Applied Machine Learning and Predictive Modelling I: Modelling Stroke Data

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Module: Applied Machine Learning and Predictive Modelling I

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1 Introduction

Use case: We are a smart watch manufacturer working on a new feature for stroke prevention. We are going to analyze survey data that we plan to ask our users, complementing it with HR (Heart Rate) and CGM (Continuous Glucose Monitoring) data that our product already measures. We hope that our feature can prevent serious health issues and motivate our users to adopt healthier lifestyles.

2 Importing Data

```
stroke_data <- read_csv('./data/healthcare-dataset-stroke-data.csv')
```

```
## Rows: 5110 Columns: 12
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (6): gender, ever_married, work_type, Residence_type, bmi, smoking_status
## dbl (6): id, age, hypertension, heart_disease, avg_glucose_level, stroke
##
## 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.
```

```
s <- spec(stroke_data)
s
```

```
## cols(
##   id = col_double(),
##   gender = col_character(),
##   age = col_double(),
##   hypertension = col_double(),
##   heart_disease = col_double(),
##   ever_married = col_character(),
##   work_type = col_character(),
##   Residence_type = col_character(),
##   avg_glucose_level = col_double(),
##   bmi = col_character(),
##   smoking_status = col_character(),
##   stroke = col_double()
## )
```

```
cols_condense(s)
```

```
## cols(
##   .default = col_character(),
##   id = col_double(),
##   age = col_double(),
##   hypertension = col_double(),
##   heart_disease = col_double(),
##   avg_glucose_level = col_double(),
##   stroke = col_double()
## )
```

```
stroke_data$bmi <- as.numeric(stroke_data$bmi)
```

```
## Warning: NAs introduced by coercion
```

```
stroke_data$bmi[is.na(stroke_data$bmi)] <- mean(stroke_data$bmi, na.rm = TRUE)
stroke_data$age <- as.integer(stroke_data$age)
```

```
stroke_data$smoking_status <- as.factor(stroke_data$smoking_status)
stroke_data$work_type <- as.factor(stroke_data$work_type)
stroke_data$gender <- as.factor(stroke_data$gender)
stroke_data$ever_married <- as.factor(stroke_data$ever_married)
stroke_data$Residence_type <- as.factor(stroke_data$Residence_type)
stroke_data$stroke_num <- as.numeric(stroke_data$stroke)
stroke_data$stroke <- as.factor(stroke_data$stroke)


stroke_data
```

```
## # A tibble: 5,110 x 13
##       id gender   age hypertension heart_disease ever_married work_type
##    <dbl> <fct>  <int>        <dbl>         <dbl> <fct>        <fct>
##  1  9046 Male      67            0             1 Yes          Private
##  2 51676 Female    61            0             0 Yes          Self-employed
##  3 31112 Male      80            0             1 Yes          Private
##  4 60182 Female    49            0             0 Yes          Private
##  5  1665 Female    79            1             0 Yes          Self-employed
##  6 56669 Male      81            0             0 Yes          Private
##  7 53882 Male      74            1             1 Yes          Private
##  8 10434 Female    69            0             0 No           Private
##  9 27419 Female    59            0             0 Yes          Private
## 10 60491 Female    78            0             0 Yes          Private
## # ... with 5,100 more rows, and 6 more variables: Residence_type <fct>,
## #   avg_glucose_level <dbl>, bmi <dbl>, smoking_status <fct>, stroke <fct>,
## #   stroke_num <dbl>
```

2.1 Summaries

```
#testing the effect of non smokers and smokers
count_by_smoke_status <- stroke_data %>%
  select(smoking_status, stroke) %>%
  group_by(smoking_status, stroke) %>%
  summarise( N = n())
```

```
## `summarise()` has grouped output by 'smoking_status'. You can override using the
## `.groups` argument.
```

```
#testing the effect of work type
 count_by_work_type <- stroke_data %>%
   select(work_type, stroke) %>%
   group_by(work_type, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'work_type'. You can override using the
## `.groups` argument.
```

```
 # testing the effects of residence type
count_by_Residence_type <- stroke_data %>%
   select(Residence_type, stroke) %>%
   group_by(Residence_type, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'Residence_type'. You can override using the
## `.groups` argument.
```

```r
 # testing the effects of gender
count_by_gender <- stroke_data %>%
   select(gender, stroke) %>%
   group_by(gender, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'gender'. You can override using the
## `.groups` argument.
```

```r
 # testing the effects of hypertension
count_by_hypertension <- stroke_data %>%
   select(hypertension, stroke) %>%
   group_by(hypertension, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'hypertension'. You can override using the
## `.groups` argument.
```

```r
# testing the effects of heart disease
count_by_heart_disease <- stroke_data %>%
   select(heart_disease, stroke) %>%
   group_by(heart_disease, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'heart_disease'. You can override using the
## `.groups` argument.
```

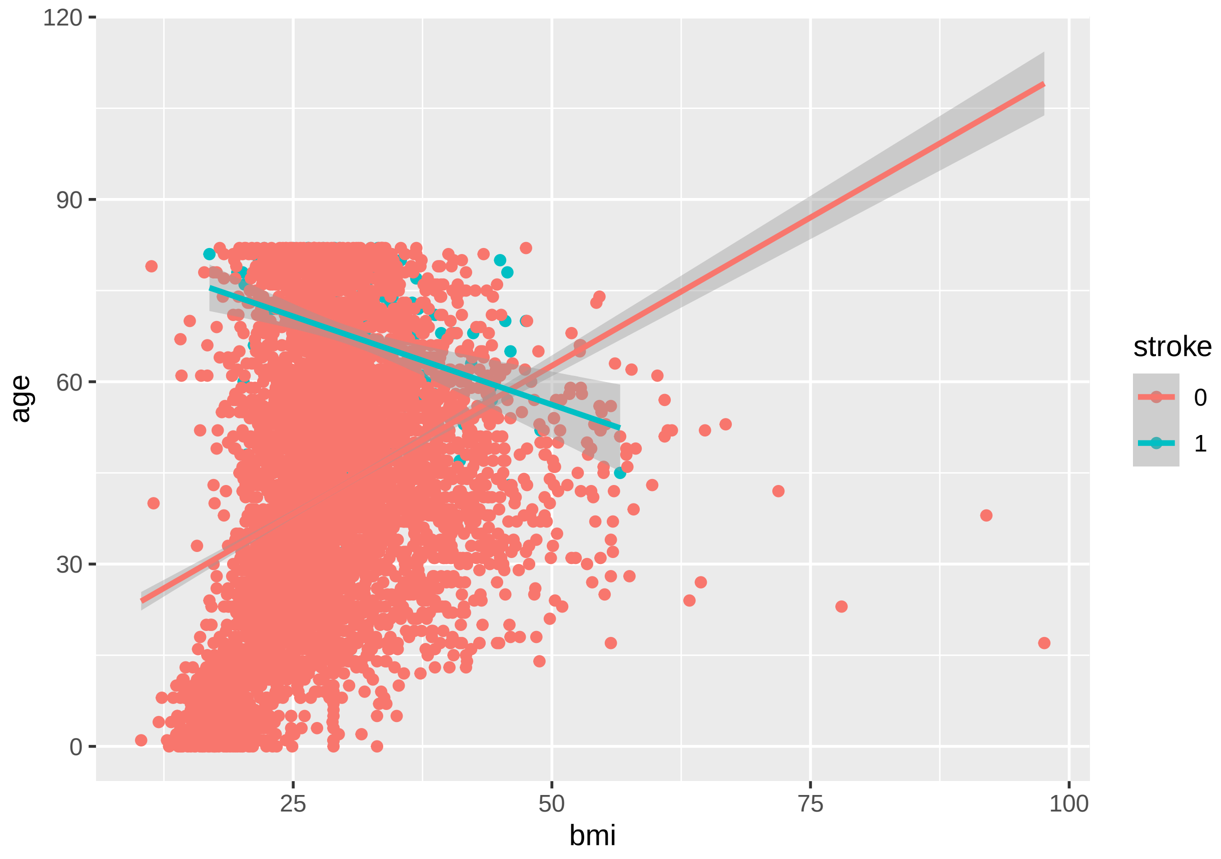
```r
# testing the effects of marriage status
count_by_marriage <- stroke_data %>%
   select(ever_married, stroke) %>%
   group_by(ever_married, stroke) %>%
   summarise( N = n())
```

```
## `summarise()` has grouped output by 'ever_married'. You can override using the
## `.groups` argument.
```

2.2 Scatterplots

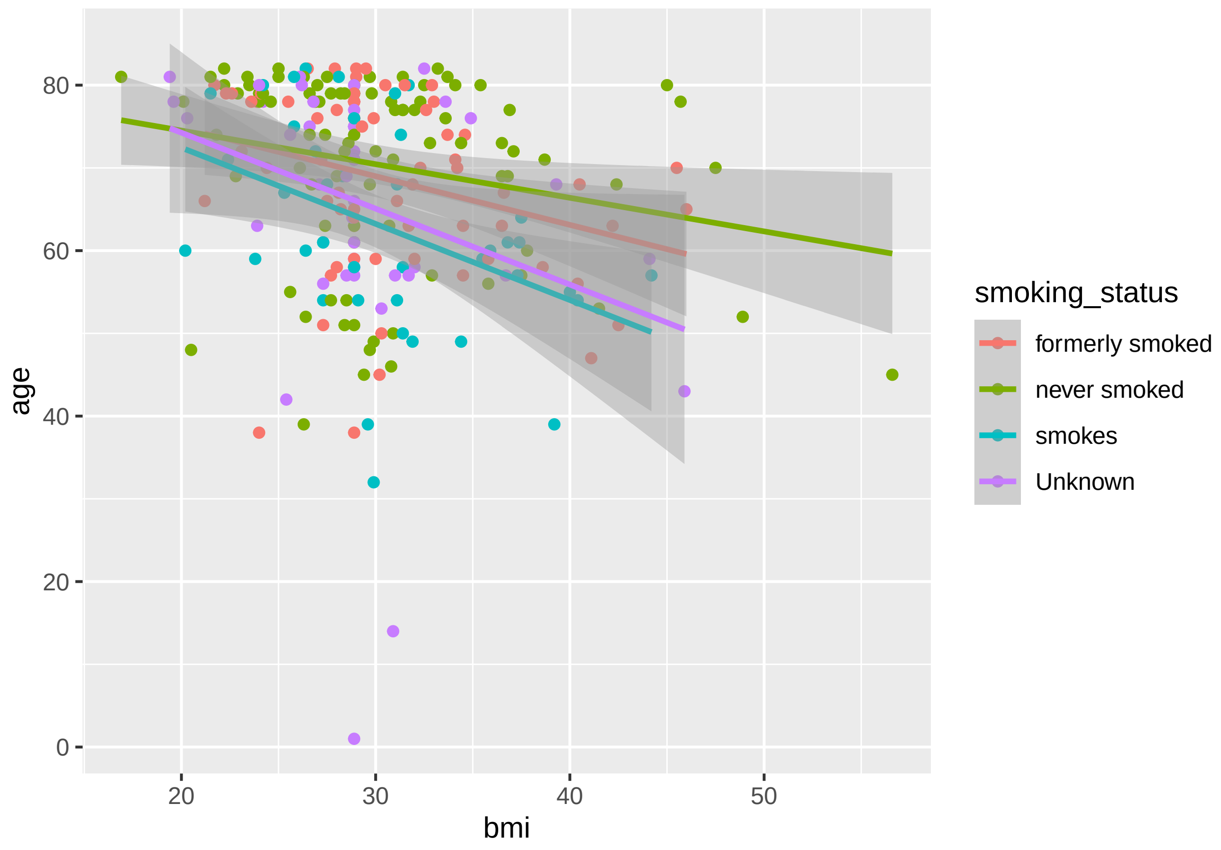
```r
stroke_data %>%
  ggplot(mapping = aes(x = bmi, y = age, color = stroke)) +
  geom_point() +
  geom_smooth(method = 'lm')
```

```
## `geom_smooth()` using formula 'y ~ x'
```



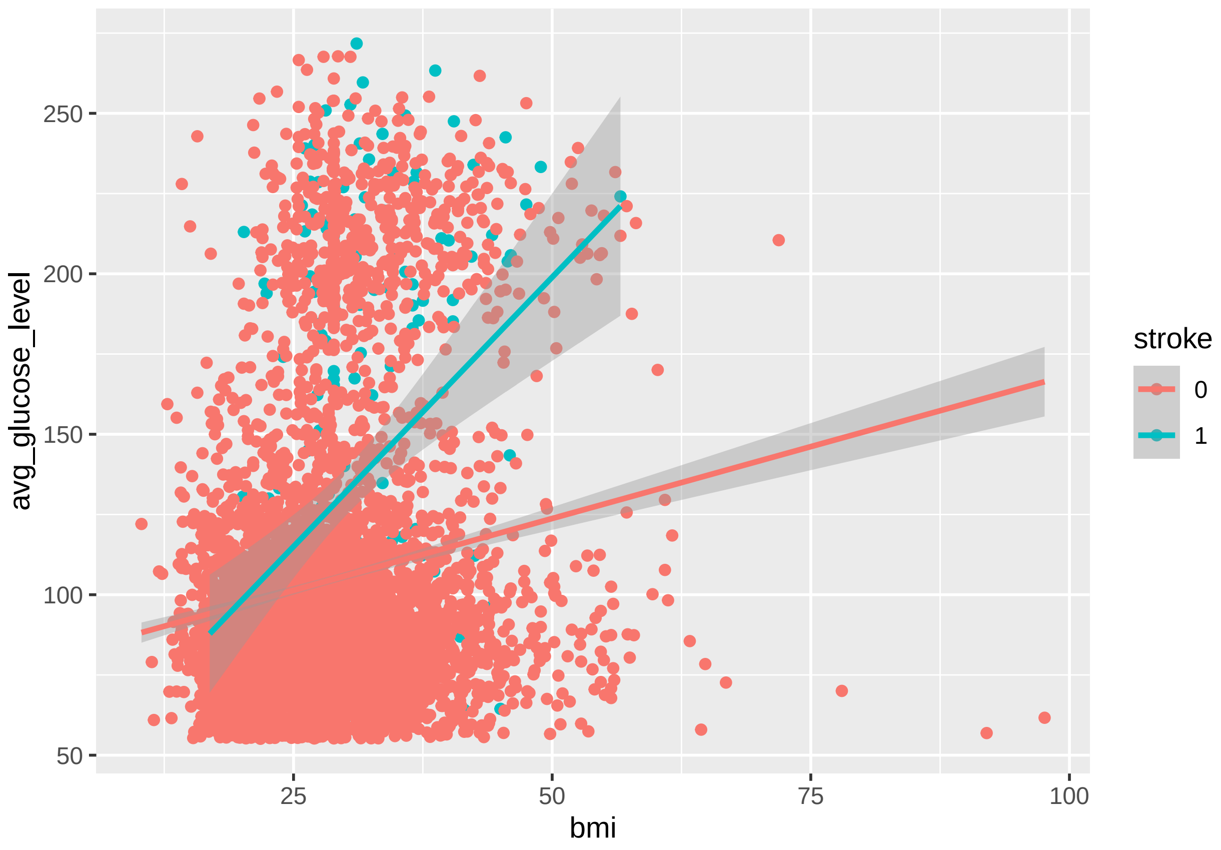
```r
stroke_data %>%
  filter(stroke == 1) %>%
  ggplot(mapping = aes(x = bmi, y = age, color = smoking_status)) +
  geom_point(method = 'lm') +
  geom_smooth(method = 'lm')
```

```
## Warning: Ignoring unknown parameters: method

## `geom_smooth()` using formula 'y ~ x'
```



```r
stroke_data %>%
  ggplot(mapping = aes(x = bmi, y = avg_glucose_level, color = stroke)) +
  geom_point() +
  geom_smooth(method = 'lm')
```

