```r
library(tidyverse)   # Data manipulation
```

```
## Warning: package 'tidyverse' was built under R version 4.4.3

## Warning: package 'readr' was built under R version 4.4.3

## Warning: package 'dplyr' was built under R version 4.4.3

## Warning: package 'forcats' was built under R version 4.4.3

## -- 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 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- 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(brms)        # Bayesian regression modeling
```

```
## Warning: package 'brms' was built under R version 4.4.3

## Loading required package: Rcpp
## Loading 'brms' package (version 2.22.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').
##
## Attaching package: 'brms'
##
## The following object is masked from 'package:stats':
##
##     ar
```

```r
library(bayesplot)   # MCMC diagnostics and posterior visualization
```

```
## Warning: package 'bayesplot' was built under R version 4.4.3

## This is bayesplot version 1.11.1
## - Online documentation and vignettes at mc-stan.org/bayesplot
## - bayesplot theme set to bayesplot::theme_default()
##    * Does _not_ affect other ggplot2 plots
##    * See ?bayesplot_theme_set for details on theme setting
##
## Attaching package: 'bayesplot'
##
## The following object is masked from 'package:brms':
##
##     rhat
```

```
library(ggplot2)
```

```
# Read the dataset from the CSV file
data <- read_csv("C:/Users/Sourav/Downloads/diabetes_data_upload.csv")
```

```
## Rows: 520 Columns: 17
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (16): Gender, Polyuria, Polydipsia, sudden weight loss, weakness, Polyph...
## dbl  (1): Age
##
## 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.
```

```
# Inspect the data
print(head(data))        # View the first few rows
```

```
## # A tibble: 6 x 17
##     Age Gender Polyuria Polydipsia ‘sudden weight loss‘ weakness Polyphagia
##   <dbl> <chr>  <chr>    <chr>      <chr>                <chr>    <chr>
## 1    40 Male   No       Yes        No                   Yes      No
## 2    58 Male   No       No         No                   Yes      No
## 3    41 Male   Yes      No         No                   Yes      Yes
## 4    45 Male   No       No         Yes                  Yes      Yes
## 5    60 Male   Yes      Yes        Yes                  Yes      Yes
## 6    55 Male   Yes      Yes        No                   Yes      Yes
## # i 10 more variables: ‘Genital thrush‘ <chr>, ‘visual blurring‘ <chr>,
## #   Itching <chr>, Irritability <chr>, ‘delayed healing‘ <chr>,
## #   ‘partial paresis‘ <chr>, ‘muscle stiffness‘ <chr>, Alopecia <chr>,
## #   Obesity <chr>, class <chr>
```

```
str(data)                # Check the structure of the data
```

```
## spc_tbl_ [520 x 17] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ Age               : num [1:520] 40 58 41 45 60 55 57 66 67 70 ...
##  $ Gender            : chr [1:520] "Male" "Male" "Male" "Male" ...
##  $ Polyuria          : chr [1:520] "No" "No" "Yes" "No" ...
##  $ Polydipsia        : chr [1:520] "Yes" "No" "No" "No" ...
##  $ sudden weight loss: chr [1:520] "No" "No" "No" "Yes" ...
##  $ weakness          : chr [1:520] "Yes" "Yes" "Yes" "Yes" ...
##  $ Polyphagia        : chr [1:520] "No" "No" "Yes" "Yes" ...
##  $ Genital thrush    : chr [1:520] "No" "No" "No" "Yes" ...
##  $ visual blurring   : chr [1:520] "No" "Yes" "No" "No" ...
##  $ Itching           : chr [1:520] "Yes" "No" "Yes" "Yes" ...
##  $ Irritability      : chr [1:520] "No" "No" "No" "No" ...
##  $ delayed healing   : chr [1:520] "Yes" "No" "Yes" "Yes" ...
##  $ partial paresis   : chr [1:520] "No" "Yes" "No" "No" ...
##  $ muscle stiffness  : chr [1:520] "Yes" "No" "Yes" "No" ...
##  $ Alopecia          : chr [1:520] "Yes" "Yes" "Yes" "No" ...
##  $ Obesity           : chr [1:520] "Yes" "No" "No" "No" ...
##  $ class             : chr [1:520] "Positive" "Positive" "Positive" "Positive" ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   Age = col_double(),
##   ..   Gender = col_character(),
##   ..   Polyuria = col_character(),
##   ..   Polydipsia = col_character(),
##   ..   ‘sudden weight loss‘ = col_character(),
##   ..   weakness = col_character(),
##   ..   Polyphagia = col_character(),
##   ..   ‘Genital thrush‘ = col_character(),
##   ..   ‘visual blurring‘ = col_character(),
##   ..   Itching = col_character(),
##   ..   Irritability = col_character(),
##   ..   ‘delayed healing‘ = col_character(),
##   ..   ‘partial paresis‘ = col_character(),
##   ..   ‘muscle stiffness‘ = col_character(),
##   ..   Alopecia = col_character(),
##   ..   Obesity = col_character(),
##   ..   class = col_character()
##   .. )
##  - attr(*, "problems")=<externalptr>
```

```
summary(data)            # Get summary statistics
```

```
##       Age           Gender            Polyuria          Polydipsia
##  Min.   :16.00   Length:520         Length:520         Length:520
##  1st Qu.:39.00   Class :character   Class :character   Class :character
##  Median :47.50   Mode  :character   Mode  :character   Mode  :character
##  Mean   :48.03
##  3rd Qu.:57.00
##  Max.   :90.00
##  sudden weight loss   weakness           Polyphagia        Genital thrush
##  Length:520         Length:520         Length:520         Length:520
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##  visual blurring      Itching          Irritability       delayed healing
##  Length:520         Length:520         Length:520         Length:520
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##  partial paresis    muscle stiffness     Alopecia            Obesity
##  Length:520         Length:520         Length:520         Length:520
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##     class
##  Length:520
##  Class :character
##  Mode  :character
##
##
##
```

```r
# Check for missing values
missing_vals <- sapply(data, function(x) sum(is.na(x)))
missing_vals
```

```
##                Age             Gender           Polyuria         Polydipsia
##                  0                  0                  0                  0
## sudden weight loss           weakness         Polyphagia     Genital thrush
##                  0                  0                  0                  0
##    visual blurring            Itching       Irritability    delayed healing
##                  0                  0                  0                  0
##    partial paresis   muscle stiffness           Alopecia            Obesity
##                  0                  0                  0                  0
##              class
##                  0
```

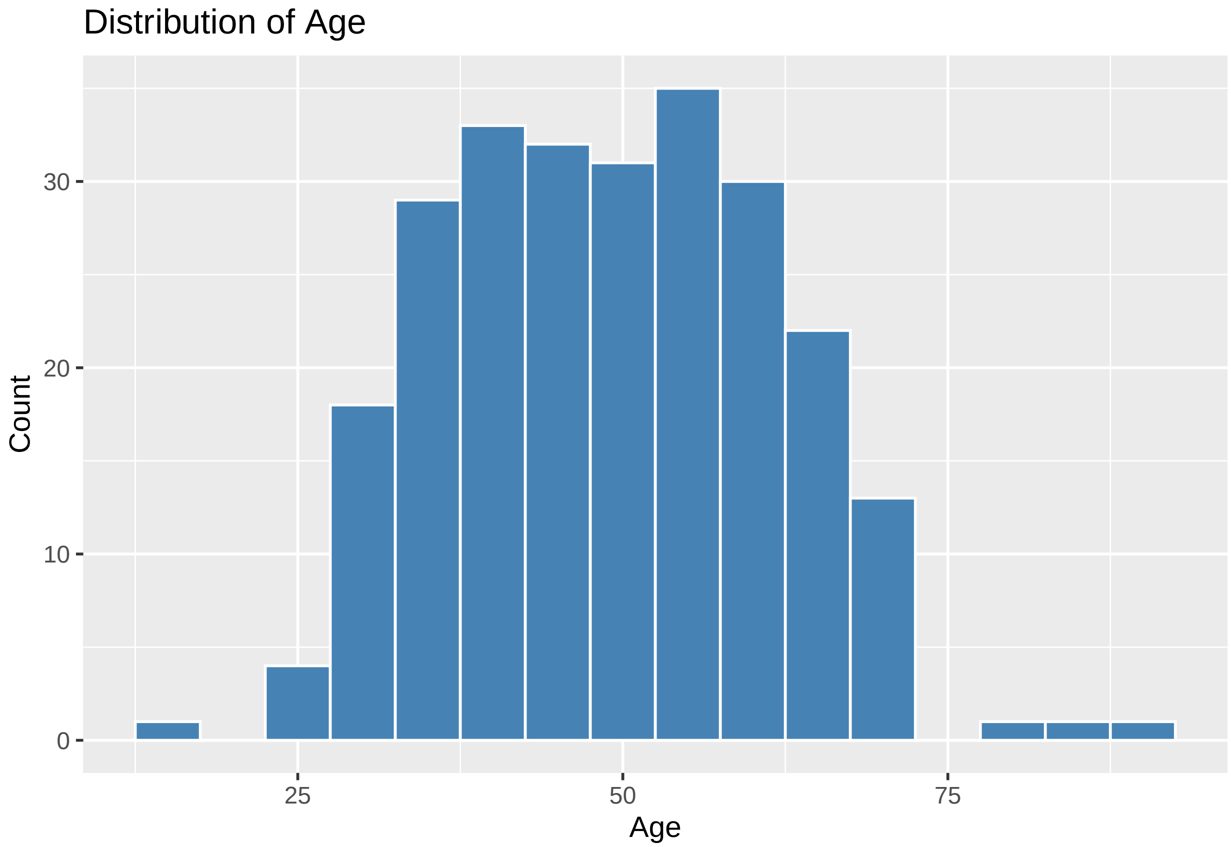
```r
# Remove duplicate rows
data <- distinct(data)

# Convert "Yes"/"No" columns to 1/0
# Identify the columns that contain Yes/No responses
yes_no_cols <- c(
  "Polyuria", "Polydipsia", "sudden weight loss", "weakness", "Polyphagia",
  "Genital thrush", "visual blurring", "Itching", "Irritability",
  "delayed healing", "partial paresis", "muscle stiffness",
  "Alopecia", "Obesity"
)

# Convert Yes -> 1, No -> 0
data[yes_no_cols] <- lapply(data[yes_no_cols], function(col) {
  ifelse(col == "Yes", 1, 0)
})

# Convert "Positive"/"Negative" in 'class' column to 1/0
data$class <- ifelse(data$class == "Positive", 1, 0)

# Inspect the transformed data
head(data)
```

```
## # A tibble: 6 x 17
##     Age Gender Polyuria Polydipsia ‘sudden weight loss‘ weakness Polyphagia
##   <dbl> <chr>     <dbl>      <dbl>                <dbl>    <dbl>      <dbl>
## 1    40 Male          0          1                    0        1          0
## 2    58 Male          0          0                    0        1          0
## 3    41 Male          1          0                    0        1          1
## 4    45 Male          0          0                    1        1          1
## 5    60 Male          1          1                    1        1          1
## 6    55 Male          1          1                    0        1          1
## # i 10 more variables: ‘Genital thrush‘ <dbl>, ‘visual blurring‘ <dbl>,
## #   Itching <dbl>, Irritability <dbl>, ‘delayed healing‘ <dbl>,
## #   ‘partial paresis‘ <dbl>, ‘muscle stiffness‘ <dbl>, Alopecia <dbl>,
## #   Obesity <dbl>, class <dbl>
```

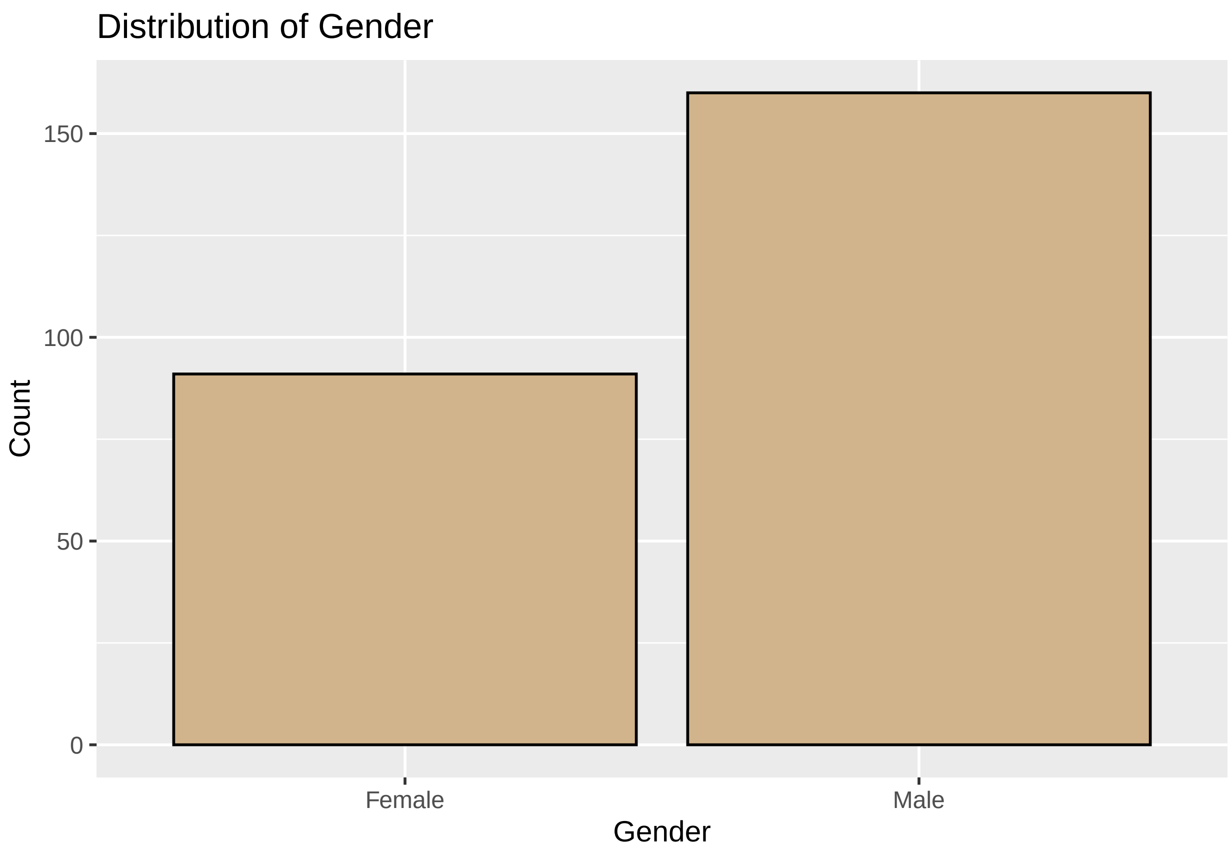
```
str(data)
```

```
## tibble [251 x 17] (S3: tbl_df/tbl/data.frame)
##  $ Age               : num [1:251] 40 58 41 45 60 55 57 66 67 70 ...
##  $ Gender            : chr [1:251] "Male" "Male" "Male" "Male" ...
##  $ Polyuria          : num [1:251] 0 0 1 0 1 1 1 1 1 0 ...
##  $ Polydipsia        : num [1:251] 1 0 0 0 1 1 1 1 1 1 ...
##  $ sudden weight loss: num [1:251] 0 0 0 1 1 0 0 1 0 1 ...
##  $ weakness          : num [1:251] 1 1 1 1 1 1 1 1 1 1 ...
##  $ Polyphagia        : num [1:251] 0 0 1 1 1 1 1 0 1 1 ...
##  $ Genital thrush    : num [1:251] 0 0 0 1 0 0 1 0 1 0 ...
##  $ visual blurring   : num [1:251] 0 1 0 0 1 1 0 1 0 1 ...
##  $ Itching           : num [1:251] 1 0 1 1 1 1 0 1 1 1 ...
##  $ Irritability      : num [1:251] 0 0 0 0 1 0 0 1 1 1 ...
##  $ delayed healing   : num [1:251] 1 0 1 1 1 1 1 0 0 0 ...
##  $ partial paresis   : num [1:251] 0 1 0 0 1 0 1 1 1 0 ...
##  $ muscle stiffness  : num [1:251] 1 0 1 0 1 1 0 1 1 0 ...
##  $ Alopecia          : num [1:251] 1 1 1 0 1 1 0 0 0 1 ...
##  $ Obesity           : num [1:251] 1 0 0 0 1 1 0 0 1 0 ...
##  $ class             : num [1:251] 1 1 1 1 1 1 1 1 1 1 ...
```

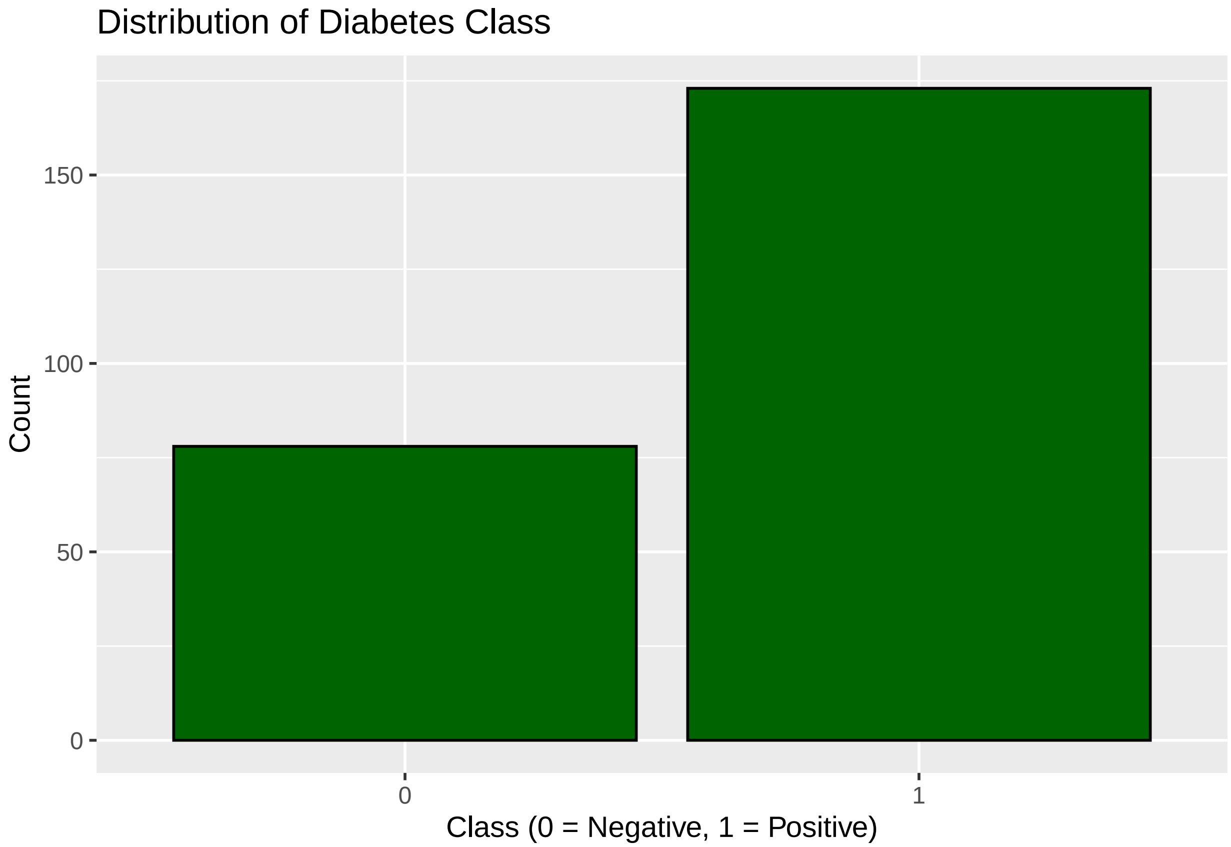
```
# Histogram of Age
ggplot(data, aes(x = Age)) +
  geom_histogram(binwidth = 5, fill = "steelblue", color = "white") +
  labs(title = "Distribution of Age", x = "Age", y = "Count")
```



```
# Bar plot of Gender (if still categorical)
# If you converted Gender to 1/0, you can factor it first or skip this step
ggplot(data, aes(x = Gender)) +
  geom_bar(fill = "tan", color = "black") +
  labs(title = "Distribution of Gender", x = "Gender", y = "Count")
```



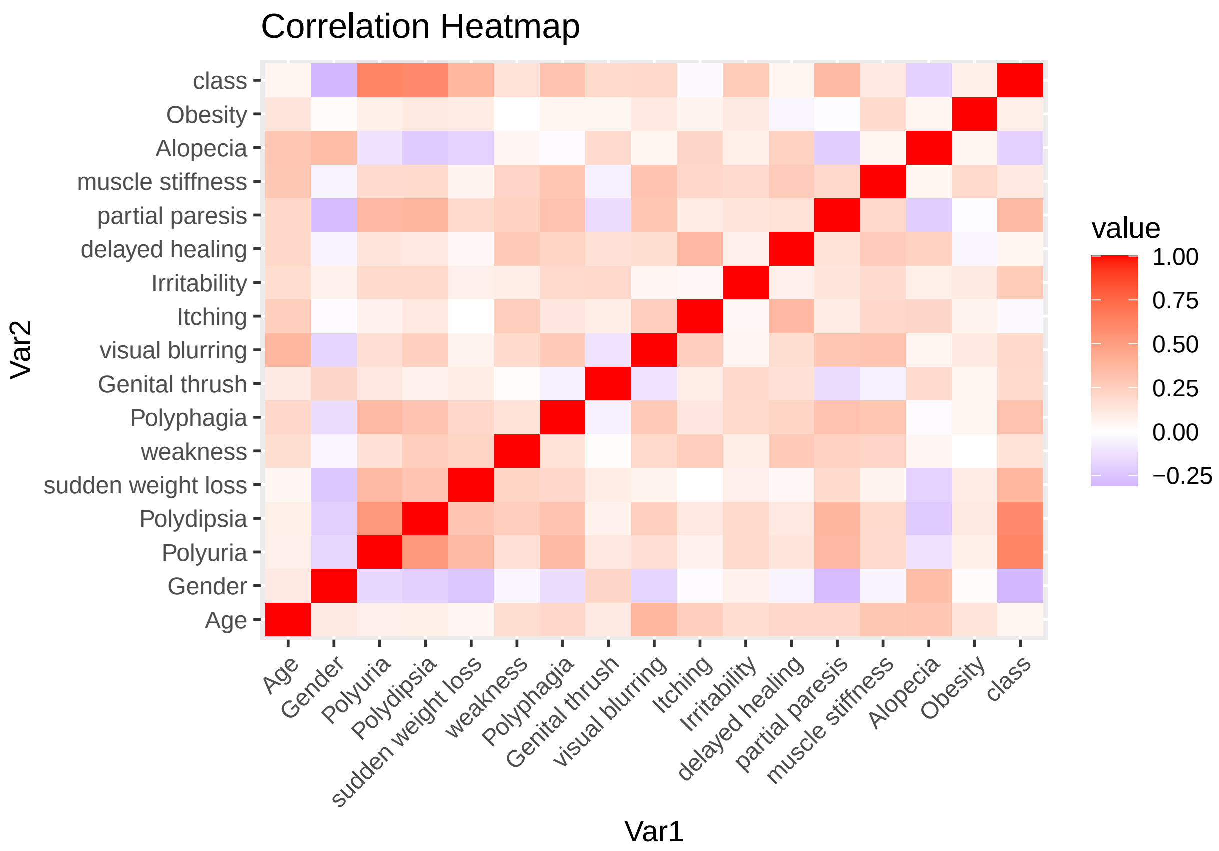
```r
# Bar plot of 'class' (after conversion to 1/0)
ggplot(data, aes(x = factor(class))) +
  geom_bar(fill = "darkgreen", color = "black") +
  labs(title = "Distribution of Diabetes Class", x = "Class (0 = Negative, 1 = Positive)", y = "Count")
```



```r
# Correlation Heatmap (Optional)
# For correlation, all columns must be numeric.
# If Gender is still categorical (M/F), convert it to 1/0 as shown above
numeric_data <- data %>%
  mutate(Gender = ifelse(Gender == "Male" | Gender == 1, 1, 0))  # ensure numeric
# Calculate correlation matrix
corr_mat <- cor(numeric_data)
# Melt the correlation matrix for ggplot
library(reshape2)
```

```
##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
##     smiths
```

```r
melted_corr <- melt(corr_mat)
# Plot heatmap
ggplot(melted_corr, aes(x = Var1, y = Var2, fill = value)) +
  geom_tile() +
  scale_fill_gradient2(low = "blue", mid = "white", high = "red", midpoint = 0) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  labs(title = "Correlation Heatmap")
```



```r
data <- data %>%
  rename(
    sudden_weight_loss = `sudden weight loss`,
    Genital_thrush = `Genital thrush`,
    visual_blurring = `visual blurring`,
    delayed_healing = `delayed healing`,
    partial_paresis = `partial paresis`,
    muscle_stiffness = `muscle stiffness`
  )

# -------------------------------------------------------------
# 1. Check Factor Levels
# -------------------------------------------------------------
table(data$class)
```

```
##
##   0   1
##  78 173
```

```r
# -------------------------------------------------------------
# 2. Define Priors
# -------------------------------------------------------------
my_priors <- c(
  set_prior("normal(0, 1)", class = "b"),          # Prior for coefficients
  set_prior("normal(0, 2.5)", class = "Intercept")  # Prior for intercept
)

# ------------------------------------------------------------
# 3. Fit the Bayesian Logit Regression Model
# ------------------------------------------------------------
fit_logit <- brm(
  formula = class ~ Age + Polyuria + Polydipsia + sudden_weight_loss + weakness + Polyphagia +
            Genital_thrush + visual_blurring + Itching + Irritability +
            delayed_healing + partial_paresis + muscle_stiffness +
            Alopecia + Obesity,
  data    = data,
  family  = bernoulli(link = "logit"),  # Logit regression for binary classification
  prior   = my_priors,
  chains  = 4,      # Number of Markov Chains
  iter    = 2000,   # Total iterations per chain
  warmup  = 1000,   # Warm-up iterations (burn-in)
  cores   = 4,      # Parallel computation
  seed    = 1234    # Ensure reproducibility
)
```

```
## Compiling Stan program...
```

```
## Start sampling
```

```
# ------------------------------------------------------------
# 4. Model Summary and Posterior Estimates
# ------------------------------------------------------------
summary(fit_logit)       # Print model summary
```

```
##  Family: bernoulli
##   Links: mu = logit
## Formula: class ~ Age + Polyuria + Polydipsia + sudden_weight_loss + weakness + Polyphagia + Genital_
##    Data: data (Number of observations: 251)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Regression Coefficients:
##                      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept               -0.80      0.90    -2.56     0.96 1.00     4519     3230
## Age                     -0.02      0.02    -0.06     0.02 1.00     4462     3211
## Polyuria                 2.26      0.49     1.33     3.27 1.00     4302     2899
## Polydipsia               2.35      0.51     1.37     3.35 1.00     4271     3176
## sudden_weight_loss       0.92      0.45     0.06     1.78 1.00     4706     3347
## weakness                 0.16      0.43    -0.69     1.00 1.00     4651     3021
## Polyphagia               0.69      0.45    -0.18     1.59 1.00     5292     3586
## Genital_thrush           1.19      0.50     0.22     2.18 1.00     4550     2884
## visual_blurring          0.83      0.50    -0.12     1.80 1.00     4265     2384
## Itching                 -0.89      0.47    -1.83     0.04 1.00     4175     2882
## Irritability             0.96      0.48     0.00     1.89 1.00     4956     3280
## delayed_healing         -0.34      0.48    -1.31     0.60 1.00     4897     3563
## partial_paresis          0.91      0.46     0.02     1.86 1.00     4927     3054
## muscle_stiffness        -0.36      0.48    -1.29     0.58 1.00     4539     2988
## Alopecia              -0.44      0.48     -1.40     0.50 1.00     4459     3040
## Obesity                0.16      0.51     -0.87     1.18 1.00     5473     2868
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```r
prior_summary(fit_logit) # Show priors used
```

```
##           prior     class                coef group resp dpar nlpar lb ub
##    normal(0, 1)         b
##    normal(0, 1)         b                 Age
##    normal(0, 1)         b            Alopecia
##    normal(0, 1)         b     delayed_healing
##    normal(0, 1)         b      Genital_thrush
##    normal(0, 1)         b        Irritability
##    normal(0, 1)         b             Itching
##    normal(0, 1)         b    muscle_stiffness
##    normal(0, 1)         b             Obesity
##    normal(0, 1)         b     partial_paresis
##    normal(0, 1)         b          Polydipsia
##    normal(0, 1)         b          Polyphagia
##    normal(0, 1)         b            Polyuria
##    normal(0, 1)         b  sudden_weight_loss
##    normal(0, 1)         b     visual_blurring
##    normal(0, 1)         b            weakness
##  normal(0, 2.5) Intercept
##        source
##          user
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##          user
```

```r
# Get fixed effects estimates (population-level effects)
fixef(fit_logit)
```

```
##                        Estimate  Est.Error         Q2.5      Q97.5
## Intercept          -0.80120297 0.89545487 -2.564210370 0.95997235
## Age                -0.01642244 0.02109202 -0.058675101 0.02391545
## Polyuria            2.26495381 0.49294825  1.332048575 3.27174866
## Polydipsia          2.35170517 0.50585099  1.369643000 3.35451904
## sudden_weight_loss  0.92497261 0.44542445  0.064998216 1.77874968
## weakness            0.16231782 0.42734848 -0.688729157 1.00453917
## Polyphagia          0.69318103 0.44988928 -0.179697091 1.59018486
## Genital_thrush      1.18862217 0.50333108  0.218080480 2.18152789
## visual_blurring     0.83076547 0.49701372 -0.123645622 1.79556494
## Itching            -0.88889485 0.47448139 -1.834356941 0.04340460
## Irritability        0.95679616 0.48175733  0.003176781 1.89471832
## delayed_healing    -0.34497595 0.48211244 -1.314430574 0.59819604
## partial_paresis     0.91112851 0.45973601  0.024564559 1.85611671
## muscle_stiffness   -0.35516524 0.48215407 -1.291760966 0.58412472
## Alopecia           -0.43707302 0.47684779 -1.401237888 0.49957054
## Obesity             0.15571816 0.51379889 -0.873471147 1.17664204
```

