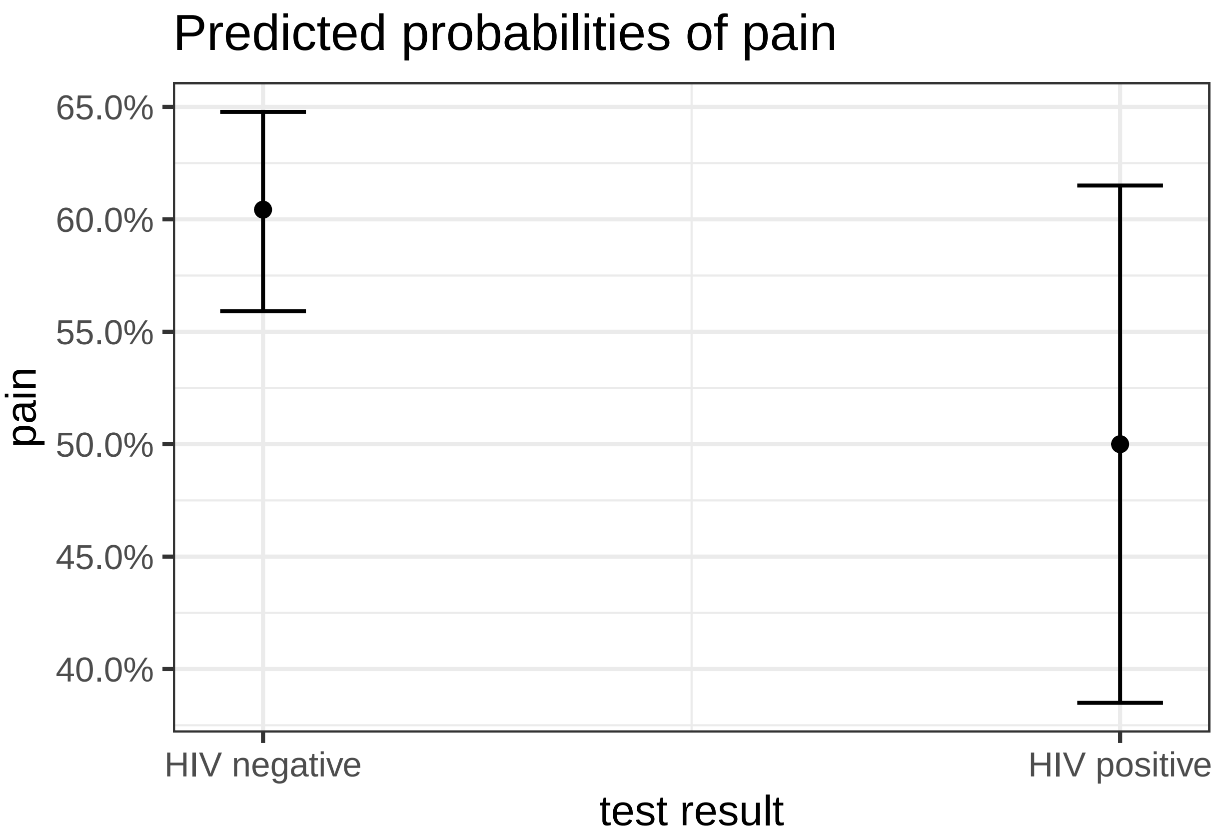
Hosmer-Lemeshow test

```
hoslem.test(x = mod_hiv$y,
            y = fitted(mod_hiv),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_hiv$y, fitted(mod_hiv)
## X-squared = 9.9918e-29, df = 8, p-value = 1
```

Plot predicted probabilities

```
plot_model(mod_hiv,
           type = 'pred')$test_result
```




```
# Publication plot
## Extract data
hiv <- plot_model(mod_hiv,
                  type = 'pred')$test_result

hiv_data <- tibble(x = factor(hiv$data$x),
                   pred = hiv$data$predicted,
                   low = hiv$data$conf.low,
                   high = hiv$data$conf.high)

## Plot
```

```r
pp_hiv <- ggplot(data = hiv_data) +
    aes(x = x,
        y = pred,
        ymin = low,
        ymax = high) +
    geom_errorbar(width = 0.3,
                  size = 1) +
    geom_point(size = 3) +
    annotate(geom = 'text',
             label = 'HIV status*',
             size = 5,
             x = 0.5,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'right') +
    scale_x_discrete(labels = c('Negative', 'Positive')) +
    labs(x = 'HIV test result') +
    theme(axis.title.y = element_blank(),
          axis.title.x = element_text(size = 17),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'))
```

Age

Build model

```r
mod_age <- glm(pain ~ age,
               data = data[!is.na(data$age), ],
               family = binomial(link = 'logit'))
```

Beta coefficients

```r
# Coefficients
coef(mod_age)
```

```
## (Intercept)         age
## 0.194494016 0.004976257
```

```r
# 95% CI of the coefficients
confint(mod_age)
```

```
##                   2.5 %     97.5 %
## (Intercept) -0.36882723 0.75671672
## age         -0.01059239 0.02075425
```

Odds ratios

```r
# OR
exp(coef(mod_age))
```

```
## (Intercept)         age
##    1.214696    1.004989
```

```r
# 95% CI of the OR
exp(confint(mod_age))
```

```
##                 2.5 %   97.5 %
## (Intercept) 0.6915449 2.131267
## age         0.9894635 1.020971
```

Overall model

```r
# Likelihood ratio test
Anova(mod_age,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##     LR Chisq Df Pr(>Chisq)
## age  0.39027  1     0.5322
```

Model terms

```r
# Summary
summary(mod_age)
```

```
##
## Call:
## glm(formula = pain ~ age, family = binomial(link = "logit"),
##     data = data[!is.na(data$age), ])
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.419  -1.324   1.002   1.034   1.065
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.194494   0.286725   0.678    0.498
## age         0.004976   0.007981   0.624    0.533
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 720.09  on 531  degrees of freedom
## Residual deviance: 719.70  on 530  degrees of freedom
## AIC: 723.7
##
## Number of Fisher Scoring iterations: 4
```

```r
# Wald test
Anova(mod_age,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
```

```
##
## Response: pain
##     Df  Chisq Pr(>Chisq)
## age  1 0.3888      0.533
```