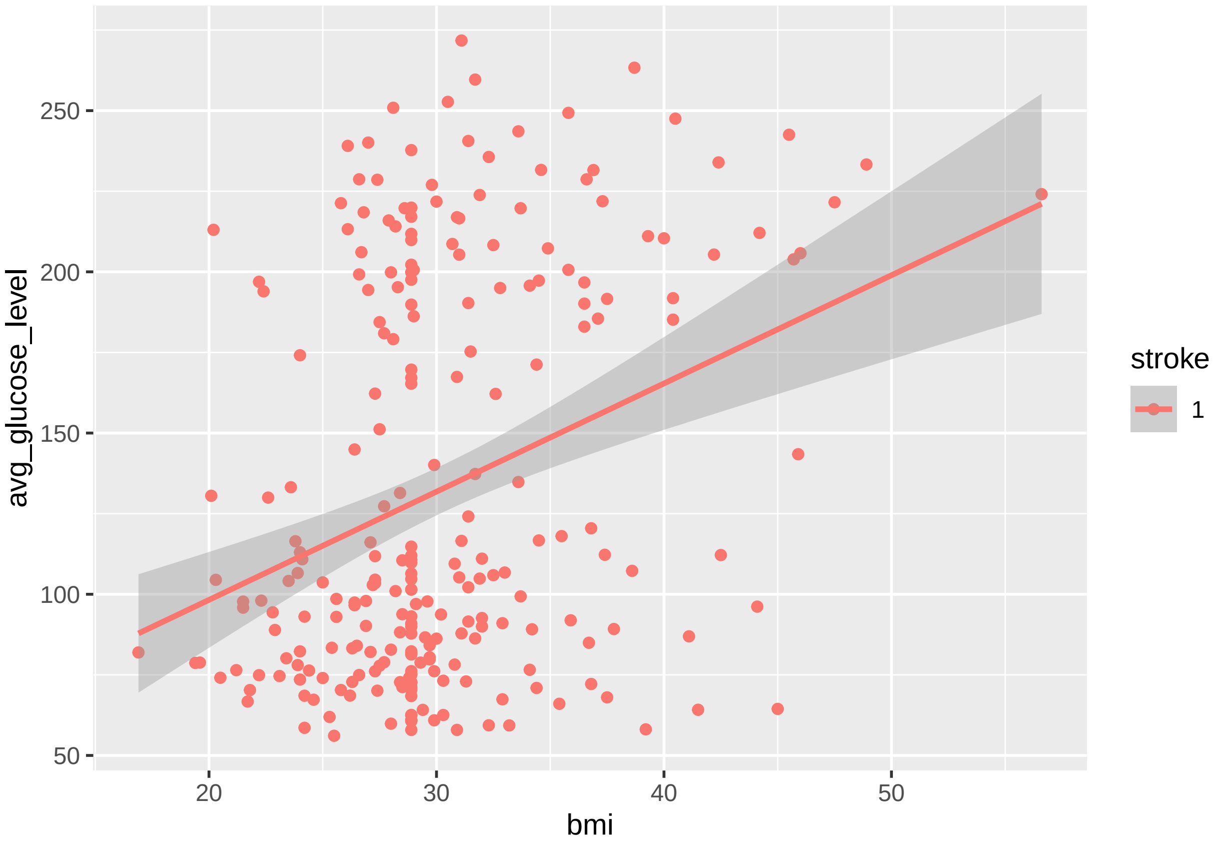
```
## `geom_smooth()` using formula 'y ~ x'
```



```
stroke_data %>%
  filter(stroke == 1) %>%
  ggplot(mapping = aes(x = bmi, y = avg_glucose_level, color = stroke)) +
  geom_point(method = 'lm') +
  geom_smooth(method = 'lm')
```

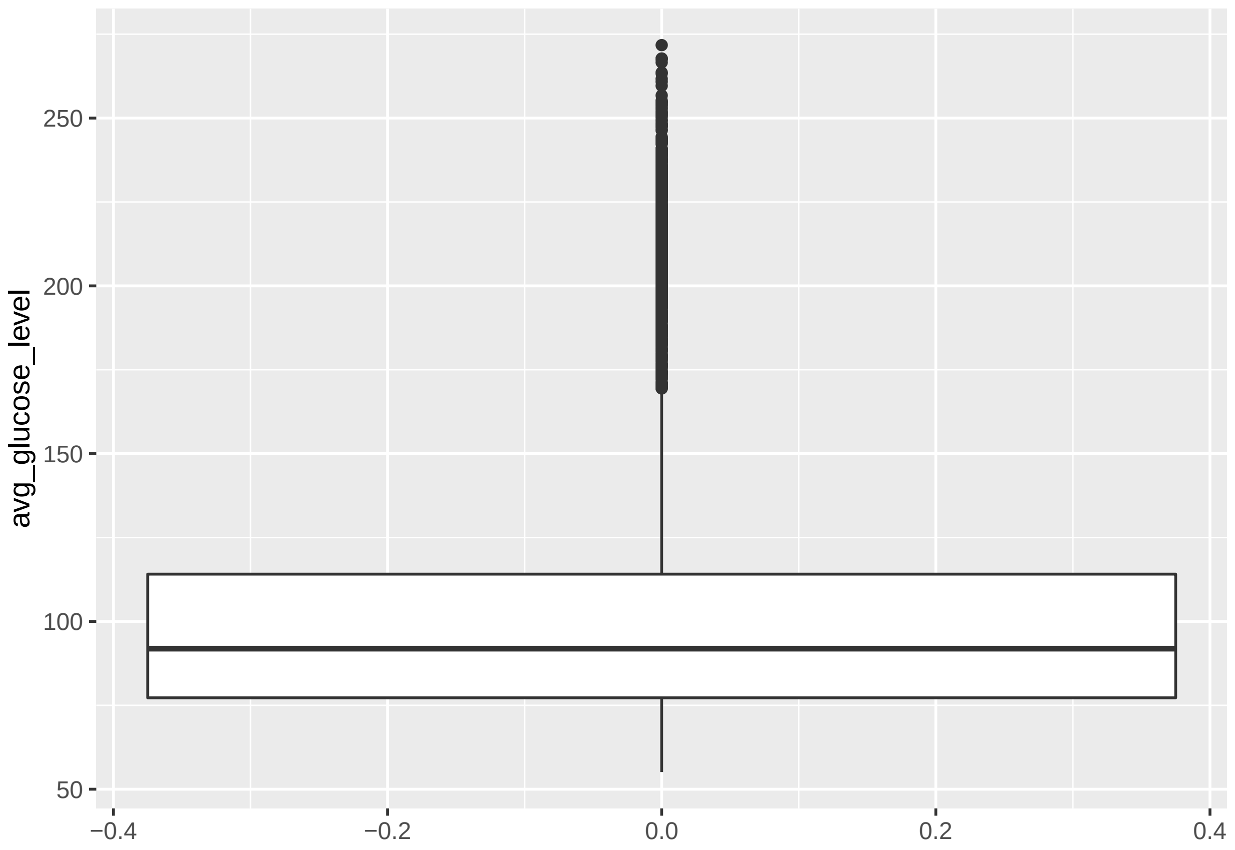
```
## Warning: Ignoring unknown parameters: method
```

```
## `geom_smooth()` using formula 'y ~ x'
```

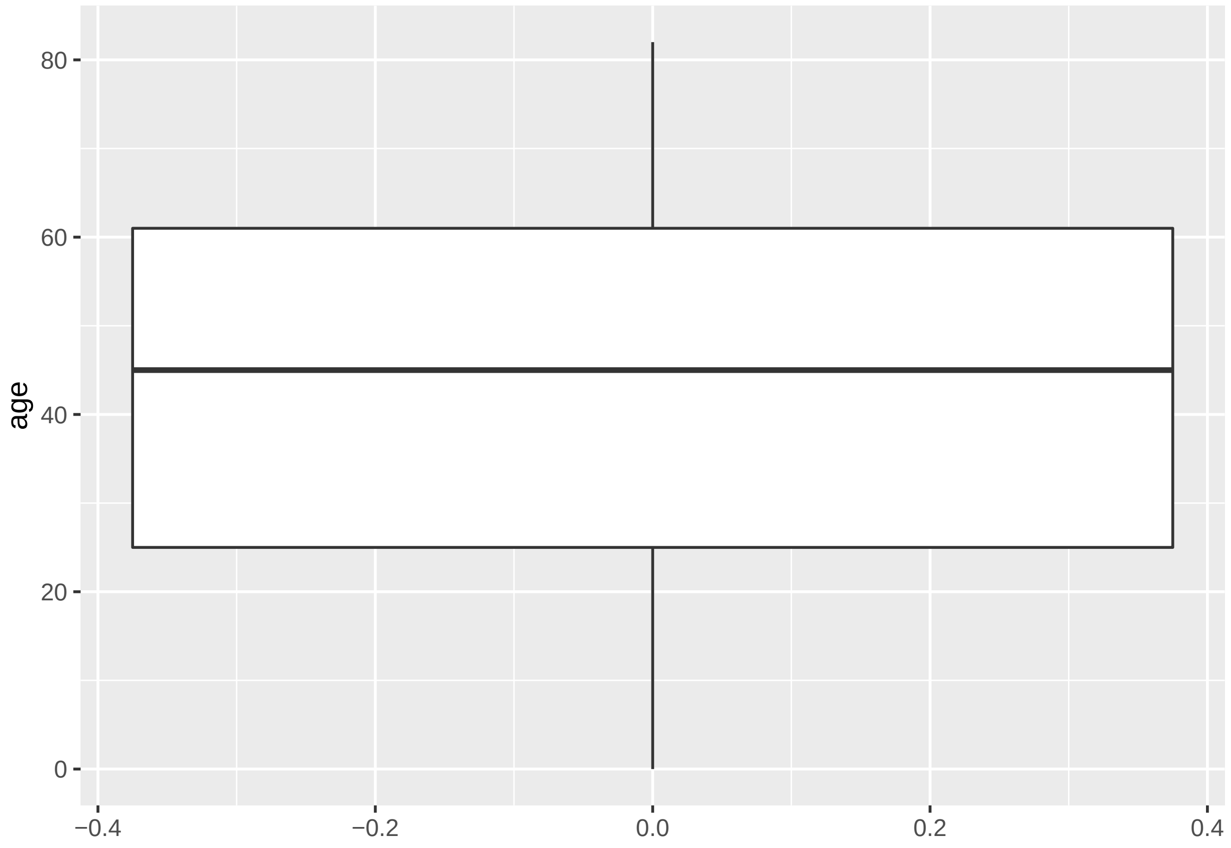


2.3 Boxplots

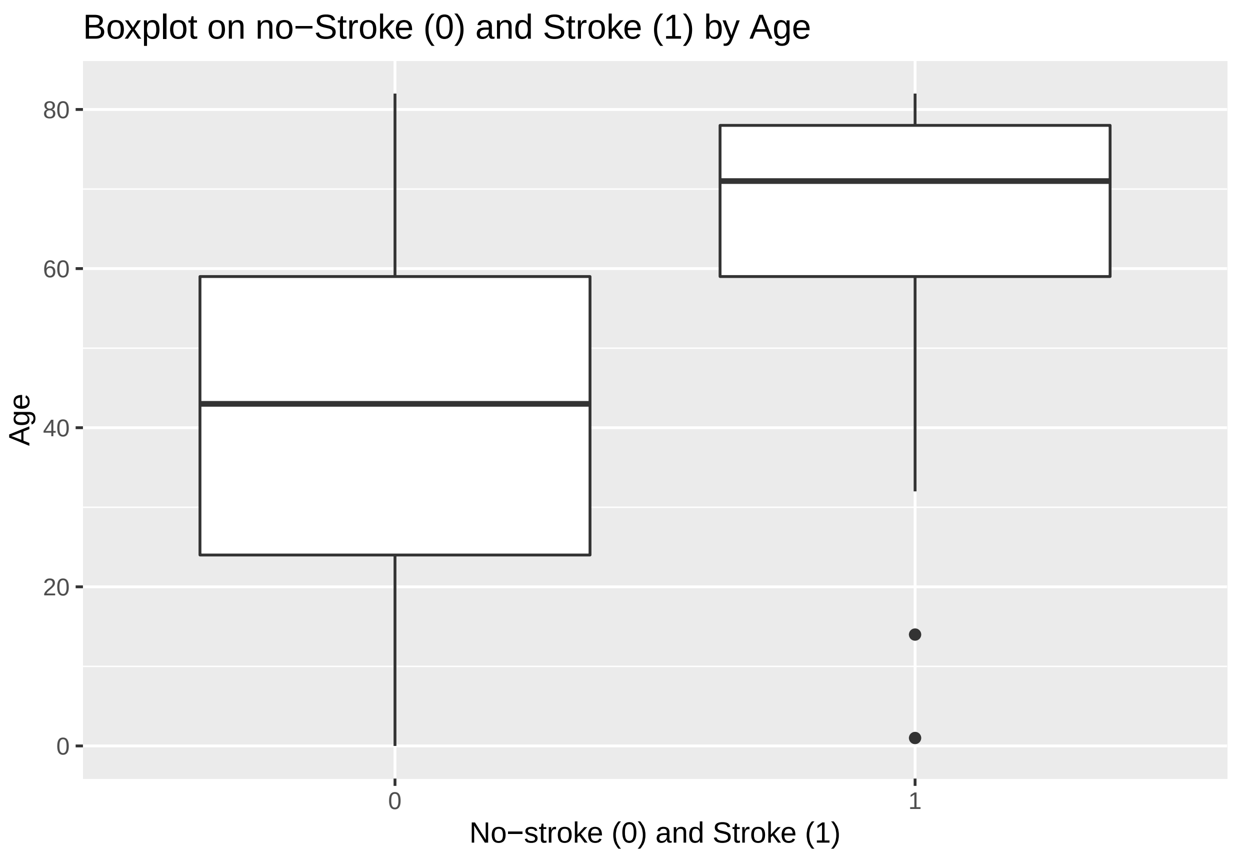
```
#Boxplot on avg. glucose_level
ggplot(stroke_data, aes(y = avg_glucose_level)) +
  geom_boxplot()
```



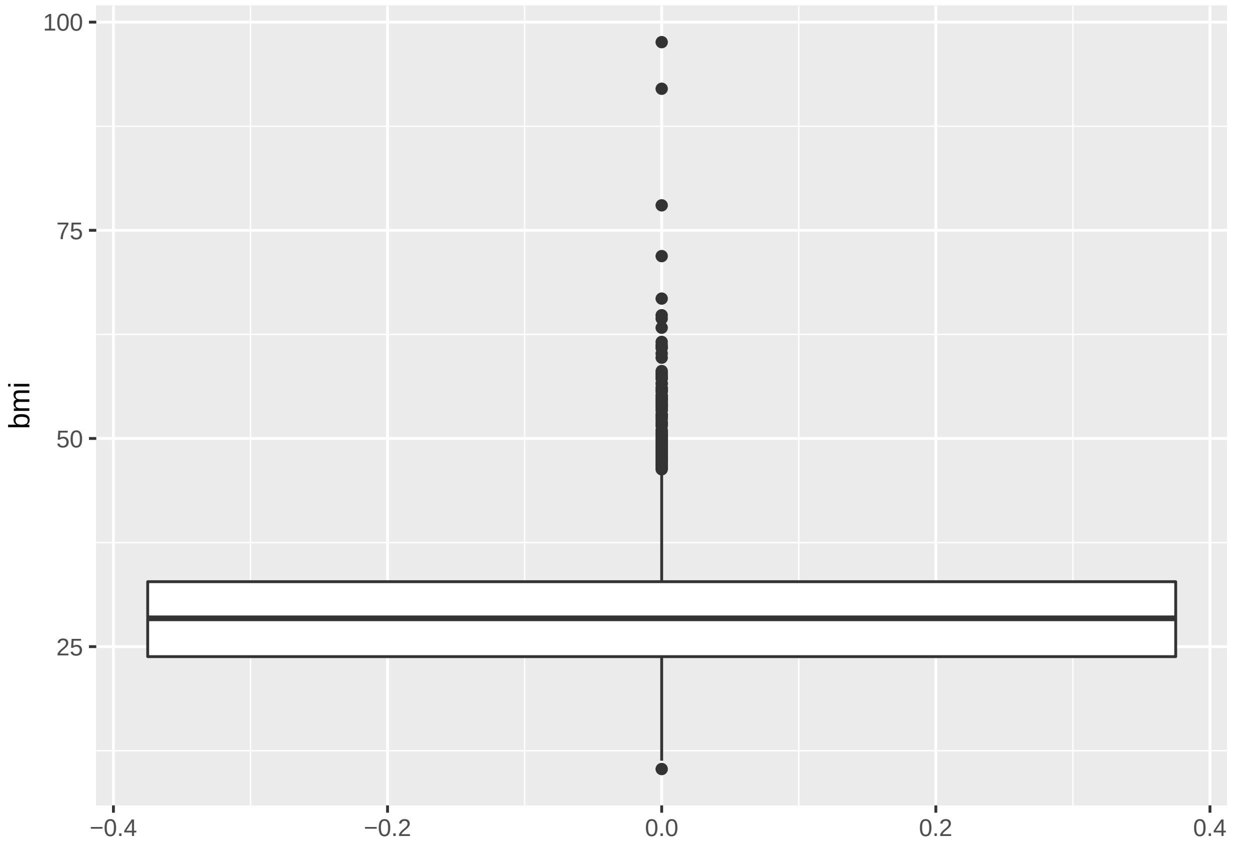
```r
#Boxplot on Age
ggplot(stroke_data, aes(y = age)) +
  geom_boxplot()
```