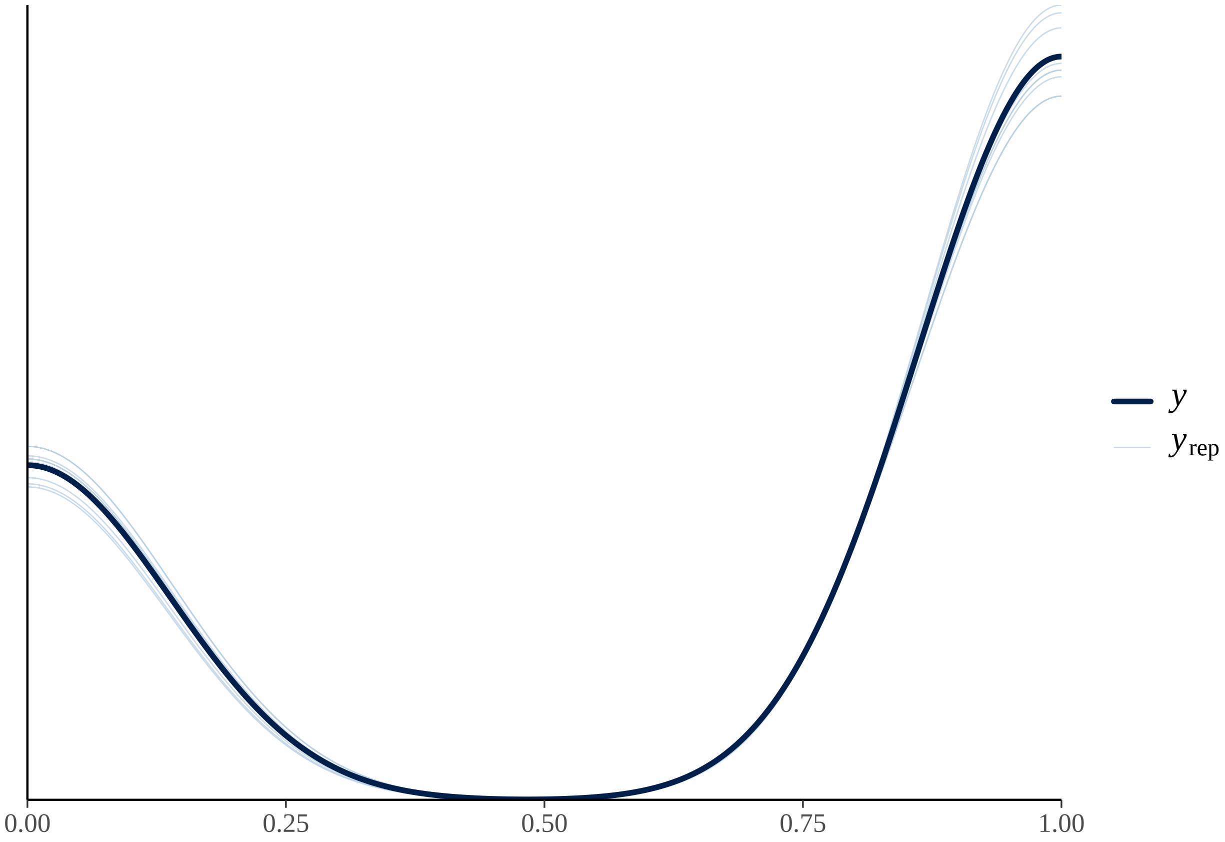
```
# Check the first few posterior samples
head(posterior_samples(fit_logit))
```

```
## Warning: Method 'posterior_samples' is deprecated. Please see ?as_draws for
## recommended alternatives.
```

```
##   b_Intercept        b_Age b_Polyuria b_Polydipsia b_sudden_weight_loss
## 1  -2.7746999  0.016796174   2.560970     2.750409            1.3507200
## 2  -2.4862688  0.013766010   1.787318     3.714879            0.5119741
## 3   0.1325893 -0.030498031   2.114115     2.484075            0.8992447
## 4  -1.9901908 -0.007830156   2.075145     2.446004            1.4587294
## 5  -0.5767134 -0.007190334   1.891896     3.050850            0.2233347
## 6  -0.4943746 -0.015838112   2.145437     1.496714            1.2706095
##   b_weakness b_Polyphagia b_Genital_thrush b_visual_blurring  b_Itching
## 1  0.5686692  0.834398978         1.560081         1.1660117 -1.3920354
## 2  0.4056039  0.703410544         0.782191         0.1179227 -0.7898869
## 3  0.2360142  0.009231634         1.100071         0.3750265 -0.4932310
## 4  0.4631474  0.681767660         1.192488         0.8414611 -0.1256065
## 5 -0.4068958  0.627008340         1.219412         1.0310804 -1.6402234
## 6  0.4799626  0.611965059         1.281859        -0.1543572 -0.9739982
##   b_Irritability b_delayed_healing b_partial_paresis b_muscle_stiffness
## 1      0.4654567        -0.1134112        0.62587769         -0.5345490
## 2      1.1950757        -0.4905190        1.56807624         -0.8861569
## 3      1.2273998        -1.1390334        2.14974964         -0.5872135
## 4      0.4324161        -1.0169647        1.48733989         -0.4318473
## 5      1.4746561         0.2520516        0.04336771         -0.0857685
## 6     -0.2742894        -0.3088282        1.58623345          0.2286505
##    b_Alopecia b_Obesity Intercept    lprior     lp__
## 1 -1.32382152 1.2147389  2.172209 -29.41375 -95.86537
## 2  0.10179489 0.1188474  2.124626 -28.03220 -97.00803
## 3 -0.03457183 0.6057120  2.321360 -26.66930 -96.61435
## 4 -0.09597170 0.5750732  1.946688 -25.52352 -93.32933
## 5 -0.69165060 0.2145607  1.970815 -26.68394 -95.20039
## 6 -0.47091246 0.1062595  1.911711 -23.23686 -96.08259
```

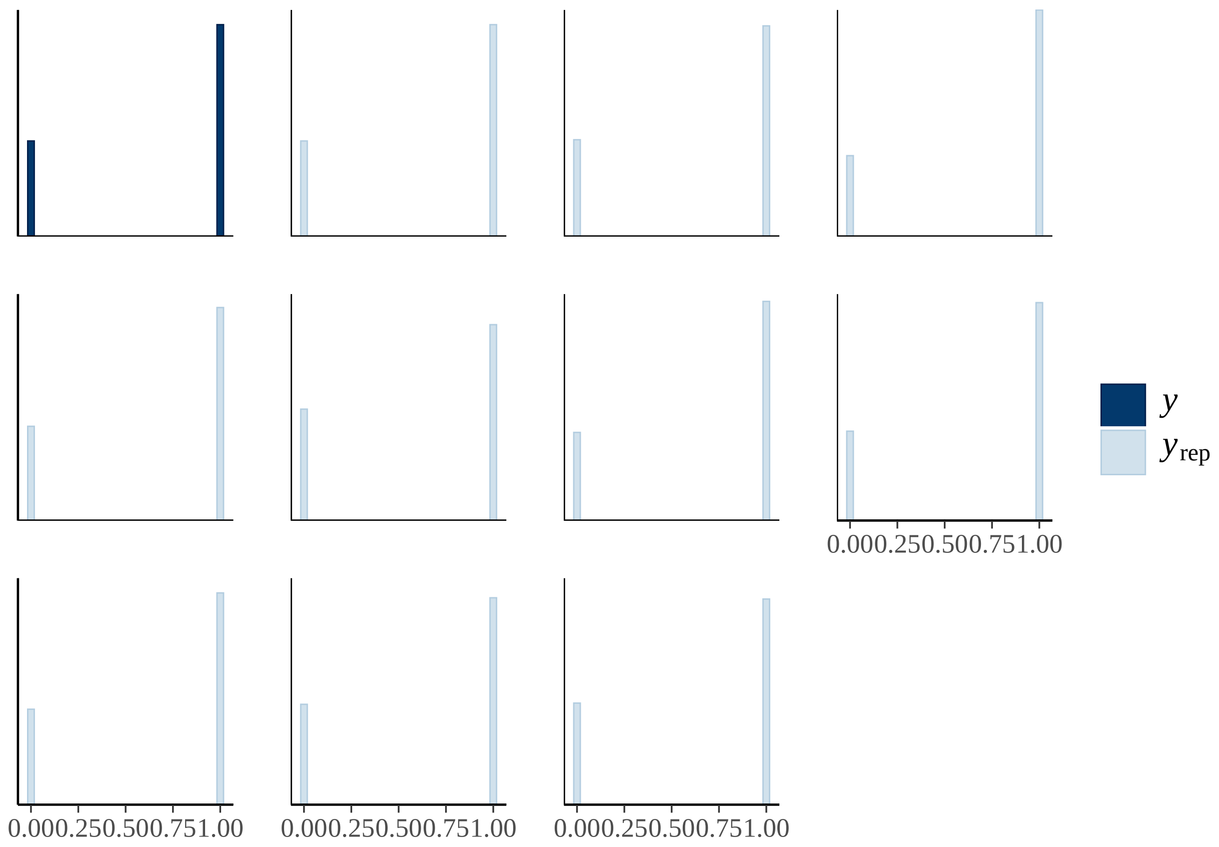
```
# -------------------------------------------------------------
# 5. Posterior Predictive Checks (Model Diagnostics)
# -------------------------------------------------------------
# Density overlay of observed vs predicted values
pp_check(fit_logit, type = "dens_overlay")
```

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



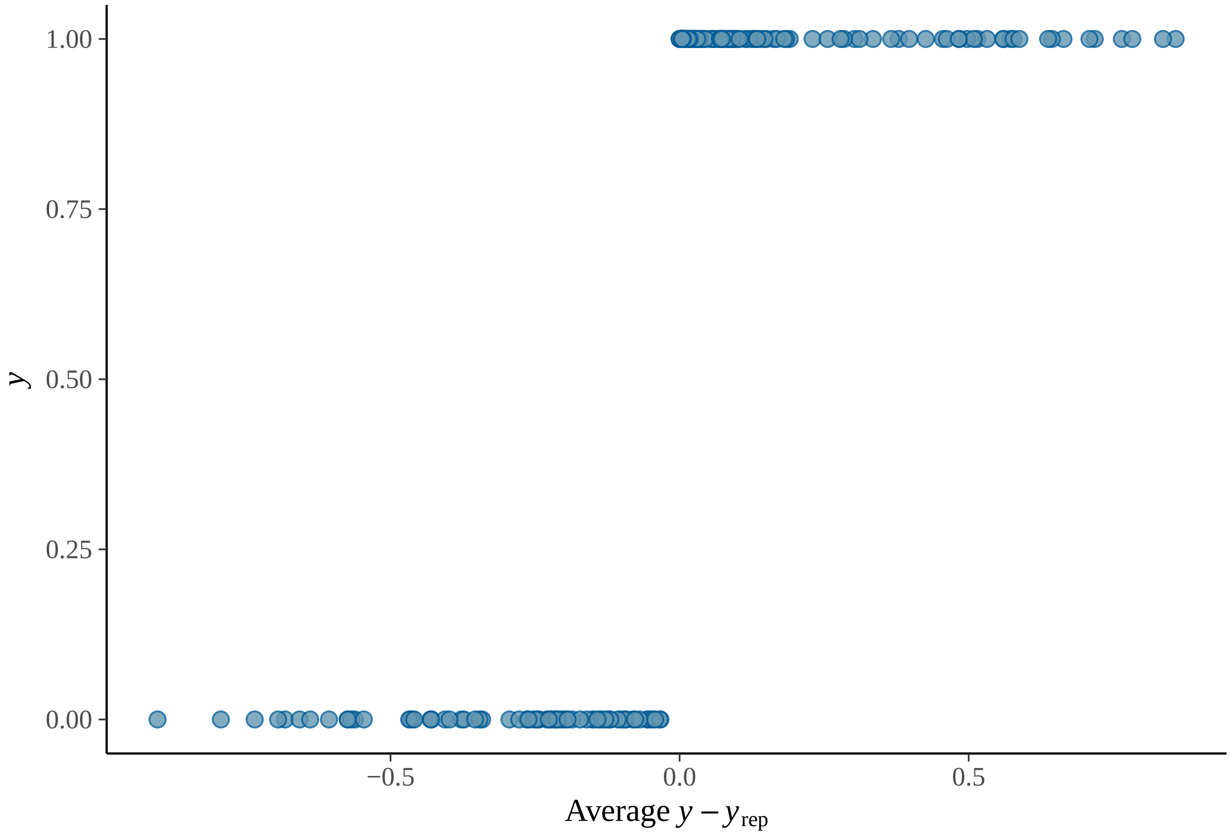
```
# Histogram of simulated posterior predictions
pp_check(fit_logit, type = "hist")
```

```
## Using 10 posterior draws for ppc type 'hist' by default.

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
pp_check(fit_logit, type = "error_scatter_avg")
```

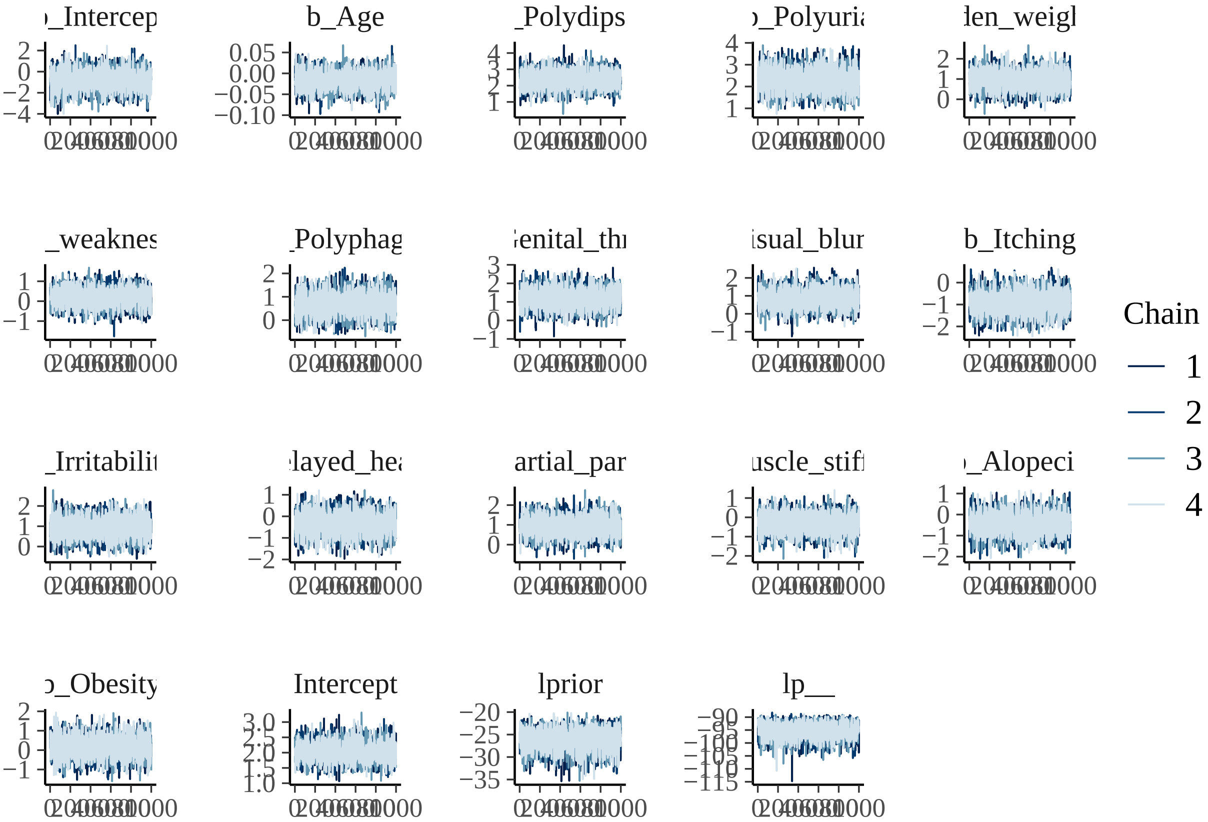
```
## Using all posterior draws for ppc type 'error_scatter_avg' by default.
```



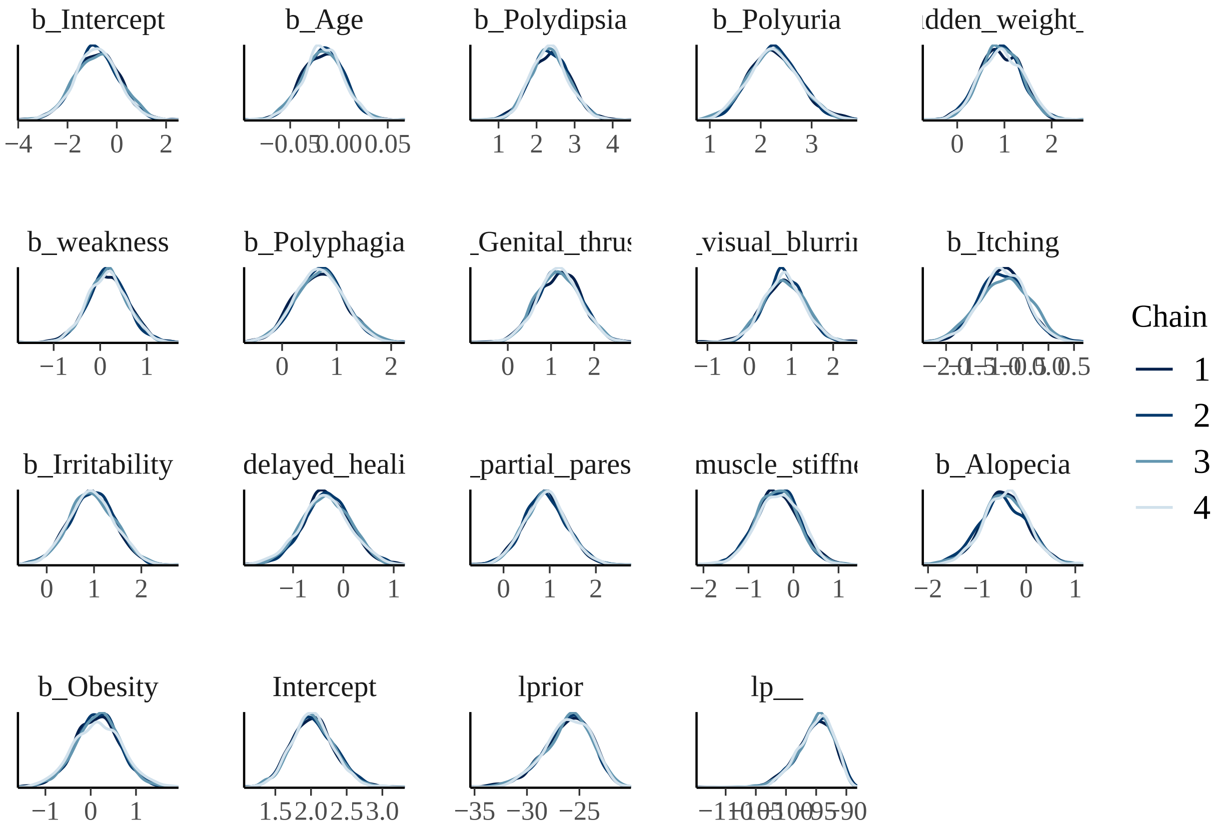
```r
# Check if chains have converged (Trace Plots)
# Get all parameter names in the model
variables(as_draws(fit_logit))
```

```
##  [1] "b_Intercept"          "b_Age"                "b_Polyuria"
##  [4] "b_Polydipsia"         "b_sudden_weight_loss" "b_weakness"
##  [7] "b_Polyphagia"         "b_Genital_thrush"     "b_visual_blurring"
## [10] "b_Itching"            "b_Irritability"       "b_delayed_healing"
## [13] "b_partial_paresis"    "b_muscle_stiffness"   "b_Alopecia"
## [16] "b_Obesity"            "Intercept"            "lprior"
## [19] "lp__"
```

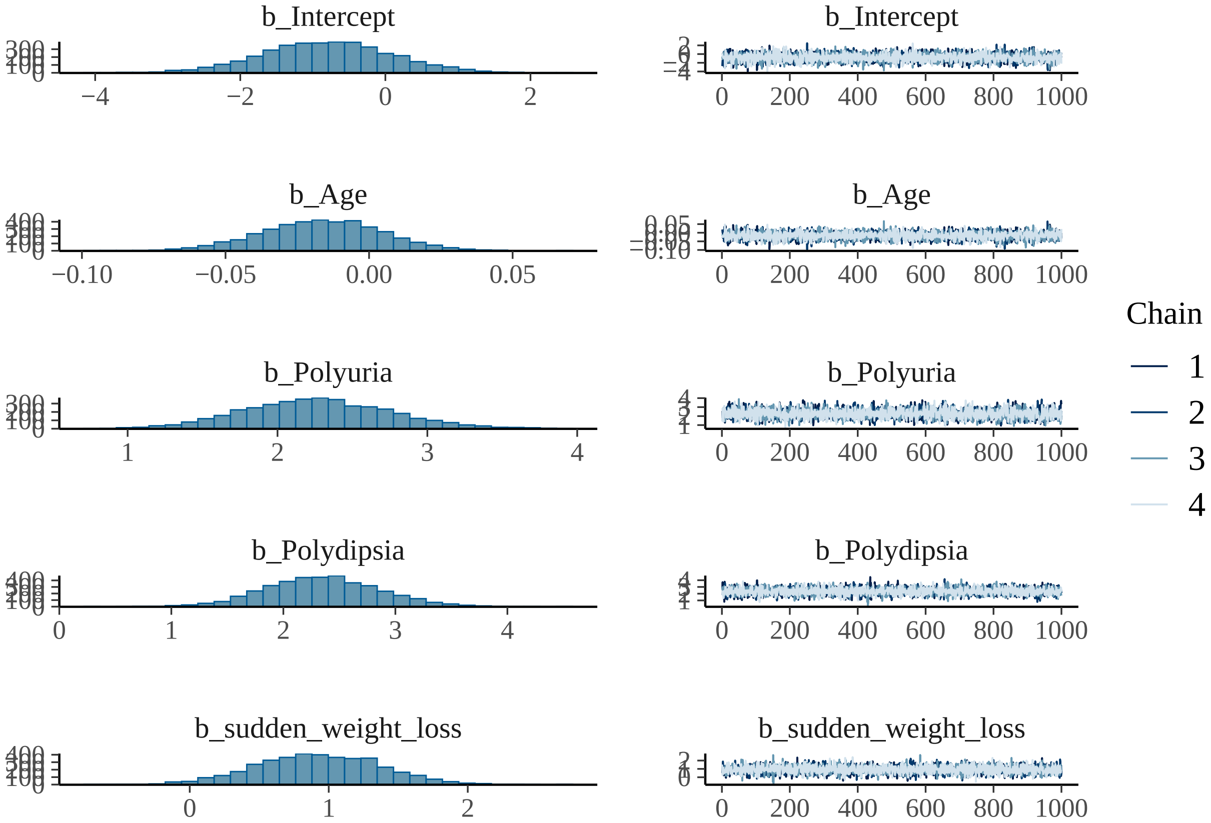
```r
mcmc_trace(as_draws(fit_logit),
           pars = c("b_Intercept" , "b_Age",  "b_Polydipsia", "b_Polyuria", "b_sudden_weight_loss", "b_w
```

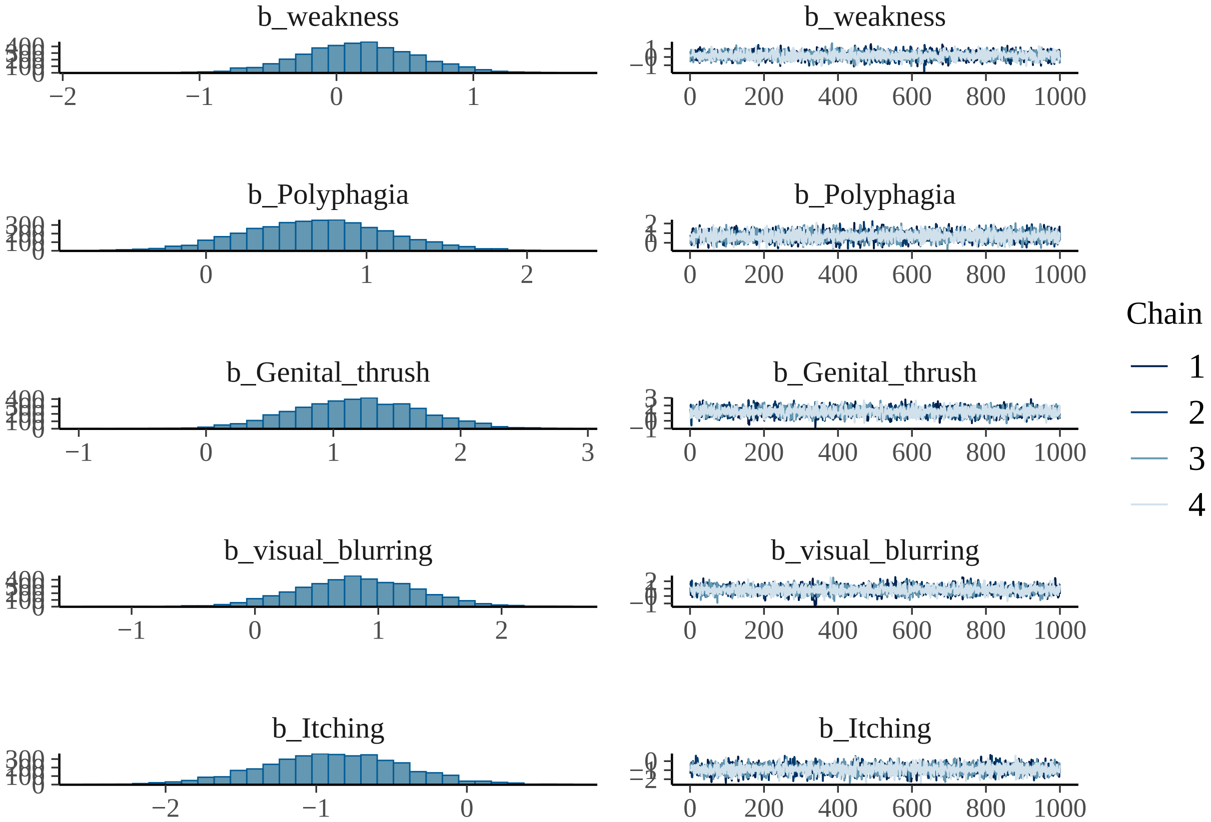


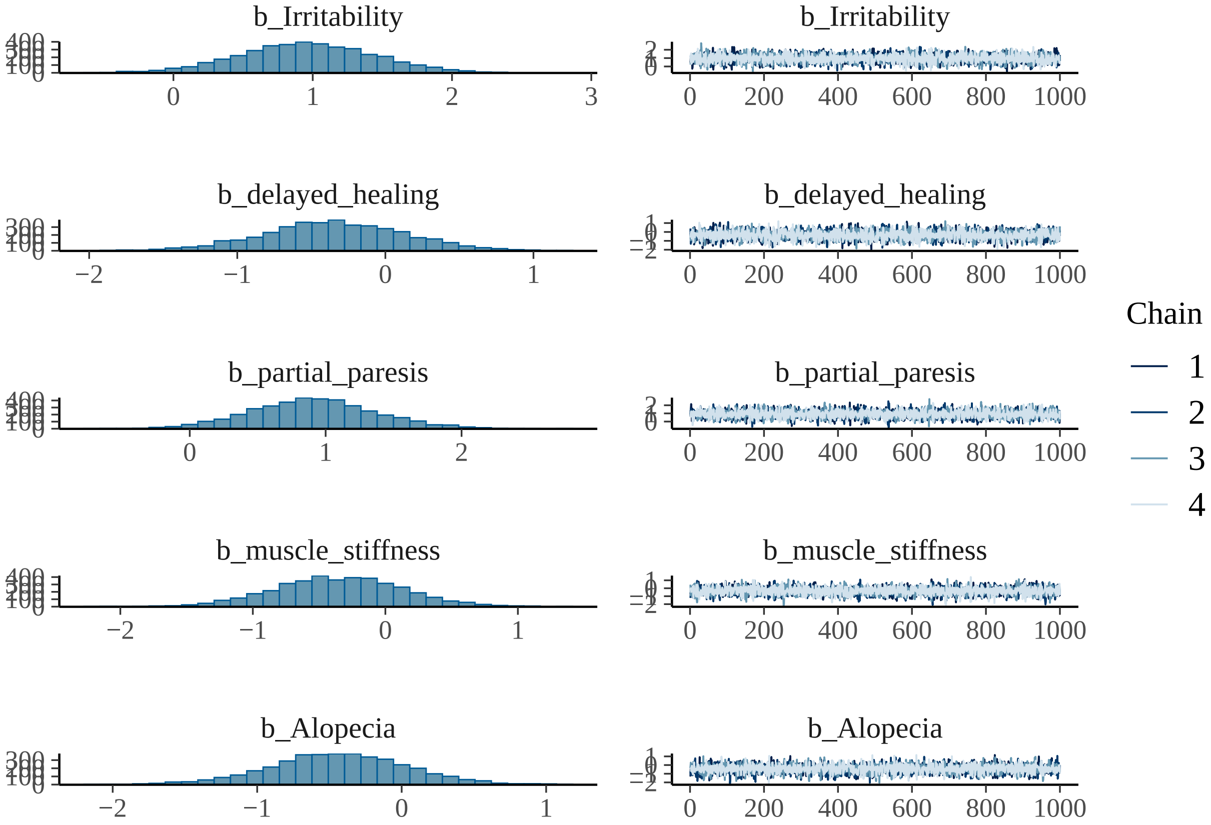
```
# Posterior Density Overlays
mcmc_dens_overlay(as.array(fit_logit),
                  pars = c("b_Intercept" , "b_Age",  "b_Polydipsia", "b_Polyuria", "b_sudden_weight_los
```

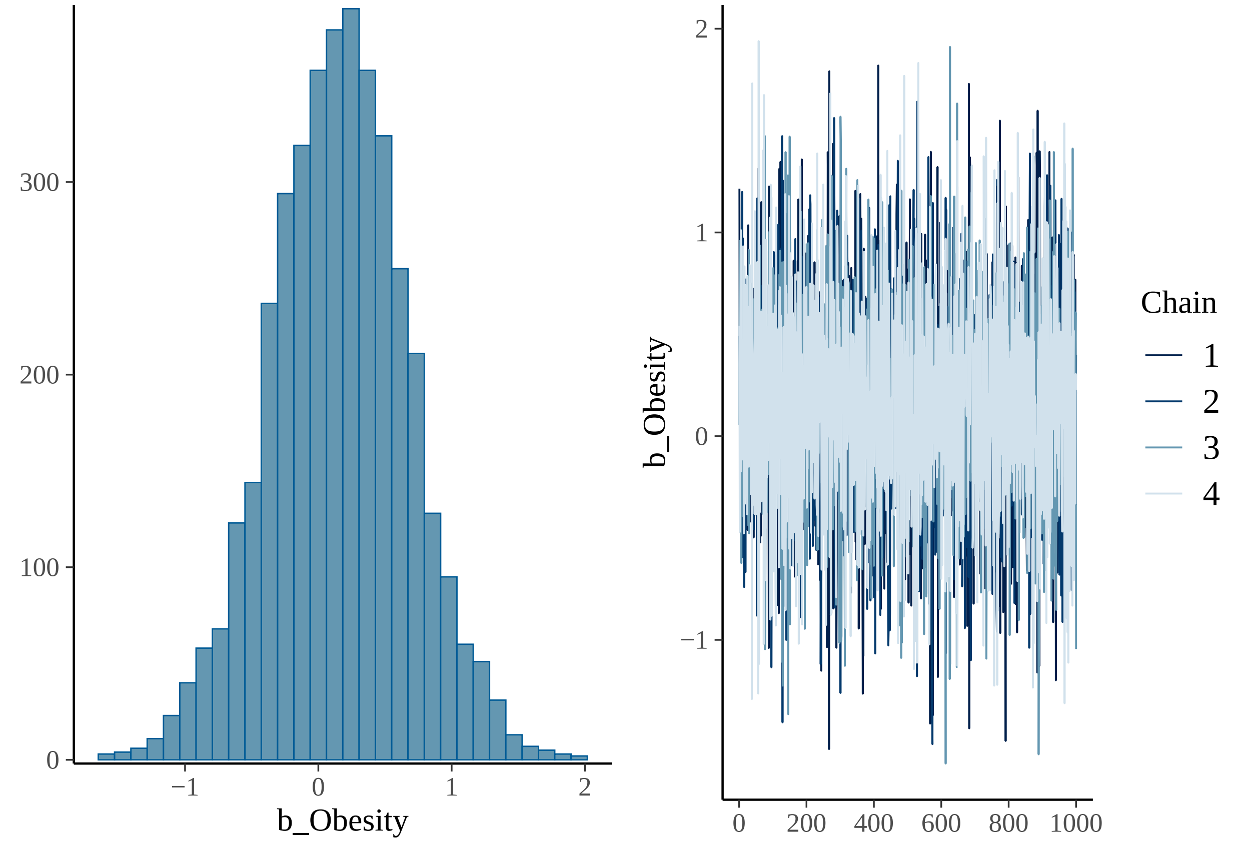


```
# Posterior Intervals
plot(fit_logit)
```