Model fit

Pseudo-R^2

```r
nagelkerke(mod_age)
```

```
## $Models
##
## Model: "glm, pain ~ age, binomial(link = \"logit\"), data[!is.na(data$age), ]"
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data[!is.na(data$age), ]"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                          0.000541979
## Cox and Snell (ML)                0.000733329
## Nagelkerke (Cragg and Uhler)      0.000988741
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff   Chisq p.value
##       -1    -0.19514 0.39027 0.53216
##
## $Number.of.observations
##
## Model: 532
## Null:  532
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

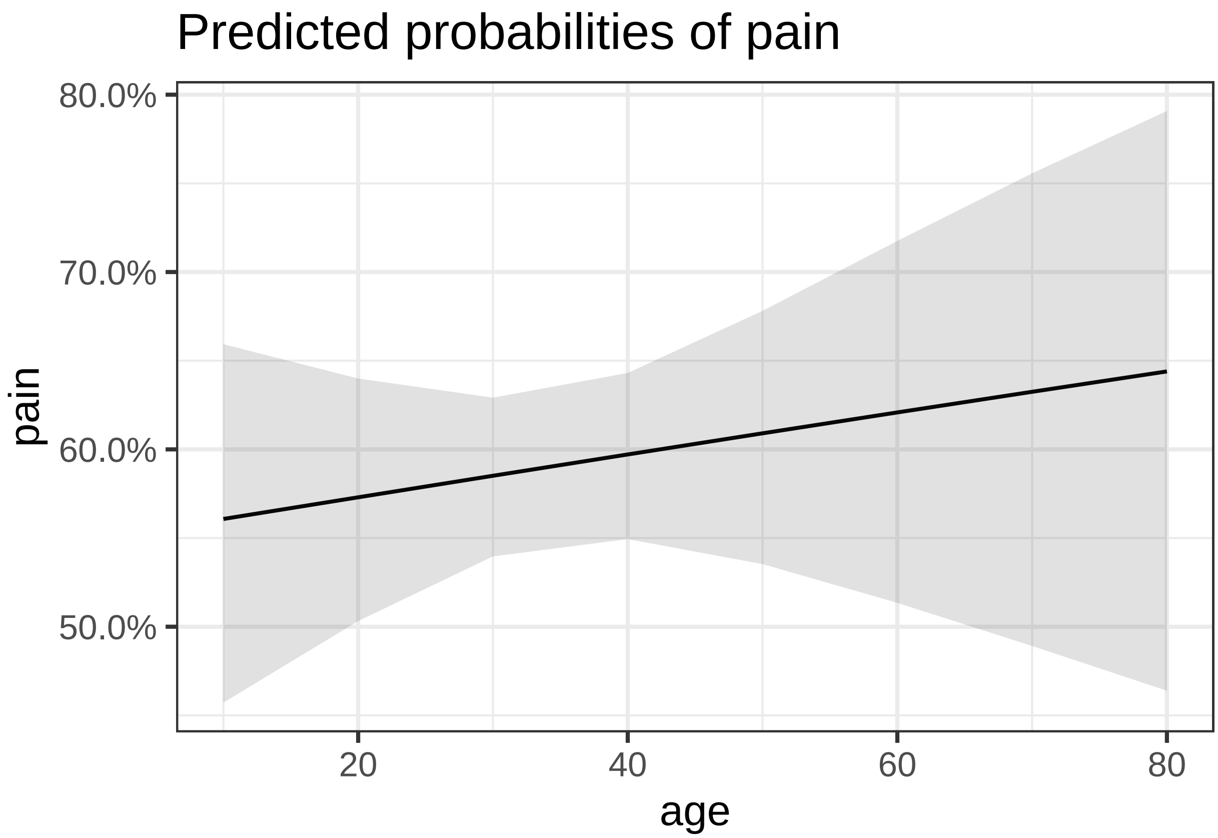
Hosmer-Lemeshow test

```r
hoslem.test(x = mod_age$y,
            y = fitted(mod_age),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_age$y, fitted(mod_age)
## X-squared = 6.6654, df = 8, p-value = 0.5731
```

Plot predicted probabilities

```r
plot_model(mod_age,
           type = 'pred')$age
```




```r
# Publication plot
## Extract data
age <- plot_model(mod_age,
                  type = 'pred')$age

age_data <- tibble(x = age$data$x,
                   pred = age$data$predicted,
                   low = age$data$conf.low,
                   high = age$data$conf.high)

## Plot
pp_age <- ggplot(data = age_data) +
    aes(x = x,
        y = pred,
        ymax = high,
        ymin = low) +
    geom_ribbon(fill = '#CCCCCC') +
    geom_line(size = 0.8) +
    annotate(geom = 'text',
             label = 'Age*',
             size = 5,
             x = 10,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'left') +
    labs(x = 'Age (years)') +
```

```
    theme(axis.title.y = element_blank(),
          axis.title.x = element_text(size = 17),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'))
```

Sex

Build model

```
mod_sex <- glm(pain ~ sex,
               data = data[!is.na(data$sex), ],
               family = binomial(link = 'logit'))
```

Beta coefficients

```
# Coefficients
coef(mod_sex)
```

```
## (Intercept)     sexmale
##   0.5920511  -0.5007013
```

```
# 95% CI of the coefficients
confint(mod_sex)
```

```
##                  2.5 %     97.5 %
## (Intercept)  0.3549933  0.8346266
## sexmale     -0.8502162 -0.1532804
```

Odds ratios

```
# OR
exp(coef(mod_sex))
```

```
## (Intercept)     sexmale
##   1.8076923   0.6061055
```

```
# 95% CI of the OR
exp(confint(mod_sex))
```

```
##                 2.5 %    97.5 %
## (Intercept) 1.4261710 2.3039535
## sexmale     0.4273226 0.8578891
```

Overall model

```
# Likelihood ratio test
Anova(mod_sex,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##     LR Chisq Df Pr(>Chisq)
## sex   7.9882  1   0.004708 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model terms

```
# Summary
summary(mod_sex)
```

```
##
## Call:
## glm(formula = pain ~ sex, family = binomial(link = "logit"),
##     data = data[!is.na(data$sex), ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4369  -1.2164   0.9384   0.9384   1.1389
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.5921     0.1222   4.845 1.27e-06 ***
## sexmale      -0.5007     0.1777  -2.818  0.00483 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 721.87  on 532  degrees of freedom
## Residual deviance: 713.88  on 531  degrees of freedom
## AIC: 717.88
##
## Number of Fisher Scoring iterations: 4
```

```
# Wald test
Anova(mod_sex,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##     Df Chisq Pr(>Chisq)
## sex  1 7.942    0.00483 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model fit

Pseudo-R^2

```r
nagelkerke(mod_sex)
```

```
## $Models
##
## Model: "glm, pain ~ sex, binomial(link = \"logit\"), data[!is.na(data$sex), ]"
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data[!is.na(data$sex), ]"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                            0.0110660
## Cox and Snell (ML)                  0.0148755
## Nagelkerke (Cragg and Uhler)        0.0200509
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff  Chisq   p.value
##       -1     -3.9941 7.9882 0.0047083
##
## $Number.of.observations
##
## Model: 533
## Null:  533
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