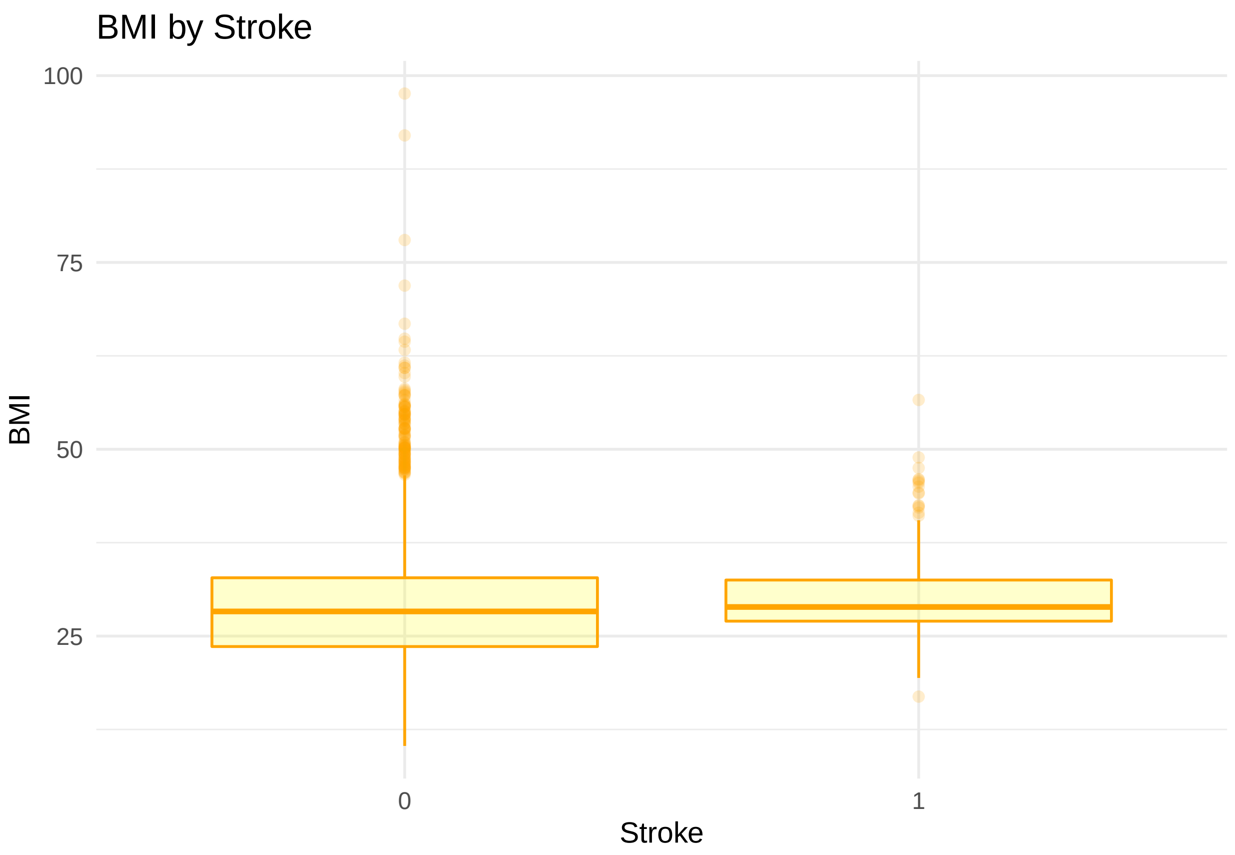
```
stroke_by_age <- stroke_data %>%
# dplyr::filter(stroke == 1) %>%
 ggplot(aes(x = stroke,
            y = age)) +
  geom_boxplot() +
  labs(title = "Boxplot on no-Stroke (0) and Stroke (1) by Age",
       x = "No-stroke (0) and Stroke (1)",
       y = "Age")
       color = "green"

stroke_by_age
```



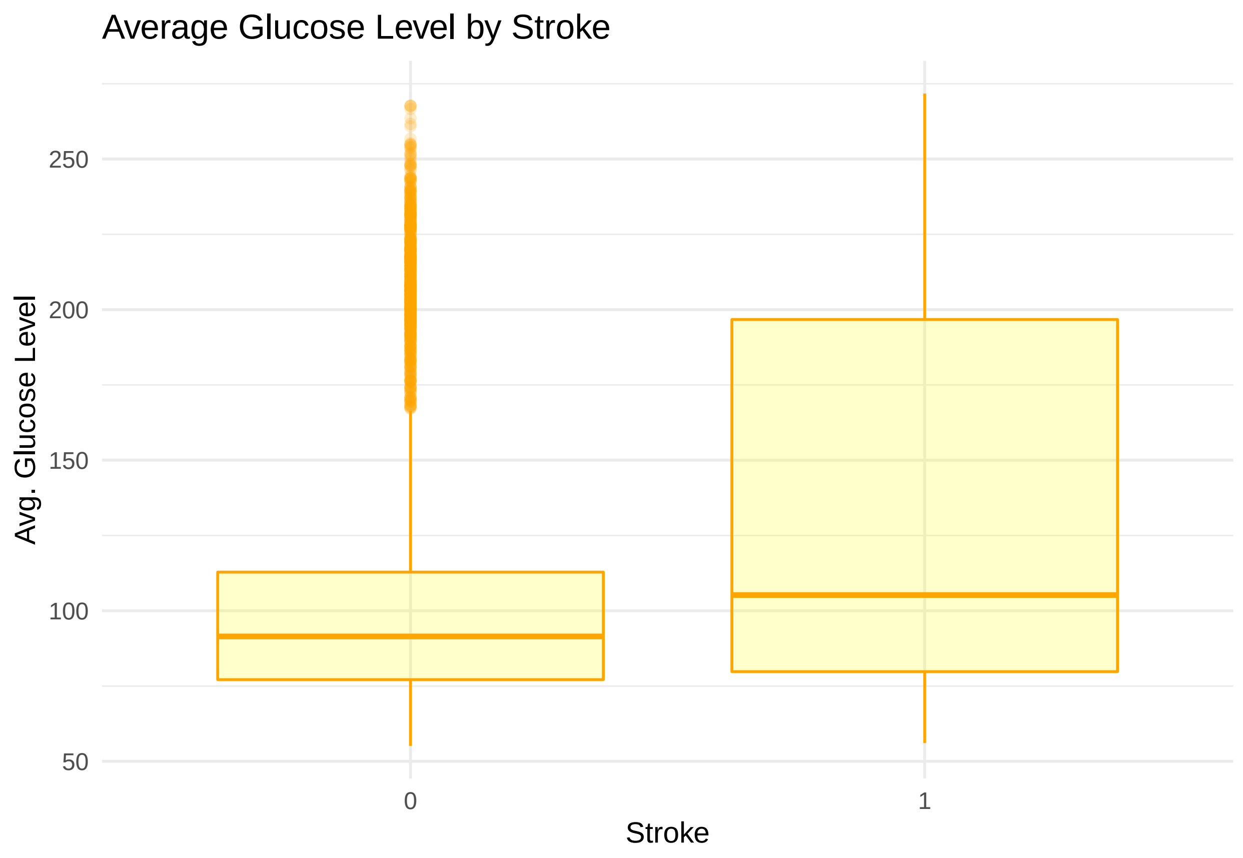
```
#Boxplot on BMI
ggplot(stroke_data, aes(y = bmi)) +
geom_boxplot()
```



```
stroke_by_bmi <- stroke_data %>%
# dplyr::filter(stroke == 1) %>%
 ggplot(aes(x = stroke,
            y = bmi)) +
  geom_boxplot(color="orange", fill="yellow", alpha=0.2) +
  ggtitle("BMI by Stroke") +
  xlab("Stroke") + ylab("BMI") +
  theme_minimal() + theme(axis.text.x = element_text(angle = 0))
stroke_by_bmi
```



```r
#boxplot by avg_glucose_level and stroke
stroke_by_avg_glucose_level <- stroke_data %>%
# dplyr::filter(stroke == 1) %>%
 ggplot(aes(x = stroke,
            y = avg_glucose_level)) +
  geom_boxplot(color="orange", fill="yellow", alpha=0.2) +
  ggtitle("Average Glucose Level by Stroke") +
  xlab("Stroke") + ylab("Avg. Glucose Level") +
  theme_minimal() + theme(axis.text.x = element_text(angle = 0))

stroke_by_avg_glucose_level
```



3 Methodology

```
set.seed(7406)
n=dim(stroke_data[1])  # number of observations in dataset
n_train=0.70*n  # training set is 70%
flag = sort(sample(1:n, size=n_train, replace=FALSE))
```

```
## Warning in 1:n: numerical expression has 2 elements: only the first used
```

```
# Use df (all data points without ID column) df_train, and df_test
# Gender, hypertension, heart disease, ever married, work type, residence type, smoking status, and str
# This should allow for the best modeling options possible for our methods.
df_train = stroke_data[flag,]
df_test = stroke_data[-flag,]
```

```
head(df_test)
```

```
## # A tibble: 6 x 13
##       id gender   age hypertension heart_disease ever_married work_type
##    <dbl> <fct>  <int>        <dbl>         <dbl> <fct>        <fct>
## 1 51676 Female    61            0             0 Yes          Self-employed
## 2 10434 Female    69            0             0 No           Private
## 3 60491 Female    78            0             0 Yes          Private
## 4 12095 Female    61            0             1 Yes          Govt_job
## 5 58202 Female    50            1             0 Yes          Self-employed
## 6 56112 Male      64            0             1 Yes          Private
## # ... with 6 more variables: Residence_type <fct>, avg_glucose_level <dbl>,
## #   bmi <dbl>, smoking_status <fct>, stroke <fct>, stroke_num <dbl>
```

```
head(df_train)
```

```
## # A tibble: 6 x 13
##      id gender   age hypertension heart_disease ever_married work_type
##   <dbl> <fct>  <int>        <dbl>         <dbl> <fct>        <fct>
## 1  9046 Male      67            0             1 Yes          Private
## 2 31112 Male      80            0             1 Yes          Private
## 3 60182 Female    49            0             0 Yes          Private
## 4  1665 Female    79            1             0 Yes          Self-employed
## 5 56669 Male      81            0             0 Yes          Private
## 6 53882 Male      74            1             1 Yes          Private
## # ... with 6 more variables: Residence_type <fct>, avg_glucose_level <dbl>,
## #   bmi <dbl>, smoking_status <fct>, stroke <fct>, stroke_num <dbl>
```

4 Linear Models

```
set.seed(7406)
n=dim(stroke_data[1])  # number of observations in dataset
n_train=0.70*n  # training set is 70%
flag = sort(sample(1:n, size=n_train, replace=FALSE))
```

```
## Warning in 1:n: numerical expression has 2 elements: only the first used
```

```
# Use df (all data points without ID column) df_train_linear, and df_test_linear
# Gender, hypertension, heart disease, ever married, work type, residence type, smoking status, and str
# This should allow for the best modeling options possible for our methods.
df_train_linear = stroke_data[flag,]
df_test_linear = stroke_data[-flag,]
```

```
head(df_test_linear)
```

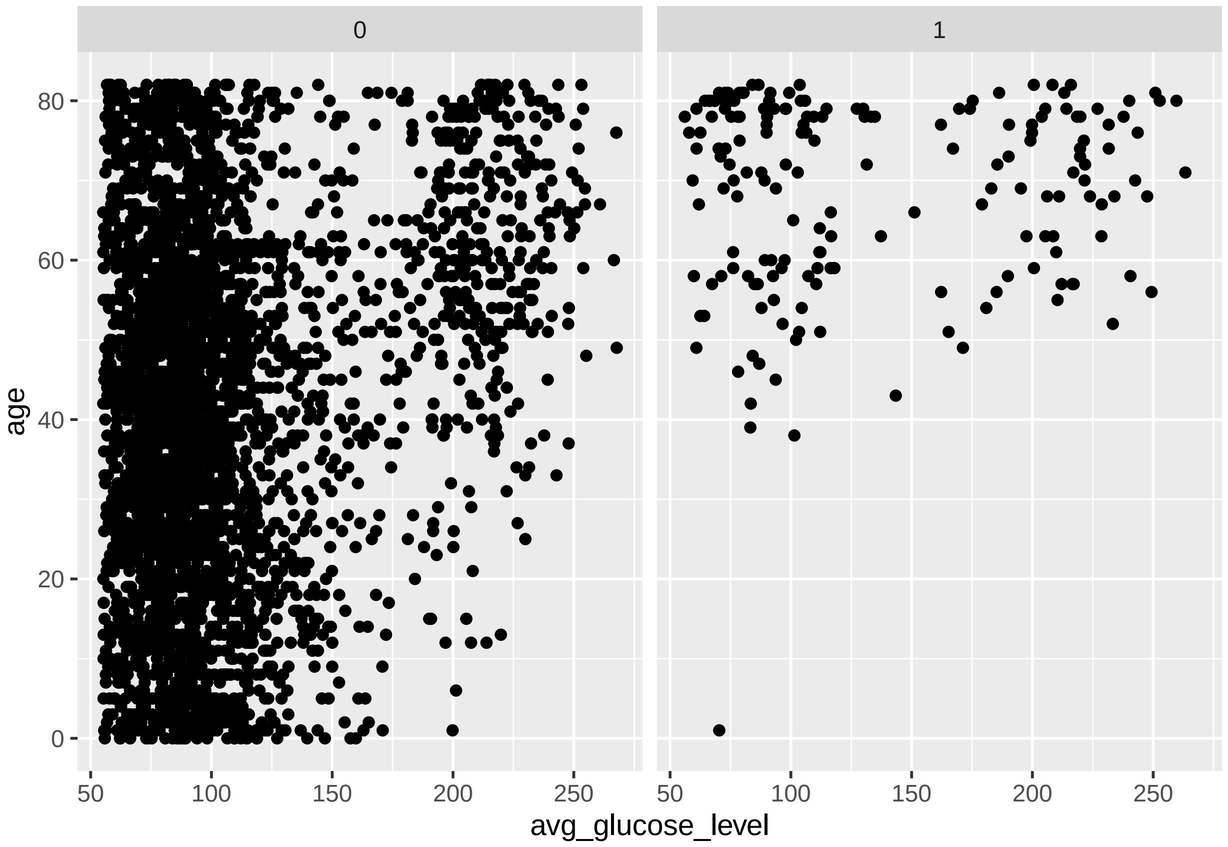
```
## # A tibble: 6 x 13
##      id gender   age hypertension heart_disease ever_married work_type
##   <dbl> <fct>  <int>        <dbl>         <dbl> <fct>        <fct>
## 1 51676 Female    61            0             0 Yes          Self-employed
## 2 10434 Female    69            0             0 No           Private
## 3 60491 Female    78            0             0 Yes          Private
## 4 12095 Female    61            0             1 Yes          Govt_job
## 5 58202 Female    50            1             0 Yes          Self-employed
## 6 56112 Male      64            0             1 Yes          Private
## # ... with 6 more variables: Residence_type <fct>, avg_glucose_level <dbl>,
## #   bmi <dbl>, smoking_status <fct>, stroke <fct>, stroke_num <dbl>
```

```
head(df_train_linear)
```

```
## # A tibble: 6 x 13
##      id gender   age hypertension heart_disease ever_married work_type
##   <dbl> <fct>  <int>        <dbl>         <dbl> <fct>        <fct>
## 1  9046 Male      67            0             1 Yes          Private
## 2 31112 Male      80            0             1 Yes          Private
## 3 60182 Female    49            0             0 Yes          Private
## 4  1665 Female    79            1             0 Yes          Self-employed
## 5 56669 Male      81            0             0 Yes          Private
## 6 53882 Male      74            1             1 Yes          Private
## # ... with 6 more variables: Residence_type <fct>, avg_glucose_level <dbl>,
## #   bmi <dbl>, smoking_status <fct>, stroke <fct>, stroke_num <dbl>
```

Our aim is to predict strokes, and the stroke variable is always our response variable of interest. However, simple or multiple linear regression is not the tool of choice, as stroke is a binary / categorical response variable. Thus in the following we will nonetheless fit a linear regression model to our data with stroke as the response variable (and another example to show that we've understood the concept). We know of the following limitations for fitting a linear regression model to a binary response variable: - - -

```
# qplot -> age/glucose level per stroke
library(ggplot2)
 qplot(y = age, x = avg_glucose_level,
       data = df_train_linear,
       facets = ~ stroke)
```