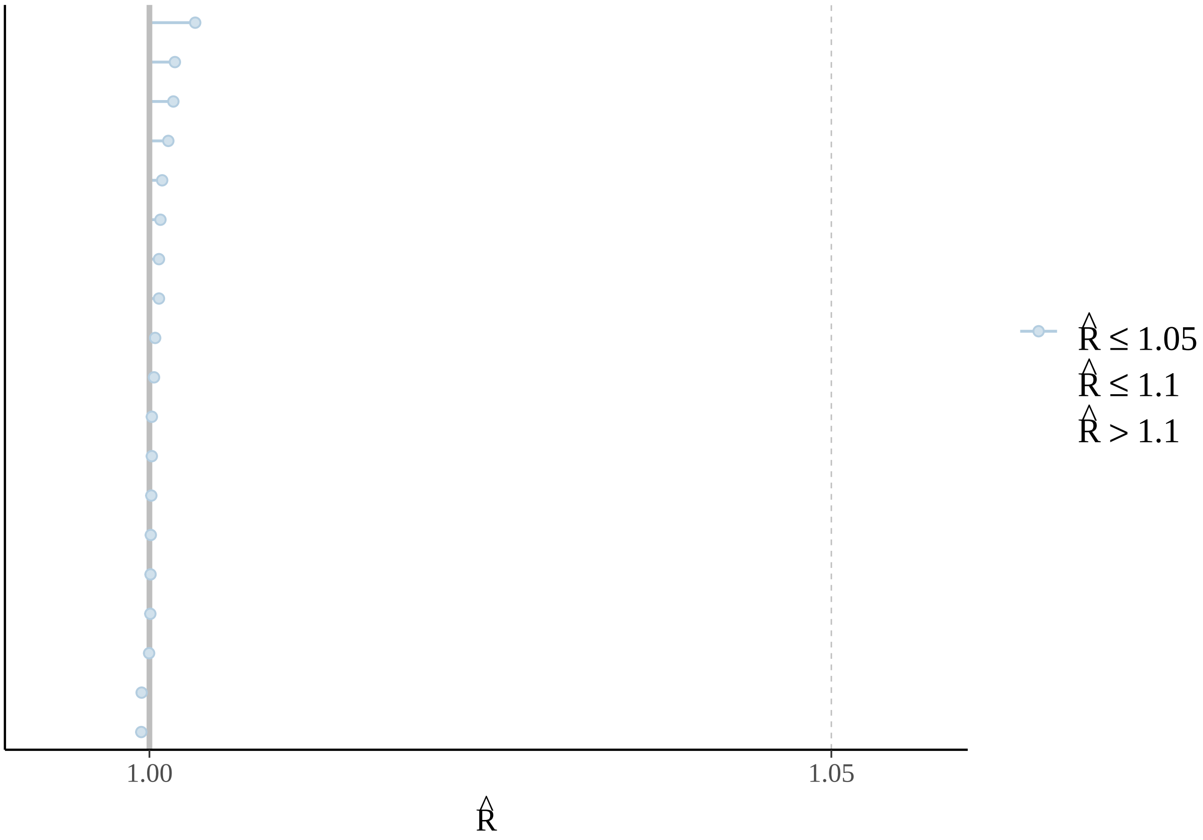

b_Intercept
300
200
100
0
−4
−2
0
2
b_Intercept
2
0
−2
−4
0
200
400
600
800
1000
b_Age
400
300
200
100
0
−0.10
−0.05
0.00
0.05
b_Age
0.05
0.00
−0.05
−0.10
0
200
400
600
800
1000
Chain
1
2
3
4
b_Polyuria
300
200
100
0
1
2
3
4
b_Polyuria
4
3
2
1
0
200
400
600
800
1000
b_Polydipsia
400
300
200
100
0
0
1
2
3
4
b_Polydipsia
4
3
2
1
0
200
400
600
800
1000
b_sudden_weight_loss
400
300
200
100
0
0
1
2
b_sudden_weight_loss
2
1
0
0
200
400
600
800
1000


b_weakness
b_weakness
−2
−1
0
1
0
200
400
600
800
1000
b_Polyphagia
b_Polyphagia
0
1
2
b_Genital_thrush
b_Genital_thrush
−1
0
1
2
3
b_visual_blurring
b_visual_blurring
b_Itching
b_Itching
Chain
1
2
3
4

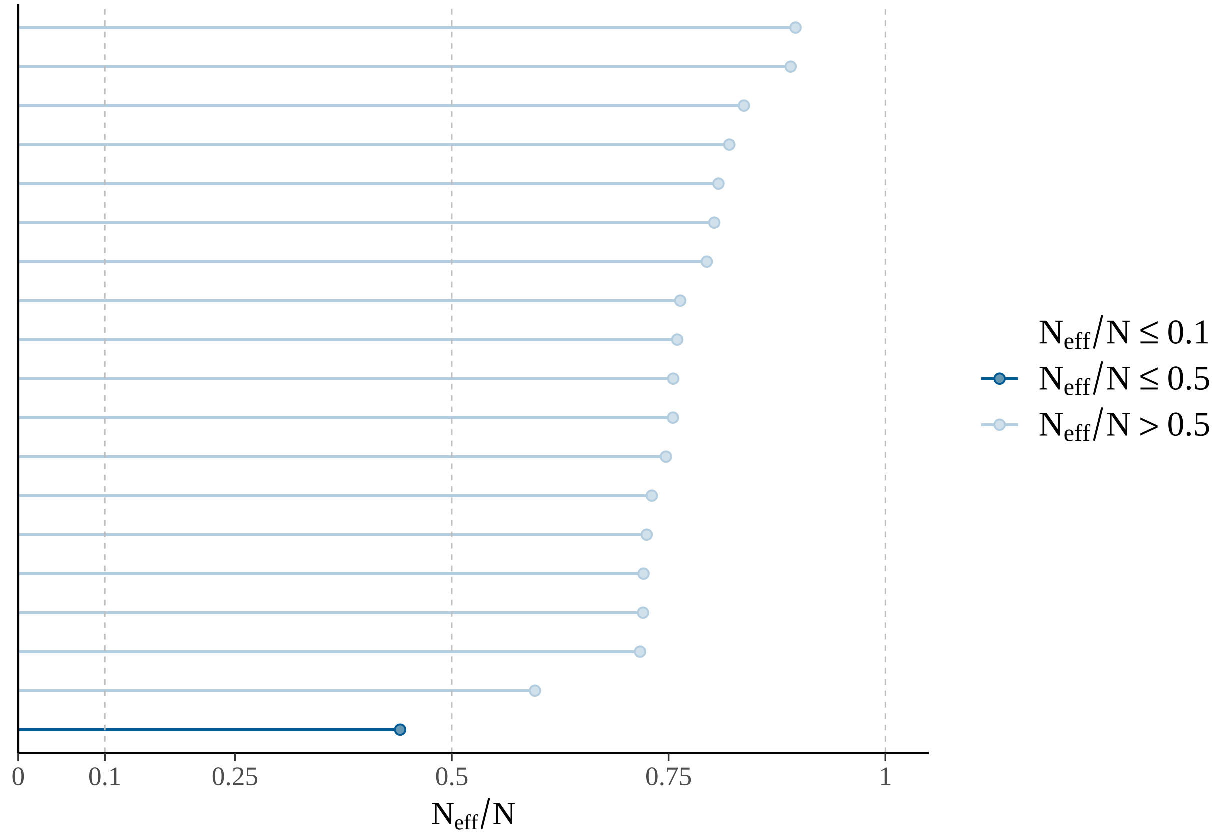

b_Irritability
400
300
200
100
0
0
1
2
3
b_Irritability
2
1
0
0
200
400
600
800
1000
b_delayed_healing
300
200
100
0
−2
−1
0
1
b_delayed_healing
1
0
−1
−2
0
200
400
600
800
1000
Chain
1
2
3
4
b_partial_paresis
400
300
200
100
0
0
1
2
b_partial_paresis
2
1
0
0
200
400
600
800
1000
b_muscle_stiffness
400
300
200
100
0
−2
−1
0
1
b_muscle_stiffness
1
0
−1
−2
0
200
400
600
800
1000
b_Alopecia
300
200
100
0
−2
−1
0
1
b_Alopecia
1
0
−1
−2
0
200
400
600
800
1000



```r
mcmc_plot(fit_logit, type = "rhat")
```



```
mcmc_plot(fit_logit, type = "neff")
```



```r
# Define parameter list
param_list <- c("b_Intercept", "b_Age", "b_Polydipsia", "b_Polyuria", "b_sudden_weight_loss",
                "b_weakness", "b_Polyphagia", "b_Genital_thrush", "b_visual_blurring",
                "b_Itching", "b_Irritability", "b_delayed_healing", "b_partial_paresis",
                "b_muscle_stiffness", "b_Alopecia", "b_Obesity", "Intercept", "lprior", "lp__")
# Open a PDF file
pdf("mcmc_diagnostics.pdf", width = 12, height = 8)

# Trace Plot
trace_plot <- mcmc_trace(as_draws(fit_logit), pars = param_list)
print(trace_plot)

# Density Overlay
dens_overlay <- mcmc_dens_overlay(as.array(fit_logit), pars = param_list)
print(dens_overlay)

# Posterior Intervals
posterior_plot <- plot(fit_logit)
print(posterior_plot)
```

```
## [[1]]

##
## [[2]]

##
```

```
## [[3]]
```

```
##
## [[4]]
```

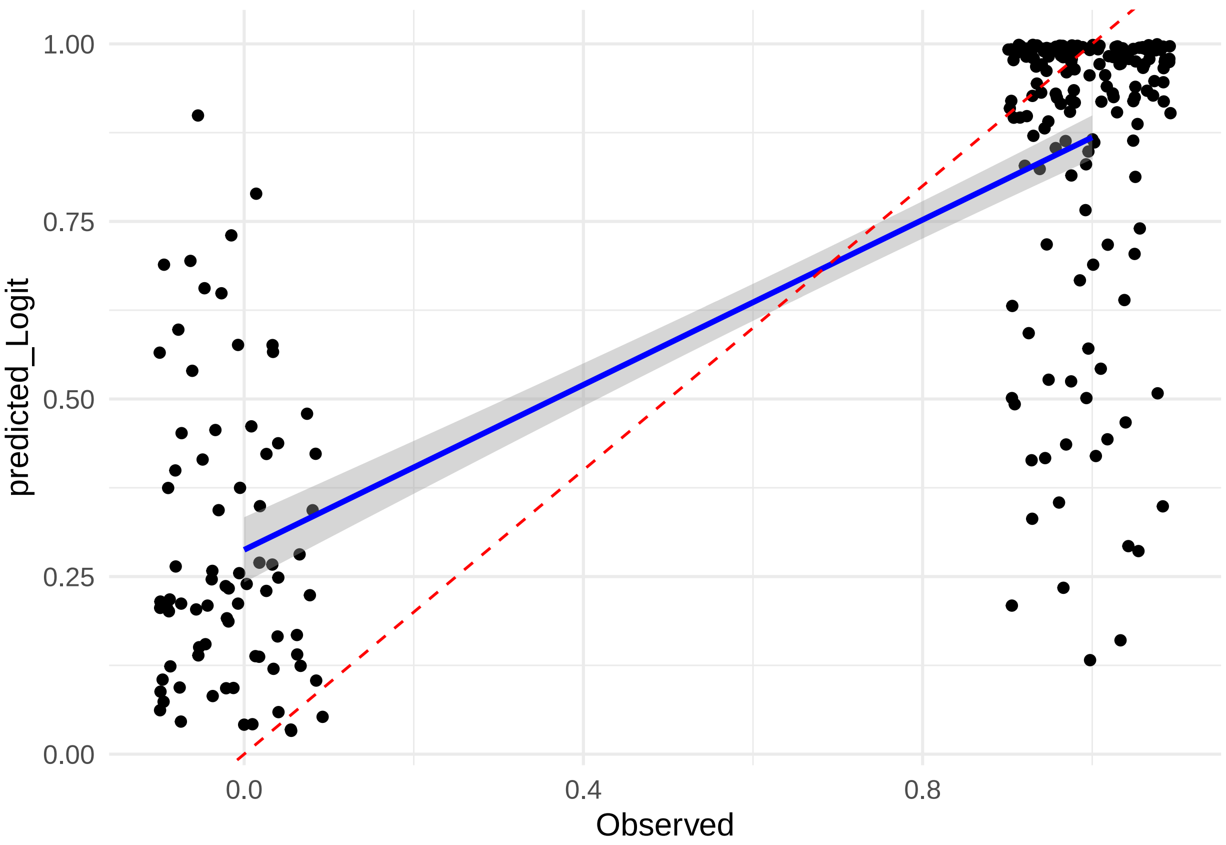
```r
# Rhat Plot
rhat_plot <- mcmc_plot(fit_logit, type = "rhat")
print(rhat_plot)

# Neff Plot
neff_plot <- mcmc_plot(fit_logit, type = "neff")
print(neff_plot)

# Close the PDF file
dev.off()
```

```
## pdf
##   2
```

```r
print("All MCMC diagnostic plots saved in mcmc_diagnostics.pdf!")
```

```
## [1] "All MCMC diagnostic plots saved in mcmc_diagnostics.pdf!"
```

```r
#Plot the relationship between observed and predicted values

data$predicted_Logit <- fitted(fit_logit)[, "Estimate"]


# Logistic Regression
ggplot(data, aes(x = class, y = predicted_Logit)) +
  geom_jitter(width = 0.1, height = 0) +
  geom_smooth(method = "lm", formula = y ~ x, color = "blue") +
  geom_abline(slope = 1, intercept = 0, color = "red", linetype = "dashed") +
  labs(x = "Observed", y = "predicted_Logit", color = "Observed Class") +
  theme_minimal(base_size = 12)
```



```
# ------------------------------------------------------------
# 4. Fit the Bayesian Probit Regression Model
# ------------------------------------------------------------
fit_probit <- brm(
  formula = class ~ Age + Polyuria + Polydipsia + sudden_weight_loss + weakness + Polyphagia +
            Genital_thrush + visual_blurring + Itching + Irritability +
            delayed_healing + partial_paresis + muscle_stiffness +
            Alopecia + Obesity,
  data    = data,
  family  = bernoulli(link = "probit"),  # Probit regression for binary classification
  prior   = my_priors,
  chains  = 4,       # Number of Markov Chains
  iter    = 2000,    # Total iterations per chain
  warmup  = 1000,    # Warm-up iterations (burn-in)
  cores   = 4,       # Parallel computation
  seed    = 1234     # Ensure reproducibility
)
```

```
## Compiling Stan program...

## Start sampling
```

```
# ------------------------------------------------------------
# 5. Model Summary and Posterior Estimates
# ------------------------------------------------------------
summary(fit_probit)       # Print model summary
```

```
##  Family: bernoulli
##   Links: mu = probit
## Formula: class ~ Age + Polyuria + Polydipsia + sudden_weight_loss + weakness + Polyphagia + Genital_
##    Data: data (Number of observations: 251)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Regression Coefficients:
##                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept             -0.53      0.57    -1.64     0.58 1.00     5206     3442
## Age                   -0.01      0.01    -0.04     0.01 1.00     5395     3139
## Polyuria               1.60      0.34     0.95     2.30 1.00     4550     3010
## Polydipsia             1.70      0.34     1.05     2.37 1.00     4499     3387
## sudden_weight_loss     0.56      0.31    -0.02     1.18 1.00     5822     3098
## weakness               0.13      0.29    -0.45     0.70 1.00     4932     3234
## Polyphagia             0.47      0.30    -0.13     1.08 1.00     6386     3272
## Genital_thrush         0.87      0.33     0.24     1.53 1.00     6027     3102
## visual_blurring        0.64      0.34    -0.04     1.32 1.00     5319     2967
## Itching               -0.78      0.33    -1.43    -0.14 1.00     4722     2975
## Irritability           0.67      0.33     0.03     1.34 1.00     5985     3448
## delayed_healing       -0.24      0.32    -0.85     0.38 1.00     5498     2668
## partial_paresis        0.58      0.31    -0.03     1.17 1.00     5641     2919
## muscle_stiffness      -0.33      0.33    -1.01     0.34 1.00     5894     2511
## Alopecia              -0.26      0.31    -0.89     0.35 1.00     5048     3124
## Obesity                0.12      0.33    -0.54     0.79 1.00     5500     2532
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
prior_summary(fit_probit) # Show priors used
```

```
##           prior     class               coef group resp dpar nlpar lb ub
##    normal(0, 1)         b
##    normal(0, 1)         b                Age
##    normal(0, 1)         b           Alopecia
##    normal(0, 1)         b    delayed_healing
##    normal(0, 1)         b     Genital_thrush
##    normal(0, 1)         b       Irritability
##    normal(0, 1)         b            Itching
##    normal(0, 1)         b   muscle_stiffness
##    normal(0, 1)         b            Obesity
##    normal(0, 1)         b    partial_paresis
##    normal(0, 1)         b         Polydipsia
##    normal(0, 1)         b         Polyphagia
##    normal(0, 1)         b           Polyuria
##    normal(0, 1)         b sudden_weight_loss
##    normal(0, 1)         b    visual_blurring
##    normal(0, 1)         b           weakness
##  normal(0, 2.5) Intercept
##        source
##          user
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##  (vectorized)
##          user
```

```
# Get fixed effects estimates (population-level effects)
fixef(fit_probit)
```

```
##                        Estimate  Est.Error        Q2.5       Q97.5
## Intercept          -0.53452942 0.56731756 -1.64310124  0.57663078
## Age                -0.01070062 0.01316401 -0.03693990  0.01478971
## Polyuria            1.60471144 0.33625137  0.95207913  2.30091760
## Polydipsia          1.69641068 0.34004485  1.04901167  2.37469578
## sudden_weight_loss  0.56396894 0.30697888 -0.01932090  1.17742260
## weakness            0.12813227 0.29127280 -0.44743340  0.69962150
## Polyphagia          0.46546691 0.30301783 -0.12577730  1.08442908
## Genital_thrush      0.86608374 0.32893101  0.23601348  1.52851692
## visual_blurring     0.63886994 0.34243295 -0.03832870  1.32410097
## Itching            -0.78015321 0.32892290 -1.43414700 -0.13770585
## Irritability        0.67462636 0.33457287  0.03219570  1.33820059
## delayed_healing    -0.24237616 0.31502753 -0.84823252  0.38315609
## partial_paresis     0.58201967 0.30695768 -0.03336033  1.16795246
## muscle_stiffness   -0.33205944 0.33449676 -1.00858332  0.33844578
## Alopecia           -0.25808505 0.31493079 -0.89113241  0.34596849
## Obesity             0.11815689 0.33278913 -0.54409066  0.78871423
```

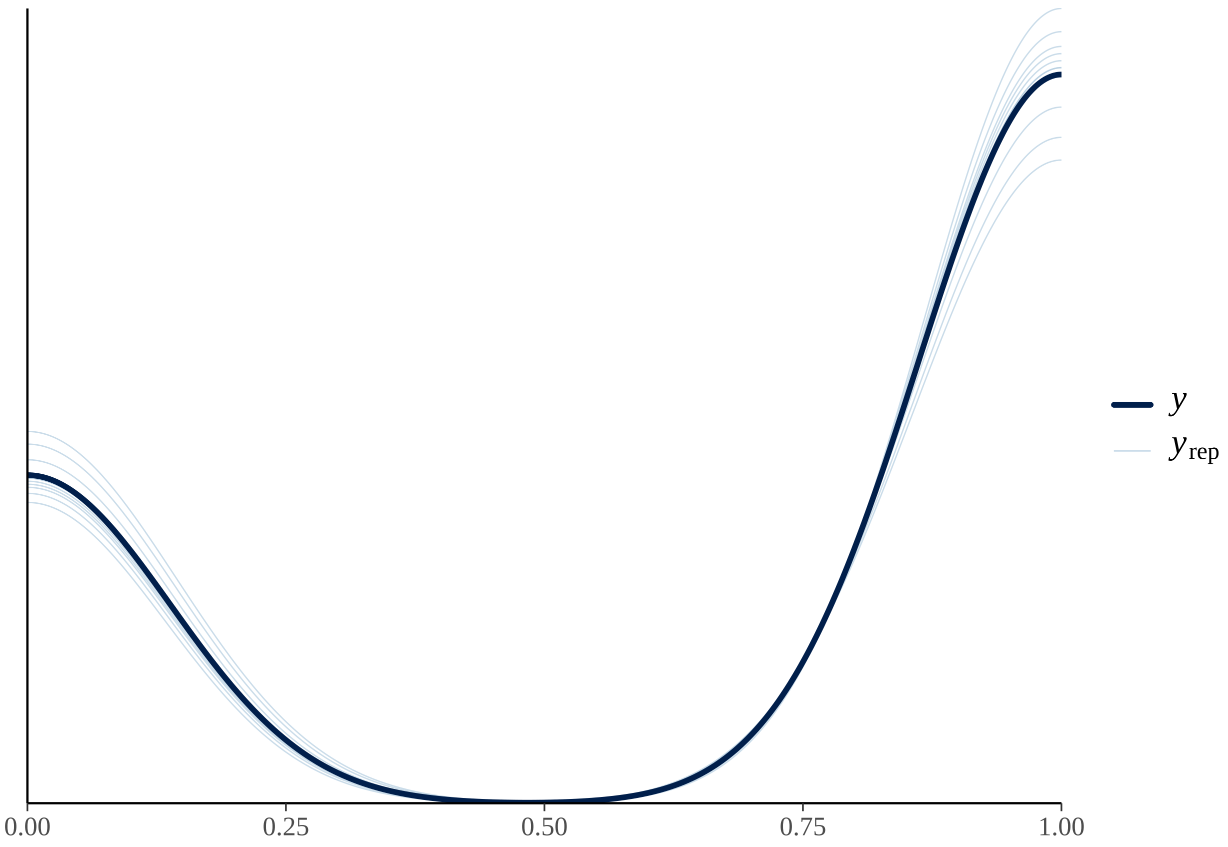
```
# Check the first few posterior samples
head(posterior_samples(fit_probit))
```

```
## Warning: Method 'posterior_samples' is deprecated. Please see ?as_draws for
## recommended alternatives.
```

```
##   b_Intercept        b_Age b_Polyuria b_Polydipsia b_sudden_weight_loss
## 1 -1.10725382  0.001805965  1.7868771    0.8840681            0.2792649
## 2 -0.22130419 -0.018690806  1.4151176    2.7402095            1.1972684
## 3 -1.24341601  0.015692296  2.5262022    2.0125813            0.2559733
## 4 -0.15634801 -0.021614720  0.5235883    1.6842997            0.5523631
## 5  0.07799193 -0.024540500  0.7798000    2.3140430            0.1945644
## 6 -0.26745868 -0.021933839  0.9479691    2.0242256            0.3724910
##    b_weakness b_Polyphagia b_Genital_thrush b_visual_blurring  b_Itching
## 1  0.33469874    0.4770060        0.9401970         0.5468016 -0.6446944
## 2 -0.06477899    0.5501483        0.6900196         0.6944521 -0.7558575
## 3  0.31764122    0.7019825        0.5515530         0.1034281 -1.1546823
## 4  0.13357991    0.5501434        1.2199354         1.3622858 -0.5841274
## 5 -0.25200574    0.6293881        1.8896803         0.8860027 -0.8895860
## 6 -0.22257127    0.9394300        1.5158065         0.8984474 -0.7533856
##   b_Irritability b_delayed_healing b_partial_paresis b_muscle_stiffness
## 1      0.1055772       -0.55724063         0.4726080        -0.09893532
## 2      1.5656869        0.17300588         0.6711435        -0.59254826
## 3      0.2637683       -0.56912282         1.0139957        -0.59143416
## 4      0.9863150       -0.04622703         0.3970872        -0.18992288
## 5      1.0047004       -0.20561502         0.7594751        -0.09084300
## 6      1.0766900       -0.28194448         0.5507098         0.06873542
##    b_Alopecia  b_Obesity Intercept    lprior      lp__
## 1  0.04169338  0.1719188  1.043817 -18.99485 -87.52820
## 2 -0.15685114 -0.4075693  2.253126 -24.15306 -94.75451
## 3  0.08254778  0.2889975  2.182370 -23.30113 -96.24380
## 4 -0.46557936 -0.2505099  1.245508 -20.17870 -91.04152
## 5 -0.41522300 -0.4253321  1.354379 -22.56521 -93.52606
## 6 -0.17085121 -0.2094797  1.370037 -21.44933 -88.71173
```

```r
# ------------------------------------------------------------
# 6. Posterior Predictive Checks (Model Diagnostics)
# ------------------------------------------------------------
# Density overlay of observed vs predicted values
pp_check(fit_probit, type = "dens_overlay")
```

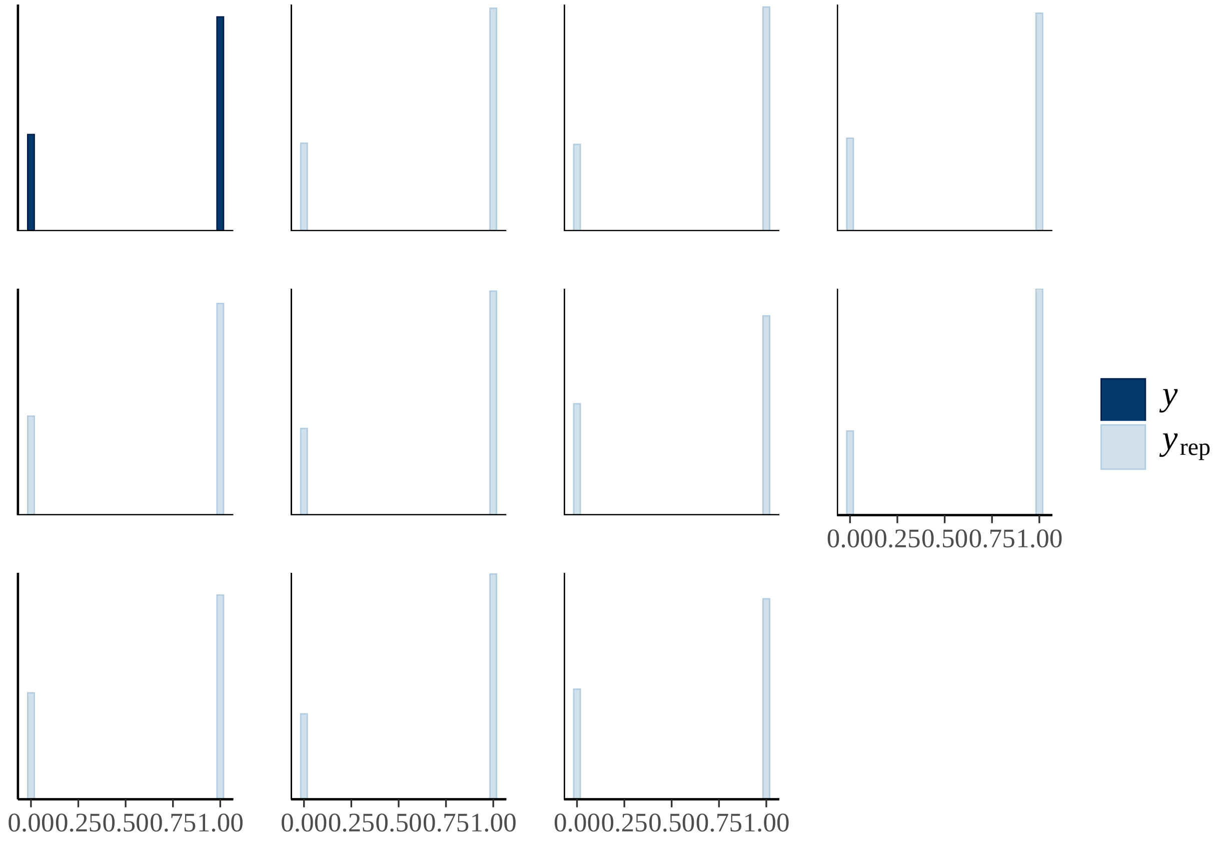
```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