Hosmer-Lemeshow test

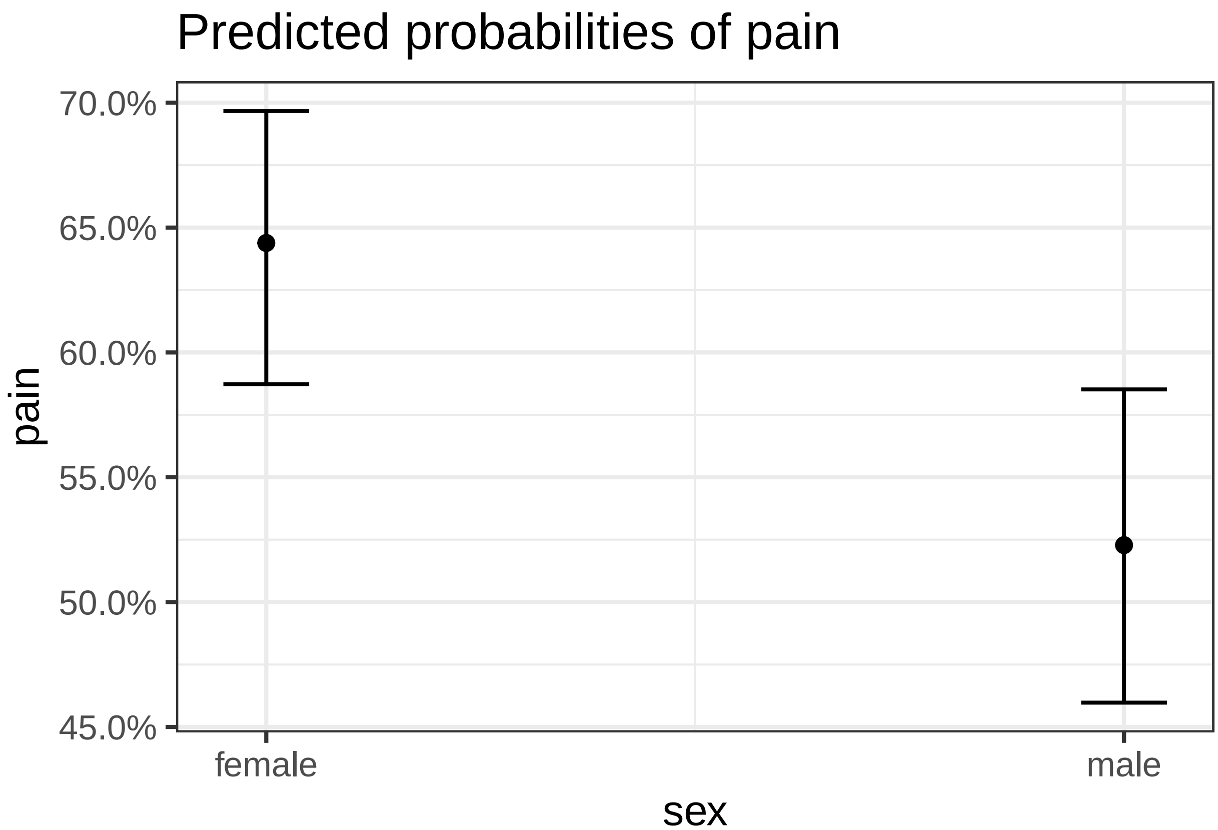
```r
hoslem.test(x = mod_sex$y,
            y = fitted(mod_sex),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_sex$y, fitted(mod_sex)
## X-squared = 4.1499e-26, df = 8, p-value = 1
```

Plot predicted probabilities

```r
plot_model(mod_sex,
           type = 'pred')
```

```
## $sex
```




```
# Publication plot
## Extract data
sex <- plot_model(mod_sex,
                  type = 'pred')$sex

sex_data <- tibble(x = factor(sex$data$x),
                   pred = sex$data$predicted,
                   low = sex$data$conf.low,
                   high = sex$data$conf.high)

## Plot
pp_sex <- ggplot(data = sex_data) +
    aes(x = x,
        y = pred,
        ymin = low,
        ymax = high) +
    geom_errorbar(width = 0.3,
                  size = 1) +
    geom_point(size = 3) +
    annotate(geom = 'text',
             label = 'Sex',
             size = 5,
             x = 0.5,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'right') +
    scale_x_discrete(labels = c('Female', 'Male')) +
```

```
    labs(x = 'Sex') +
    theme(axis.title.y = element_blank(),
          axis.title.x = element_text(size = 17),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'))
```

Educational level

Build model

```
mod_school <- glm(pain ~ educational_level,
                  data = data[!is.na(data$educational_level), ],
                  family = binomial(link = 'logit'))
```

Beta coefficients

```
# Coefficients
coef(mod_school)
```

```
##         (Intercept) educational_level.L educational_level.Q
##          0.31072492          0.21947500          0.02822161
```

```
# 95% CI of the coefficients
confint(mod_school)
```

```
##                           2.5 %    97.5 %
## (Intercept)          0.01507632 0.6117129
## educational_level.L -0.39956640 0.8277941
## educational_level.Q -0.36608050 0.4276322
```

Odds ratios

```
# OR
exp(coef(mod_school))
```

```
##         (Intercept) educational_level.L educational_level.Q
##            1.364414            1.245423            1.028624
```

```
# 95% CI of the OR
exp(confint(mod_school))
```

```
##                         2.5 %   97.5 %
## (Intercept)         1.0151905 1.843587
## educational_level.L 0.6706108 2.288265
## educational_level.Q 0.6934470 1.533622
```

Overall model

```
# Likelihood ratio test
Anova(mod_school,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##                   LR Chisq Df Pr(>Chisq)
## educational_level   1.1781  2     0.5548
```

Model terms

```r
# Summary
summary(mod_school)
```

```
##
## Call:
## glm(formula = pain ~ educational_level, family = binomial(link = "logit"),
##     data = data[!is.na(data$educational_level), ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3857  -1.3018   0.9825   1.0579   1.1073
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.31072    0.15081   2.060   0.0394 *
## educational_level.L  0.21948    0.30985   0.708   0.4787
## educational_level.Q  0.02822    0.20114   0.140   0.8884
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 706.98  on 520  degrees of freedom
## Residual deviance: 705.80  on 518  degrees of freedom
## AIC: 711.8
##
## Number of Fisher Scoring iterations: 4
```

```r
# Wald test
Anova(mod_school,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##                   Df  Chisq Pr(>Chisq)
## educational_level  2 1.1729     0.5563
```

Model fit

Pseudo-R^2

```r
nagelkerke(mod_school)
```

```
## $Models
```

```
##
## Model: "glm, pain ~ educational_level, binomial(link = \"logit\"), data[!is.na(data$educational_leve
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data[!is.na(data$educational_level), ]"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                           0.00166642
## Cox and Snell (ML)                 0.00225873
## Nagelkerke (Cragg and Uhler)       0.00304181
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff  Chisq p.value
##       -2    -0.58906 1.1781 0.55485
##
## $Number.of.observations
##
## Model: 521
## Null:  521
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

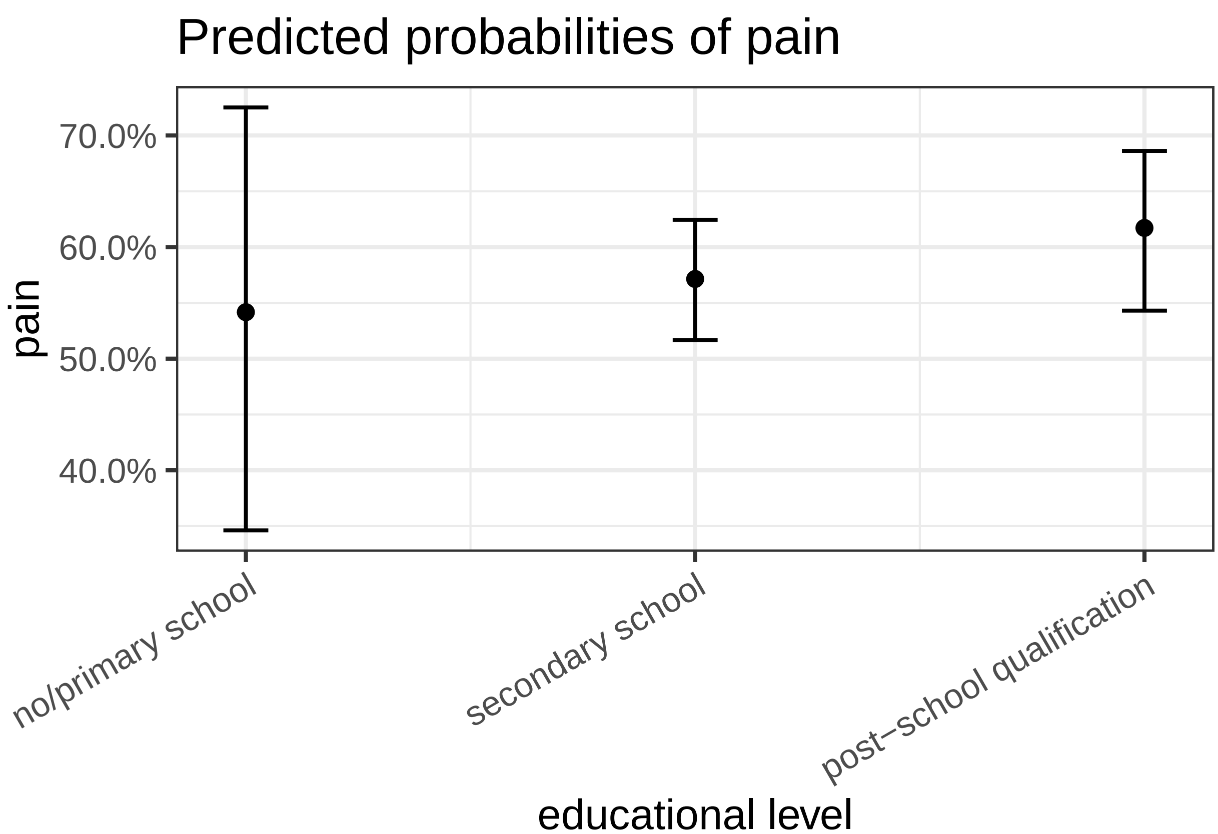
Hosmer-Lemeshow test