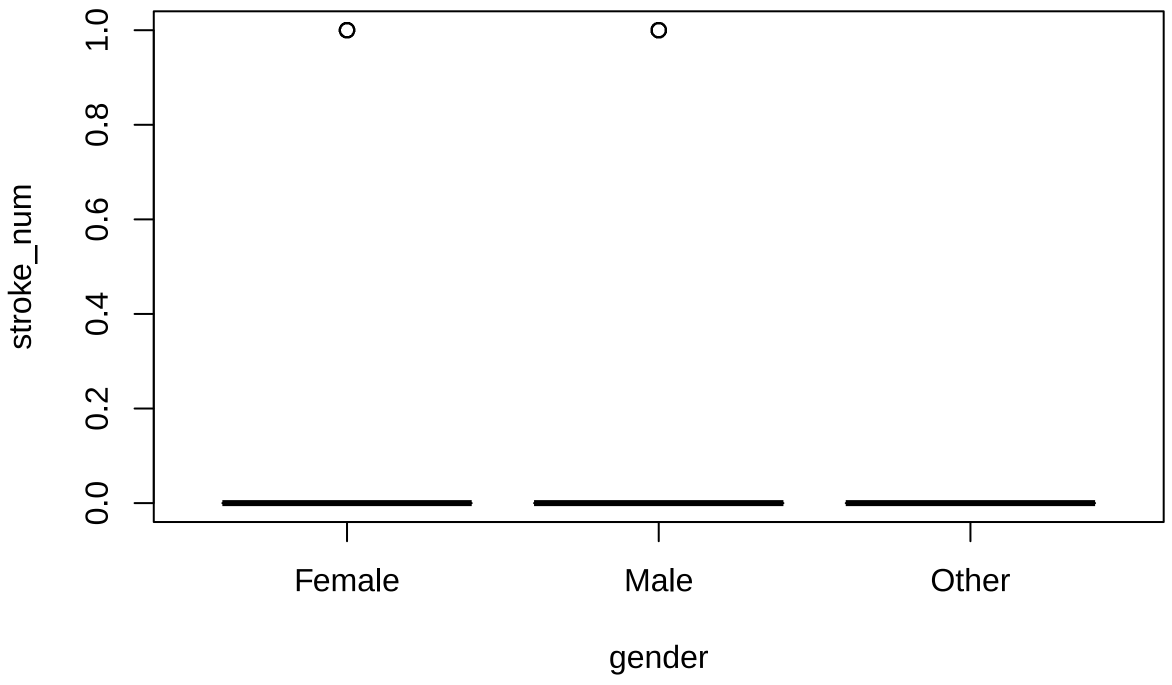


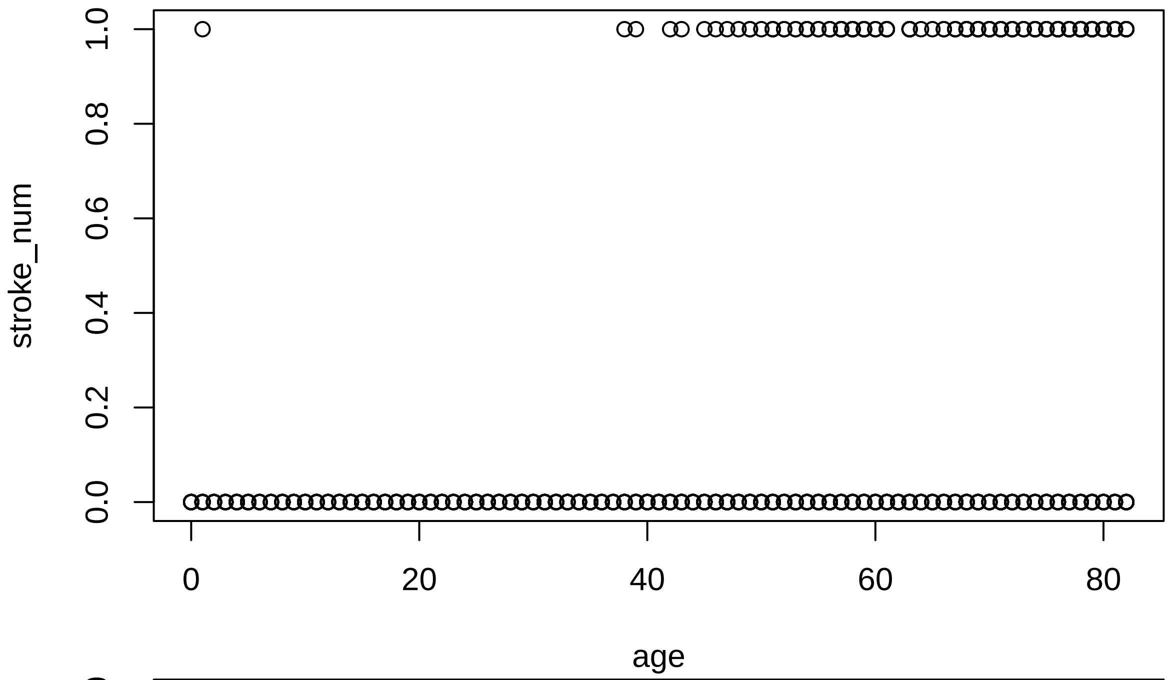
```
# fitting models for simple regression model
lm.stroke <- lm(stroke_num ~ gender + age + hypertension + heart_disease + ever_married + work_type + Re
summary(lm.stroke)
```

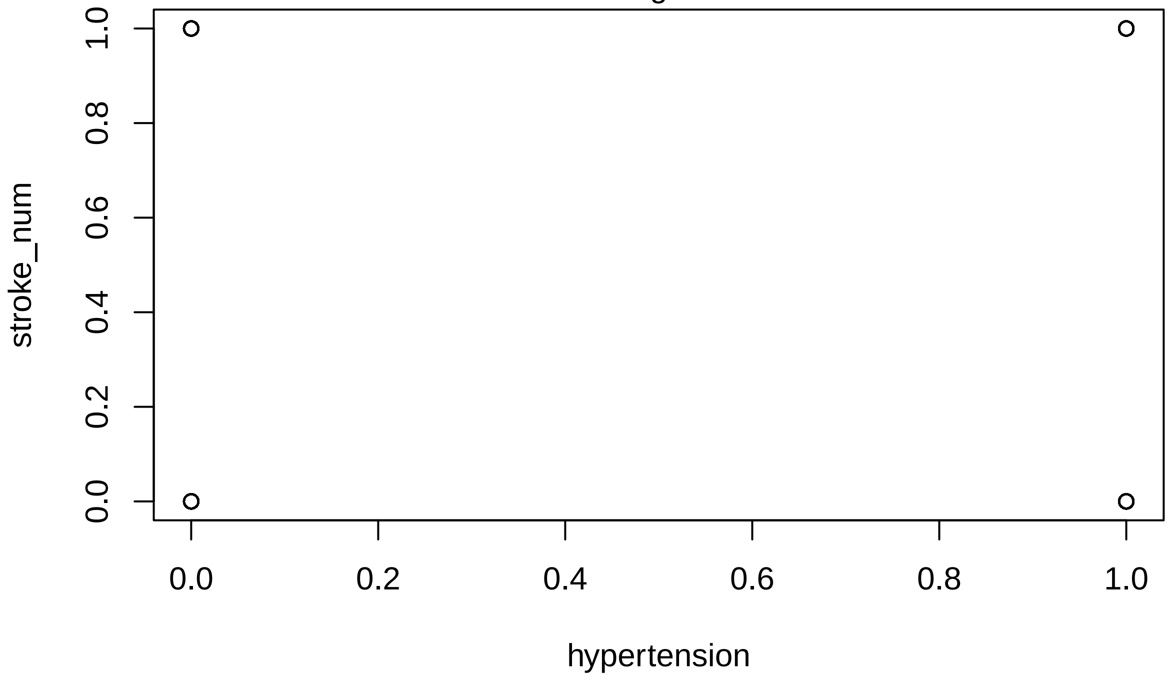
```
##
## Call:
## lm(formula = stroke_num ~ gender + age + hypertension + heart_disease +
##     ever_married + work_type + Residence_type + avg_glucose_level +
##     bmi + smoking_status, data = df_train_linear)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.33328 -0.08333 -0.02421  0.00834  1.03042
##
```

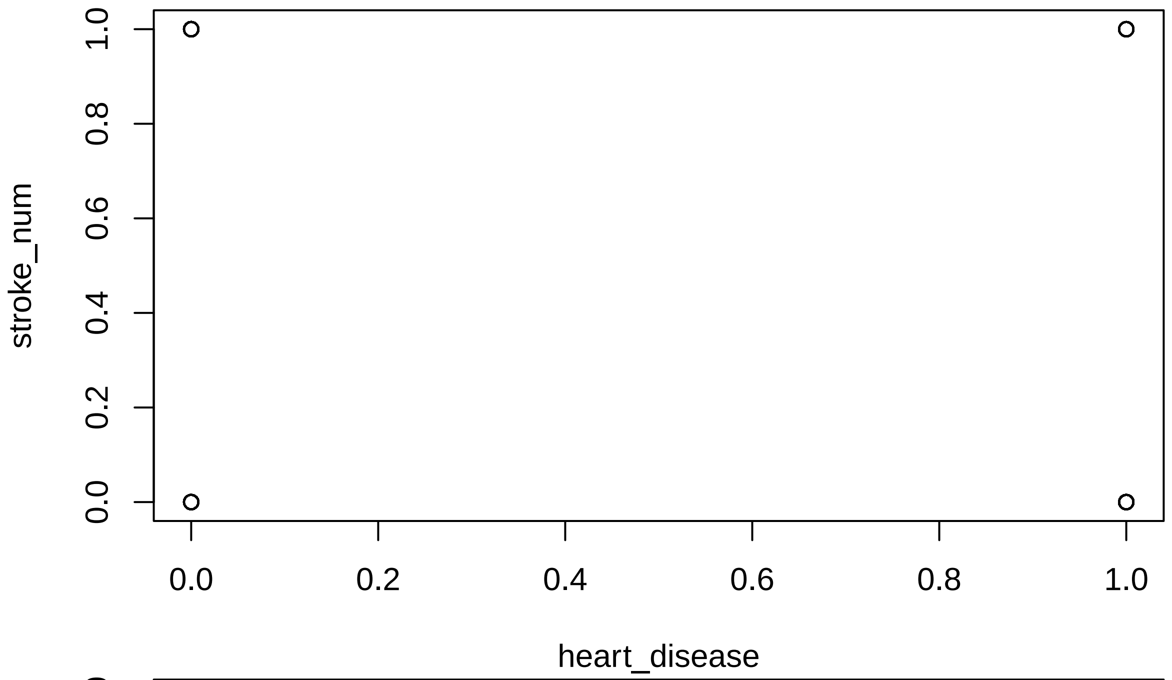
```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                 -3.812e-02  2.009e-02  -1.898 0.057814 .  
## genderMale                   4.560e-03  7.220e-03   0.632 0.527713    
## genderOther                 -2.698e-02  2.099e-01  -0.129 0.897733    
## age                          3.302e-03  2.617e-04  12.620  < 2e-16 ***
## hypertension                 3.704e-02  1.210e-02   3.062 0.002218 ** 
## heart_disease                7.191e-02  1.598e-02   4.500 7.01e-06 ***
## ever_marriedYes             -3.888e-02  1.045e-02  -3.721 0.000202 ***
## work_typeGovt_job           -6.863e-02  1.854e-02  -3.701 0.000218 ***
## work_typeNever_worked       -2.941e-02  5.372e-02  -0.548 0.584045    
## work_typePrivate            -5.075e-02  1.558e-02  -3.256 0.001139 ** 
## work_typeSelf-employed      -8.413e-02  1.892e-02  -4.447 8.99e-06 ***
## Residence_typeUrban          6.466e-04  7.016e-03   0.092 0.926575    
## avg_glucose_level            2.898e-04  8.024e-05   3.612 0.000308 ***
## bmi                         -5.155e-04  5.197e-04  -0.992 0.321284    
## smoking_statusnever smoked -7.336e-03  1.040e-02  -0.705 0.480548    
## smoking_statussmokes        -5.882e-03  1.240e-02  -0.474 0.635307    
## smoking_statusUnknown       -1.745e-03  1.163e-02  -0.150 0.880725    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2095 on 3560 degrees of freedom
## Multiple R-squared:  0.09588,    Adjusted R-squared:  0.09181
## F-statistic: 23.59 on 16 and 3560 DF,  p-value: < 2.2e-16
```

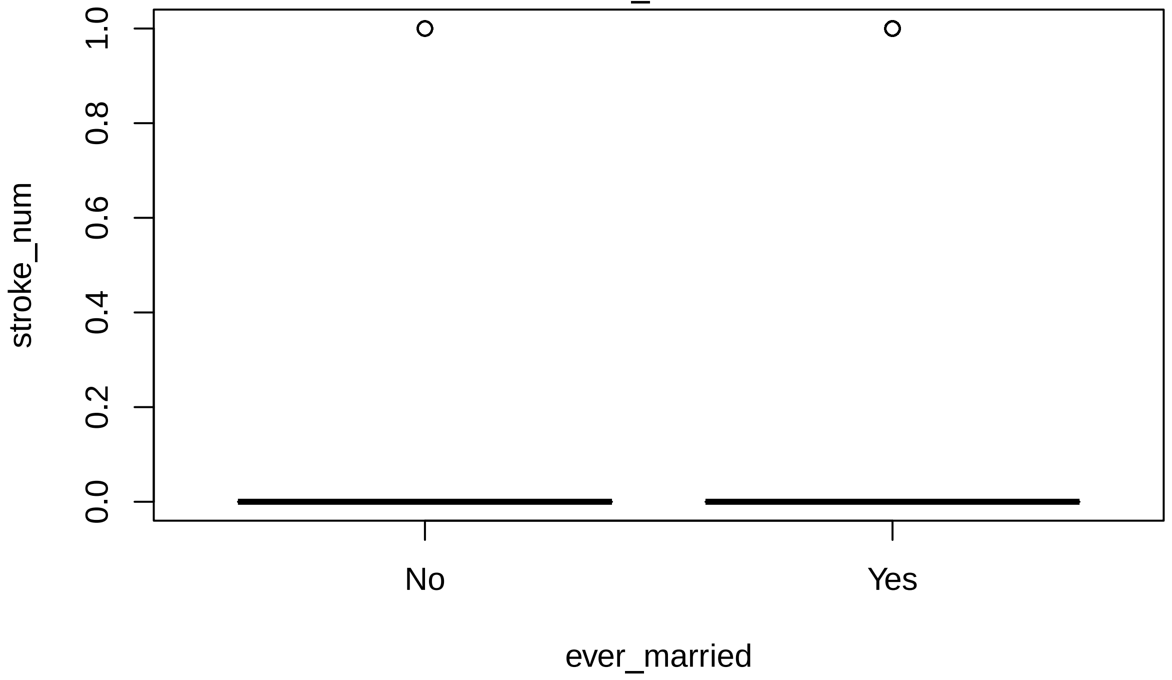
```r
plot(stroke_num ~ gender + age + hypertension + heart_disease + ever_married + work_type + Residence_typ
```