```
# Histogram of simulated posterior predictions
pp_check(fit_probit, type = "hist")
```

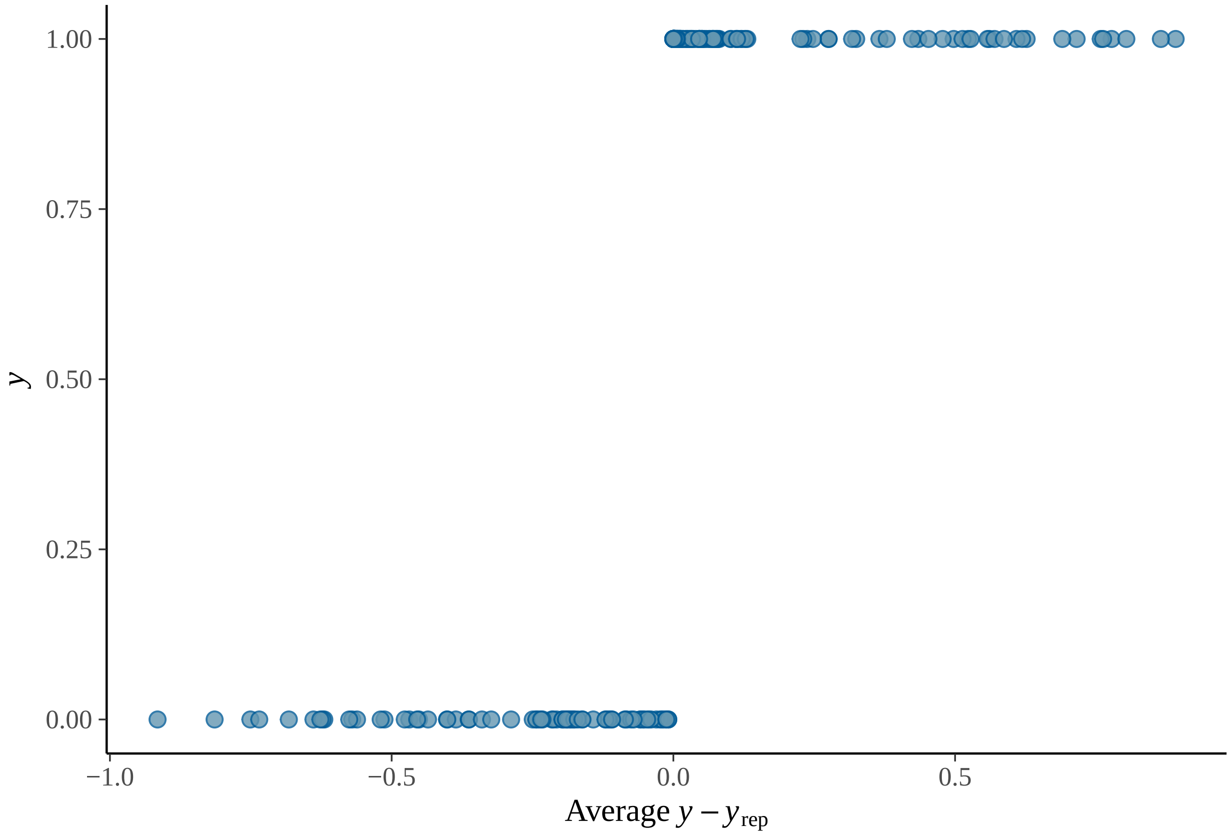
```
## Using 10 posterior draws for ppc type 'hist' by default.
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
pp_check(fit_probit, type = "error_scatter_avg")
```

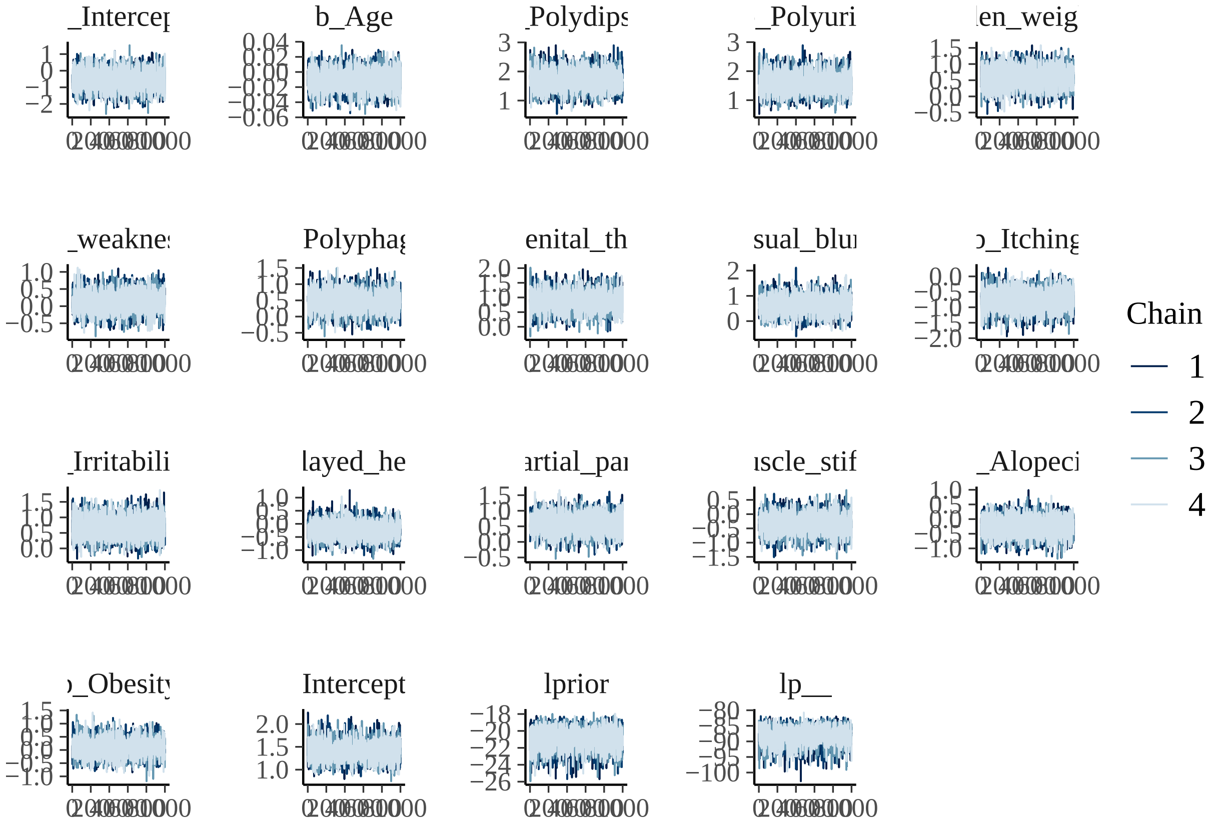
```
## Using all posterior draws for ppc type 'error_scatter_avg' by default.
```



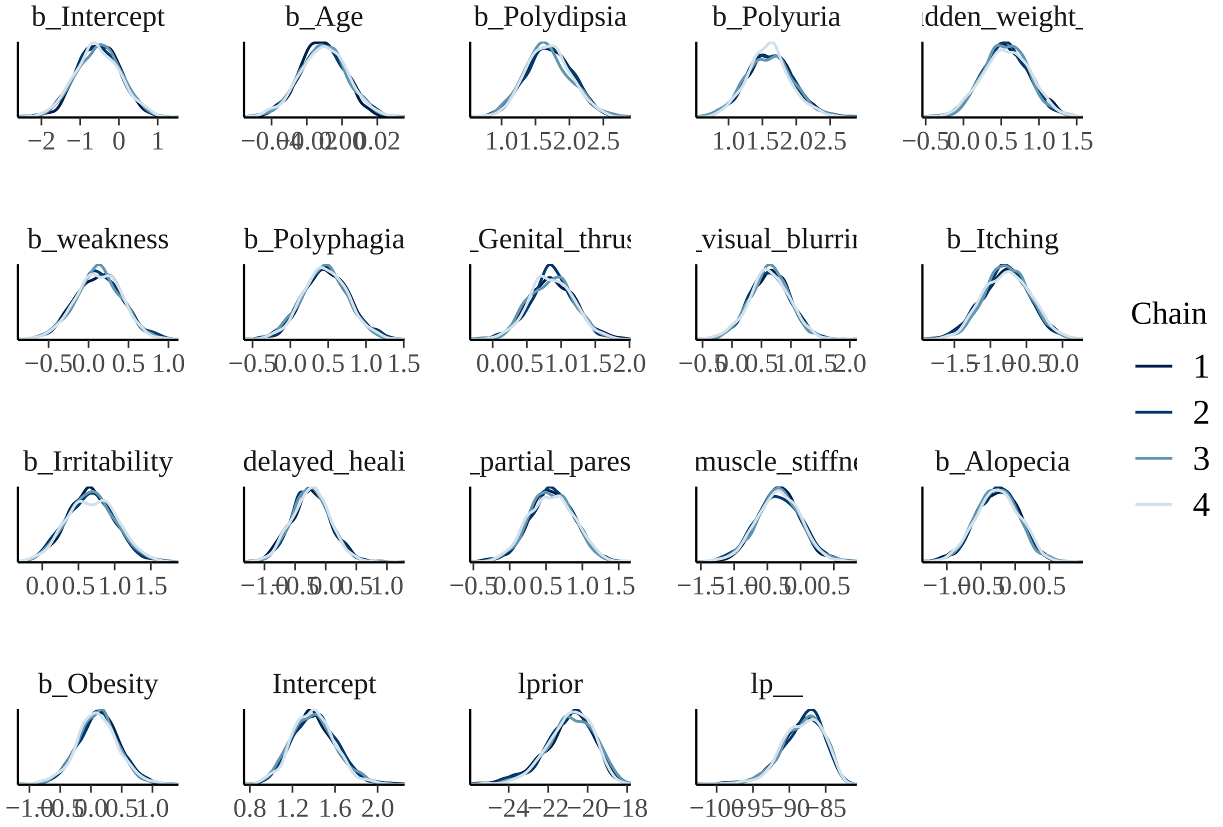
```r
# ---------------------------------------------------------------
# 7. Convergence Diagnostics and Visualization
# ---------------------------------------------------------------
# Check if chains have converged (Trace Plots)
# Get all parameter names in the model
variables(as_draws(fit_probit))
```

```
##  [1] "b_Intercept"          "b_Age"                "b_Polyuria"
##  [4] "b_Polydipsia"         "b_sudden_weight_loss" "b_weakness"
##  [7] "b_Polyphagia"         "b_Genital_thrush"     "b_visual_blurring"
## [10] "b_Itching"            "b_Irritability"       "b_delayed_healing"
## [13] "b_partial_paresis"    "b_muscle_stiffness"   "b_Alopecia"
## [16] "b_Obesity"            "Intercept"            "lprior"
## [19] "lp__"
```

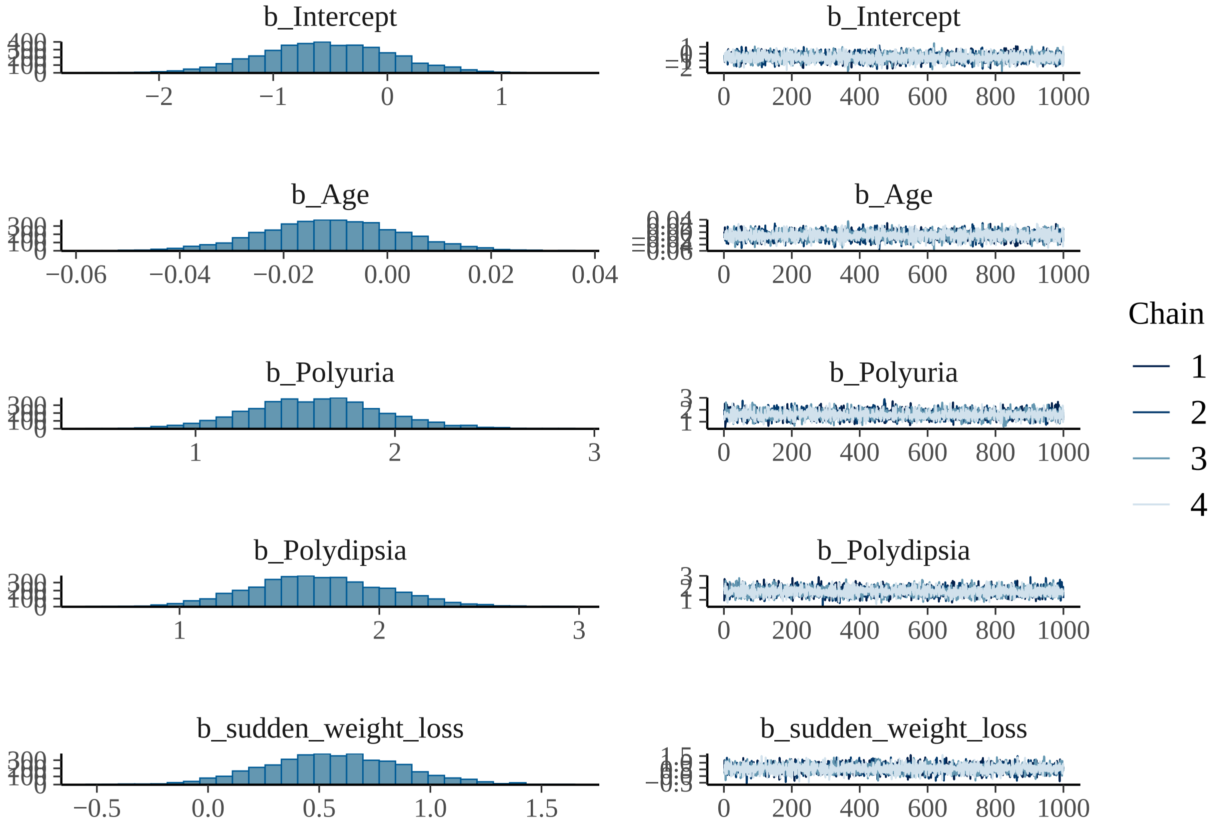
```r
mcmc_trace(as_draws(fit_probit),
           pars = c("b_Intercept" , "b_Age",  "b_Polydipsia", "b_Polyuria", "b_sudden_weight_loss", "b_
```

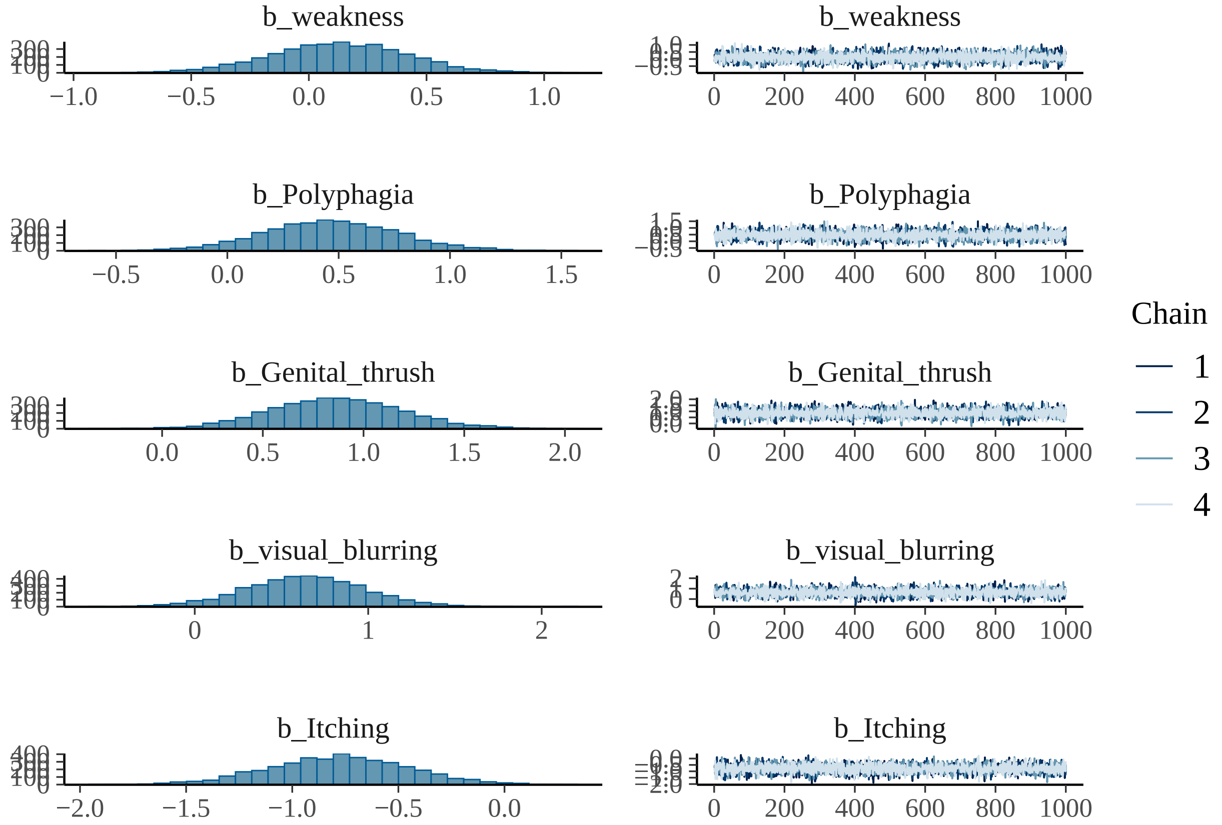


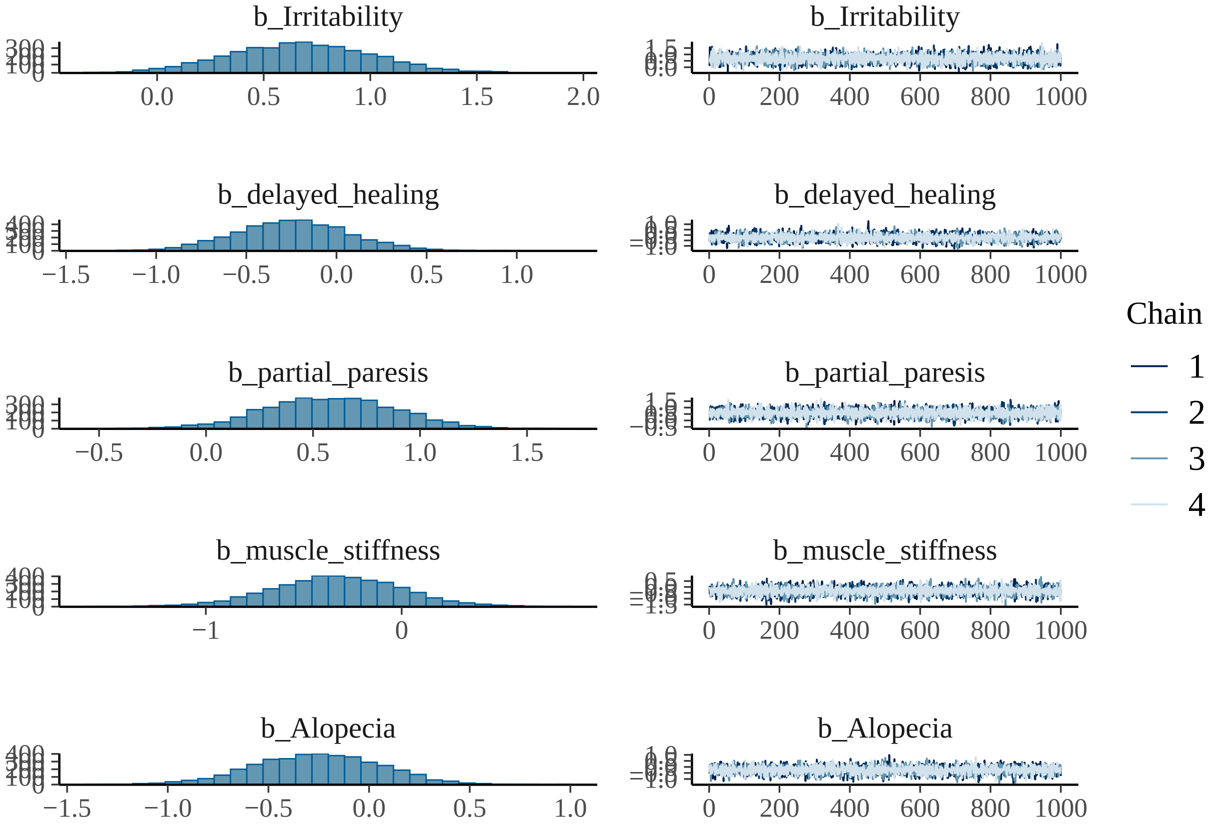
```r
# Posterior Density Overlays
mcmc_dens_overlay(as.array(fit_probit),
                  pars = c("b_Intercept" , "b_Age",  "b_Polydipsia", "b_Polyuria", "b_sudden_weight_los
```

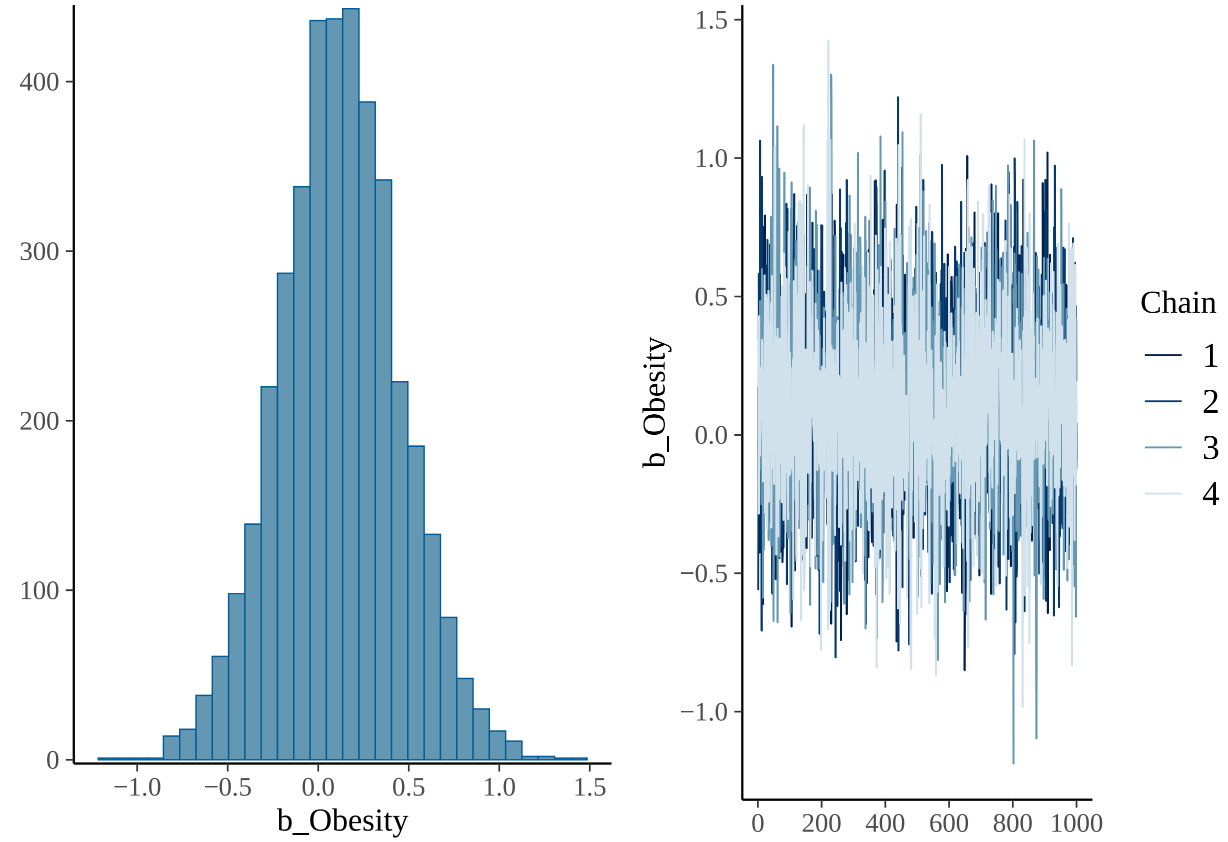


```r
# Posterior Intervals
plot(fit_probit)
```

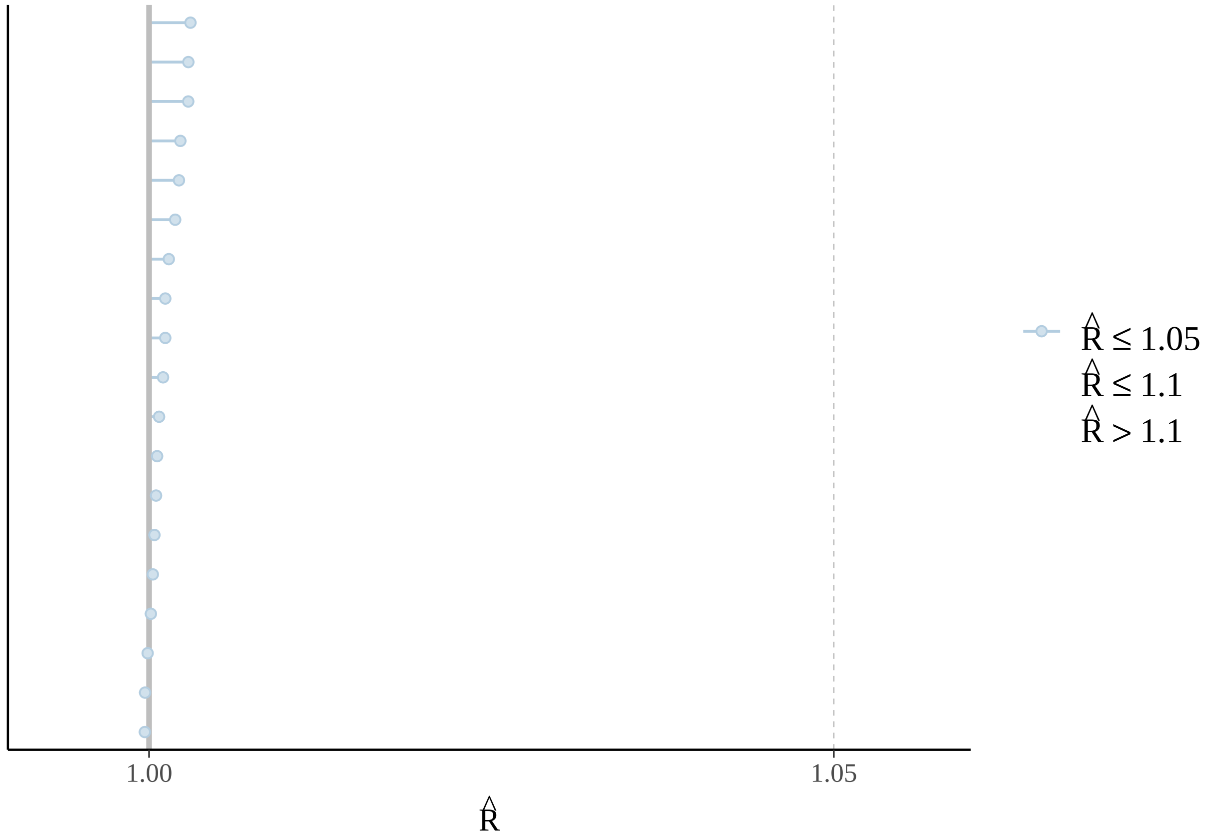

b_Intercept
400
300
200
100
0
−2
−1
0
1
b_Intercept
1
0
−1
−2
0
200
400
600
800
1000
b_Age
300
200
100
0
−0.06
−0.04
−0.02
0.00
0.02
0.04
b_Age
0.04
0.02
0.00
−0.02
−0.04
−0.06
0
200
400
600
800
1000
Chain
1
2
3
4
b_Polyuria
300
200
100
0
1
2
3
b_Polyuria
3
2
1
0
200
400
600
800
1000
b_Polydipsia
300
200
100
0
1
2
3
b_Polydipsia
3
2
1
0
200
400
600
800
1000
b_sudden_weight_loss
300
200
100
0
−0.5
0.0
0.5
1.0
1.5
b_sudden_weight_loss
1.5
1.0
0.5
0.0
−0.5
0
200
400
600
800
1000


b_weakness
300
200
100
0
−1.0
−0.5
0.0
0.5
1.0
b_weakness
1.0
0.5
0.0
−0.5
0
200
400
600
800
1000
b_Polyphagia
300
200
100
0
−0.5
0.0
0.5
1.0
1.5
b_Polyphagia
1.5
1.0
0.5
0.0
−0.5
0
200
400
600
800
1000
Chain
1
2
3
4
b_Genital_thrush
300
200
100
0
0.0
0.5
1.0
1.5
2.0
b_Genital_thrush
2.0
1.5
1.0
0.5
0.0
0
200
400
600
800
1000
b_visual_blurring
400
300
200
100
0
0
1
2
b_visual_blurring
2
1
0
0
200
400
600
800
1000
b_Itching
400
300
200
100
0
−2.0
−1.5
−1.0
−0.5
0.0
b_Itching
0.0
−0.5
−1.0
−1.5
−2.0
0
200
400
600
800
1000

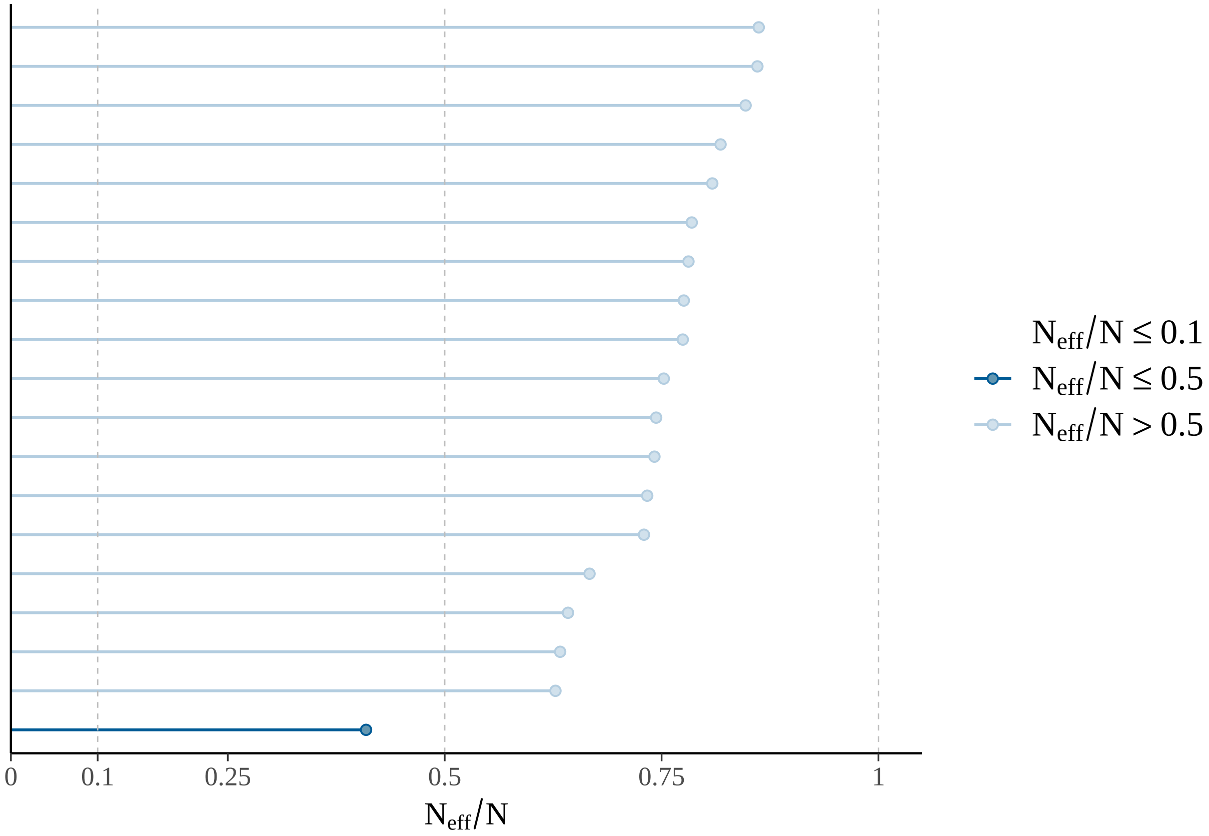

b_Irritability
0.0
0.5
1.0
1.5
2.0
b_delayed_healing
−1.5
−1.0
−0.5
0.0
0.5
1.0
b_partial_paresis
−0.5
0.0
0.5
1.0
1.5
b_muscle_stiffness
−1
0
b_Alopecia
−1.5
−1.0
−0.5
0.0
0.5
1.0
0
200
400
600
800
1000
Chain
1
2
3
4



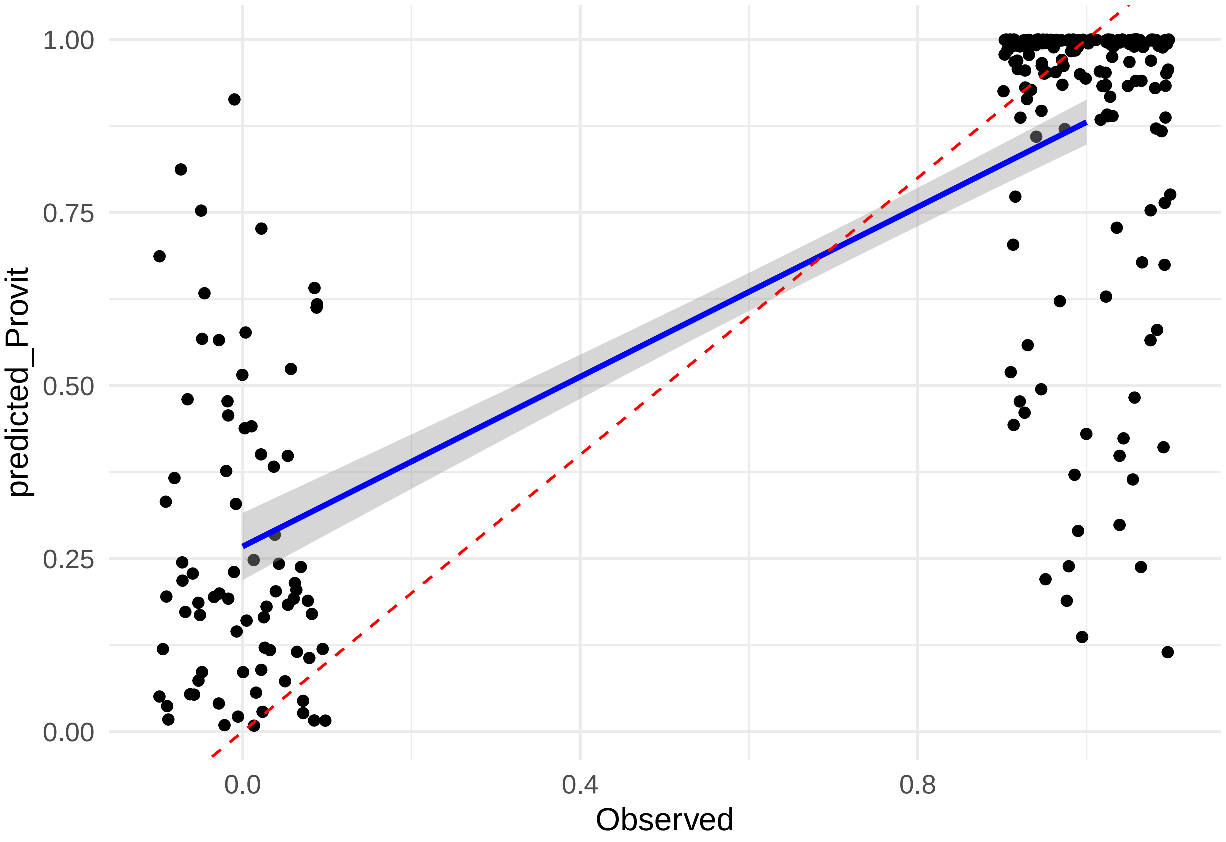
```r
mcmc_plot(fit_probit, type = "rhat")
```



```r
mcmc_plot(fit_probit, type = "neff")
```



```
#Plot the relationship between observed and predicted values

data$predicted_Provit <- fitted(fit_probit)[, "Estimate"]


# Logistic Regression
ggplot(data, aes(x = class, y = predicted_Provit)) +
  geom_jitter(width = 0.1, height = 0) +
  geom_smooth(method = "lm", formula = y ~ x, color = "blue") +
  geom_abline(slope = 1, intercept = 0, color = "red", linetype = "dashed") +
  labs(x = "Observed", y = "predicted_Provit", color = "Observed Class") +
  theme_minimal(base_size = 12)
```



```
# Compute Leave-One-Out Cross-Validation (LOO) for each model
loo_probit <- loo(fit_probit,moment_match = TRUE,reloo = TRUE)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.