```
hoslem.test(x = mod_school$y,
            y = fitted(mod_school),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_school$y, fitted(mod_school)
## X-squared = 7.384e-28, df = 8, p-value = 1
```

Plot predicted probabilities

```
plot_model(mod_school,
           type = 'pred')$educational_level +
    theme(axis.text.x = element_text(angle = 30,
                                     hjust = 1))
```




```
# Publication plot
## Extract data
edu <- plot_model(mod_school,
                  type = 'pred')$educational_level

edu_data <- tibble(x = factor(edu$data$x),
                   pred = edu$data$predicted,
                   low = edu$data$conf.low,
                   high = edu$data$conf.high)

## Plot
pp_edu <- ggplot(data = edu_data) +
    aes(x = x,
        y = pred,
        ymin = low,
        ymax = high) +
    geom_errorbar(width = 0.3,
                  size = 1) +
    geom_point(size = 3) +
    annotate(geom = 'text',
             label = 'Education*',
             size = 5,
             x = 0.5,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'left') +
    scale_x_discrete(labels = c('0-7', '8-12', '>12')) +
```

```
    labs(x = 'School grade') +
    theme(axis.title.y = element_blank(),
          axis.title.x = element_text(size = 17),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'))
```

Employment

Build model

```
mod_employment <- glm(pain ~ employment,
                      data = data[!is.na(data$employment), ],
                      family = binomial(link = 'logit'))
```

Beta coefficients

```
# Coefficients
coef(mod_employment)
```

```
##          (Intercept)   employmentemployed employmentunemployed
##            1.0296194           -0.7467566           -0.6333710
```

```
# 95% CI of the coefficients
confint(mod_employment)
```

```
##                            2.5 %    97.5 %
## (Intercept)           0.06891139 2.1592545
## employmentemployed   -1.90174775 0.2485792
## employmentunemployed -1.78608566 0.3589340
```

Odds ratios

```
# OR
exp(coef(mod_employment))
```

```
##          (Intercept)   employmentemployed employmentunemployed
##            2.8000000            0.4739011            0.5307995
```

```
# 95% CI of the OR
exp(confint(mod_employment))
```

```
##                          2.5 %   97.5 %
## (Intercept)          1.0713413 8.664676
## employmentemployed   0.1493074 1.282202
## employmentunemployed 0.1676150 1.431802
```

Overall model

```
# Likelihood ratio test
Anova(mod_employment,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##            LR Chisq Df Pr(>Chisq)
## employment   2.2454  2     0.3254
```

Model terms

```
# Summary
summary(mod_employment)
```

```
##
## Call:
## glm(formula = pain ~ employment, family = binomial(link = "logit"),
##     data = data[!is.na(data$employment), ])
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.634  -1.300   1.014   1.060   1.060
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.0296     0.5210   1.976   0.0481 *
## employmentemployed    -0.7468     0.5369  -1.391   0.1643
## employmentunemployed  -0.6334     0.5355  -1.183   0.2369
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 720.09  on 531  degrees of freedom
## Residual deviance: 717.84  on 529  degrees of freedom
## AIC: 723.84
##
## Number of Fisher Scoring iterations: 4
```

```
# Wald test
Anova(mod_employment,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##            Df Chisq Pr(>Chisq)
## employment  2  2.09     0.3517
```

Model fit

Pseudo-R^2

```
nagelkerke(mod_employment)
```

```
## $Models
```

```
##
## Model: "glm, pain ~ employment, binomial(link = \"logit\"), data[!is.na(data$employment), ]"
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data[!is.na(data$employment), ]"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                           0.00311829
## Cox and Snell (ML)                 0.00421187
## Nagelkerke (Cragg and Uhler)       0.00567883
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff  Chisq p.value
##       -2     -1.1227 2.2454 0.32539
##
## $Number.of.observations
##
## Model: 532
## Null:  532
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

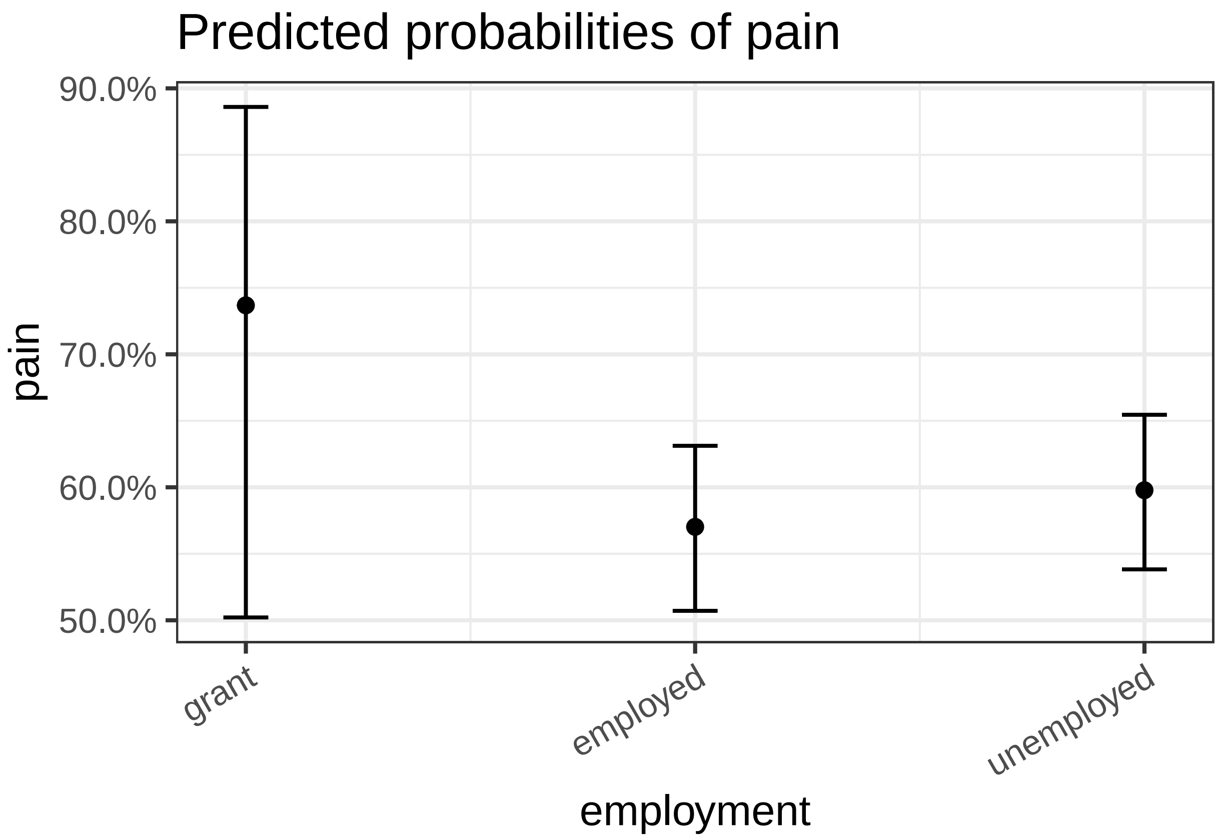
Hosmer-Lemeshow test

```
hoslem.test(x = mod_employment$y,
            y = fitted(mod_employment),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_employment$y, fitted(mod_employment)
## X-squared = 3.1778e-23, df = 8, p-value = 1
```