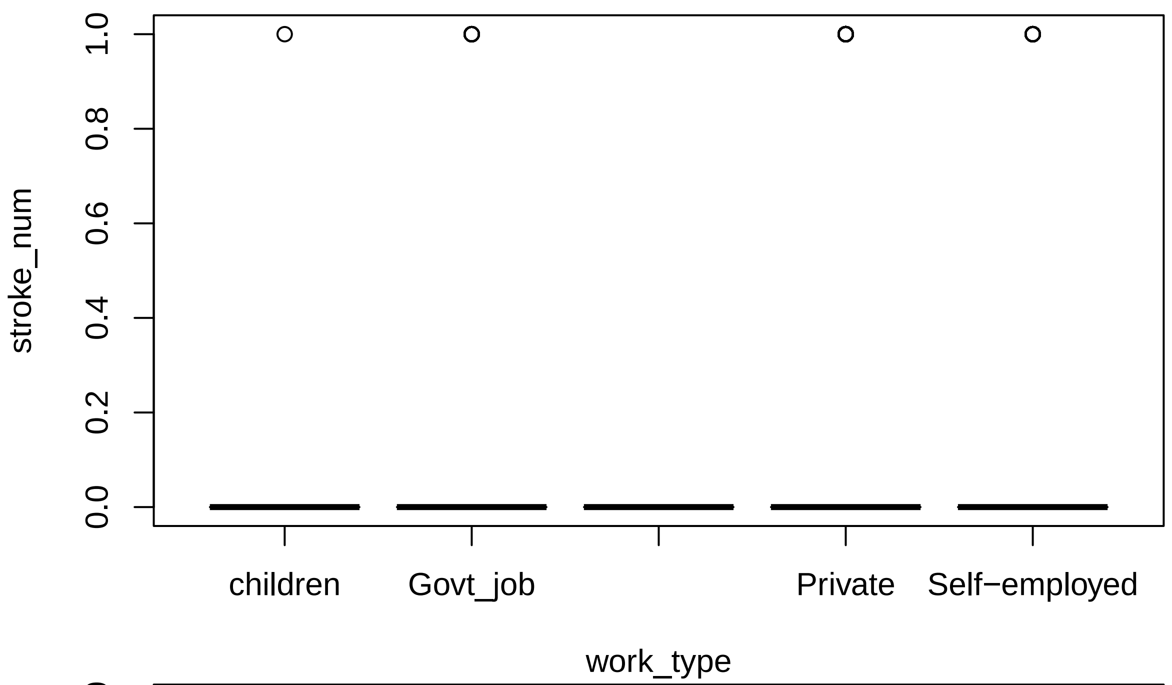


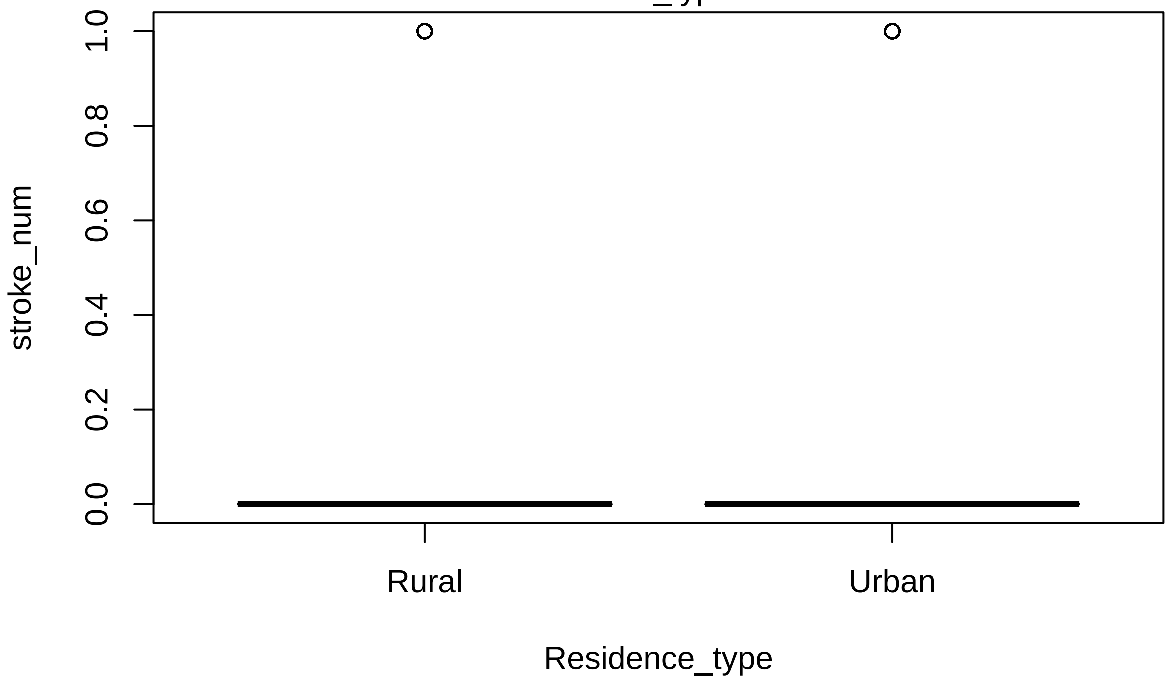

stroke_num
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
age

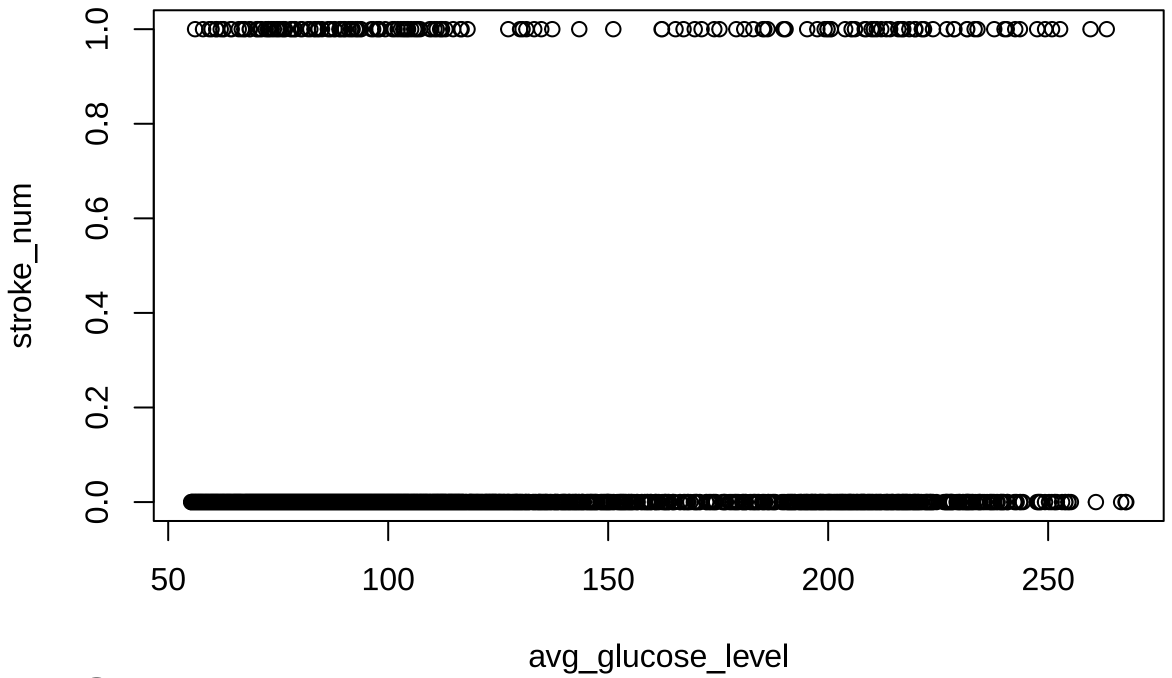

stroke_num
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
hypertension

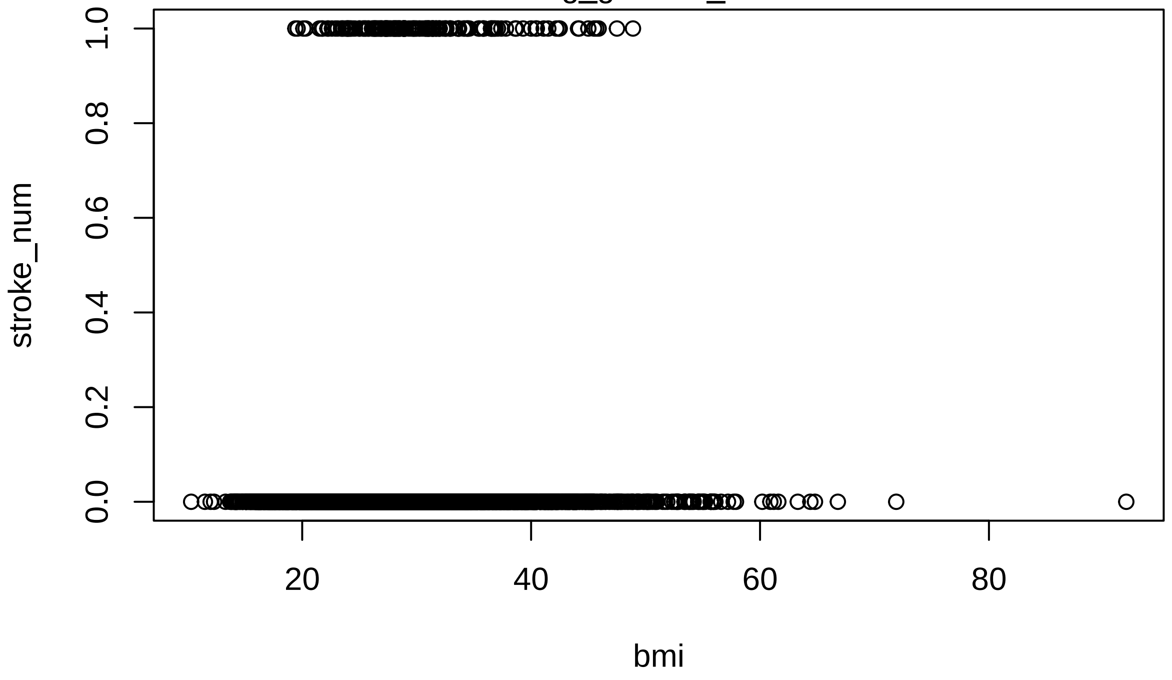

stroke_num
0.0
0.2
0.4
0.6
0.8
1.0
heart_disease


stroke_num
0.0
0.2
0.4
0.6
0.8
1.0
No
Yes
ever_married


stroke_num
0.0
0.2
0.4
0.6
0.8
1.0
children
Govt_job
Private
Self−employed
work_type

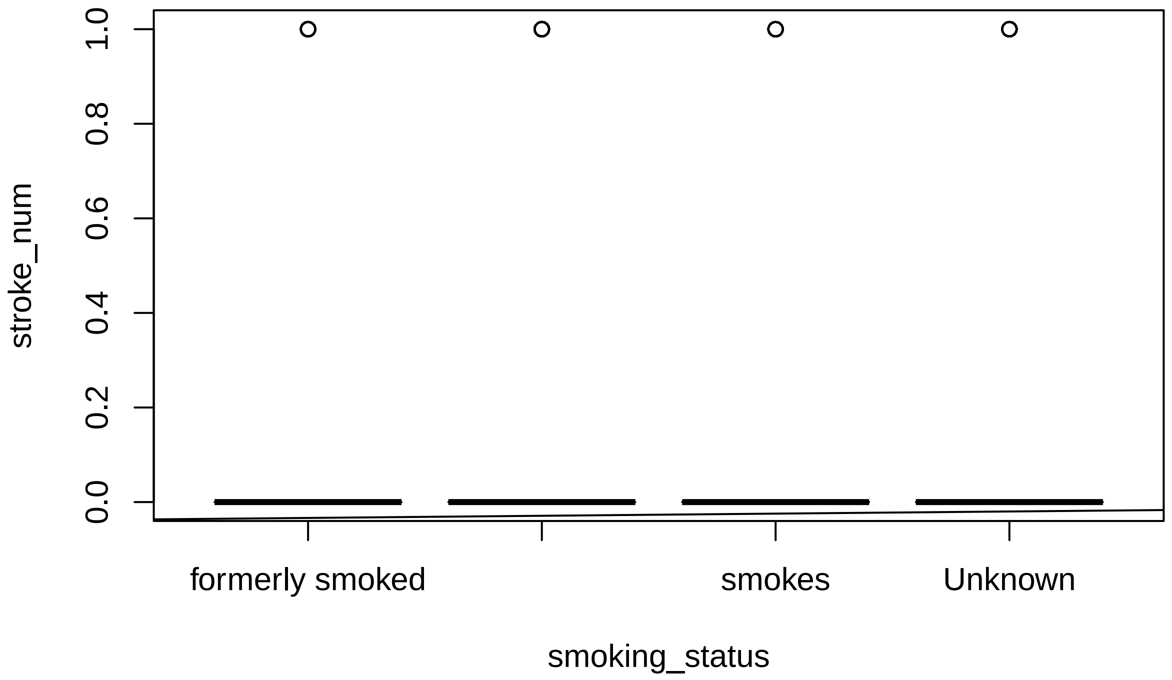

stroke_num
0.0
0.2
0.4
0.6
0.8
1.0
Rural
Urban
Residence_type





```
abline(lm.stroke)
```

```
## Warning in abline(lm.stroke): only using the first two of 17 regression
## coefficients
```

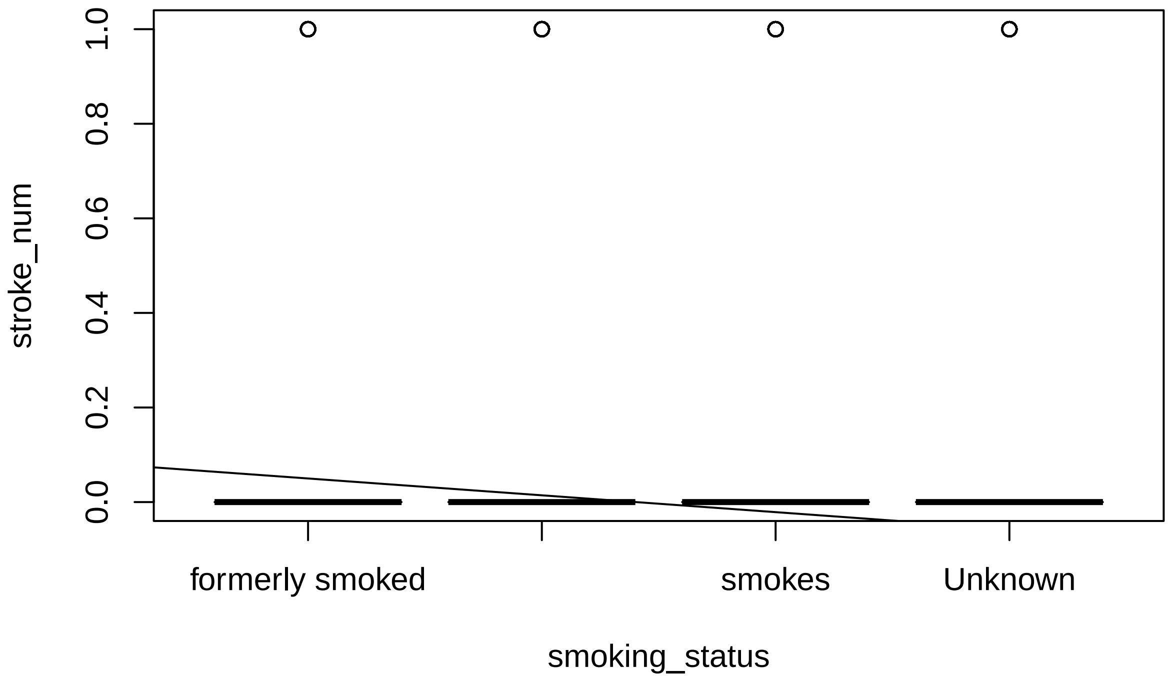


```r
# fitting models for simple regression model
lm.stroke.smoking <- lm(stroke_num ~ smoking_status , data = df_train_linear)
summary(lm.stroke.smoking)
```

```
##
## Call:
## lm(formula = stroke_num ~ smoking_status, data = df_train_linear)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08548 -0.05244 -0.04989 -0.03145  0.96855
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 0.085484   0.008801   9.713  < 2e-16 ***
## smoking_statusnever smoked -0.035597   0.010666  -3.338 0.000854 ***
## smoking_statussmokes       -0.033043   0.012818  -2.578 0.009981 **
## smoking_statusUnknown      -0.054032   0.011040  -4.894 1.03e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2191 on 3573 degrees of freedom
## Multiple R-squared:  0.006675,	Adjusted R-squared:  0.005841
## F-statistic: 8.004 on 3 and 3573 DF,  p-value: 2.579e-05
```

```r
plot(stroke_num ~ smoking_status, data = df_train_linear)
abline(lm.stroke.smoking)
```

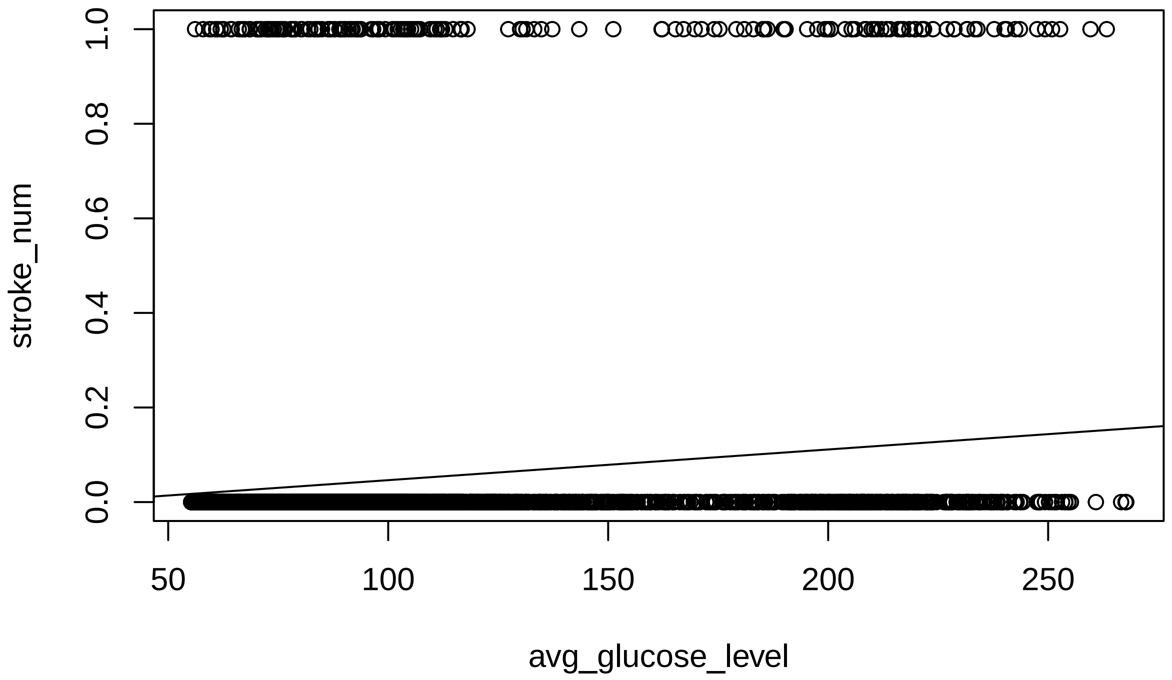
```
## Warning in abline(lm.stroke.smoking): only using the first two of 4 regression
## coefficients
```



```r
# fitting models for simple regression model
lm.stroke.glucose <- lm(stroke_num ~ avg_glucose_level , data = df_train_linear)
summary(lm.stroke.smoking)
```

```
##
## Call:
## lm(formula = stroke_num ~ smoking_status, data = df_train_linear)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08548 -0.05244 -0.04989 -0.03145  0.96855
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  0.085484   0.008801   9.713  < 2e-16 ***
## smoking_statusnever smoked -0.035597   0.010666  -3.338 0.000854 ***
## smoking_statussmokes       -0.033043   0.012818  -2.578 0.009981 **
## smoking_statusUnknown      -0.054032   0.011040  -4.894 1.03e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2191 on 3573 degrees of freedom
## Multiple R-squared:  0.006675,   Adjusted R-squared:  0.005841
## F-statistic: 8.004 on 3 and 3573 DF,  p-value: 2.579e-05
```