## 5 problematic observation(s) found.
## The model will be refit 5 times.

##
## Fitting model 1 out of 5 (leaving out observation 30)

## Start sampling

##
## Fitting model 2 out of 5 (leaving out observation 32)

## Start sampling

##
## Fitting model 3 out of 5 (leaving out observation 51)

## Start sampling
```

```
##
## Fitting model 4 out of 5 (leaving out observation 111)

## Start sampling

##
## Fitting model 5 out of 5 (leaving out observation 156)

## Start sampling
```

```
loo_logit  <- loo(fit_logit,moment_match = TRUE,reloo = TRUE)
```

```
## No problematic observations found. Returning the original 'loo' object.
```

```
# Compare models
loo_compare(loo_probit, loo_logit)
```

```
##            elpd_diff se_diff
## fit_logit   0.0       0.0
## fit_probit -0.4       1.4
```

```
#Compare Model Coefficients (Fixed Effects Estimates)
# Extract fixed effects (posterior means & intervals)
logit_coef <- fixef(fit_logit)
probit_coef <- fixef(fit_probit)

# Print comparison of coefficients
print("Logit Model Coefficients:")
```

```
## [1] "Logit Model Coefficients:"
```

```
print(logit_coef)
```

```
##                       Estimate  Est.Error         Q2.5      Q97.5
## Intercept          -0.80120297 0.89545487 -2.564210370 0.95997235
## Age                -0.01642244 0.02109202 -0.058675101 0.02391545
## Polyuria            2.26495381 0.49294825  1.332048575 3.27174866
## Polydipsia          2.35170517 0.50585099  1.369643000 3.35451904
## sudden_weight_loss  0.92497261 0.44542445  0.064998216 1.77874968
## weakness            0.16231782 0.42734848 -0.688729157 1.00453917
## Polyphagia          0.69318103 0.44988928 -0.179697091 1.59018486
## Genital_thrush      1.18862217 0.50333108  0.218080480 2.18152789
## visual_blurring     0.83076547 0.49701372 -0.123645622 1.79556494
## Itching            -0.88889485 0.47448139 -1.834356941 0.04340460
## Irritability        0.95679616 0.48175733  0.003176781 1.89471832
## delayed_healing    -0.34497595 0.48211244 -1.314430574 0.59819604
## partial_paresis     0.91112851 0.45973601  0.024564559 1.85611671
## muscle_stiffness   -0.35516524 0.48215407 -1.291760966 0.58412472
## Alopecia           -0.43707302 0.47684779 -1.401237888 0.49957054
## Obesity             0.15571816 0.51379889 -0.873471147 1.17664204
```

```
print("Probit Model Coefficients:")
```

```
## [1] "Probit Model Coefficients:"
```

```
print(probit_coef)
```

```
##                      Estimate  Est.Error        Q2.5       Q97.5
## Intercept         -0.53452942 0.56731756 -1.64310124  0.57663078
## Age               -0.01070062 0.01316401 -0.03693990  0.01478971
## Polyuria           1.60471144 0.33625137  0.95207913  2.30091760
## Polydipsia         1.69641068 0.34004485  1.04901167  2.37469578
## sudden_weight_loss  0.56396894 0.30697888 -0.01932090  1.17742260
## weakness           0.12813227 0.29127280 -0.44743340  0.69962150
## Polyphagia         0.46546691 0.30301783 -0.12577730  1.08442908
## Genital_thrush     0.86608374 0.32893101  0.23601348  1.52851692
## visual_blurring    0.63886994 0.34243295 -0.03832870  1.32410097
## Itching           -0.78015321 0.32892290 -1.43414700 -0.13770585
## Irritability       0.67462636 0.33457287  0.03219570  1.33820059
## delayed_healing   -0.24237616 0.31502753 -0.84823252  0.38315609
## partial_paresis    0.58201967 0.30695768 -0.03336033  1.16795246
## muscle_stiffness  -0.33205944 0.33449676 -1.00858332  0.33844578
## Alopecia          -0.25808505 0.31493079 -0.89113241  0.34596849
## Obesity            0.11815689 0.33278913 -0.54409066  0.78871423
```

```
#Compare Model Fit (LOO & WAIC)
# Compute model fit criteria
logit_fit <- loo(fit_logit)
probit_fit <- loo(fit_probit)
```

```
## Warning: Found 5 observations with a pareto_k > 0.7 in model 'fit_probit'. We
## recommend to set 'moment_match = TRUE' in order to perform moment matching for
## problematic observations.
```

```
waic_logit <- waic(fit_logit)
```

```
## Warning:
## 3 (1.2%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
waic_probit <- waic(fit_probit)
```