Plot predicted probabilities

```
plot_model(mod_employment,
           type = 'pred')$employment +
    theme(axis.text.x = element_text(angle = 30,
                                     hjust = 1))
```




```r
# Publication plot
## Extract data
emp <- plot_model(mod_employment,
                  type = 'pred')$employment

emp_data <- tibble(x = factor(emp$data$x),
                   pred = emp$data$predicted,
                   low = emp$data$conf.low,
                   high = emp$data$conf.high)

## Plot
pp_emp <- ggplot(data = emp_data) +
    aes(x = x,
        y = pred,
        ymin = low,
        ymax = high) +
    geom_errorbar(width = 0.3,
                  size = 1) +
    geom_point(size = 3) +
    annotate(geom = 'text',
             label = 'Employment',
             size = 5,
             x = 0.5,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'right') +
```

```
    scale_x_discrete(labels = c('Grant', 'Employed', 'Unemployed')) +
    labs(x = 'Employment status') +
    theme(axis.title.y = element_blank(),
          axis.title.x = element_text(size = 17),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'))
```

HSCL25 (total score)

Build model

```
mod_hscl <- glm(pain ~ total_score,
                data = data[!is.na(data$total_score), ],
                family = binomial(link = 'logit'))
```

Beta coefficients

```
# Coefficients
coef(mod_hscl)
```

```
## (Intercept) total_score
##   -1.856534    1.367989
```

```
# 95% CI of the coefficients
confint(mod_hscl)
```

```
##                 2.5 %    97.5 %
## (Intercept) -2.512401 -1.231110
## total_score  0.988773  1.775077
```

Odds ratios

```
# Odds ratio
exp(coef(mod_hscl))
```

```
## (Intercept) total_score
##   0.1562131   3.9274441
```

```
# 95% CI of the OR
exp(confint(mod_hscl))
```

```
##                  2.5 %    97.5 %
## (Intercept) 0.08107334 0.2919683
## total_score 2.68793445 5.9007362
```

Overall model

```
# Likelihood ratio test
Anova(mod_hscl,
      test = 'LR')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##             LR Chisq Df Pr(>Chisq)
## total_score   59.271  1  1.374e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model terms

```
# Summary
summary(mod_hscl)
```

```
##
## Call:
## glm(formula = pain ~ total_score, family = binomial(link = "logit"),
##     data = data[!is.na(data$total_score), ])
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.389  -1.110   0.594   1.040   1.391
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.8565     0.3264  -5.687 1.29e-08 ***
## total_score   1.3680     0.2003   6.830 8.50e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 717.25  on 529  degrees of freedom
## Residual deviance: 657.98  on 528  degrees of freedom
## AIC: 661.98
##
## Number of Fisher Scoring iterations: 4
```

```
# Wald test
Anova(mod_hscl,
      type = 'II',
      test = 'Wald')
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pain
##             Df  Chisq Pr(>Chisq)
## total_score  1 46.647  8.499e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model fit

Pseudo-R^2

```
nagelkerke(mod_hscl)
```

```
## $Models
##
## Model: "glm, pain ~ total_score, binomial(link = \"logit\"), data[!is.na(data$total_score), ]"
## Null:  "glm, pain ~ 1, binomial(link = \"logit\"), data[!is.na(data$total_score), ]"
##
## $Pseudo.R.squared.for.model.vs.null
##                              Pseudo.R.squared
## McFadden                             0.082637
## Cox and Snell (ML)                   0.105806
## Nagelkerke (Cragg and Uhler)         0.142670
##
## $Likelihood.ratio.test
##  Df.diff LogLik.diff  Chisq    p.value
##       -1     -29.636 59.271 1.3736e-14
##
## $Number.of.observations
##
## Model: 530
## Null:  530
##
## $Messages
## [1] "Note: For models fit with REML, these statistics are based on refitting with ML"
##
## $Warnings
## [1] "None"
```

Hosmer-Lemeshow test

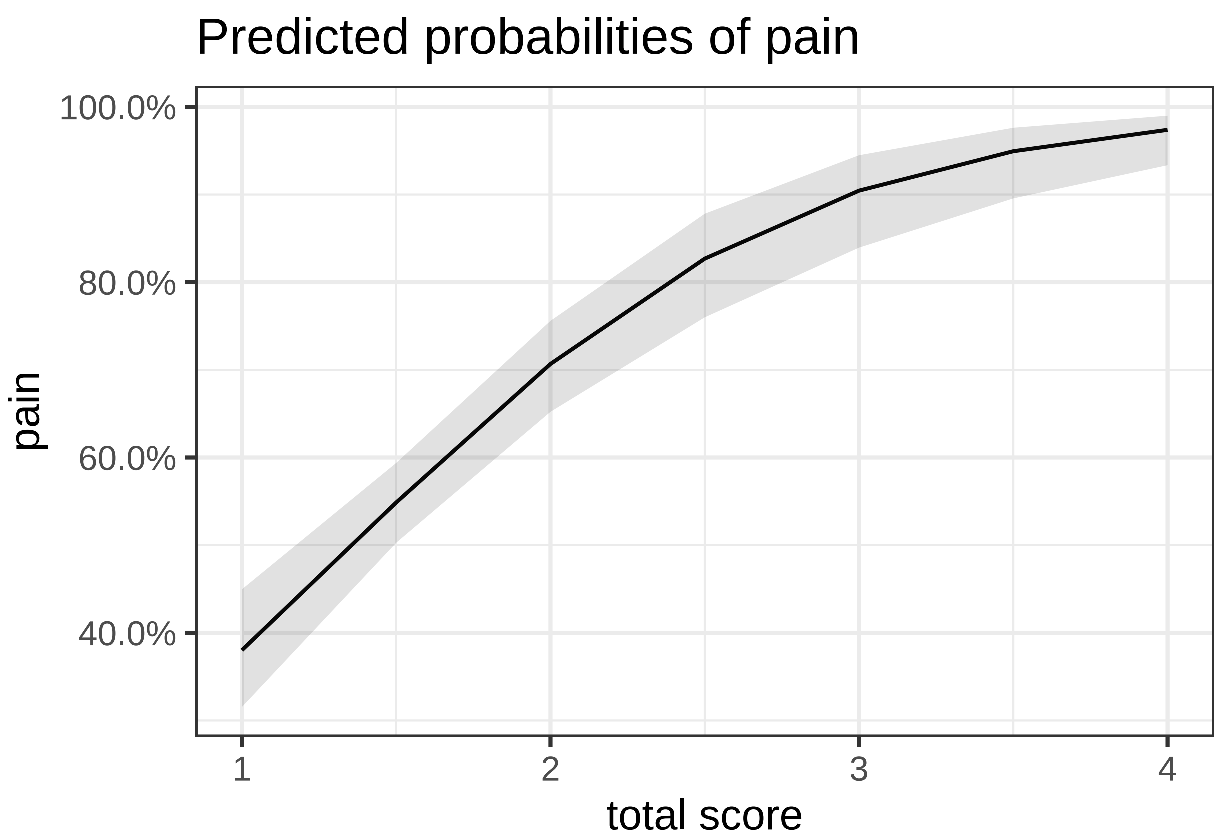
```
hoslem.test(x = mod_hscl$y,
            y = fitted(mod_hscl),
            g = 10)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  mod_hscl$y, fitted(mod_hscl)
## X-squared = 4.6332, df = 8, p-value = 0.796
```