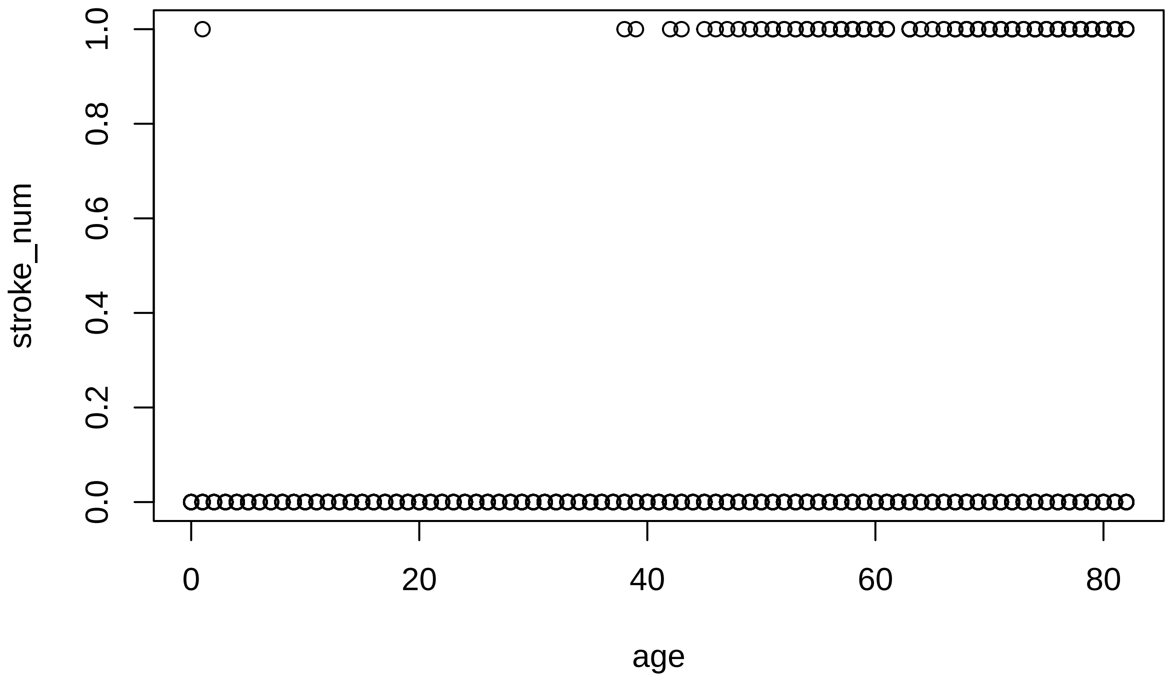
```r
plot(stroke_num ~ avg_glucose_level, data = df_train_linear)
abline(lm.stroke.glucose)
```



```r
# fitting models for simple regression model
pred_var  <-

lm.stroke.glucose <- lm(stroke_num ~ age + gender , data = df_train_linear)
summary(lm.stroke.smoking)
```

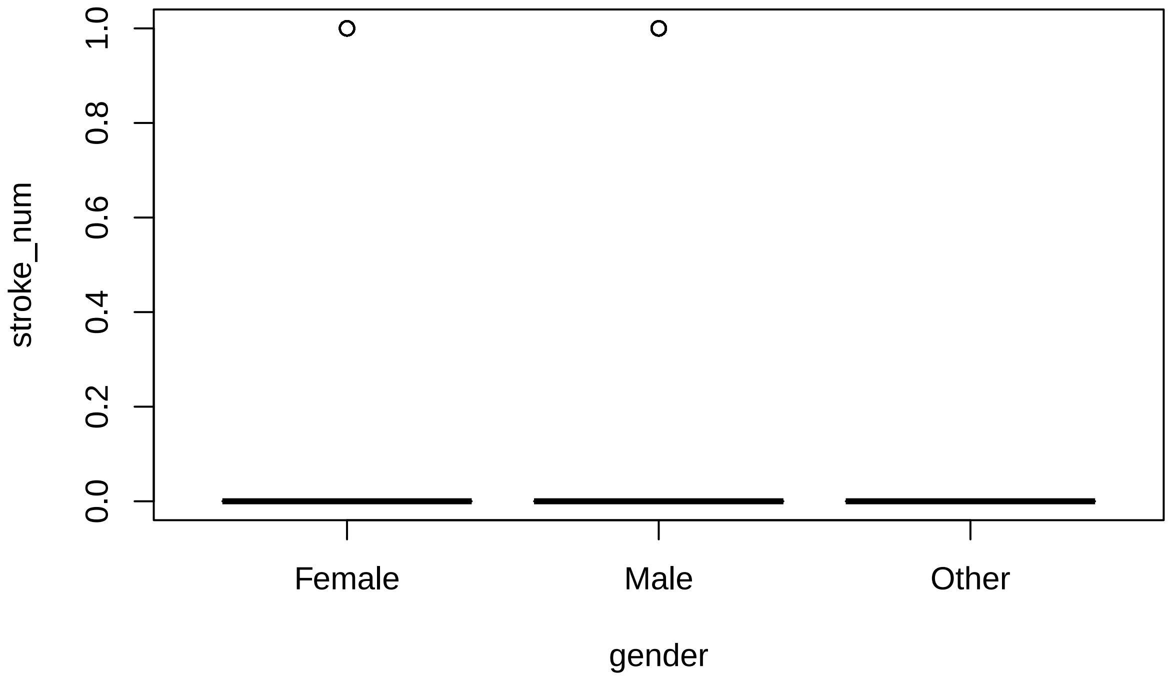
```
##
## Call:
## lm(formula = stroke_num ~ smoking_status, data = df_train_linear)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08548 -0.05244 -0.04989 -0.03145  0.96855
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  0.085484   0.008801   9.713  < 2e-16 ***
## smoking_statusnever smoked -0.035597   0.010666  -3.338 0.000854 ***
## smoking_statussmokes       -0.033043   0.012818  -2.578 0.009981 **
## smoking_statusUnknown      -0.054032   0.011040  -4.894 1.03e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2191 on 3573 degrees of freedom
## Multiple R-squared:  0.006675,   Adjusted R-squared:  0.005841
## F-statistic: 8.004 on 3 and 3573 DF,  p-value: 2.579e-05
```

```r
plot(stroke_num ~ age + gender, data = df_train_linear)
```



```r
abline(lm.stroke.glucose)
```

```
## Warning in abline(lm.stroke.glucose): only using the first two of 4 regression
## coefficients
```

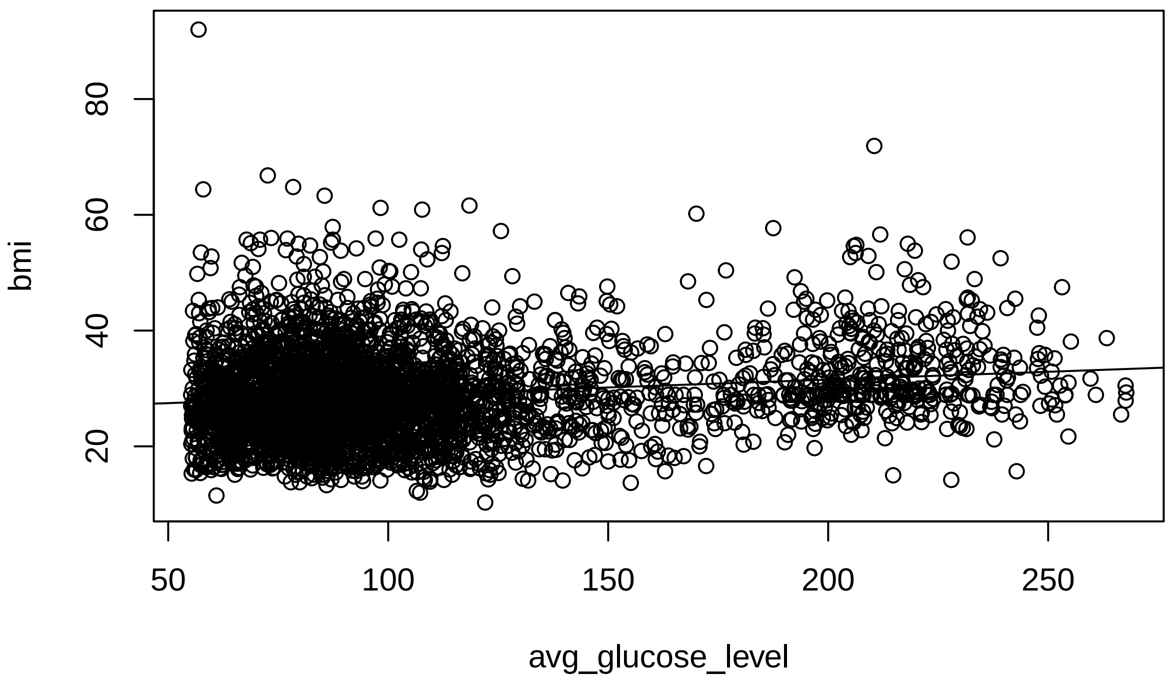


```r
# fitting models for simple regression model
 lm.stroke.bmi <- lm(bmi ~ avg_glucose_level, data = df_train_linear)
 summary(lm.stroke.bmi)
```

```
##
## Call:
## lm(formula = bmi ~ avg_glucose_level, data = df_train_linear)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -19.116  -4.919  -0.754   3.807  64.349
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       26.109983   0.320458  81.477   <2e-16 ***
## avg_glucose_level  0.027086   0.002752   9.843   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.554 on 3575 degrees of freedom
## Multiple R-squared:  0.02639,    Adjusted R-squared:  0.02612
## F-statistic: 96.89 on 1 and 3575 DF,  p-value: < 2.2e-16
```

```
plot(bmi ~ avg_glucose_level, data = df_train_linear)
abline(lm.stroke.bmi)
```



5 Generalised Linear Model with family set to Poisson

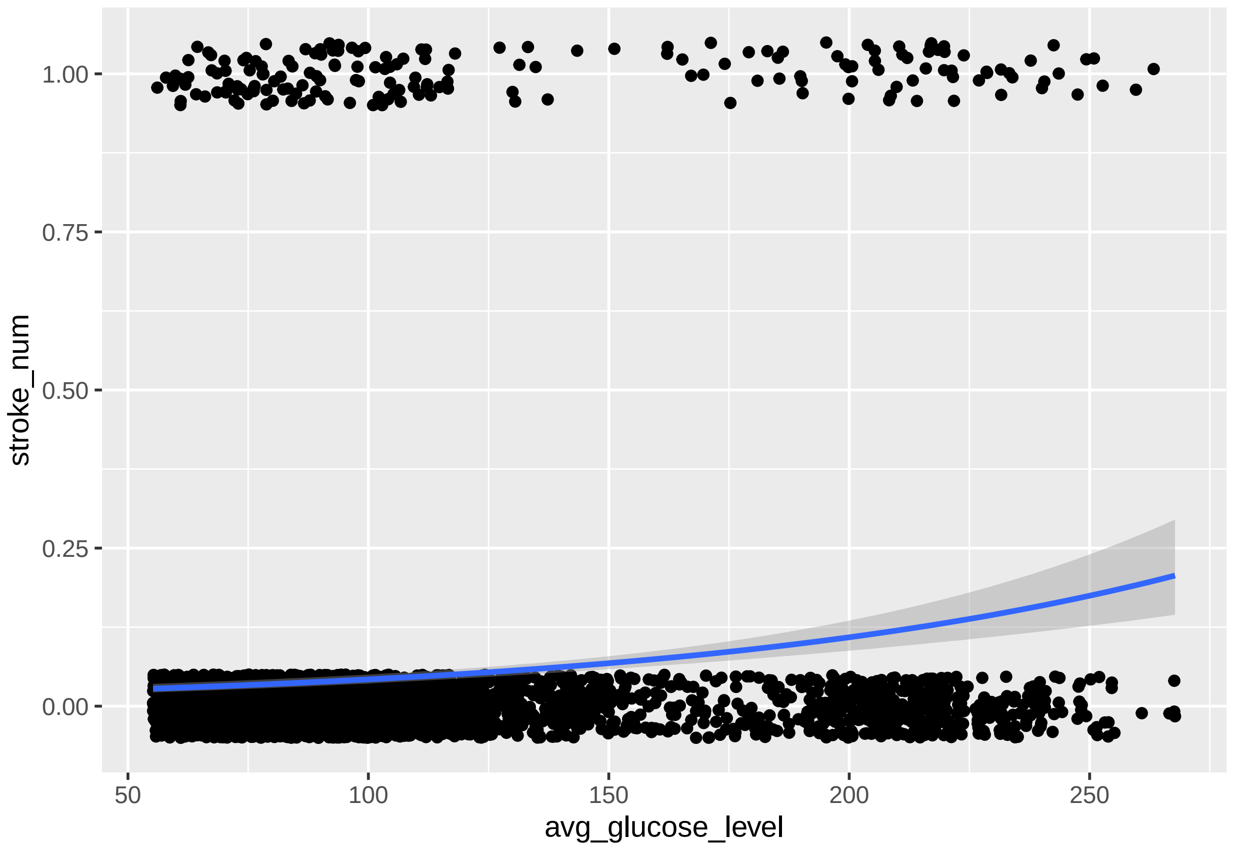
```
# text
glm.stroke.poisson <- glm(stroke_num ~ age + heart_disease + hypertension + avg_glucose_level,
family = "poisson",
data = df_train_linear)
summary(glm.stroke.poisson)
```

```
##
## Call:
## glm(formula = stroke_num ~ age + heart_disease + hypertension +
##     avg_glucose_level, family = "poisson", data = df_train_linear)
##
```

```
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0558  -0.3142  -0.1712  -0.0831   3.4861
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -7.384780   0.413043 -17.879  < 2e-16 ***
## age               0.066499   0.005875  11.319  < 2e-16 ***
## heart_disease     0.356522   0.186276   1.914  0.05563 .
## hypertension      0.296479   0.168541   1.759  0.07856 .
## avg_glucose_level 0.003448   0.001222   2.823  0.00476 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 1084.09  on 3576  degrees of freedom
## Residual deviance:  795.51  on 3572  degrees of freedom
## AIC: 1169.5
##
## Number of Fisher Scoring iterations: 7
```

```
#plot(stroke_num ~ age + heart_disease + hypertension + avg_glucose_level, data = df_train_linear)
#abline(glm.stroke_poisson)
ggplot(data = df_train_linear, aes(x = avg_glucose_level, y = stroke_num)) +
  geom_jitter(width = 0, height = 0.05) +
  geom_smooth(method = "glm", method.args = list(family = "poisson"))
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
# Evaluating model fit poisson

# fitted(glm.stroke.poisson)
fitted.glm.stroke.poisson <- ifelse(fitted(glm.stroke.poisson) < 0.08, yes = 0, no = 1)
head(fitted.glm.stroke.poisson)
```

```
## 1 2 3 4 5 6
## 1 1 0 1 1 1
```

```
obs.fitted.comp.poisson <- data.frame(obs = df_train_linear$stroke_num, fitted = fitted.glm.stroke.pois

table(obs = obs.fitted.comp.poisson$obs, fit = obs.fitted.comp.poisson$fitted)
```

```
##    fit
## obs    0    1
##   0 2809  586
##   1   51  131
```

```
table(obs = obs.fitted.comp.poisson$obs, fit = obs.fitted.comp.poisson$fitted) %>%
  prop.table() %>%
  round(digits = 2)
```

```
##    fit
## obs    0    1
##   0 0.79 0.16
##   1 0.01 0.04
```

6 Generalised Linear Model with family set to Binomial

Since we are essentially dealing with a classification issue, using logistic regression in the form of a GLM with family set to "binomial" is the best method to apply out of all the models introduced so far. For this reason, we shall go into more detail here.