```
## Warning:
## 8 (3.2%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

```
# Compare LOO scores
print("Logit Model LOO Score:")
```

```
## [1] "Logit Model LOO Score:"
```

```r
print(logit_fit)
```

```
##
## Computed from 4000 by 251 log-likelihood matrix.
##
##          Estimate   SE
## elpd_loo    -75.5  7.5
## p_loo        11.7  1.5
## looic       151.1 14.9
## ------
## MCSE of elpd_loo is 0.1.
## MCSE and ESS estimates assume MCMC draws (r_eff in [0.5, 1.6]).
##
## All Pareto k estimates are good (k < 0.7).
## See help(’pareto-k-diagnostic’) for details.
```

```r
print("Probit Model LOO Score:")
```

```
## [1] "Probit Model LOO Score:"
```

```r
print(probit_fit)
```

```
##
## Computed from 4000 by 251 log-likelihood matrix.
##
##          Estimate   SE
## elpd_loo    -76.0  8.6
## p_loo        14.9  2.2
## looic       151.9 17.2
## ------
## MCSE of elpd_loo is NA.
## MCSE and ESS estimates assume MCMC draws (r_eff in [0.6, 1.8]).
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. ESS
## (-Inf, 0.7]   (good)     246   98.0%   335
##    (0.7, 1]   (bad)        5    2.0%   <NA>
##    (1, Inf)   (very bad)   0    0.0%   <NA>
## See help(’pareto-k-diagnostic’) for details.
```

```r
# Compare WAIC scores
print("Logit Model WAIC Score:")
```

```
## [1] "Logit Model WAIC Score:"
```

```r
print(waic_logit)
```

```
##
## Computed from 4000 by 251 log-likelihood matrix.
##
```

```
##           Estimate   SE
## elpd_waic    -75.4  7.4
## p_waic        11.5  1.5
## waic         150.8 14.9
##
## 3 (1.2%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

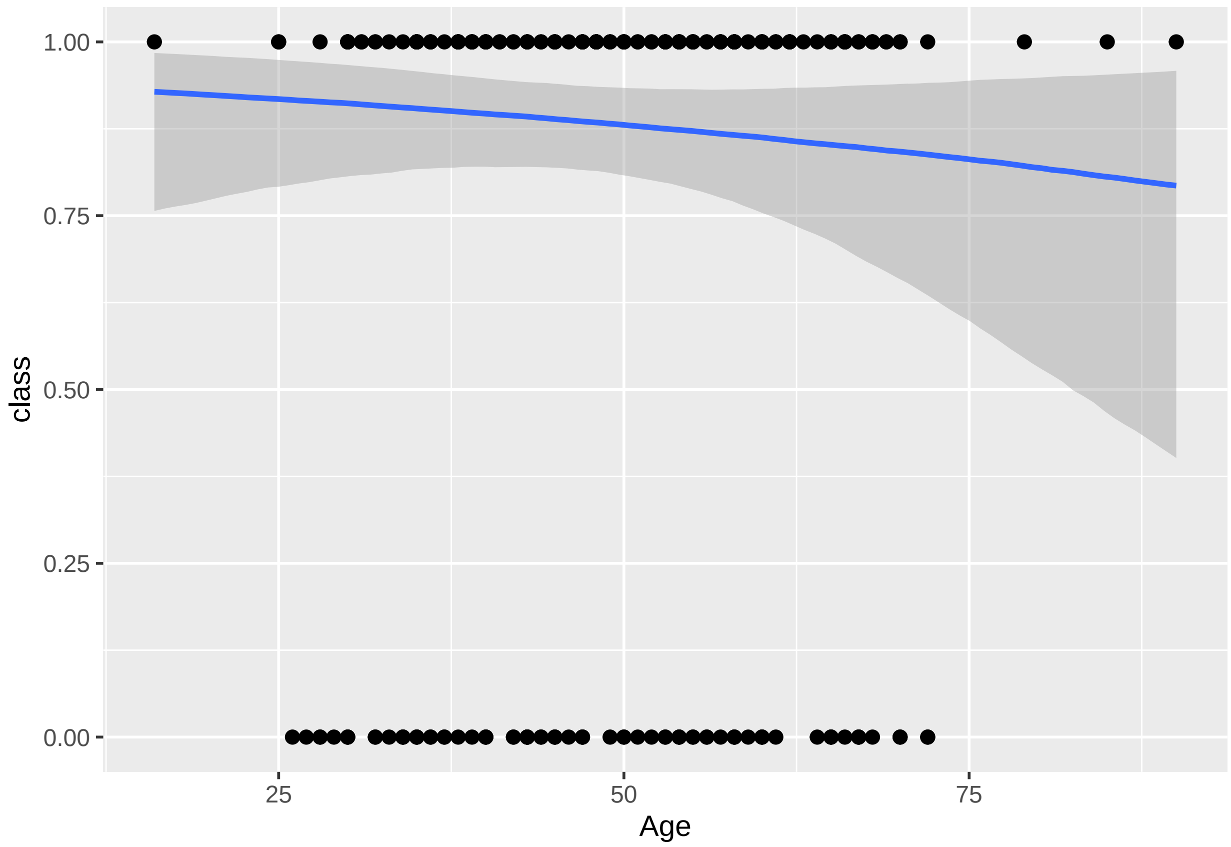
```
print("Probit Model WAIC Score:")
```

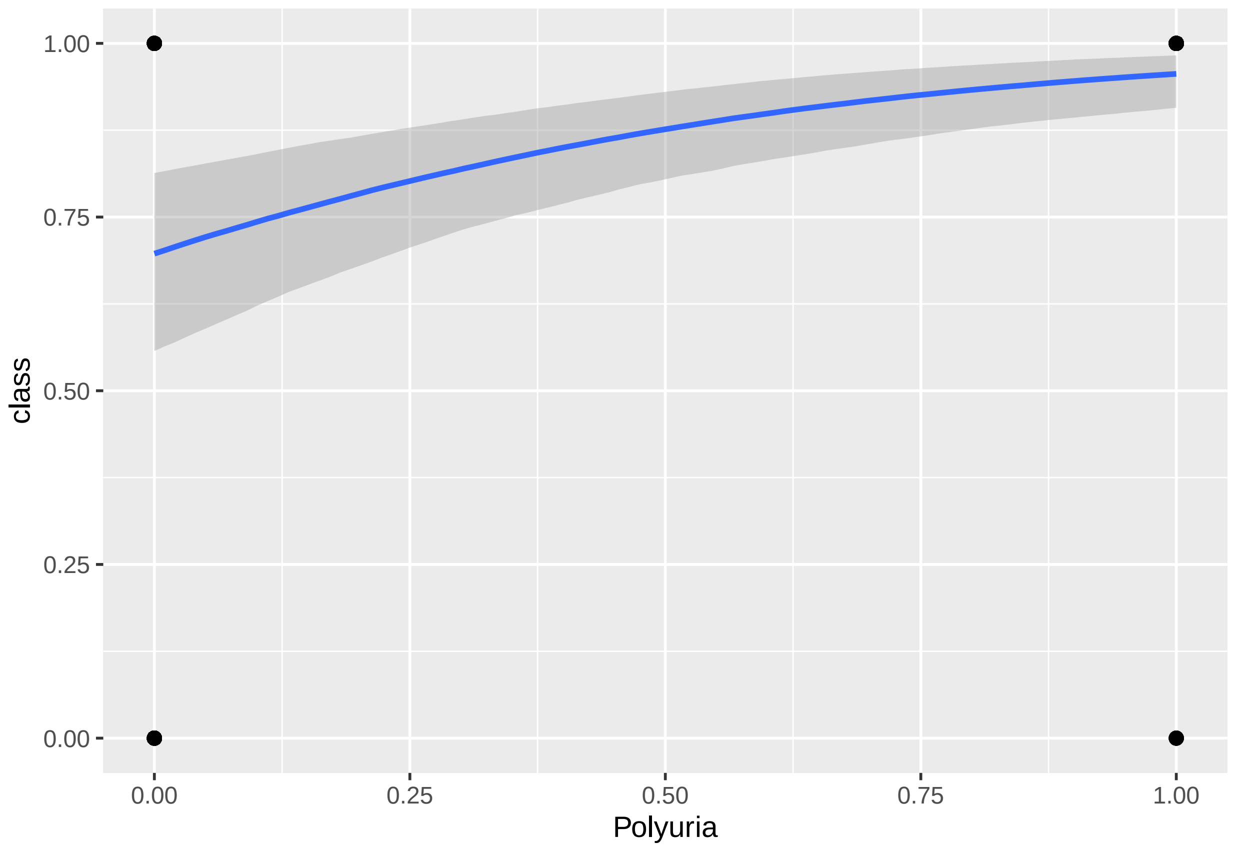
```
## [1] "Probit Model WAIC Score:"
```

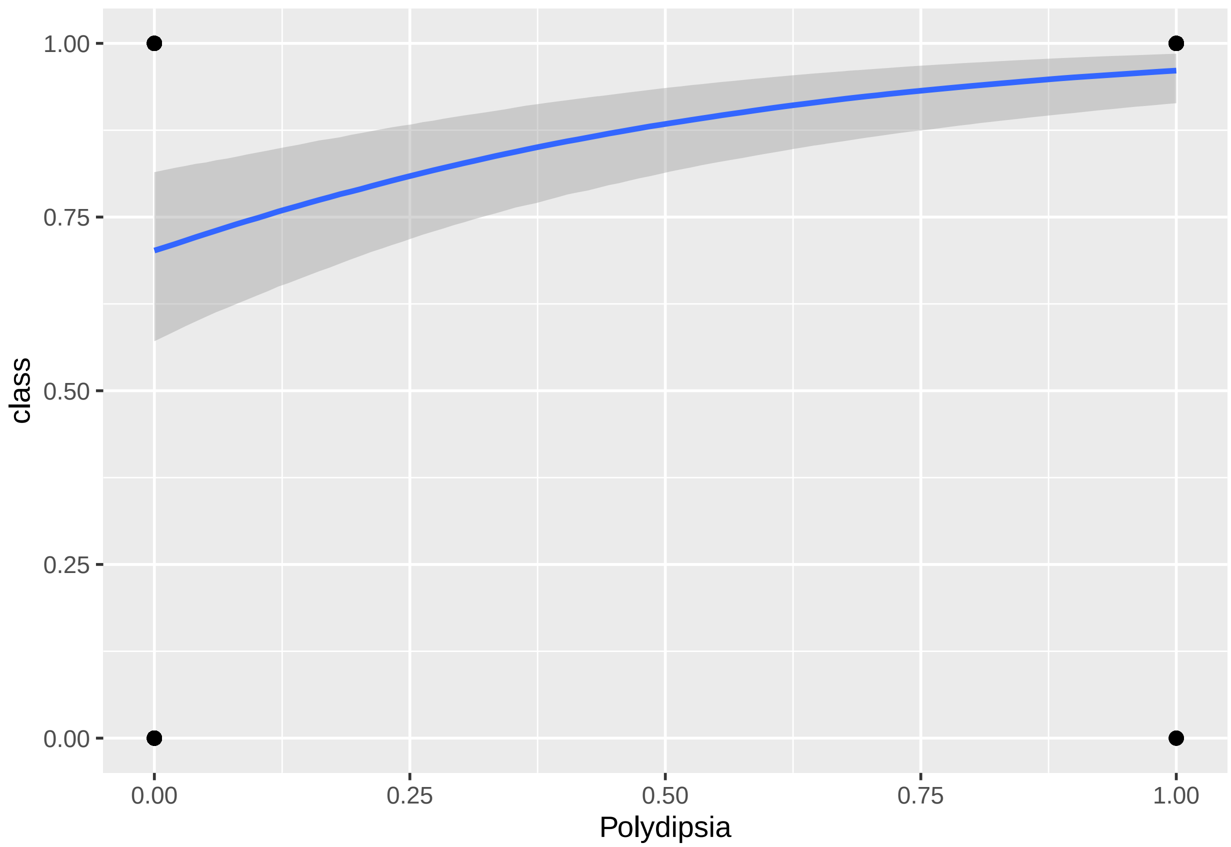
```
print(waic_probit)
```

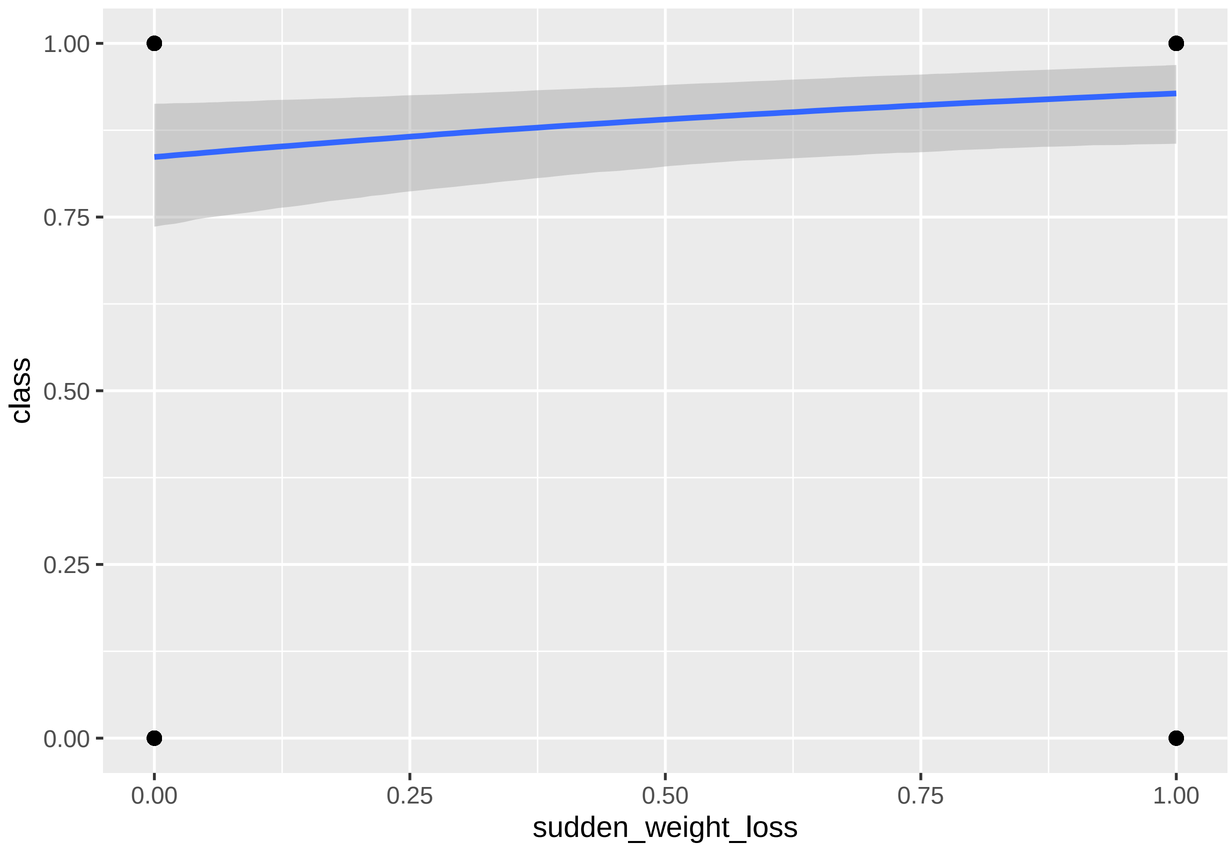
```
##
## Computed from 4000 by 251 log-likelihood matrix.
##
##           Estimate   SE
## elpd_waic    -75.5  8.5
## p_waic        14.4  2.1
## waic         150.9 17.0
##
## 8 (3.2%) p_waic estimates greater than 0.4. We recommend trying loo instead.
```

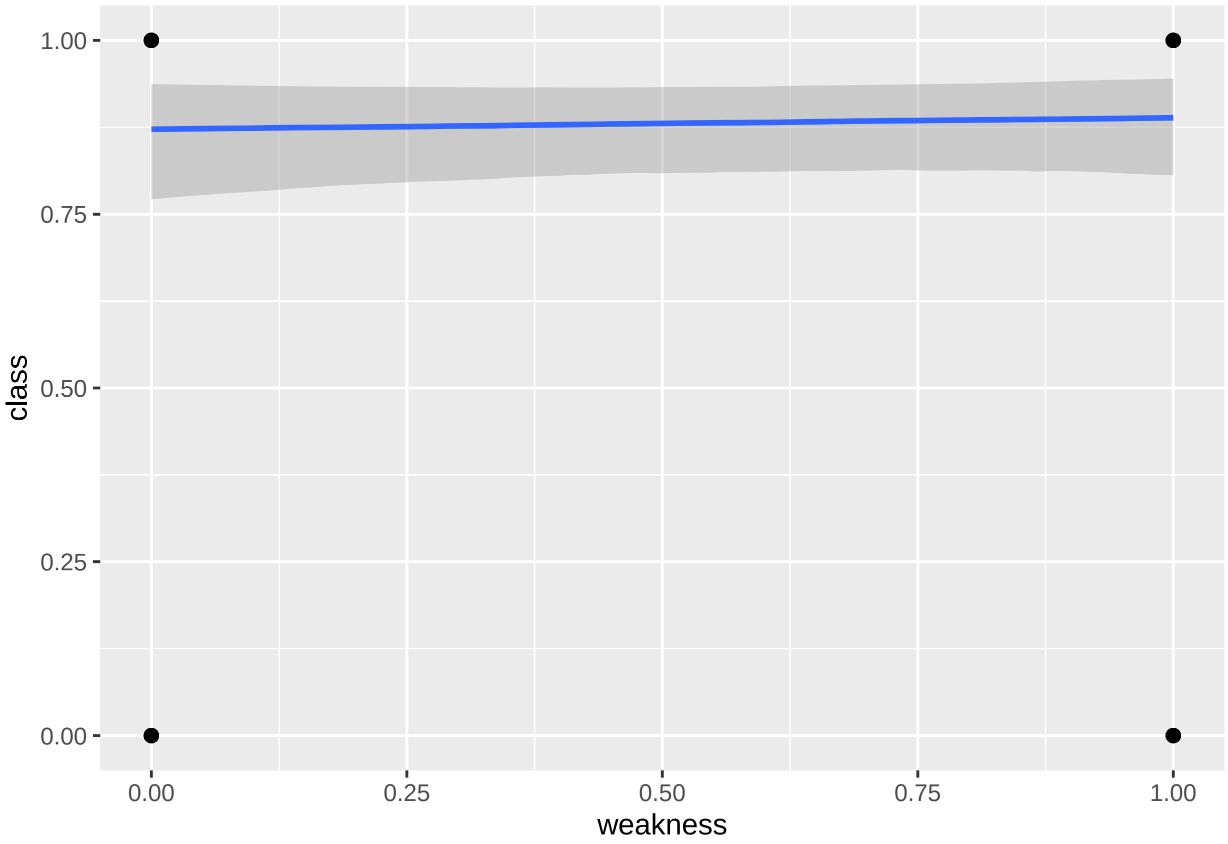
```
#Compare Marginal Effects
# Marginal effects for Logit Model
plot(conditional_effects(fit_logit), points = TRUE)
```

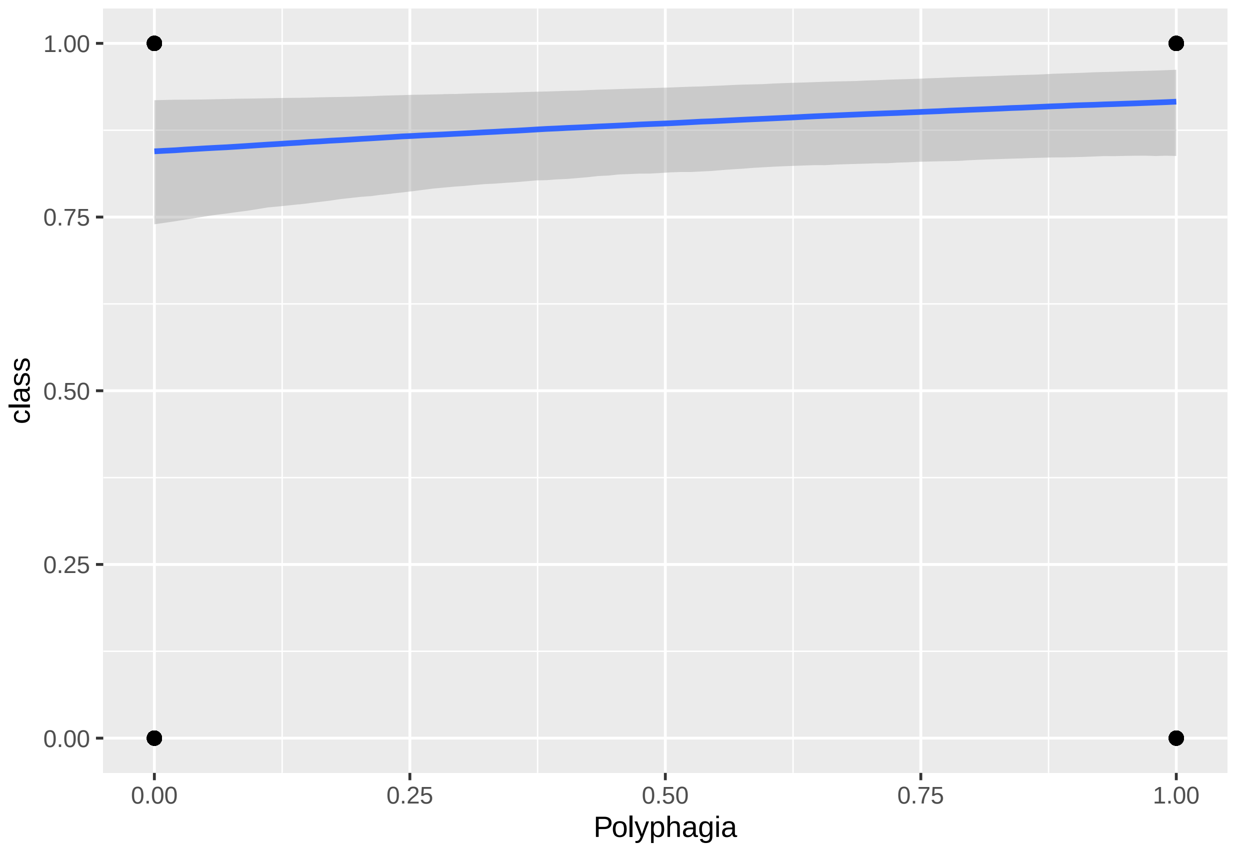


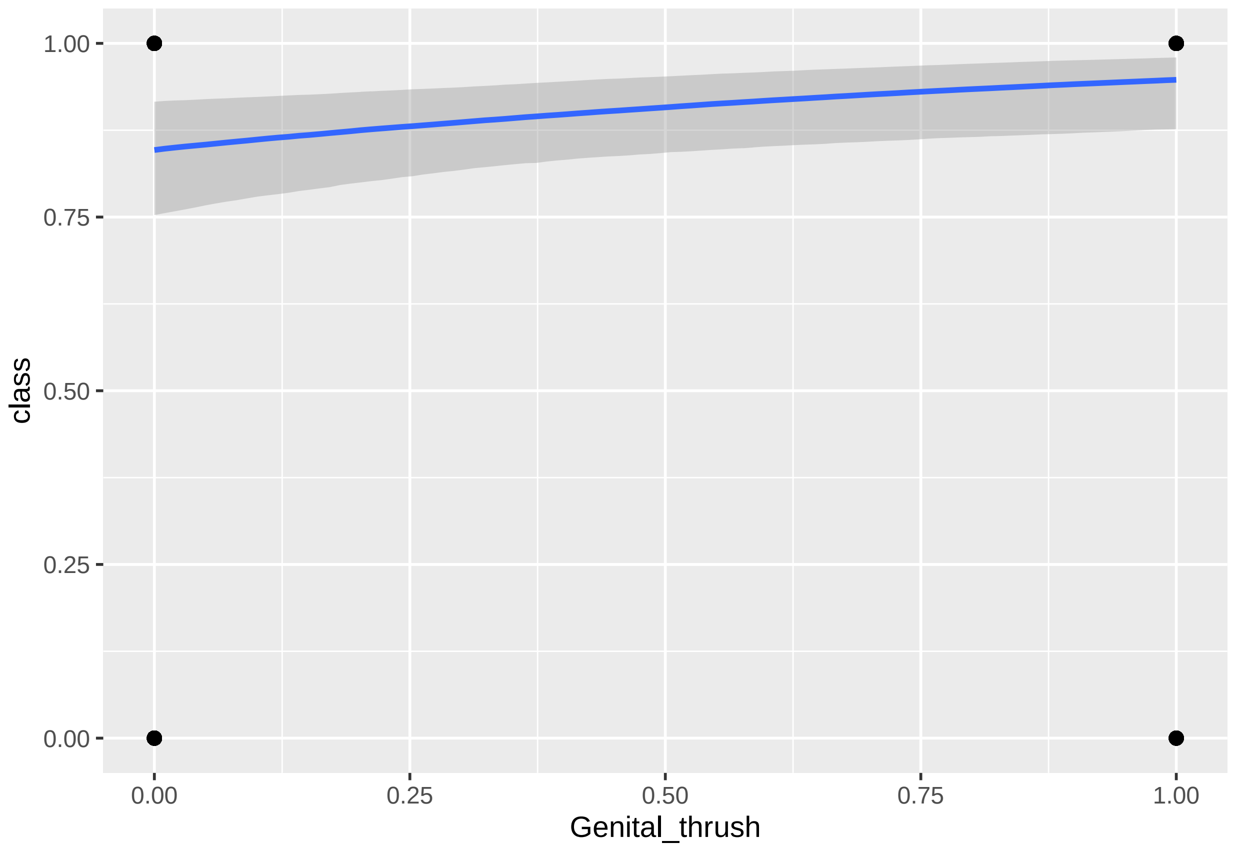

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Polyuria

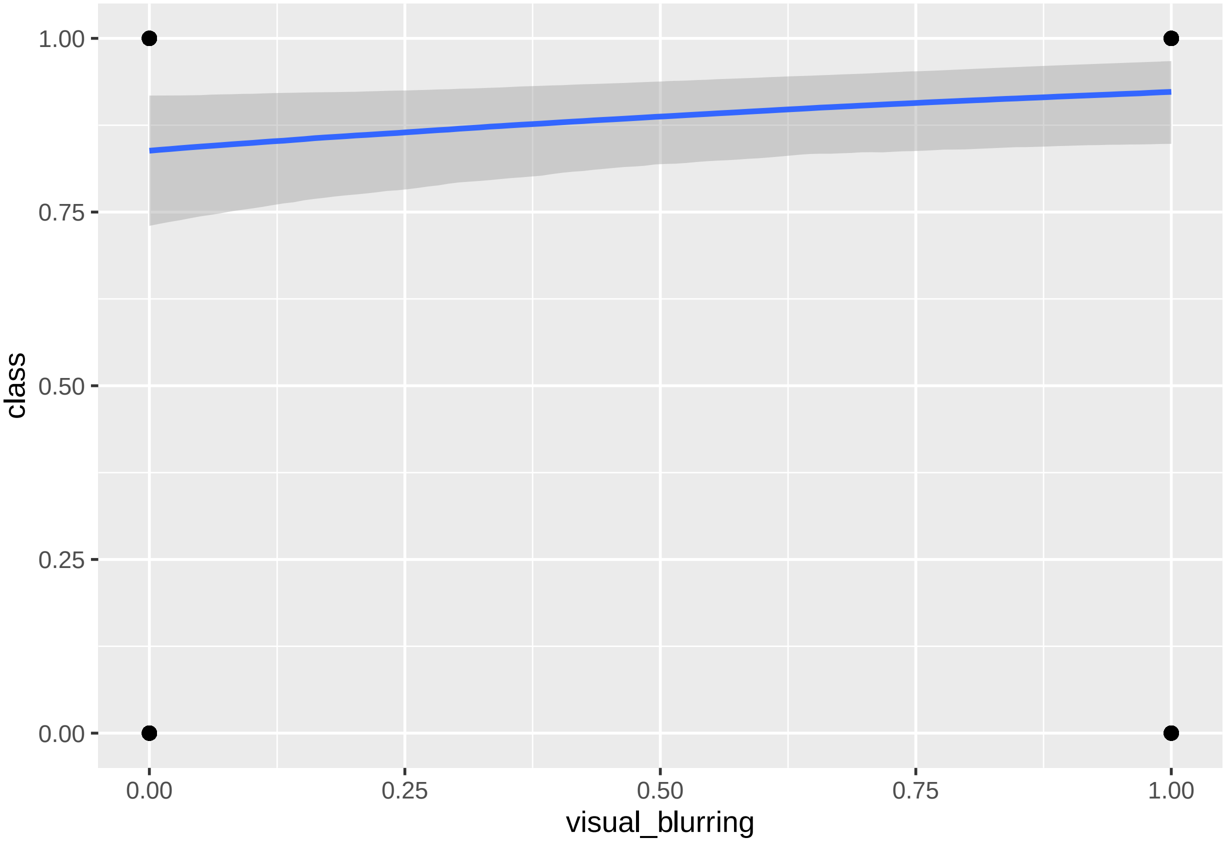

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Polydipsia

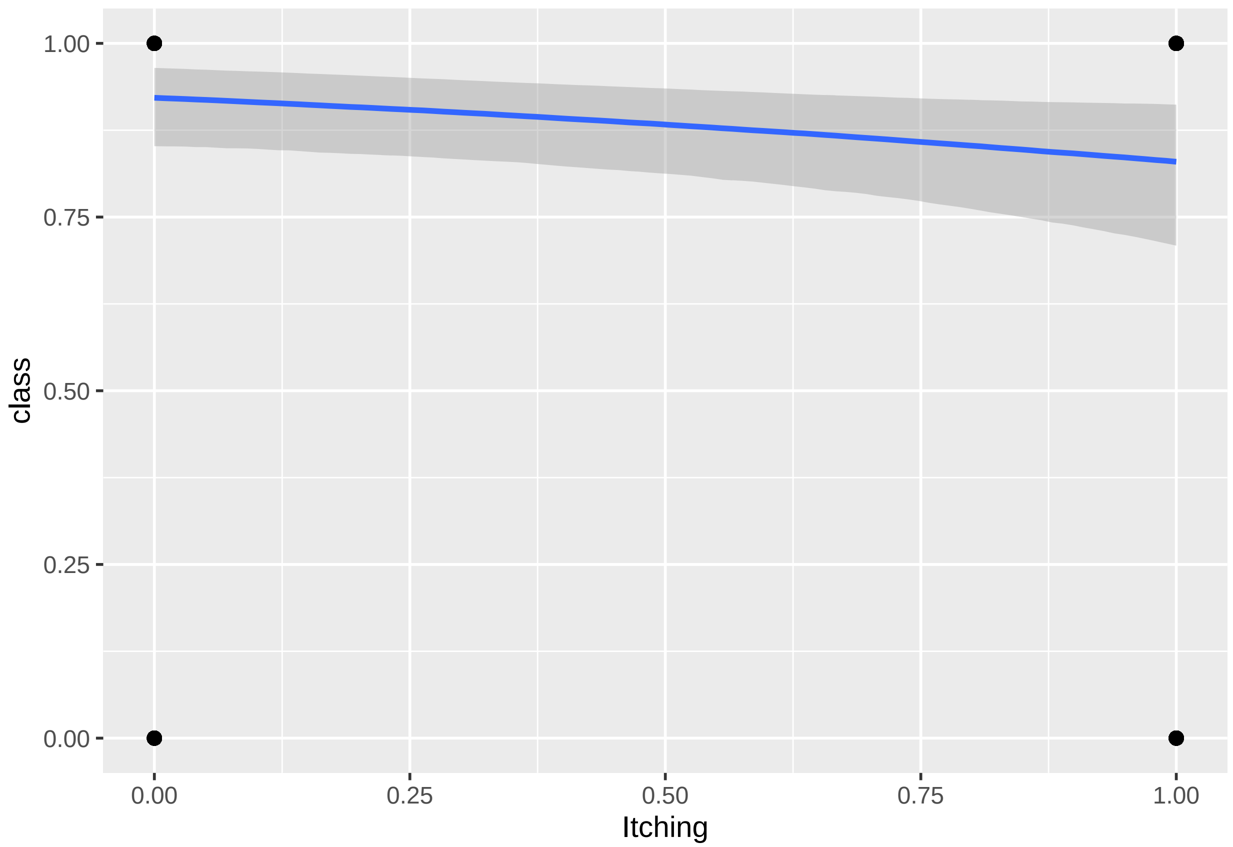

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
sudden_weight_loss

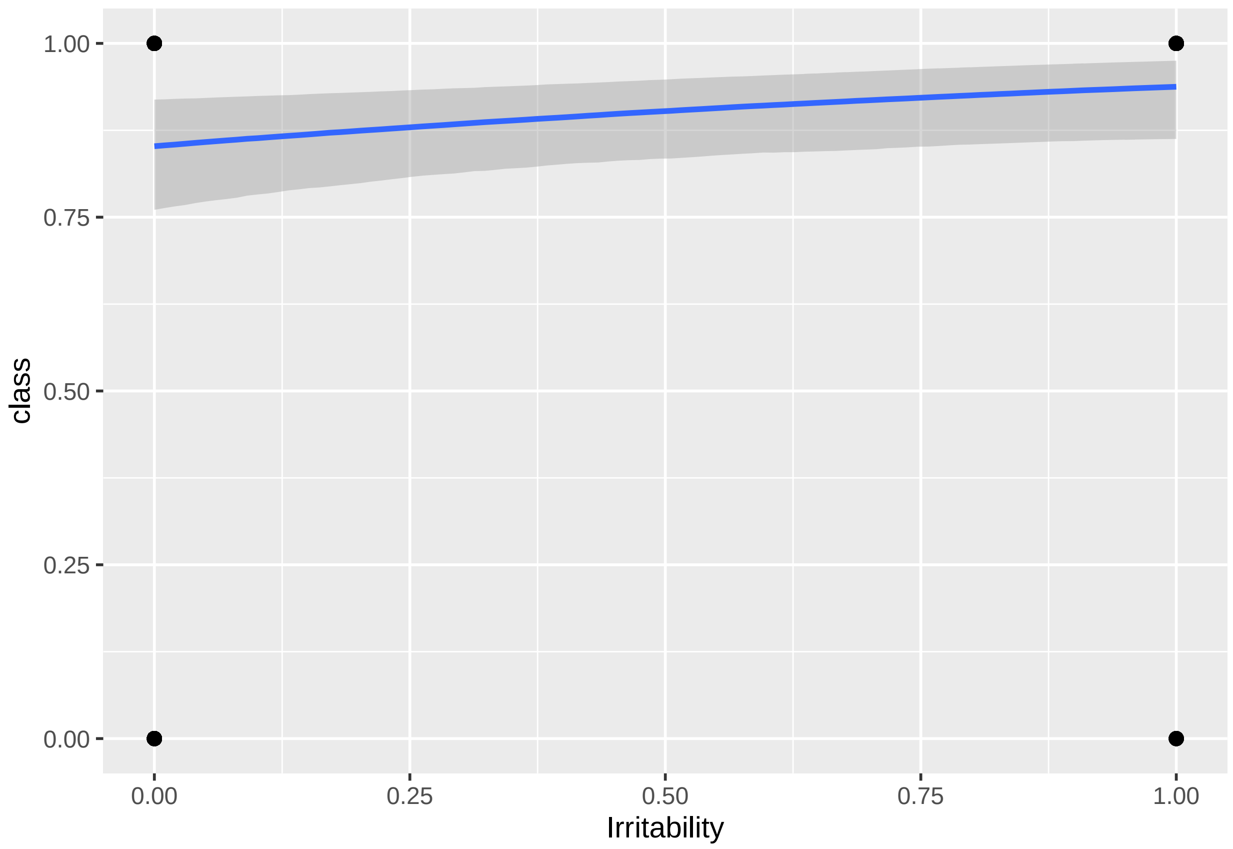

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