Plot predicted probabilities

```
plot_model(mod_hscl,
           type = 'pred')
```

```
## $total_score
```




```r
# Publication plot
## Extract data
hscl <- plot_model(mod_hscl,
                   type = 'pred')$total_score

hscl_data <- tibble(x = hscl$data$x,
                    pred = hscl$data$predicted,
                    low = hscl$data$conf.low,
                    high = hscl$data$conf.high)

## Plot
pp_hscl <- ggplot(data = hscl_data) +
    aes(x = x,
        y = pred,
        ymax = high,
        ymin = low) +
    geom_ribbon(fill = '#CCCCCC') +
    geom_line(size = 0.8) +
    annotate(geom = 'text',
             label = 'HSCL-25',
             size = 5,
             x = 1,
             y = 0.97,
             hjust = 0) +
    scale_y_continuous(limits = c(0, 1),
                       position = 'left') +
    labs(x = 'HSCL-25 total score') +
    theme(axis.title.y = element_blank(),
```

```r
        axis.title.x = element_text(size = 17),
        panel.grid = element_blank(),
        axis.text = element_text(colour = '#000000'))
```

Variable selection

Using backward selection

Prepare data

```r
# Extract complete cases and refactor educational levels
complete <- data %>%
    filter(complete.cases(.)) %>%
    mutate(educational_level = fct_recode(educational_level,
                                         `1` = 'no/primary school',
                                         `2` = 'secondary school',
                                         `3` = 'post-school qualification'))
```

Generate full model

```r
fit <- lrm(pain ~ age + sex + test_result + total_score + educational_level + employment,
           data = complete,
           x = TRUE, y = TRUE)
```

Inspect full model coefficients

```r
# Model summary
fit
```

```
## Logistic Regression Model
##
##  lrm(formula = pain ~ age + sex + test_result + total_score +
##      educational_level + employment, data = complete, x = TRUE,
##      y = TRUE)
##
##                        Model Likelihood     Discrimination    Rank Discrim.
##                           Ratio Test           Indexes           Indexes
##  Obs           509    LR chi2      66.59    R2       0.165    C       0.694
##   no           212    d.f.             8    g        0.945    Dxy     0.389
##   yes          297    Pr(> chi2) <0.0001    gr       2.574    gamma   0.389
##  max |deriv| 1e-05                          gp       0.196    tau-a   0.189
##                                             Brier    0.215
##
##                             Coef    S.E.   Wald Z Pr(>|Z|)
##  Intercept                 -2.0239 1.3132 -1.54  0.1233
##  age                        0.0146 0.0102  1.43  0.1529
##  sex=male                  -0.2267 0.2020 -1.12  0.2617
##  test_result=HIV positive -0.5788 0.2890 -2.00  0.0452
##  total_score                1.3575 0.2124  6.39  <0.0001
##  educational_level          0.1672 0.4710  0.35  0.7226
```

```
##   educational_level=3       0.1483 0.5387  0.28  0.7831
##   employment=employed      -0.6190 0.6179 -1.00  0.3164
##   employment=unemployed    -0.6071 0.6315 -0.96  0.3364
##
```

```r
# Betas
coef(fit)
```

```
##                Intercept                    age                sex=male
##              -2.02389051             0.01456871             -0.22670243
## test_result=HIV positive            total_score       educational_level
##              -0.57878625             1.35754122              0.16718303
##      educational_level=3    employment=employed   employment=unemployed
##               0.14830149            -0.61902785             -0.60705114
```

```r
confint.default(fit)
```

```
##                                 2.5 %      97.5 %
## Intercept                -4.597807803  0.55002677
## age                      -0.005409784  0.03454720
## sex=male                 -0.622609005  0.16920414
## test_result=HIV positive -1.145218451 -0.01235405
## total_score               0.941190974  1.77389147
## educational_level        -0.755930631  1.09029670
## educational_level=3      -0.907552917  1.20415590
## employment=employed      -1.829999930  0.59194424
## employment=unemployed    -1.844865102  0.63076283
```

```r
# OR
exp(coef(fit))
```

```
##                Intercept                    age                sex=male
##                0.1321404              1.0146754               0.7971580
## test_result=HIV positive            total_score       educational_level
##                0.5605784              3.8866252               1.1819706
##      educational_level=3    employment=employed   employment=unemployed
##                1.1598625              0.5384677               0.5449555
```

```r
exp(confint.default(fit))
```

```
##                              2.5 %    97.5 %
## Intercept                0.0100739 1.7332994
## age                      0.9946048 1.0351509
## sex=male                 0.5365428 1.1843619
## test_result=HIV positive 0.3181544 0.9877219
## total_score              2.5630321 5.8937441
## educational_level        0.4695734 2.9751567
## educational_level=3      0.4035104 3.3339437
## employment=employed      0.1604136 1.8074992
## employment=unemployed    0.1580466 1.8790434
```

Perform backward selection on full model

```r
# Perform selection
(bw  <- fastbw(fit))
```

```
##
##   Deleted           Chi-Sq d.f. P      Residual d.f. P      AIC
```

```
##  employment        1.01   2    0.6049  1.01    2    0.6049 -2.99
##  educational_level 2.36   2    0.3069  3.37    4    0.4982 -4.63
##  sex               1.52   1    0.2171  4.89    5    0.4292 -5.11
##  age               2.86   1    0.0905  7.76    6    0.2565 -4.24
##  test_result       3.81   1    0.0511 11.56    7    0.1159 -2.44
##
## Approximate Estimates after Deleting Factors
##
##               Coef   S.E. Wald Z         P
## Intercept   -1.778 0.3329 -5.340 9.303e-08
## total_score  1.296 0.2034  6.372 1.862e-10
##
## Factors in Final Model
##
## [1] total_score
```

```
# Betas
coef(bw)
```

```
##   Intercept total_score
##   -1.777667    1.295831
```

```
confint.default(bw)
```

```
##                  2.5 %    97.5 %
## Intercept   -2.4301535 -1.125181
## total_score  0.8972649  1.694396
```

```
# OR
exp(coef(bw))
```

```
##   Intercept total_score
##    0.169032    3.654030
```

```
exp(confint.default(bw))
```

```
##                  2.5 %    97.5 %
## Intercept   0.08802332 0.3245936
## total_score 2.45288512 5.4433594
```