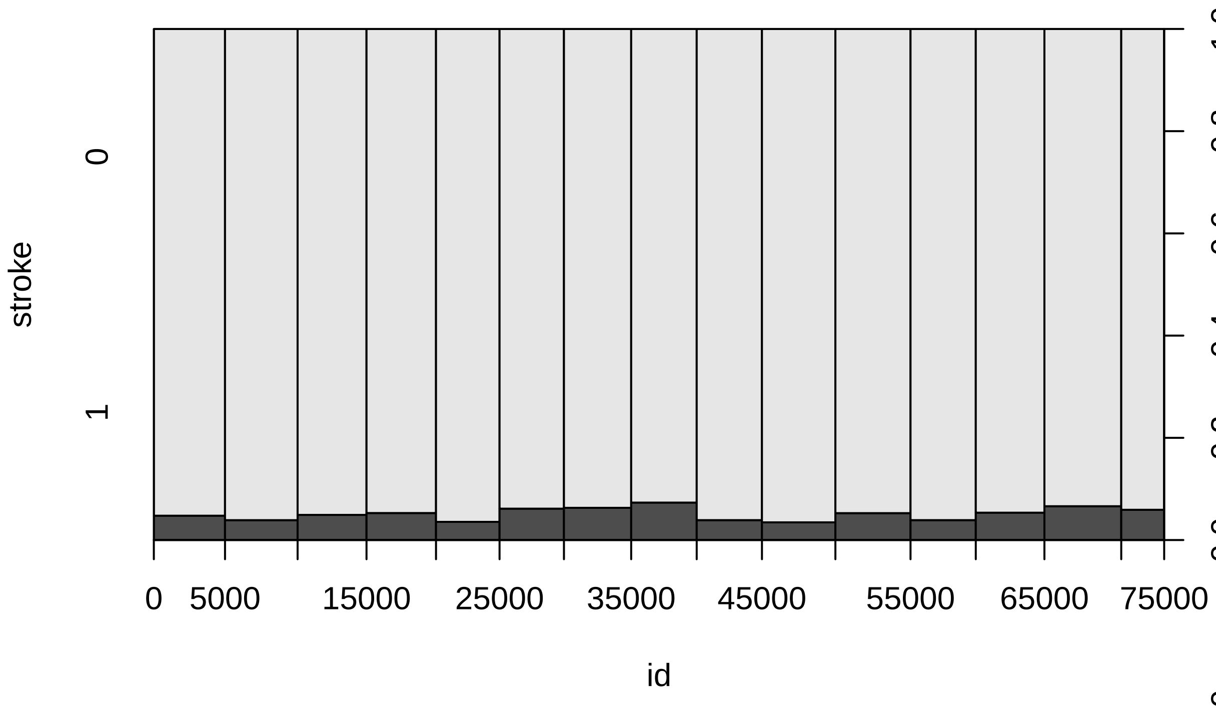
```
# Include all variables to start variable selection
# Plot all of them for visual analysis
glm.stroke.binomial <- glm(stroke ~ .,
family = "binomial",
data = df_train_linear)
```

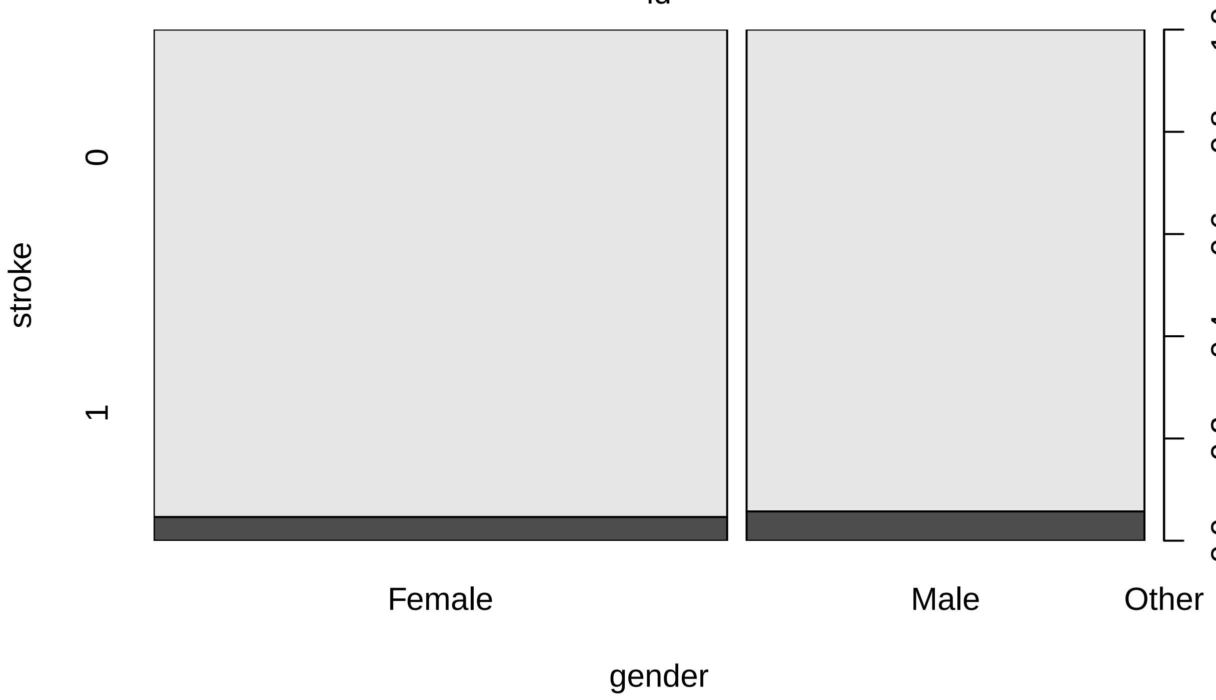
```
## Warning: glm.fit: algorithm did not converge
```

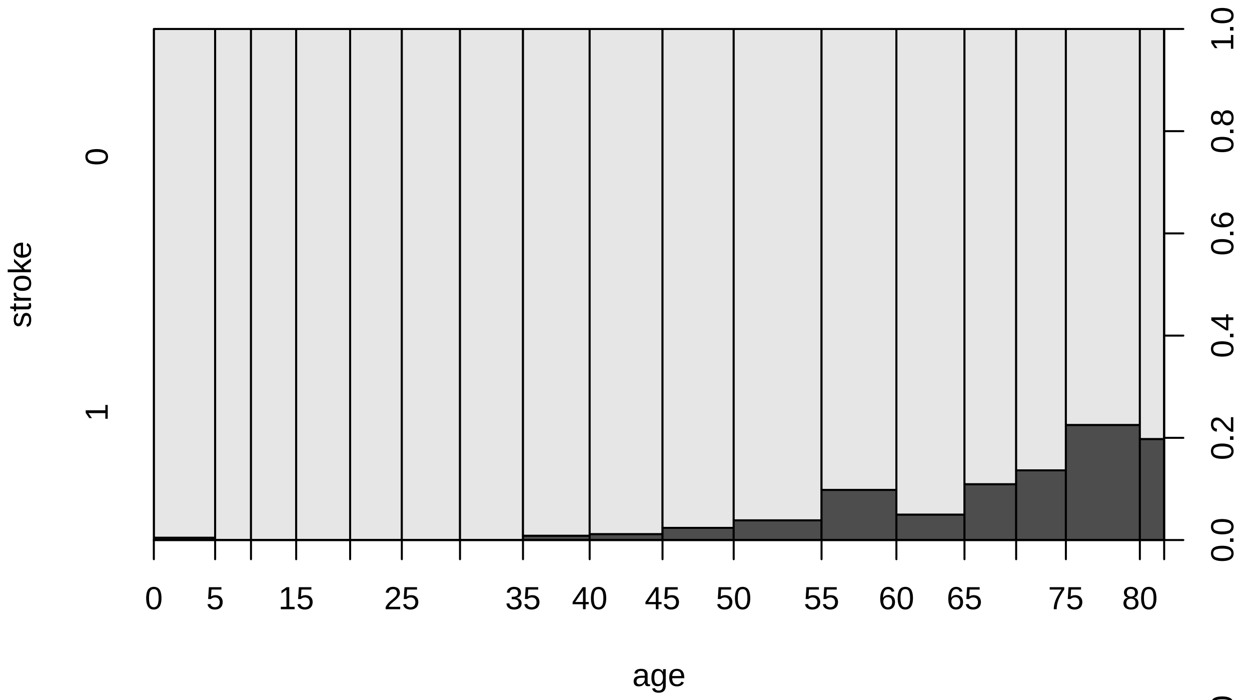
```
summary(glm.stroke.binomial)
```

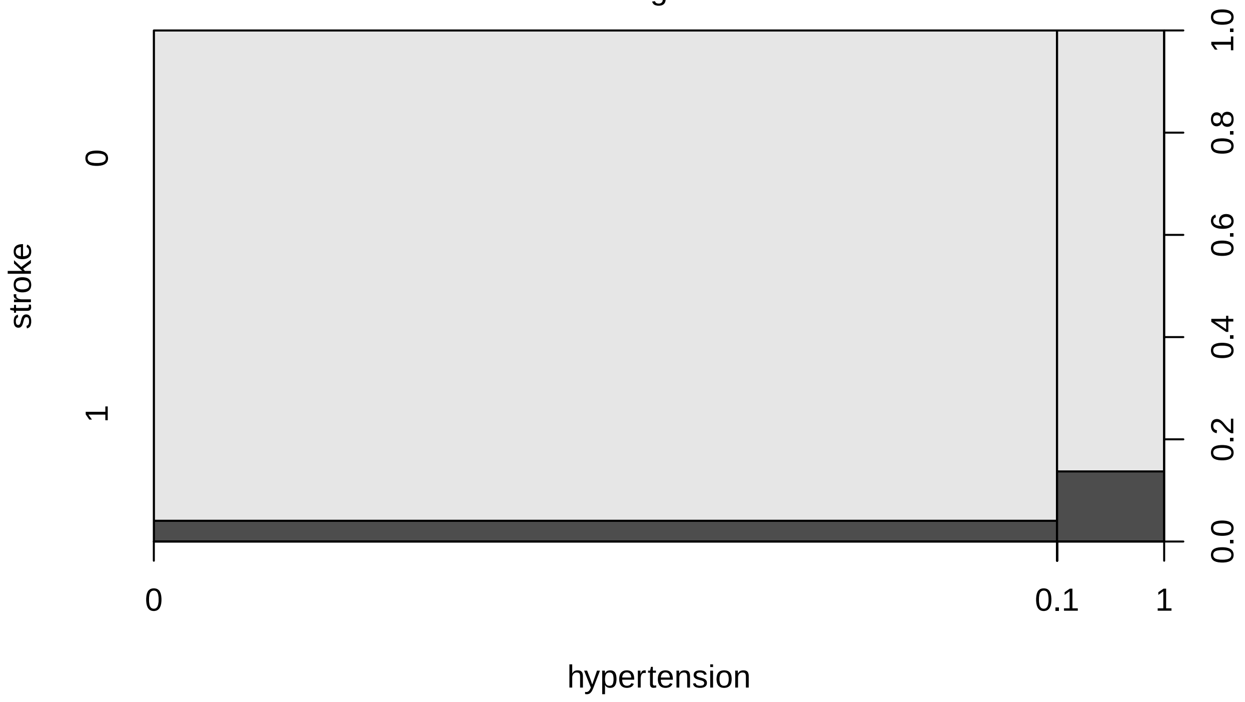
```
##
## Call:
## glm(formula = stroke ~ ., family = "binomial", data = df_train_linear)
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -2.409e-06  -2.409e-06  -2.409e-06  -2.409e-06   2.409e-06
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -2.657e+01  3.576e+04  -0.001    0.999
## id                          3.753e-17  2.789e-01   0.000    1.000
## genderMale                 -1.296e-12  1.228e+04   0.000    1.000
## genderOther                -1.930e-12  3.569e+05   0.000    1.000
## age                        -5.937e-13  4.548e+02   0.000    1.000
## hypertension               -1.935e-11  2.060e+04   0.000    1.000
## heart_disease               2.369e-10  2.725e+04   0.000    1.000
## ever_marriedYes             2.975e-13  1.780e+04   0.000    1.000
## work_typeGovt_job           1.343e-11  3.160e+04   0.000    1.000
## work_typeNever_worked       4.315e-12  9.134e+04   0.000    1.000
## work_typePrivate            1.297e-11  2.654e+04   0.000    1.000
## work_typeSelf-employed      1.753e-12  3.226e+04   0.000    1.000
## Residence_typeUrban         7.404e-12  1.193e+04   0.000    1.000
## avg_glucose_level           1.803e-13  1.367e+02   0.000    1.000
## bmi                         9.729e-14  8.838e+02   0.000    1.000
## smoking_statusnever smoked  4.215e-12  1.768e+04   0.000    1.000
## smoking_statussmokes        1.480e-11  2.109e+04   0.000    1.000
## smoking_statusUnknown       6.158e-12  1.978e+04   0.000    1.000
## stroke_num                  5.313e+01  2.850e+04   0.002    0.999
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.4387e+03  on 3576  degrees of freedom
## Residual deviance: 2.0752e-08  on 3558  degrees of freedom
## AIC: 38
##
## Number of Fisher Scoring iterations: 25
```

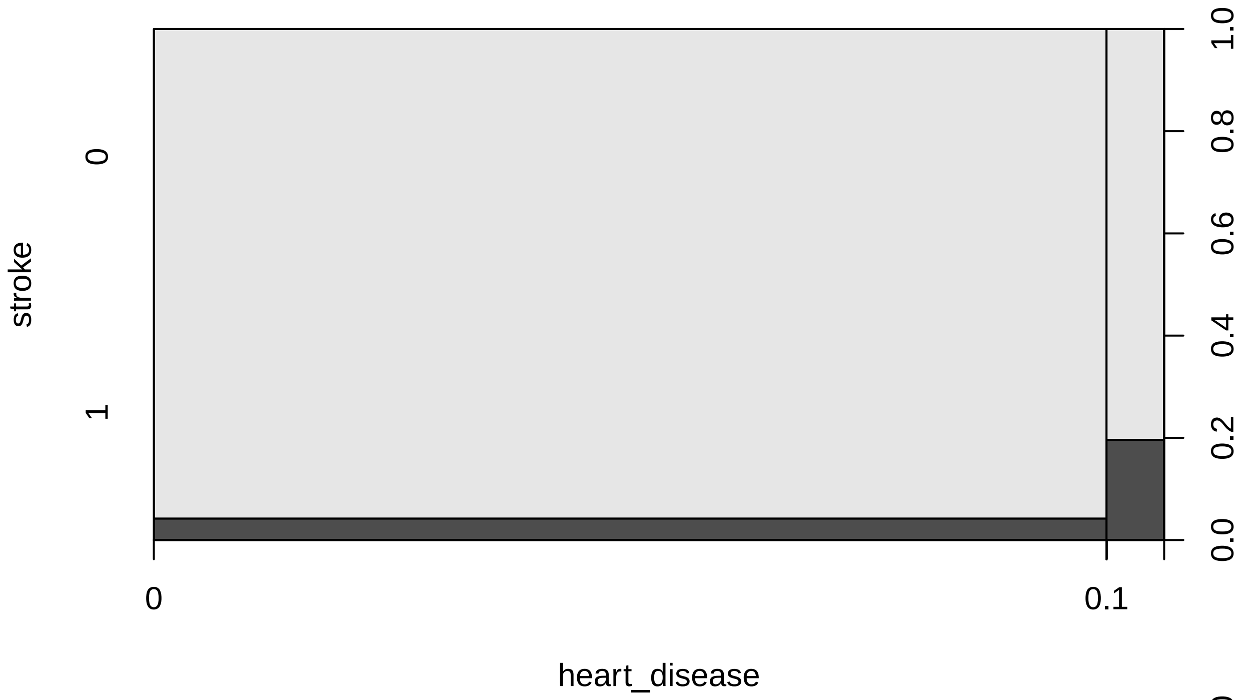
```
plot(stroke ~ ., data = df_train_linear)
```

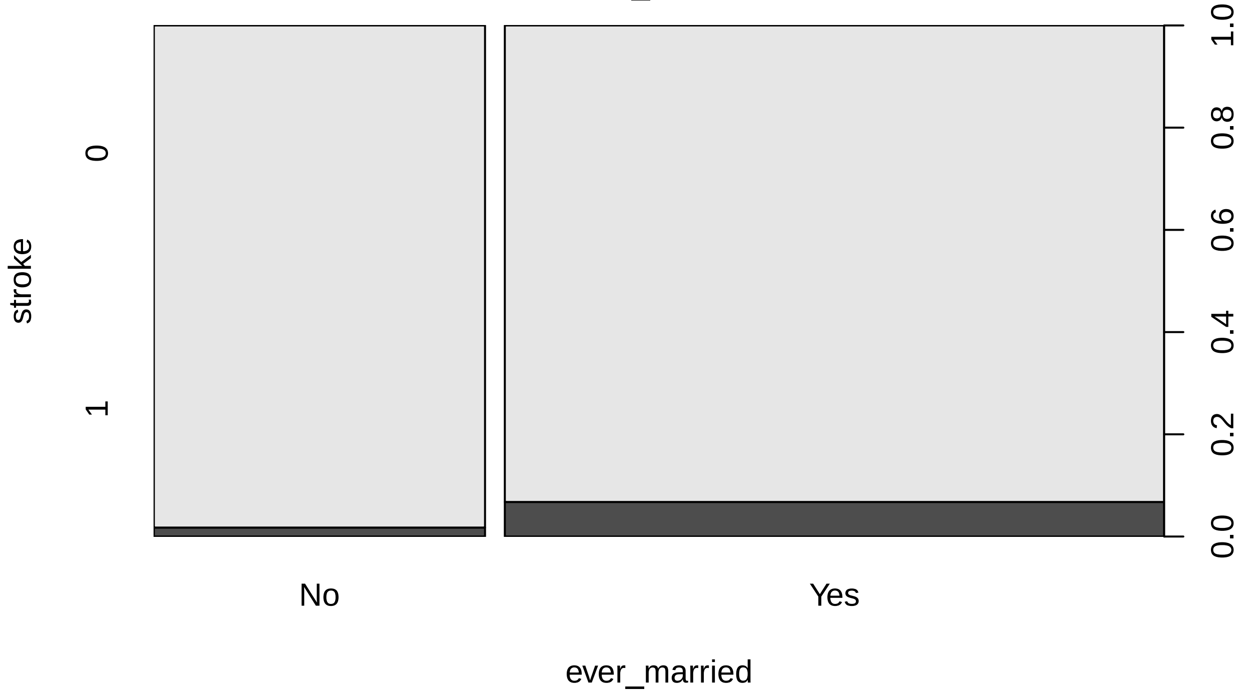

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
5000
15000
25000
35000
45000
55000
65000
75000
id