weakness

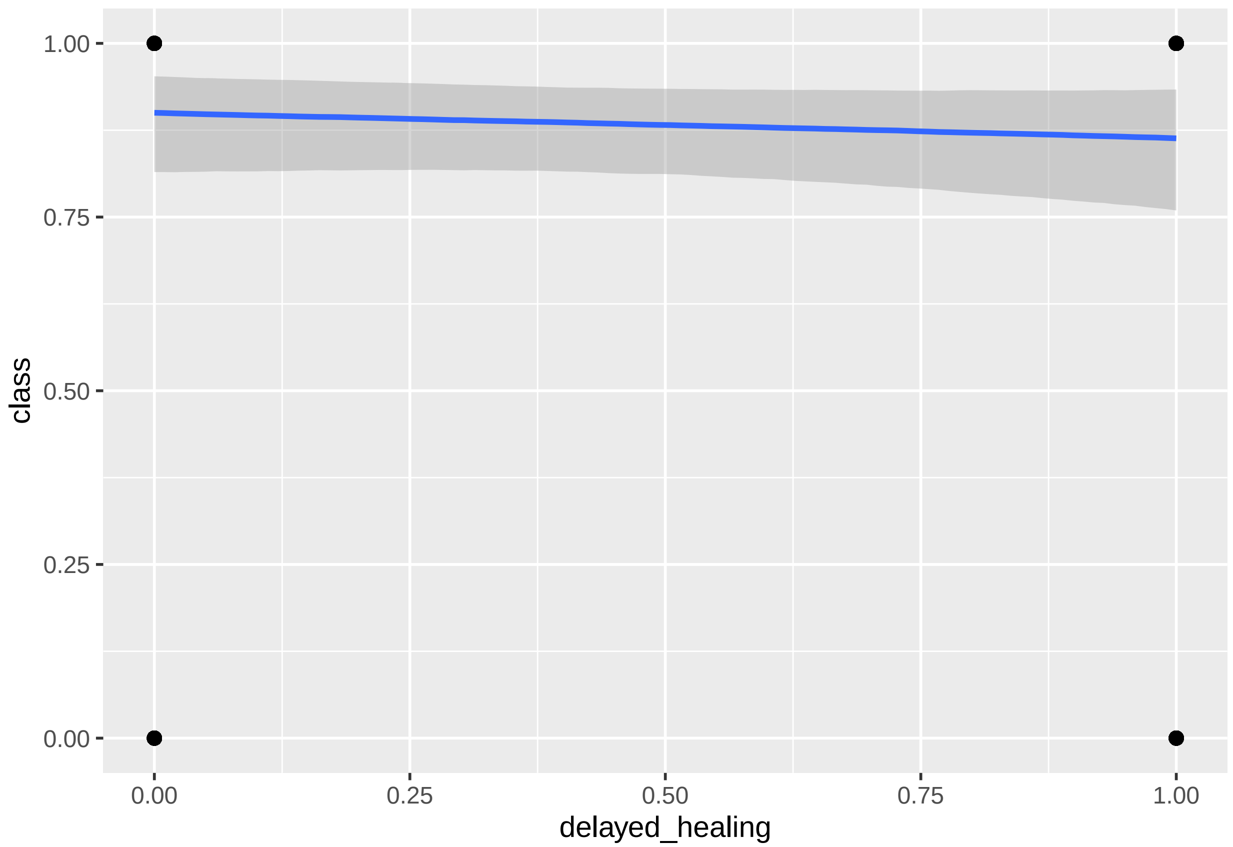

class
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
Polyphagia

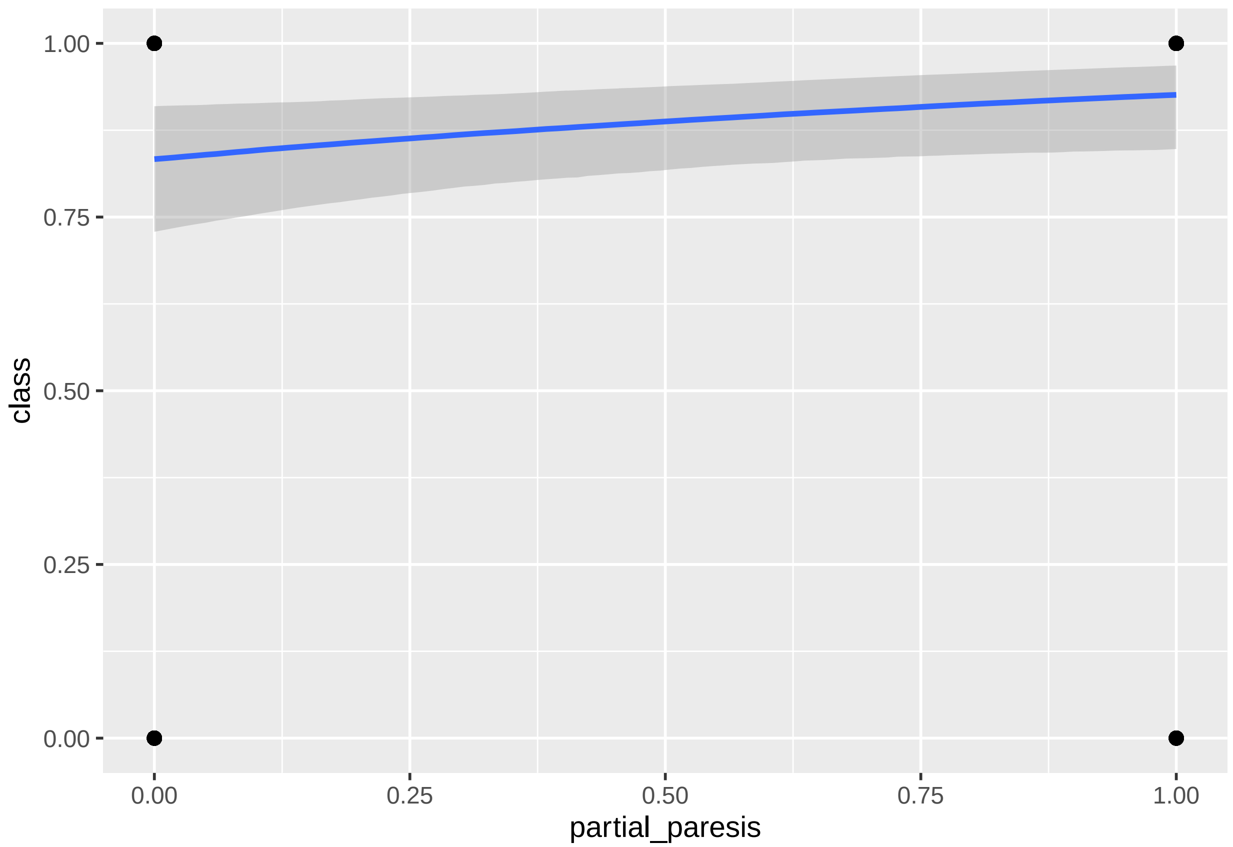

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Genital_thrush

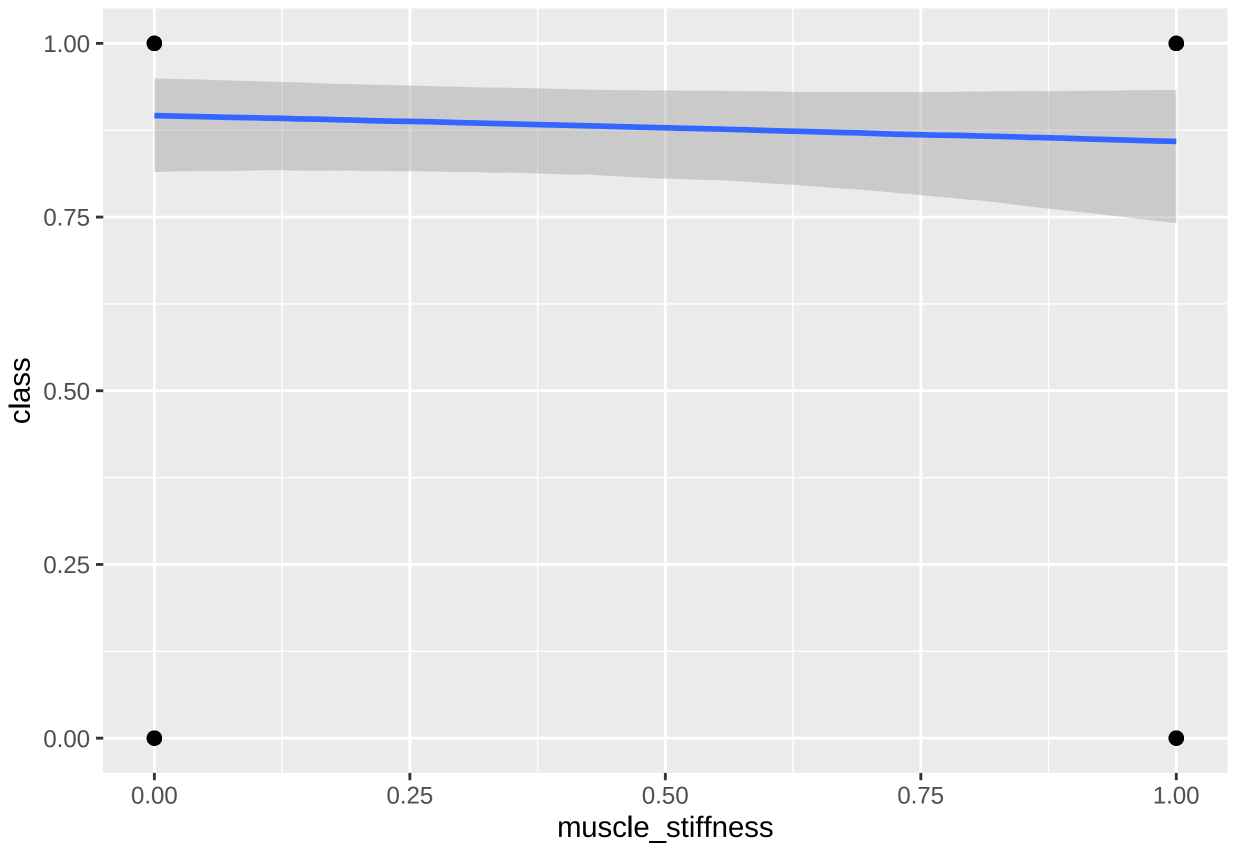

class
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
visual_blurring

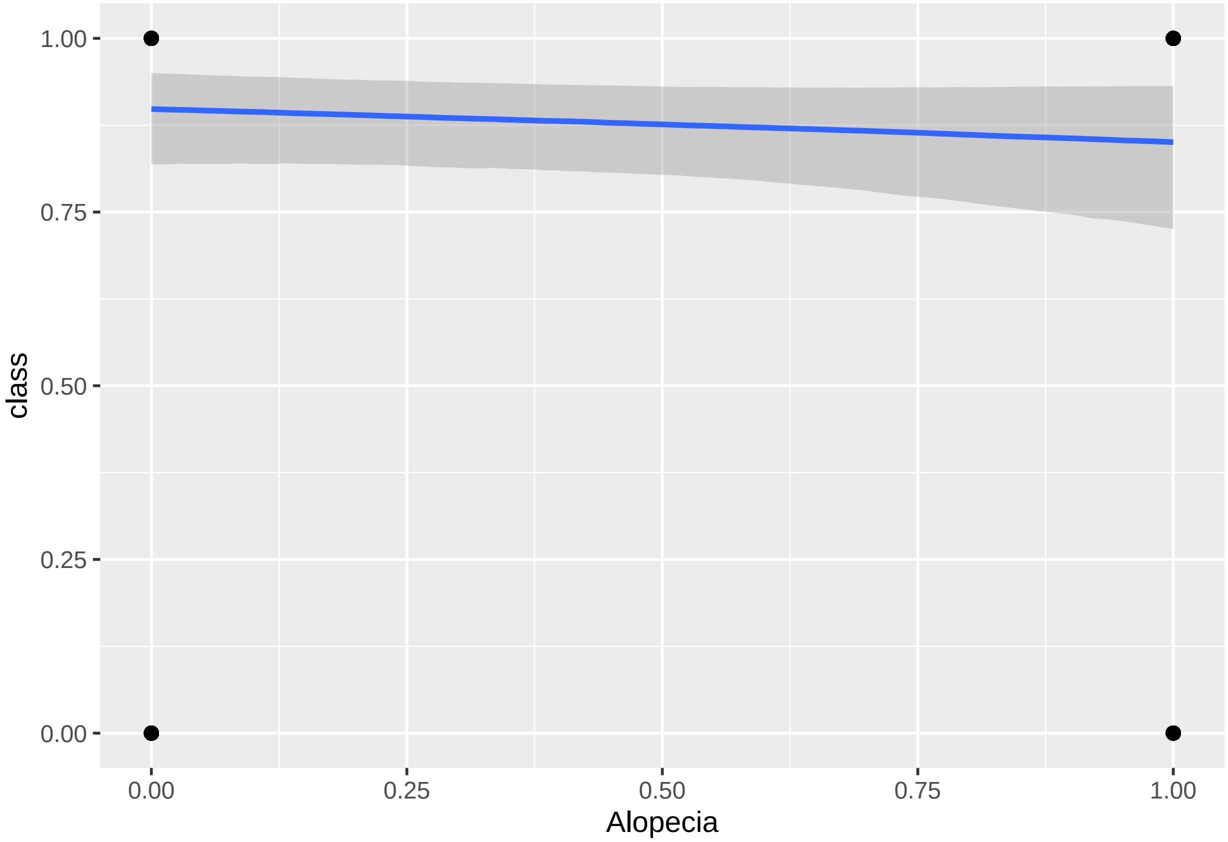

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Itching

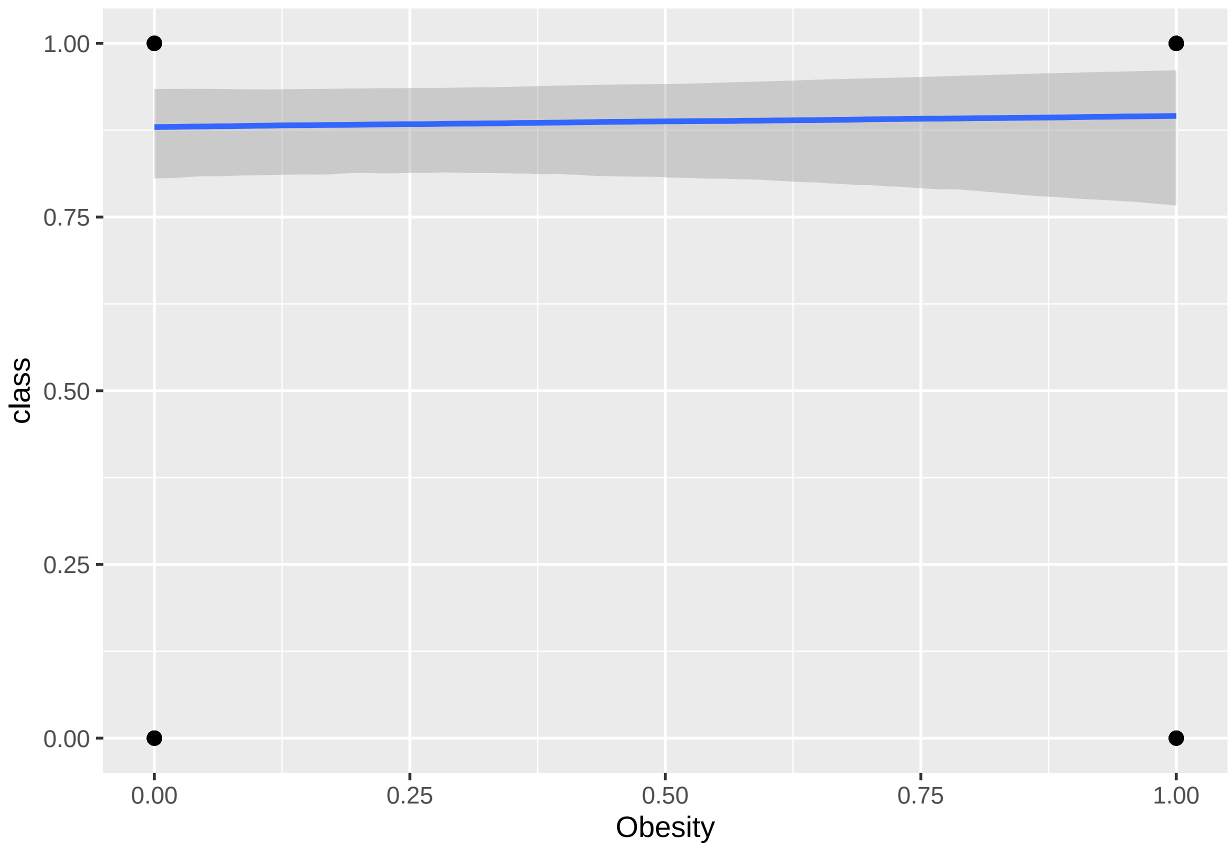

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Irritability


1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
delayed_healing

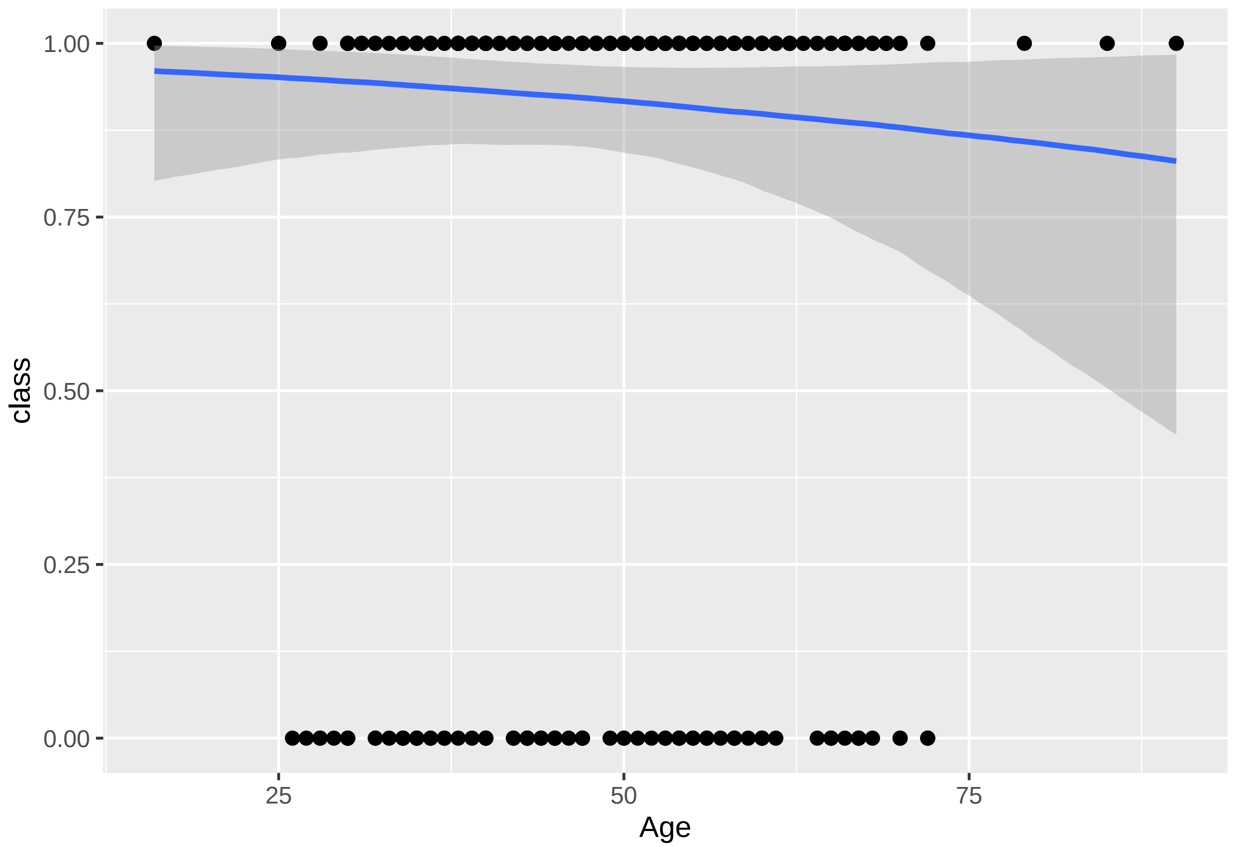

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
partial_paresis

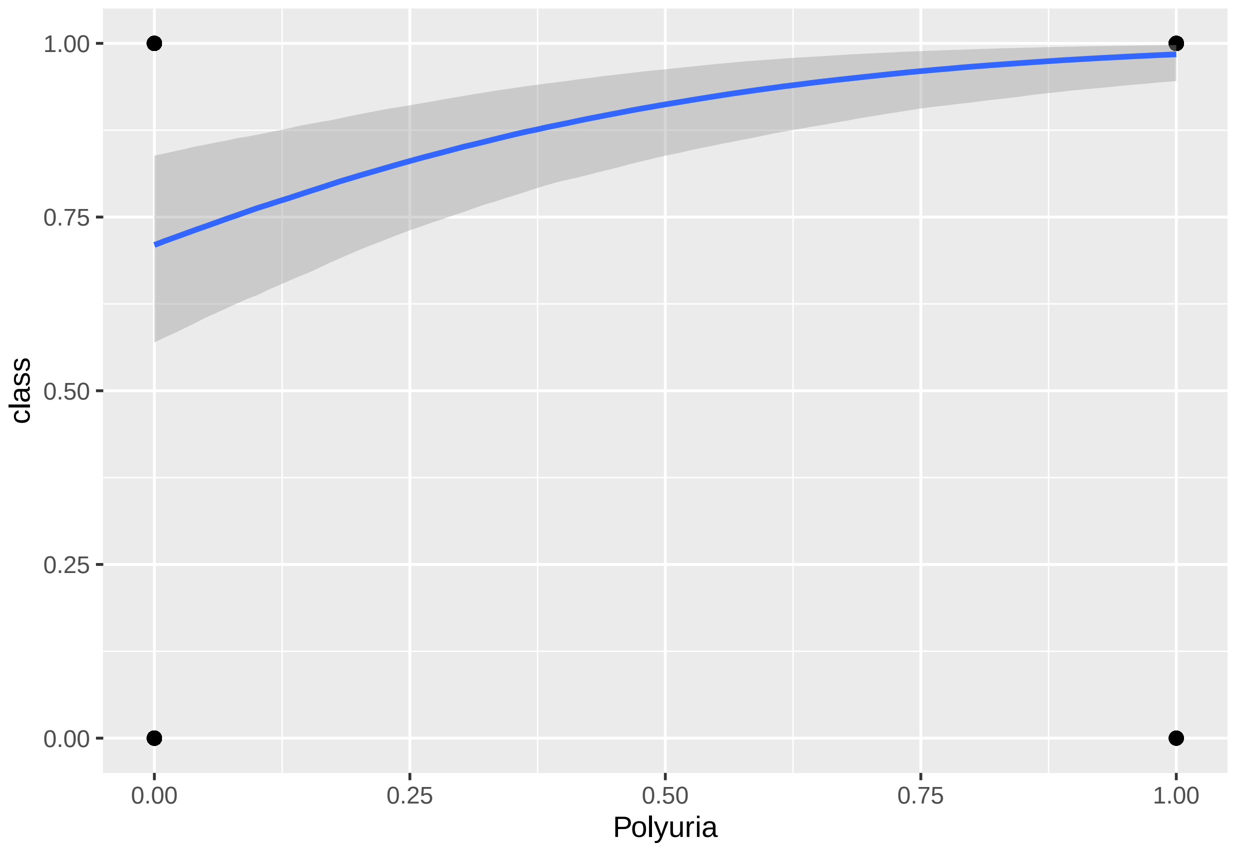

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
muscle_stiffness

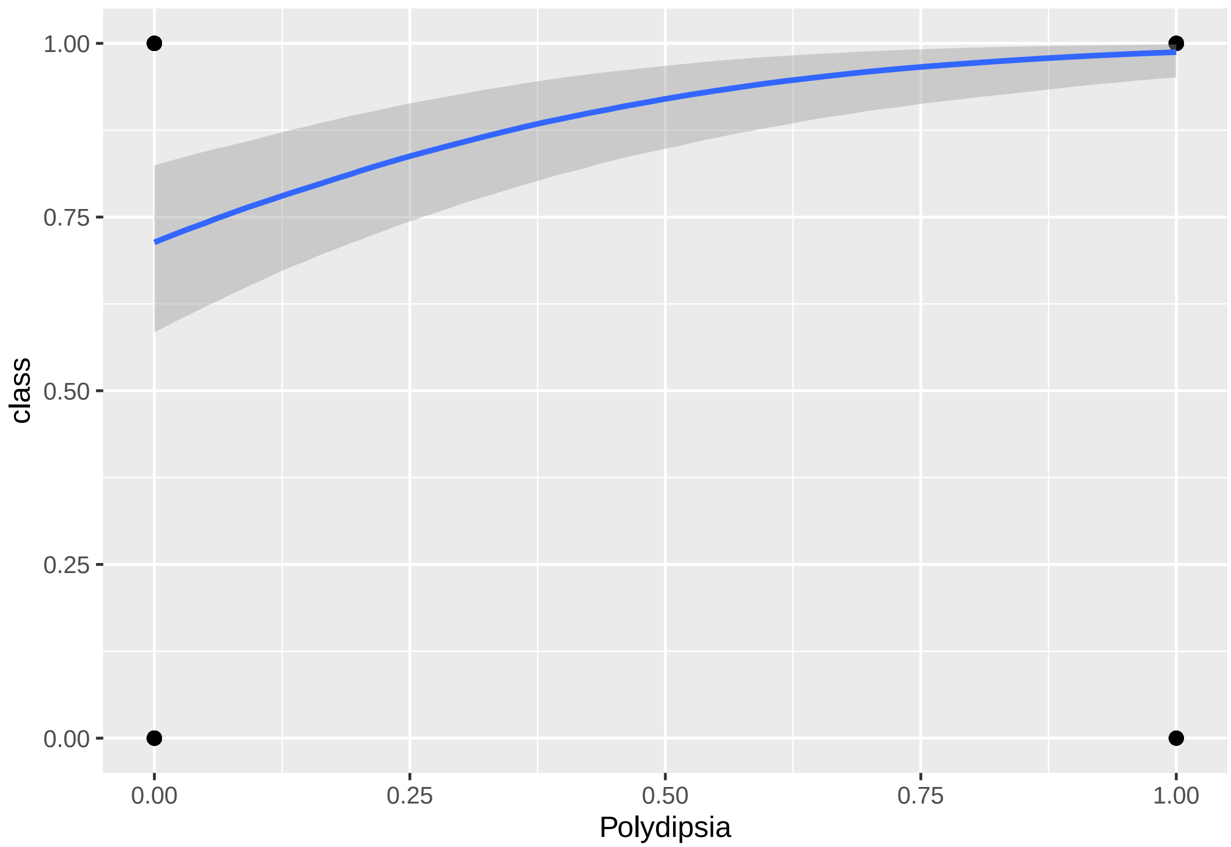

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Alopecia

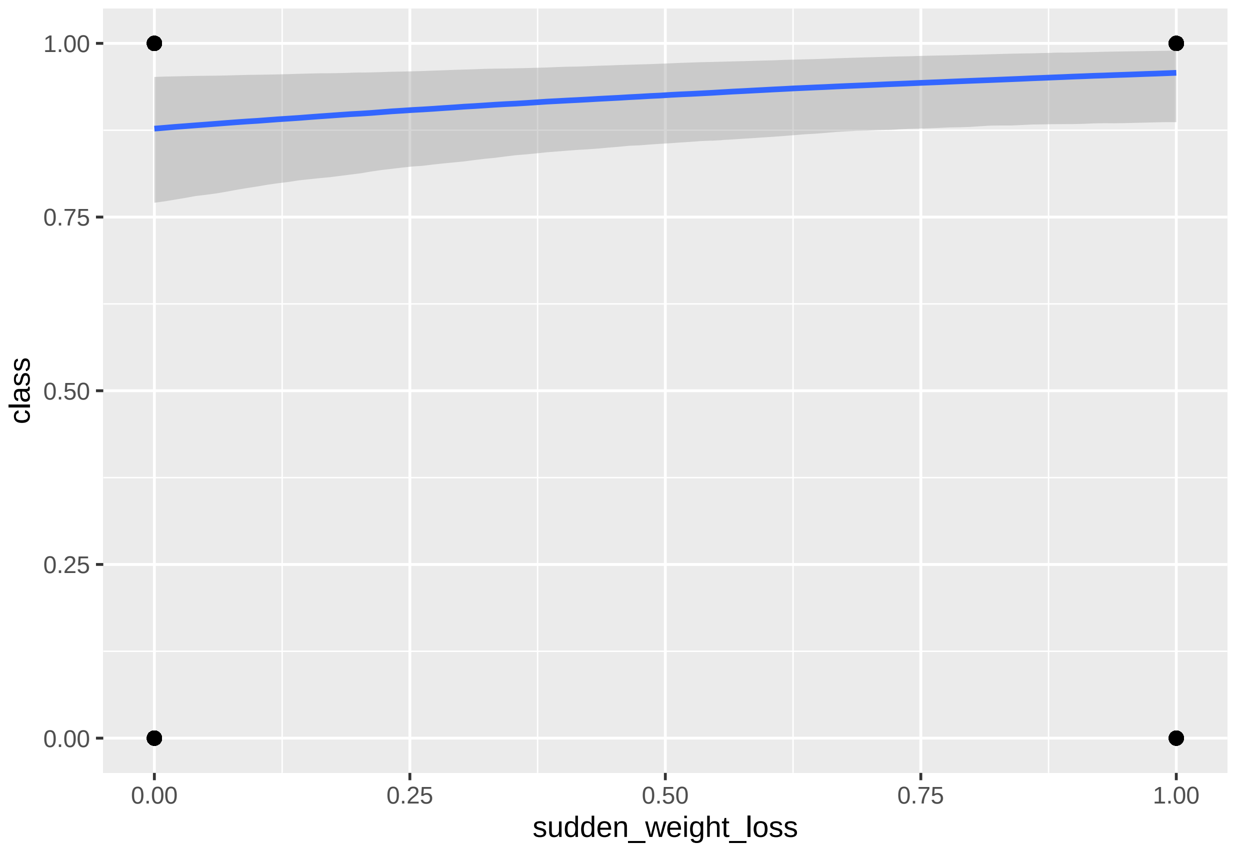


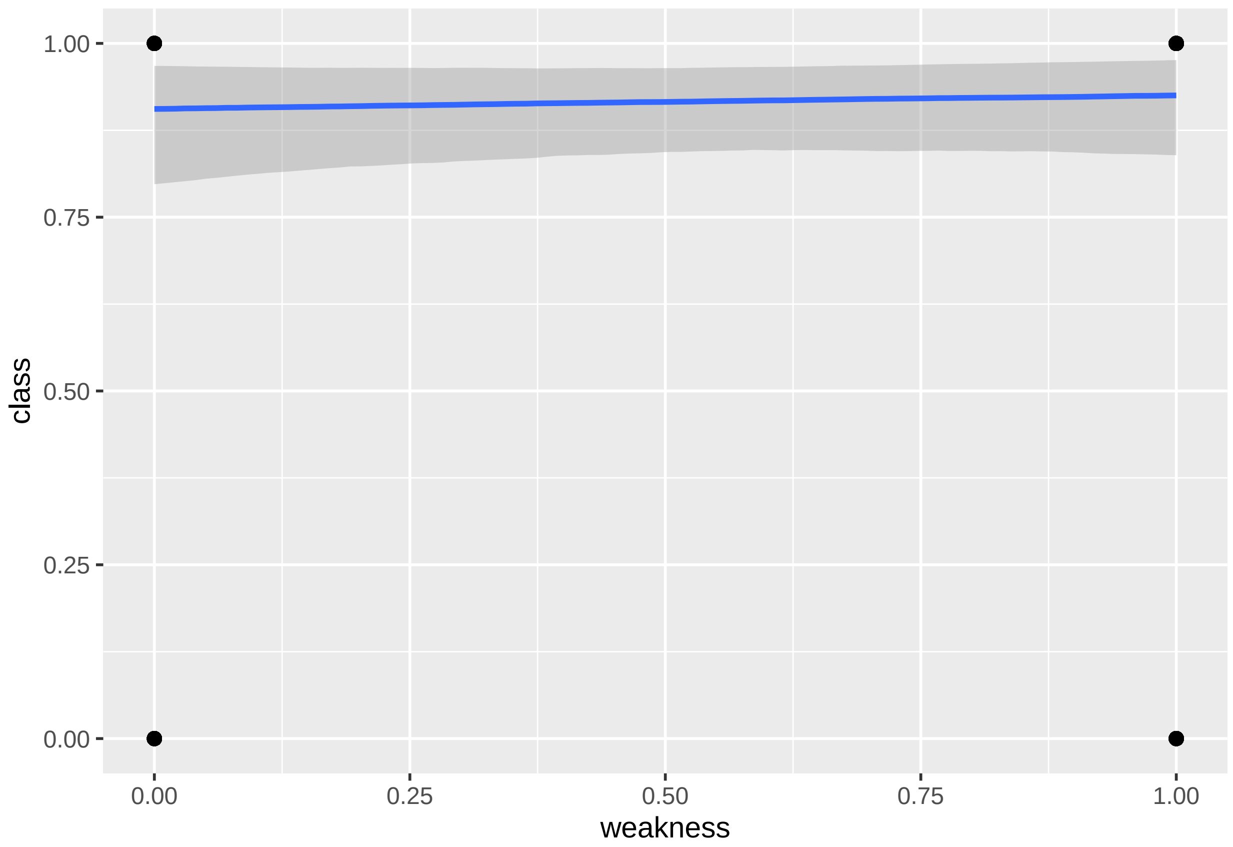
```
# Marginal effects for Probit Model
plot(conditional_effects(fit_probit), points = TRUE)
```

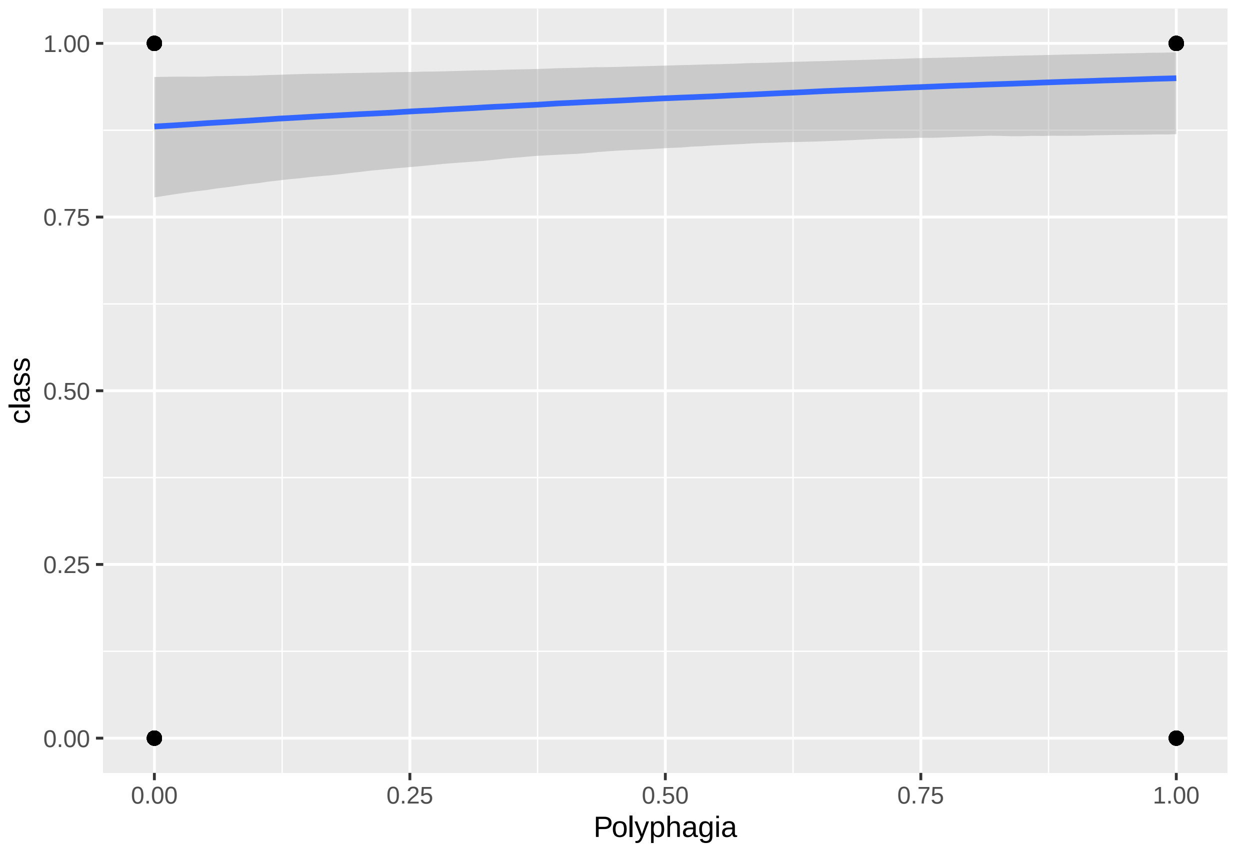

1.00
0.75
0.50
0.25
0.00
class
25
50
75
Age

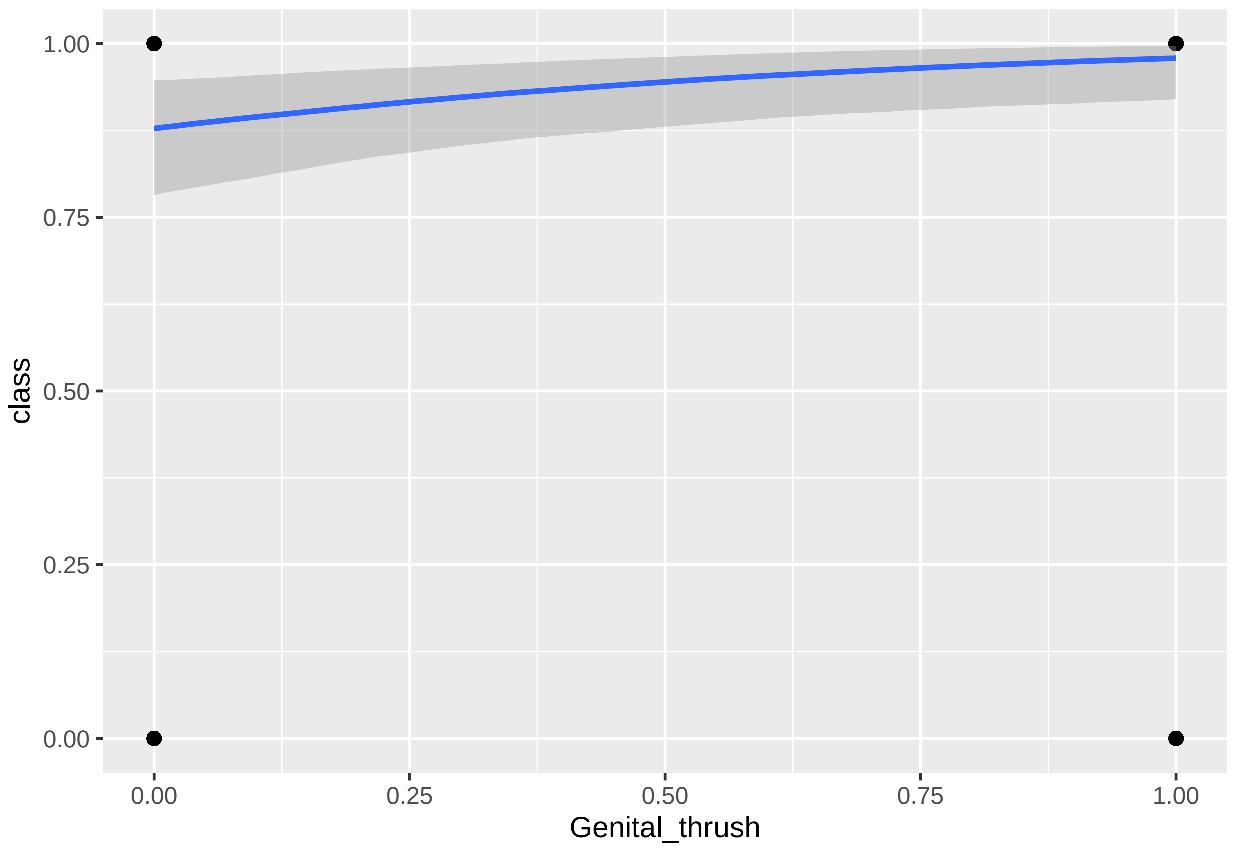

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Polyuria

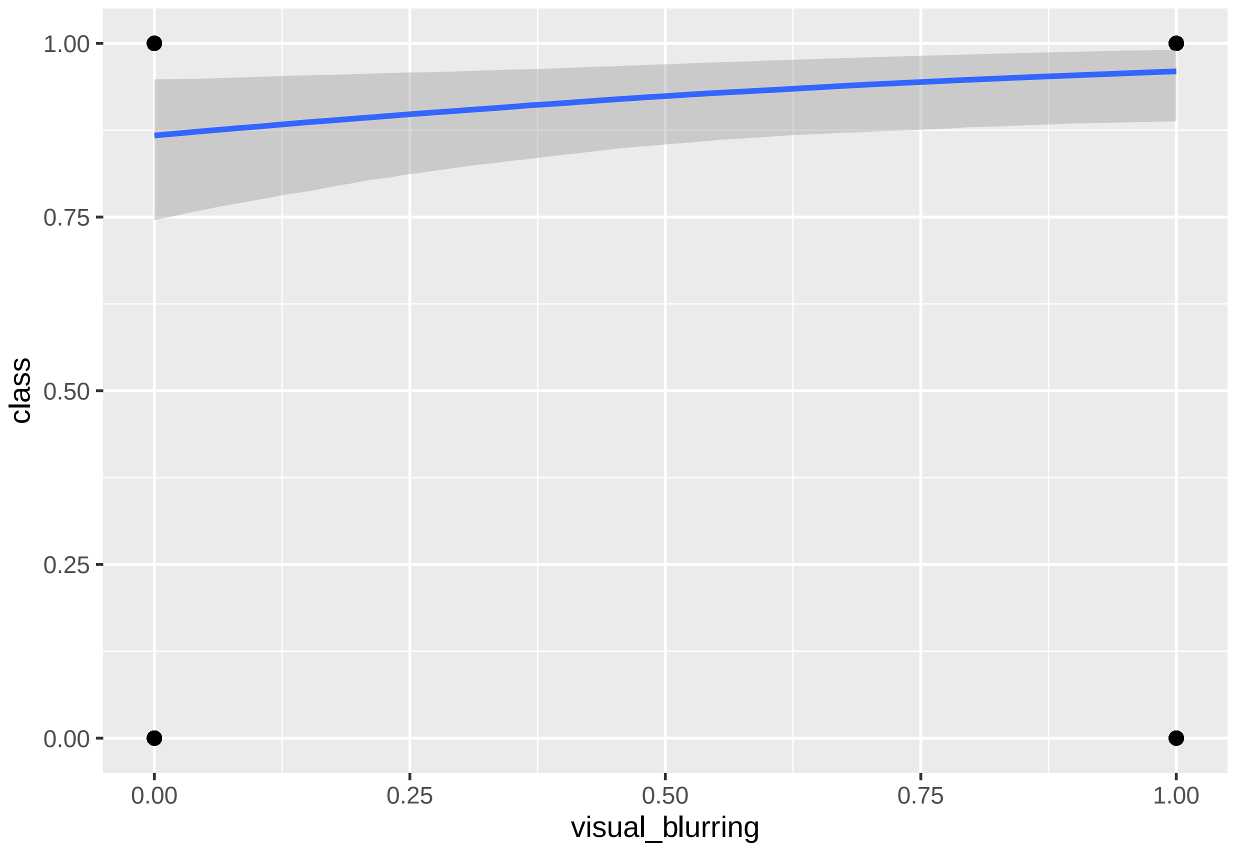

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Polydipsia

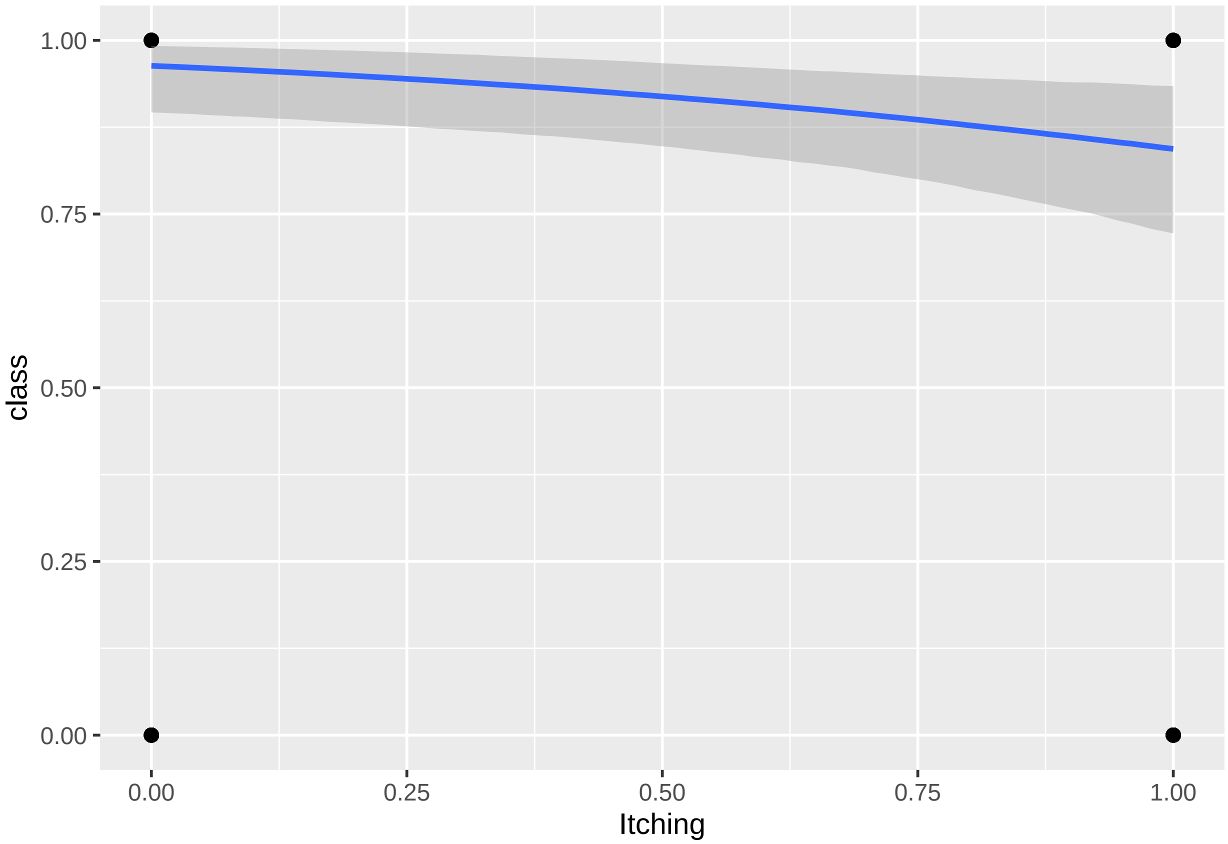

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
sudden_weight_loss

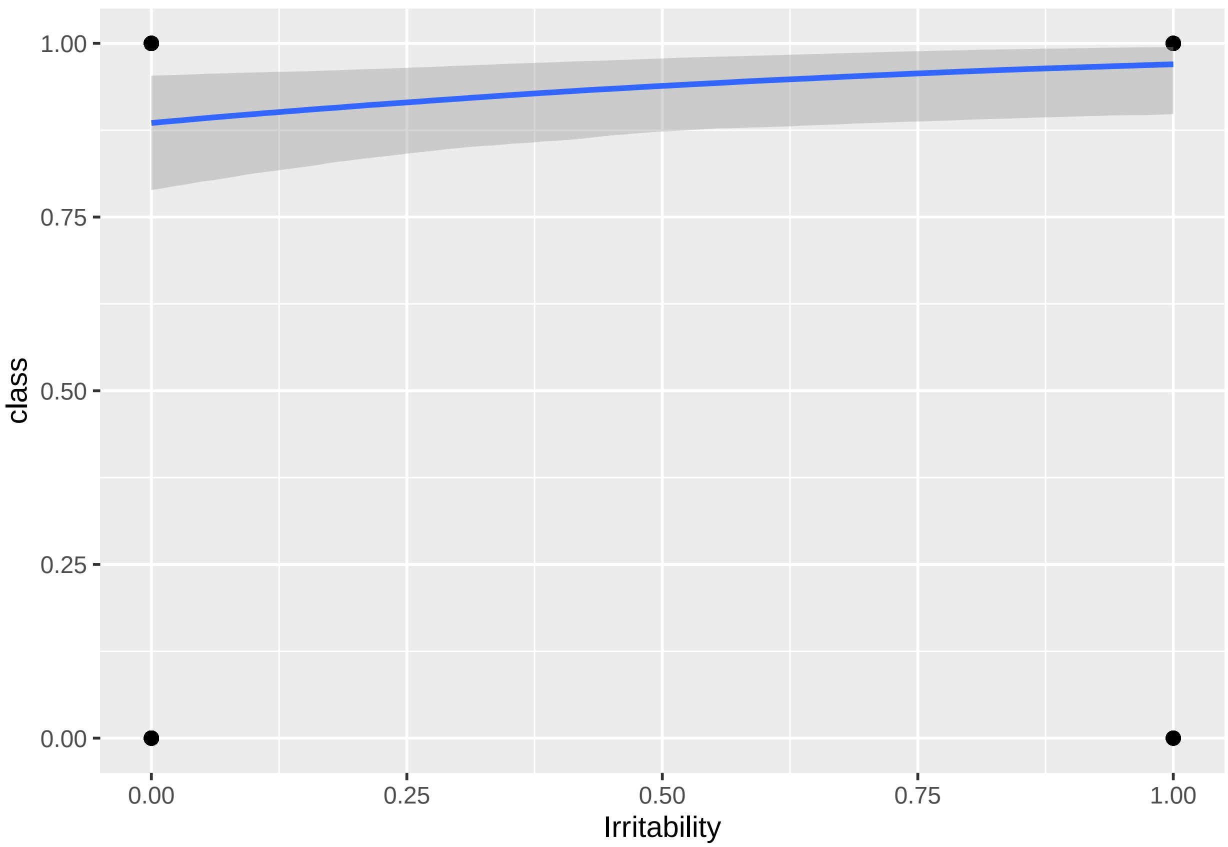

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
weakness

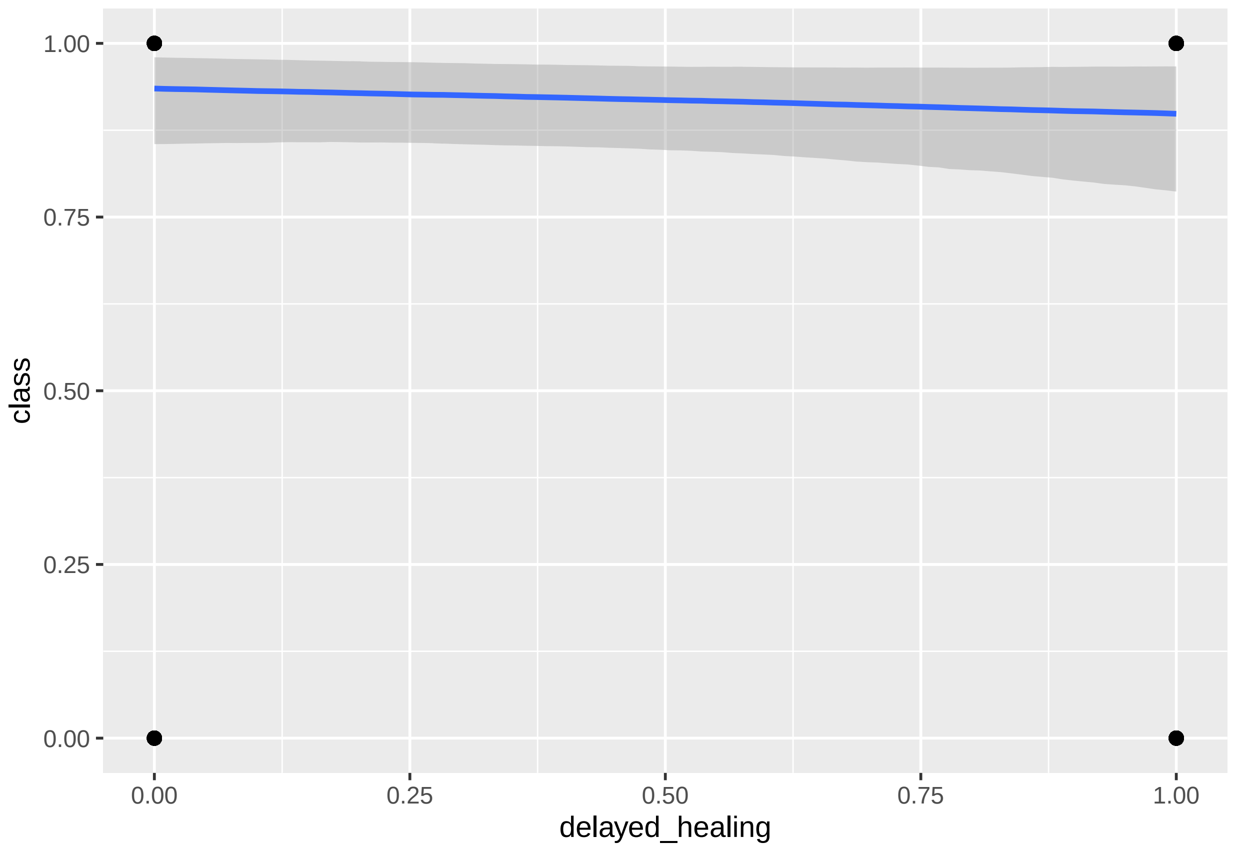

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Polyphagia

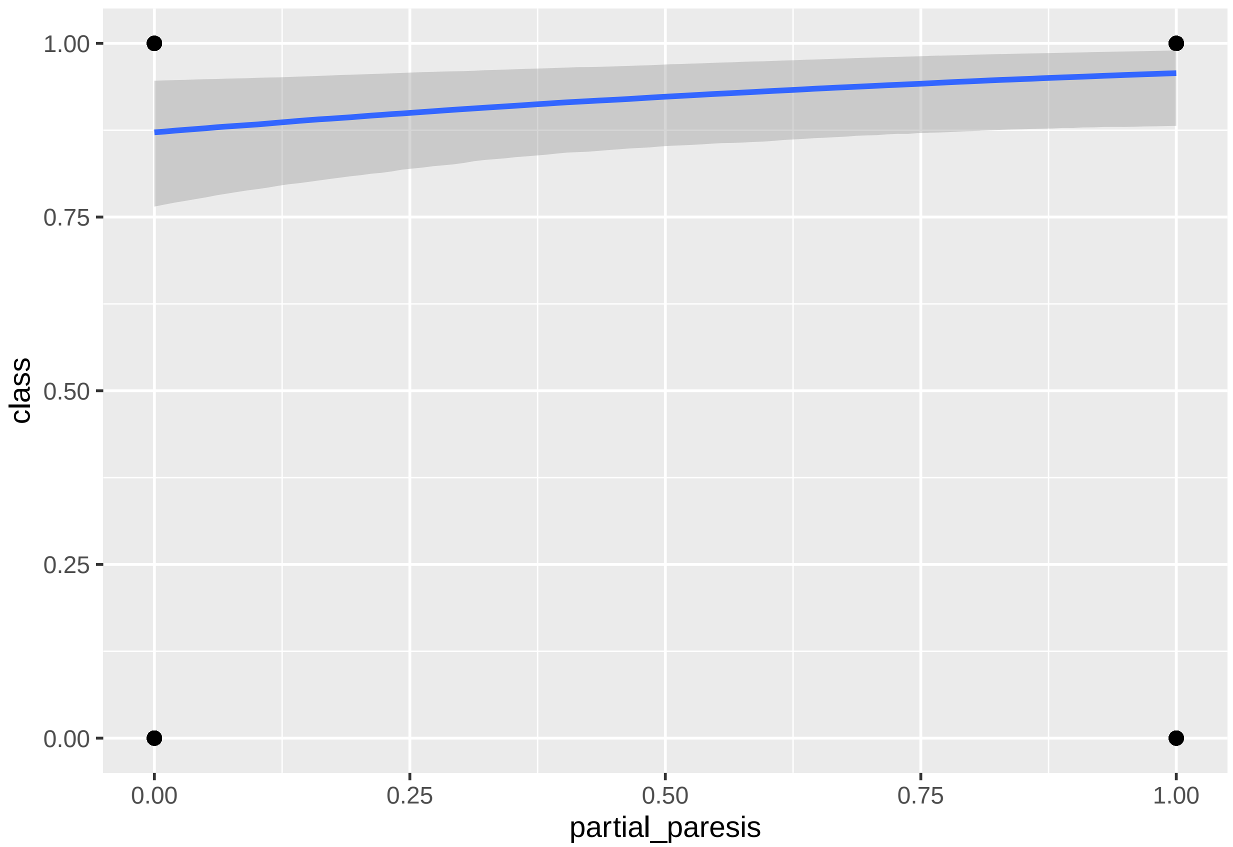

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Genital_thrush

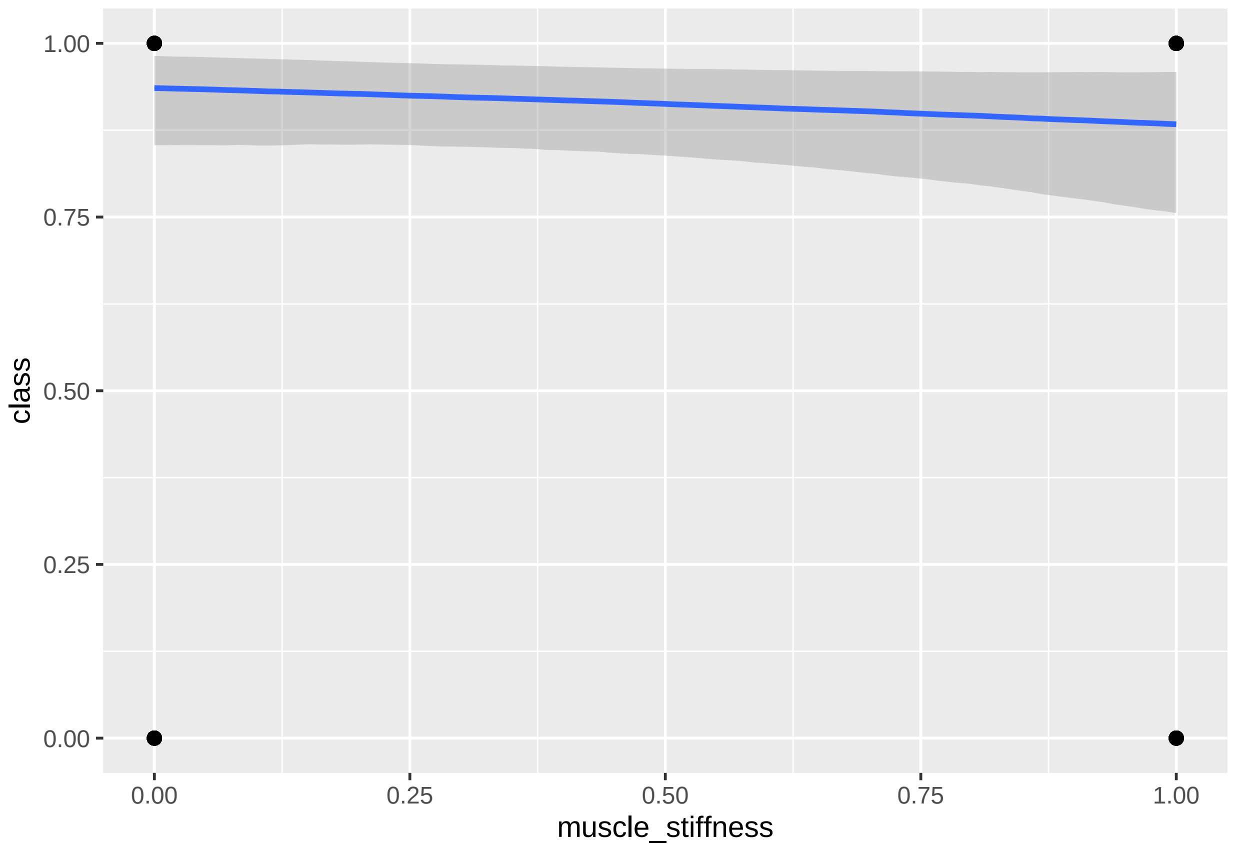

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
visual_blurring


class
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
Itching

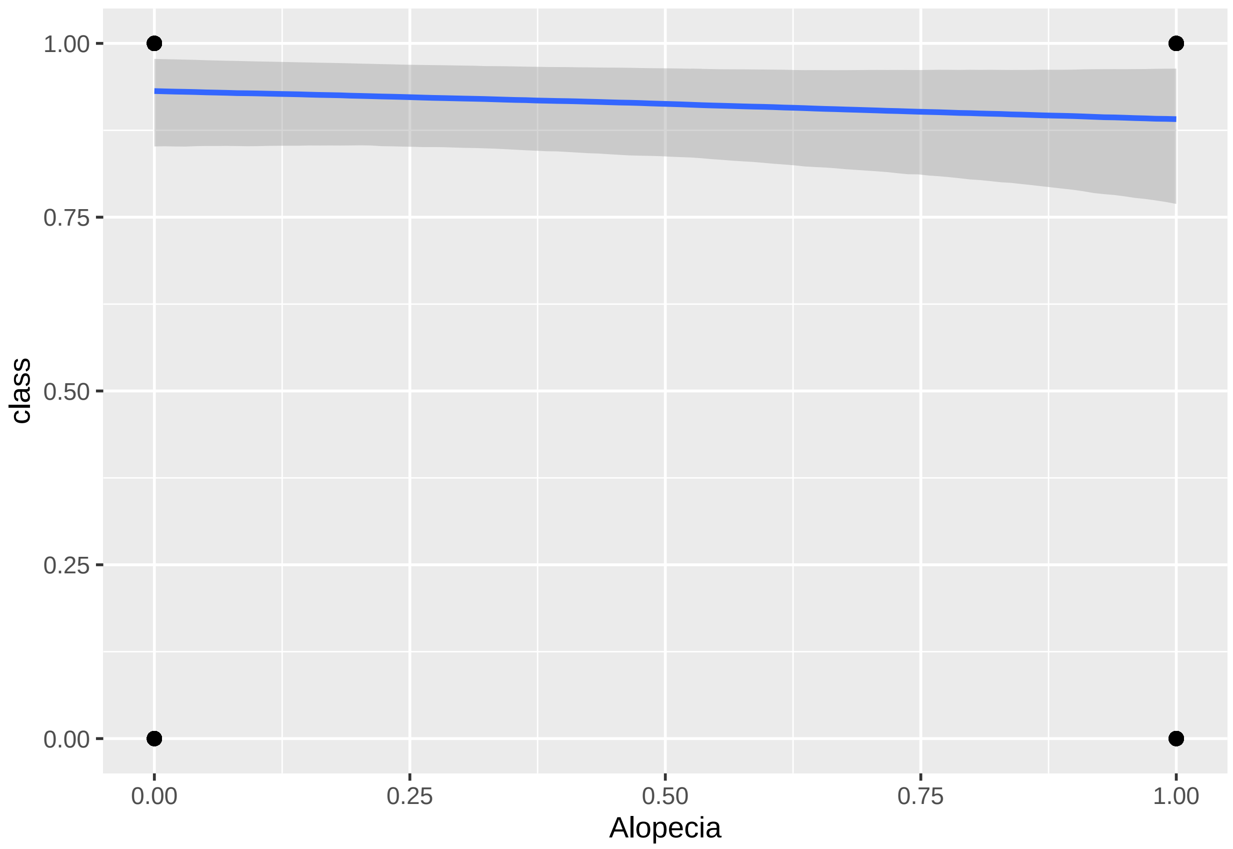

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Irritability

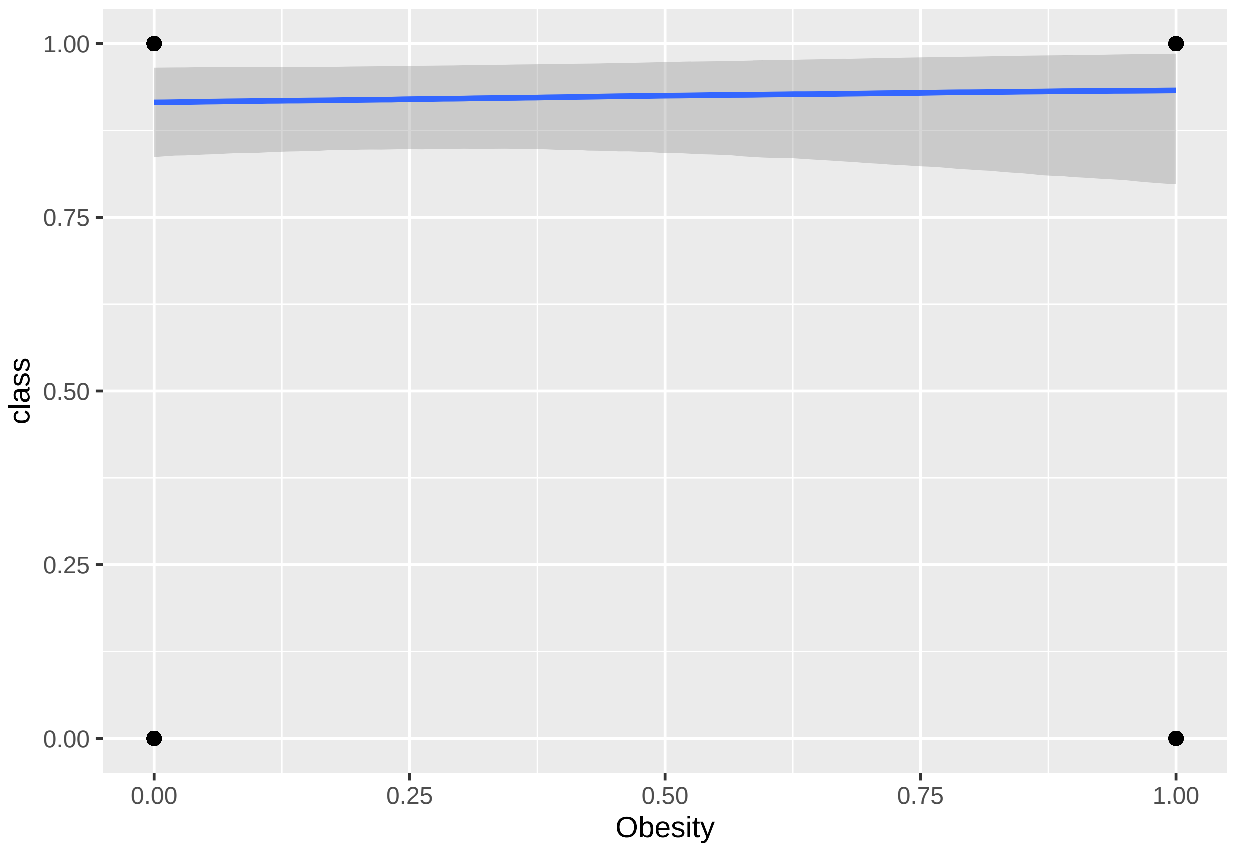

1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
delayed_healing


1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
partial_paresis



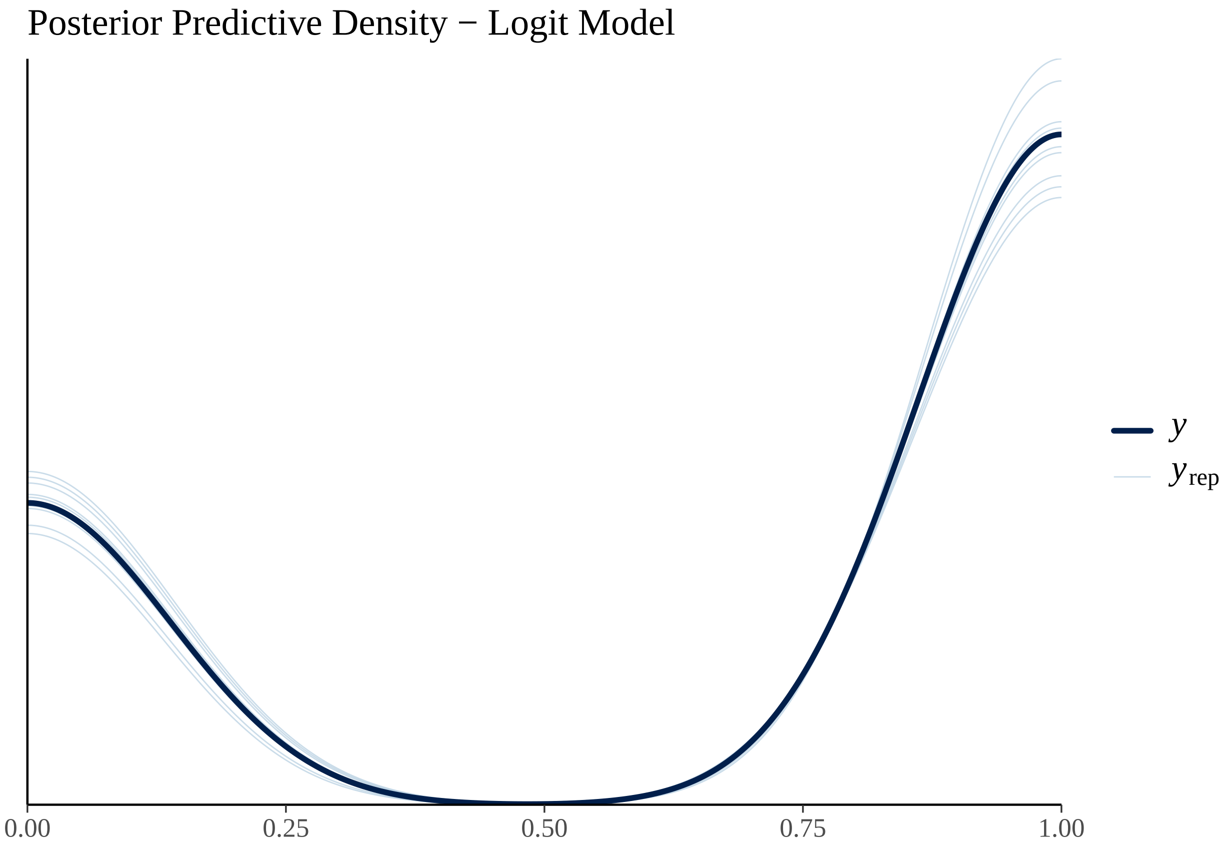
class
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
muscle_stiffness


1.00
0.75
0.50
0.25
0.00
class
0.00
0.25
0.50
0.75
1.00
Alopecia



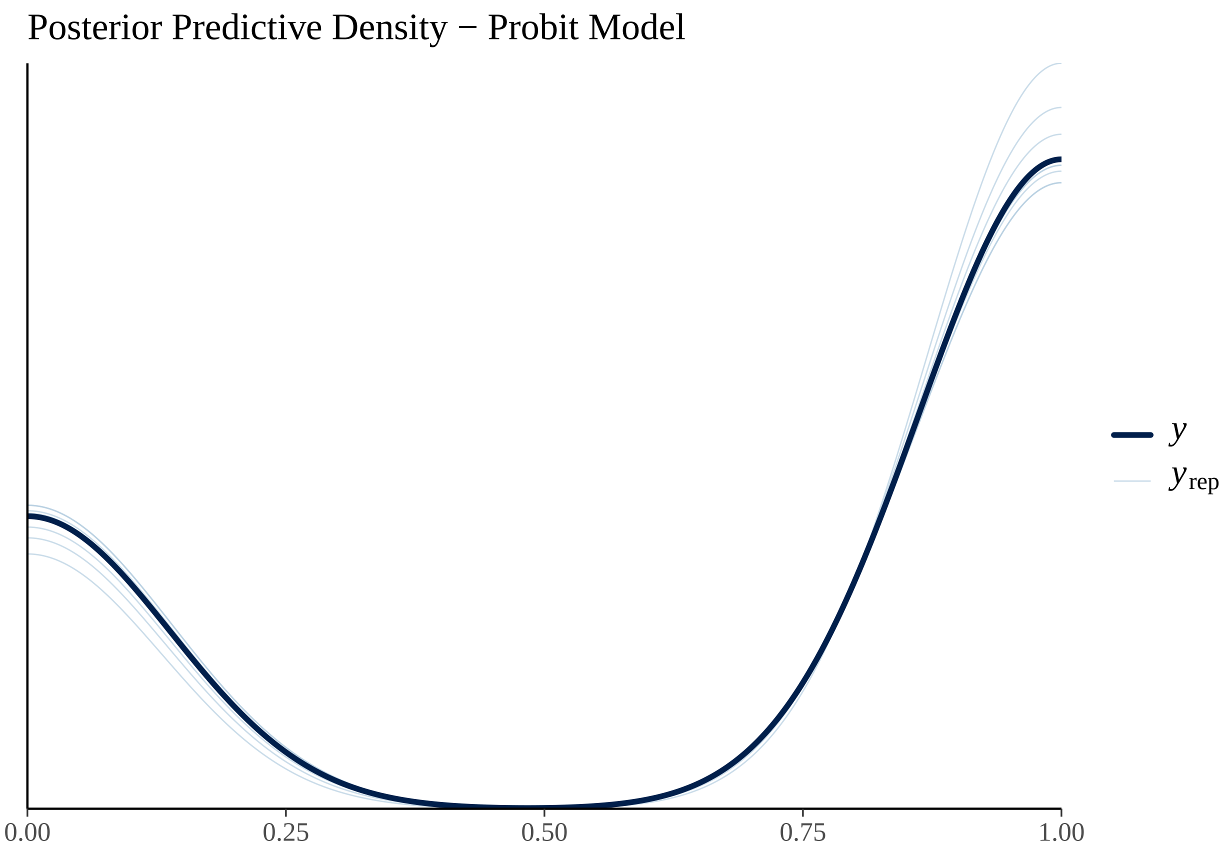
```
# Generate posterior predictive samples for both models
pp_logit <- posterior_predict(fit_logit)
pp_probit <- posterior_predict(fit_probit)