Check model stability

100 bootstrapped resamples.

```
validate(fit, B = 100, bw = TRUE)
```

```
##
##      Backwards Step-down - Original Model
##
##  Deleted           Chi-Sq d.f. P      Residual d.f. P      AIC
##  employment        1.01   2    0.6049  1.01    2    0.6049 -2.99
##  educational_level 2.36   2    0.3069  3.37    4    0.4982 -4.63
##  sex               1.52   1    0.2171  4.89    5    0.4292 -5.11
##  age               2.86   1    0.0905  7.76    6    0.2565 -4.24
##  test_result       3.81   1    0.0511 11.56    7    0.1159 -2.44
##
## Approximate Estimates after Deleting Factors
##
```

```
##              Coef   S.E. Wald Z        P
## Intercept   -1.778 0.3329 -5.340 9.303e-08
## total_score  1.296 0.2034  6.372 1.862e-10
##
## Factors in Final Model
##
## [1] total_score
```

```
##           index.orig training   test optimism index.corrected   n
## Dxy           0.3501   0.3864 0.3545   0.0320          0.3182 100
## R2            0.1366   0.1666 0.1396   0.0270          0.1096 100
## Intercept     0.0000   0.0000 0.0298  -0.0298          0.0298 100
## Slope         1.0000   1.0000 0.9006   0.0994          0.9006 100
## Emax          0.0000   0.0000 0.0282   0.0282          0.0282 100
## D             0.1050   0.1306 0.1076   0.0230          0.0820 100
## U            -0.0039  -0.0039 0.0015  -0.0054          0.0015 100
## Q             0.1089   0.1345 0.1061   0.0284          0.0805 100
## B             0.2193   0.2141 0.2201  -0.0060          0.2253 100
## g             0.8313   0.9476 0.8422   0.1054          0.7260 100
## gp            0.1748   0.1946 0.1784   0.0161          0.1587 100
##
## Factors Retained in Backwards Elimination
##
##  age sex test_result total_score educational_level employment
##  *       *           *
##                      *           *
##                      *
##          *           *
##  *   *   *           *           *                 *
##                      *
##                      *
##          *           *
##  *   *   *           *           *
##  *       *           *           *
##                      *
##                      *
##                      *
##                      *
##                      *
##          *           *
##  *   *   *           *           *
##                      *
##          *           *           *                 *
##          *           *
##                      *
##          *           *
##          *           *
##                      *
##                      *
##      *               *           *
##                      *
##          *           *                             *
##  *                   *           *
##          *           *
```

```
##  *       *           *
##          *           *                              *
##  *       *           *
##  *                   *           *
##  *   *   *           *
##          *           *           *                  *
##          *           *
##          *           *
##                      *
##  *       *           *           *
##                      *
##                      *
##  *   *               *           *
##  *   *   *           *
##                      *
##      *               *           *                  *
##  *   *   *           *           *
##  *                   *
##  *       *           *           *
##                      *
##  *   *   *           *           *
##                      *
##  *       *           *           *
##                      *
##  *                   *           *
##                      *
##                      *
##  *       *           *                              *
##          *           *
##  *   *   *           *           *
##                      *
##          *           *
##                      *
##  *                   *
##                      *
##                      *
##                      *
##  *                   *
##                      *
##  *                   *           *
##                      *
##  *   *   *           *
##                      *
##                      *           *                  *
##          *           *
##          *           *           *
##          *           *
##          *           *
##          *           *
##          *           *
##                      *                              *
##          *           *
##                      *           *
##  *   *               *
```

```
##      *               *
##      *               *
##                      *                             *
##                      *
##      *   *           *
##                      *                             *
##  *   *               *           *
##  *   *   *           *
##  *                   *
##  *                   *
##  *       *           *
##                      *
##      *   *           *           *
##                      *
##          *           *
##          *           *
##
## Frequencies of Numbers of Factors Retained
##
##  1  2  3  4  5  6
## 33 31 15 15  5  1
```

Using LASSO

LASSO is a regression method that performs both variable selection and regularization in order to enhance the prediction accuracy and interpretability of the statistical model it produces.

The process involves performing a 10-fold cross validation to find the optimal *lambda* (penalization parameter). And then running the analysis and extracting the model based on the best lambda.

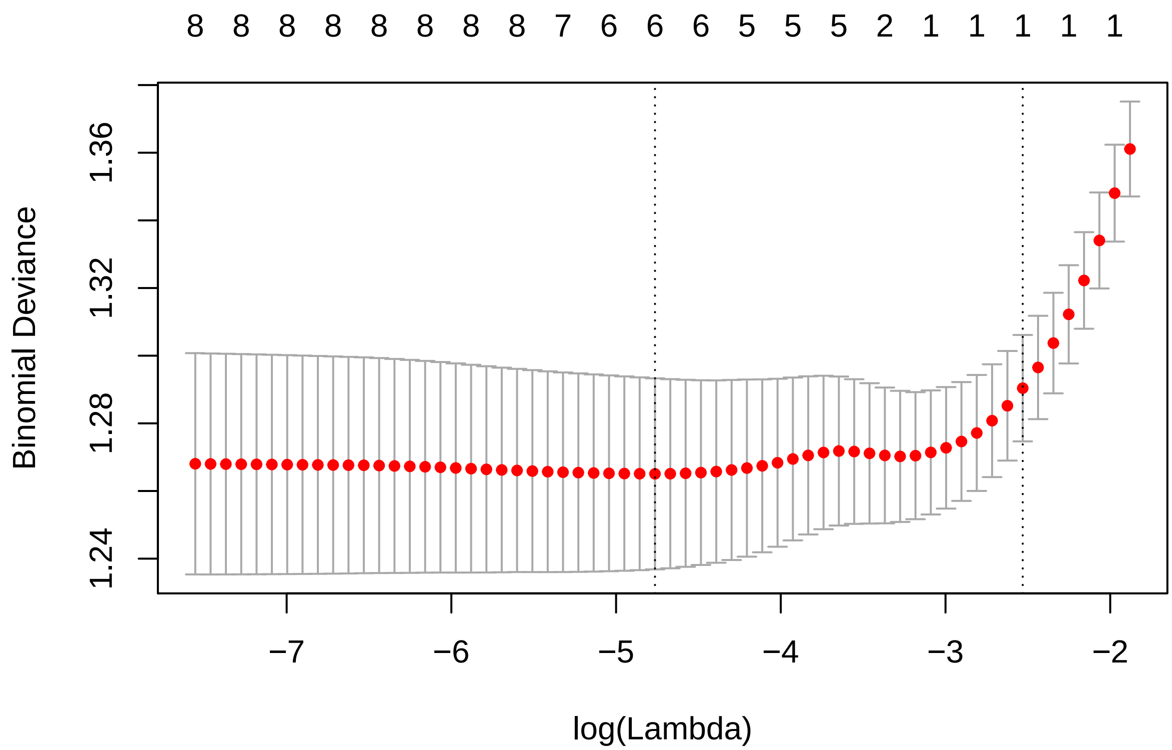
- *lambda.min* is the value of lambda that gives minimum mean cross-validated error.
- *lambda.1se*, is the value of lambda that gives the most regularized model such that error is within one standard error of the minimum

Generate a model matrix

```
# Extract complete cases
complete2 <- data %>%
    filter(complete.cases(.))

# Dependent variable
y <- ifelse(complete2$pain == 'yes', yes = 1, no = 0)

# Predictor variables
## Factor variables
xfactor <- model.matrix(complete2$pain ~ complete2$test_result + complete2$sex +
                            complete2$educational_level + complete2$employment)[, -1]

## Combine with continuous variables
x <- as.matrix(data.frame(complete2$age, complete2$total_score, xfactor))
```

Find the best minimum and 1SE lambda value using cross-validation

```
# Set seed
set.seed(2019)

# Calculate lambda (alpha = 1, lasso)
cv.lasso <- cv.glmnet(x = x, y = y,
                      nfolds = 10,
                      alpha = 1,
                      family = "binomial")

# Plot
plot(cv.lasso)
```



Lambda values

Lambda min

```
cv.lasso$lambda.min
```

```
## [1] 0.008532659
```

Lambda 1se

```
cv.lasso$lambda.1se
```

```
## [1] 0.07957586
```

Inspect the model coefficients

Lambda min

```r
# Betas
coef(cv.lasso, s = "lambda.min")
```

```
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                                             1
## (Intercept)                       -2.04768463
## complete2.age                      0.01313481
## complete2.total_score              1.24556316
## complete2.test_resultHIV.positive -0.45009074
## complete2.sexmale                 -0.16187709
## complete2.educational_level.L      0.23690209
## complete2.educational_level.Q      0.02224888
## complete2.employmentemployed       .
## complete2.employmentunemployed     .
```

```r
# OR
exp(coef(cv.lasso, s = "lambda.min"))
```

```
## 9 x 1 Matrix of class "dgeMatrix"
##                                           1
## (Intercept)                       0.1290333
## complete2.age                     1.0132215
## complete2.total_score             3.4748912
## complete2.test_resultHIV.positive 0.6375703
## complete2.sexmale                 0.8505457
## complete2.educational_level.L     1.2673170
## complete2.educational_level.Q     1.0224982
## complete2.employmentemployed      1.0000000
## complete2.employmentunemployed    1.0000000
```

Lambda 1se

```r
# Betas
coef(cv.lasso, s = "lambda.1se")
```

```
## 9 x 1 sparse Matrix of class "dgCMatrix"
##                                            1
## (Intercept)                       -0.5727692
## complete2.age                      .
## complete2.total_score              0.5481293
## complete2.test_resultHIV.positive  .
## complete2.sexmale                  .
## complete2.educational_level.L      .
## complete2.educational_level.Q      .
## complete2.employmentemployed       .
## complete2.employmentunemployed     .
```

```r
# OR
exp(coef(cv.lasso, s = "lambda.1se"))
```

```
## 9 x 1 Matrix of class "dgeMatrix"
##                                           1
## (Intercept)                       0.5639615
```

```
## complete2.age                         1.0000000
## complete2.total_score                 1.7300136
## complete2.test_resultHIV.positive 1.0000000
## complete2.sexmale                     1.0000000
## complete2.educational_level.L         1.0000000
## complete2.educational_level.Q         1.0000000
## complete2.employmentemployed          1.0000000
## complete2.employmentunemployed        1.0000000
```

Publication plot

```
composite_plot <- pp_hscl + pp_sex + pp_age + pp_hiv + pp_edu + pp_emp +
    plot_layout(ncol = 2, nrow = 3)

ggsave(filename = 'figures/supp-figure-original.png',
       plot = composite_plot,
       height = 10,
       width = 8)
```

Session information

```
sessionInfo()
```

```
## R version 3.6.0 (2019-04-26)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] rms_5.1-3.1           SparseM_1.77
##  [3] Hmisc_4.2-0           Formula_1.2-3
##  [5] survival_2.44-1.1     lattice_0.20-38
##  [7] patchwork_0.0.1       ResourceSelection_0.3-5
##  [9] glmnet_2.0-18         foreach_1.4.7
## [11] Matrix_1.2-17         sjPlot_2.7.0
## [13] car_3.0-3             carData_3.0-2
## [15] rcompanion_2.2.2      DataExplorer_0.8.0
## [17] magrittr_1.5          forcats_0.4.0
## [19] stringr_1.4.0         dplyr_0.8.3
```

```
## [21] purrr_0.3.2            readr_1.3.1
## [23] tidyr_0.8.99.9000      tibble_2.1.3
## [25] ggplot2_3.2.1          tidyverse_1.2.1
##
## loaded via a namespace (and not attached):
##   [1] readxl_1.3.1        backports_1.1.4     plyr_1.8.4
##   [4] igraph_1.2.4.1      lazyeval_0.2.2      TMB_1.7.15
##   [7] splines_3.6.0       TH.data_1.0-10      digest_0.6.20
##  [10] htmltools_0.3.6     fansi_0.4.0         checkmate_1.9.4
##  [13] cluster_2.1.0       openxlsx_4.1.0.1    modelr_0.1.5
##  [16] matrixStats_0.54.0  sandwich_2.5-1      colorspace_1.4-1
##  [19] rvest_0.3.4         ggrepel_0.8.1       haven_2.1.1
##  [22] xfun_0.8            crayon_1.3.4        jsonlite_1.6
##  [25] libcoin_1.0-4       lme4_1.1-21         zeallot_0.1.0
##  [28] zoo_1.8-6           iterators_1.0.12    glue_1.3.1
##  [31] gtable_0.3.0        emmeans_1.4         MatrixModels_0.4-1
##  [34] sjstats_0.17.5      sjmisc_2.8.1        abind_1.4-5
##  [37] scales_1.0.0        mvtnorm_1.0-11      ggeffects_0.11.0
##  [40] Rcpp_1.0.2          xtable_1.8-4        performance_0.3.0
##  [43] htmlTable_1.13.1    foreign_0.8-72      stats4_3.6.0
##  [46] htmlwidgets_1.3     httr_1.4.1          RColorBrewer_1.1-2
##  [49] acepack_1.4.1       modeltools_0.2-22   pkgconfig_2.0.2
##  [52] manipulate_1.0.1    nnet_7.3-12         multcompView_0.1-7
##  [55] utf8_1.1.4          labeling_0.3        tidyselect_0.2.5
##  [58] rlang_0.4.0         munsell_0.5.0       cellranger_1.1.0
##  [61] tools_3.6.0         cli_1.1.0           generics_0.0.2
##  [64] sjlabelled_1.1.0    broom_0.5.2         evaluate_0.14
##  [67] EMT_1.1             yaml_2.2.0          knitr_1.24
##  [70] zip_2.0.3           coin_1.3-0          nlme_3.1-141
##  [73] quantreg_5.51       xml2_1.2.2          compiler_3.6.0
##  [76] rstudioapi_0.10     curl_4.0            DescTools_0.99.28
##  [79] stringi_1.4.3       psych_1.8.12        nloptr_1.2.1
##  [82] vctrs_0.2.0         pillar_1.4.2        lifecycle_0.1.0
##  [85] networkD3_0.4       lmtest_0.9-37       estimability_1.3
##  [88] data.table_1.12.2   insight_0.4.1       R6_2.4.0
##  [91] latticeExtra_0.6-28 gridExtra_2.3       rio_0.5.16
##  [94] codetools_0.2-16    polspline_1.1.15    boot_1.3-23
##  [97] MASS_7.3-51.4       assertthat_0.2.1    withr_2.1.2.9000
## [100] nortest_1.0-4       mnormt_1.5-5        multcomp_1.4-10
## [103] bayestestR_0.2.5    expm_0.999-4        parallel_3.6.0
## [106] hms_0.5.0           grid_3.6.0          rpart_4.1-15
## [109] coda_0.19-3         glmmTMB_0.2.3       minqa_1.2.4
## [112] snakecase_0.11.0    rmarkdown_1.14      lubridate_1.7.4
## [115] base64enc_0.1-3
```