# Create density overlay plots for individual models
pp_check(fit_logit, type = "dens_overlay") +
  ggtitle("Posterior Predictive Density - Logit Model")
```

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



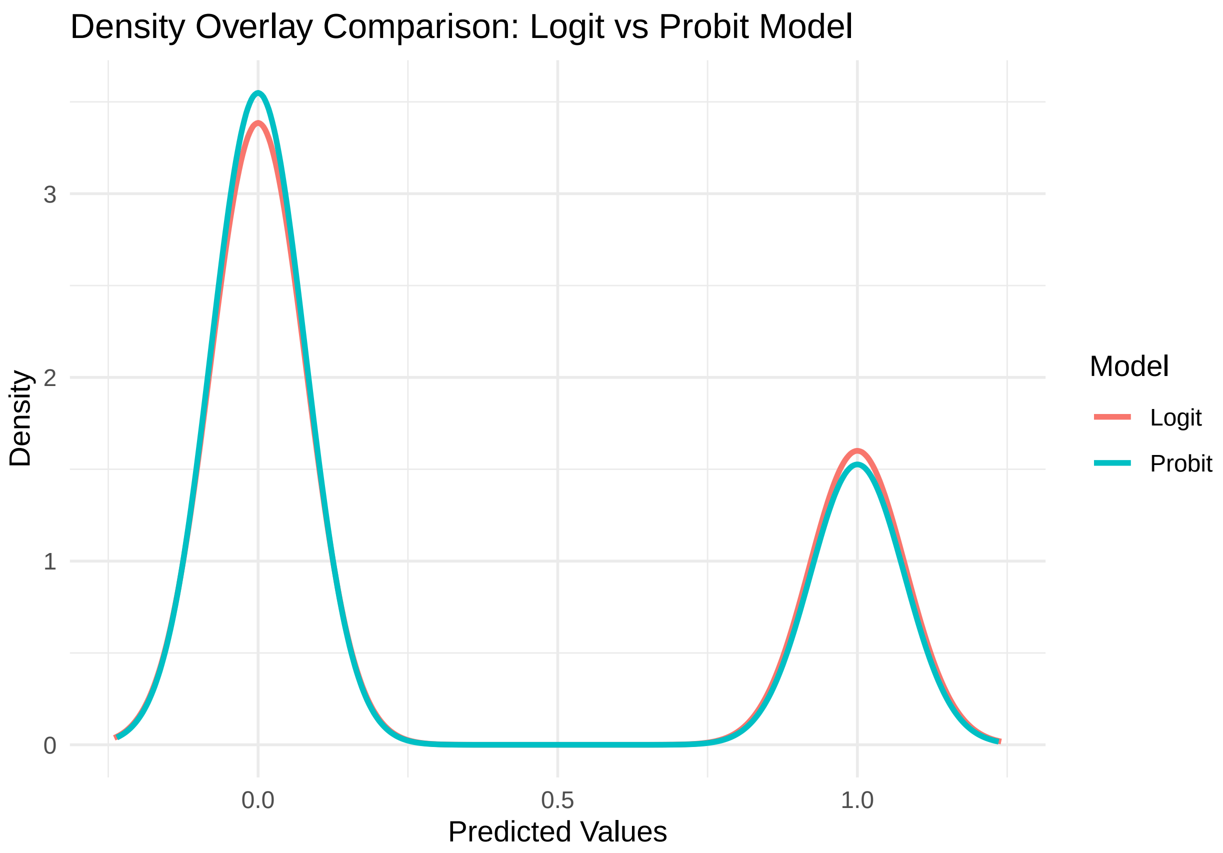
```
ggsave("DensityOverlay_Logit.png", width = 8, height = 5)

pp_check(fit_probit, type = "dens_overlay") +
  ggtitle("Posterior Predictive Density - Probit Model")
```

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



```
ggsave("DensityOverlay_Probit.png", width = 8, height = 5)

# Extract predictive samples for combined density plot
logit_density <- apply(pp_logit, 2, density)
probit_density <- apply(pp_probit, 2, density)

# Convert to data frames for ggplot2
logit_df <- data.frame(x = logit_density[[1]]$x, y = logit_density[[1]]$y, Model = "Logit")
probit_df <- data.frame(x = probit_density[[1]]$x, y = probit_density[[1]]$y, Model = "Probit")
combined_df <- rbind(logit_df, probit_df)

# Create comparison density plot
ggplot(combined_df, aes(x = x, y = y, color = Model)) +
  geom_line(size = 1) +
  labs(title = "Density Overlay Comparison: Logit vs Probit Model",
       x = "Predicted Values",
       y = "Density") +
  theme_minimal()
```

```
## Warning: Using ‘size‘ aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use ‘linewidth‘ instead.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.
```



```r
# Save the combined density plot
ggsave("DensityOverlay_Comparison.png", width = 8, height = 5)
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.