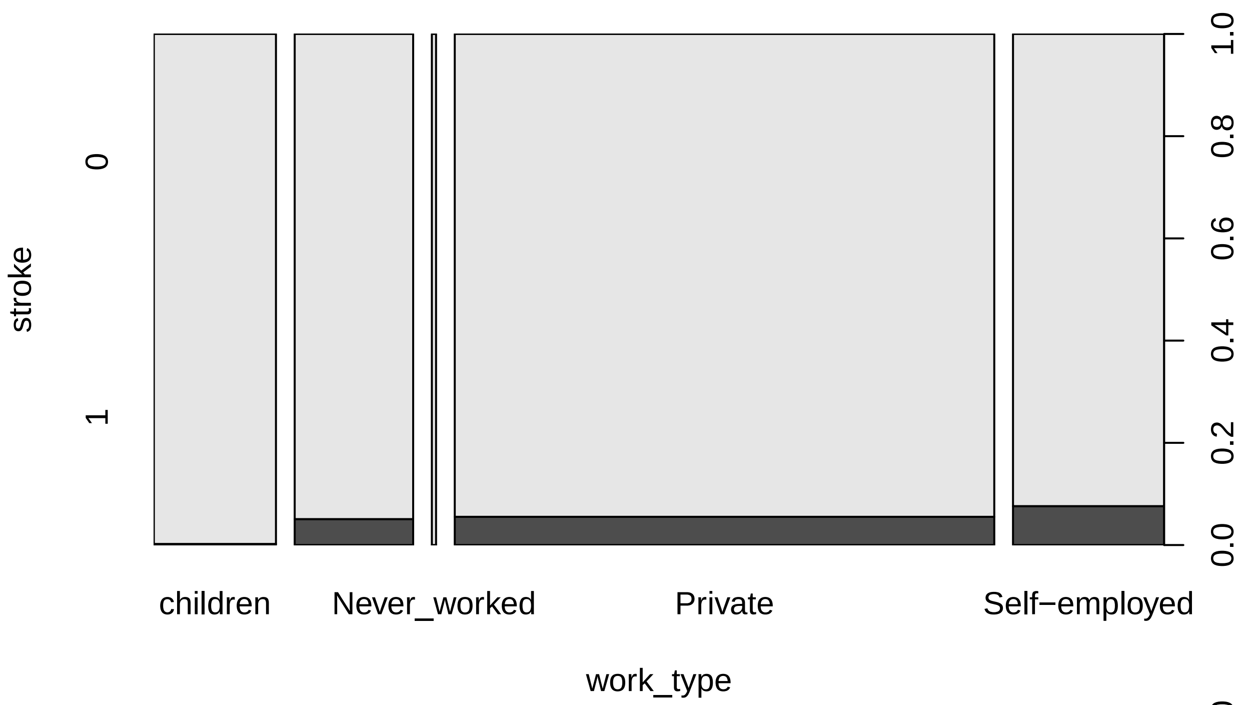

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
Female
Male
Other
gender

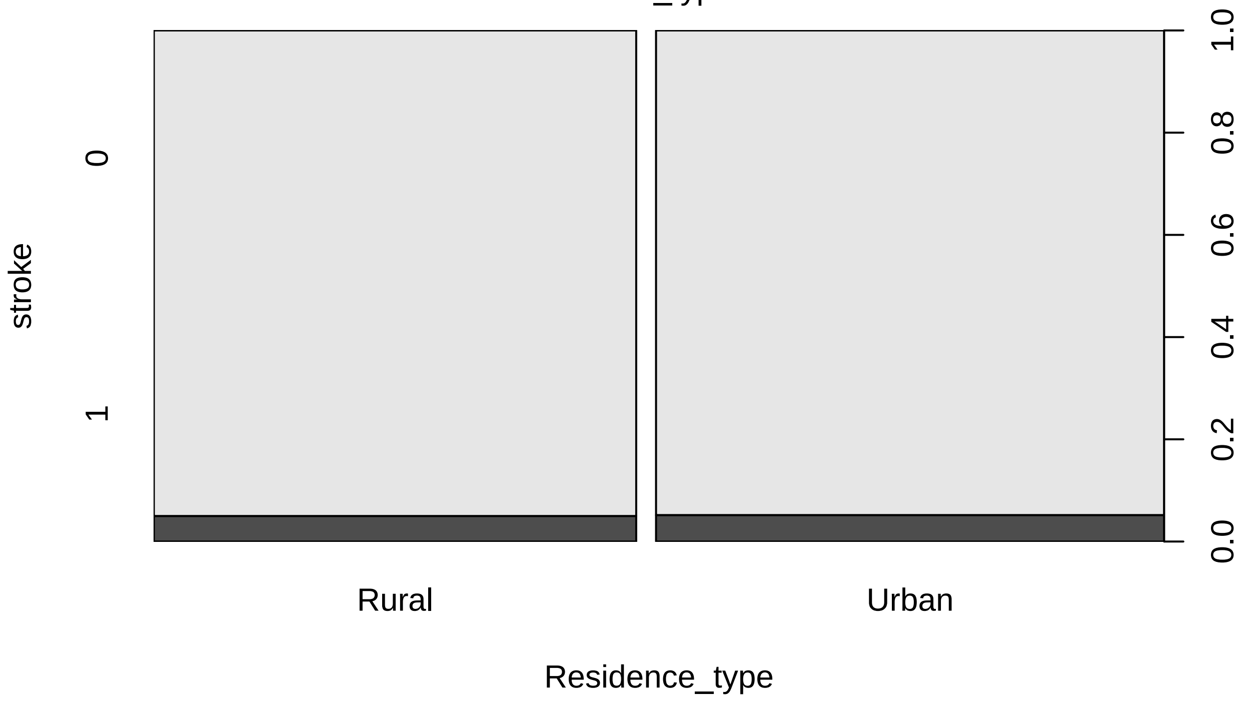

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
5
15
25
35
40
45
50
55
60
65
75
80
age

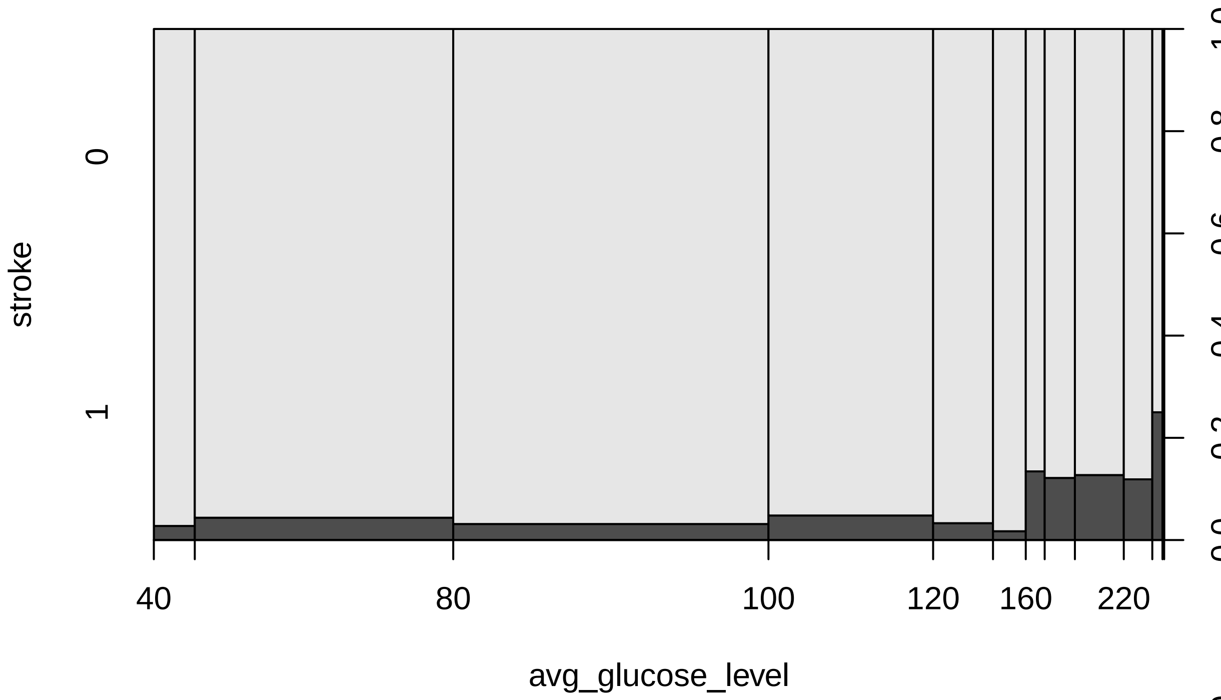

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
0.1
1
hypertension

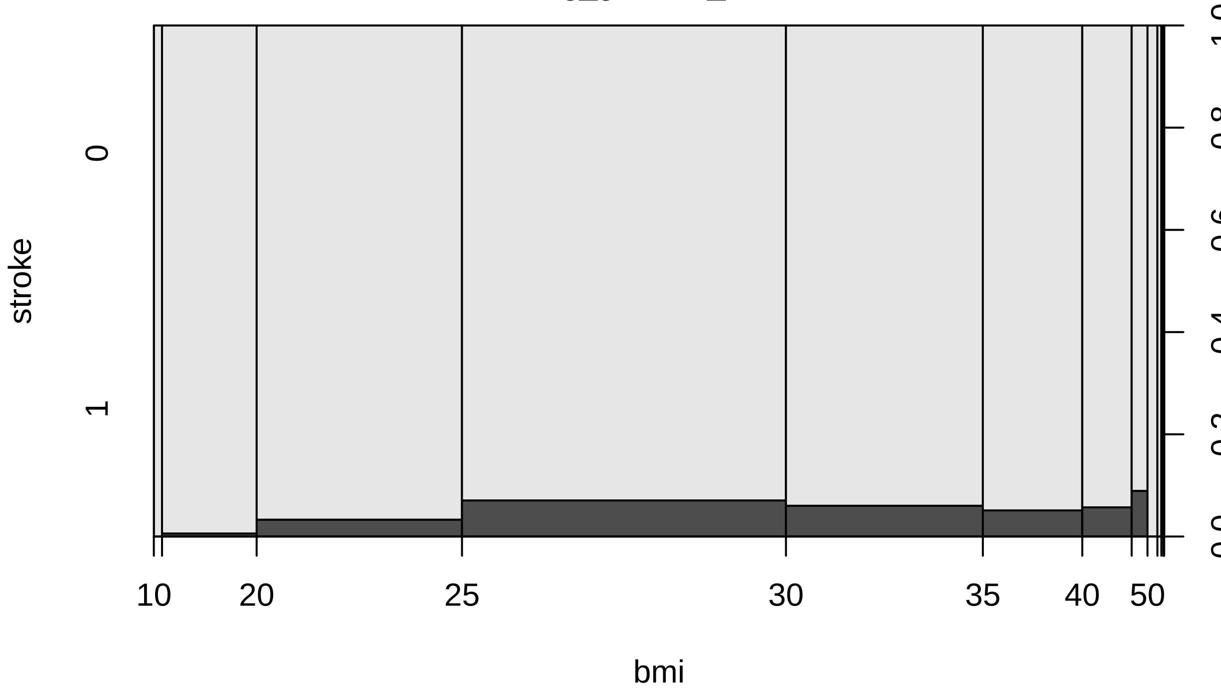

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
0.1
heart_disease

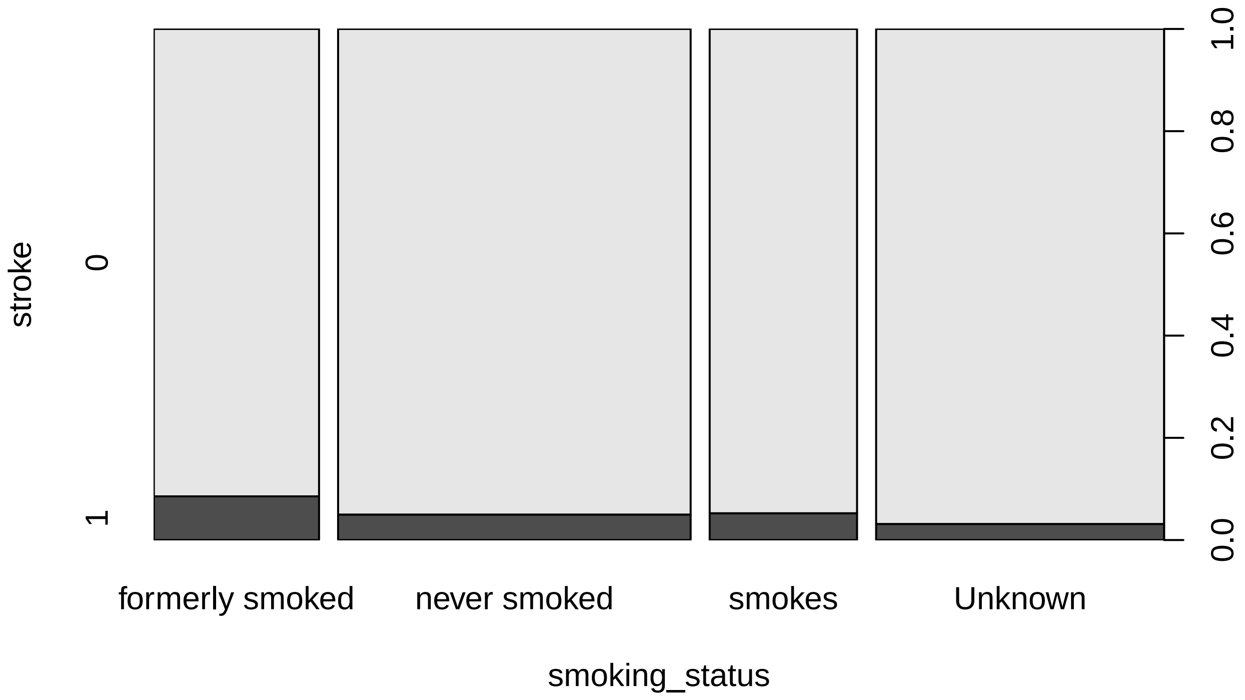

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
No
Yes
ever_married


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
children
Never_worked
Private
Self−employed
work_type


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
Rural
Urban
Residence_type

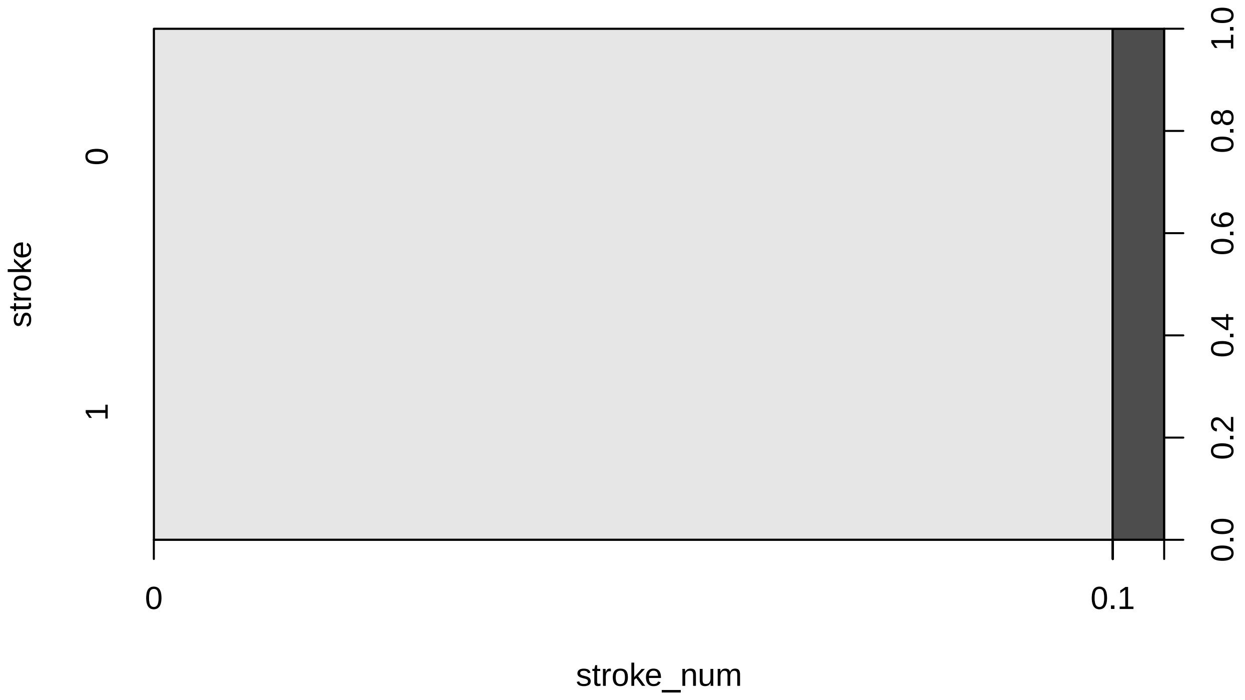

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
40
80
100
120
160
220
avg_glucose_level


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
10
20
25
30
35
40
50
bmi



```
abline(glm.stroke.binomial)
```

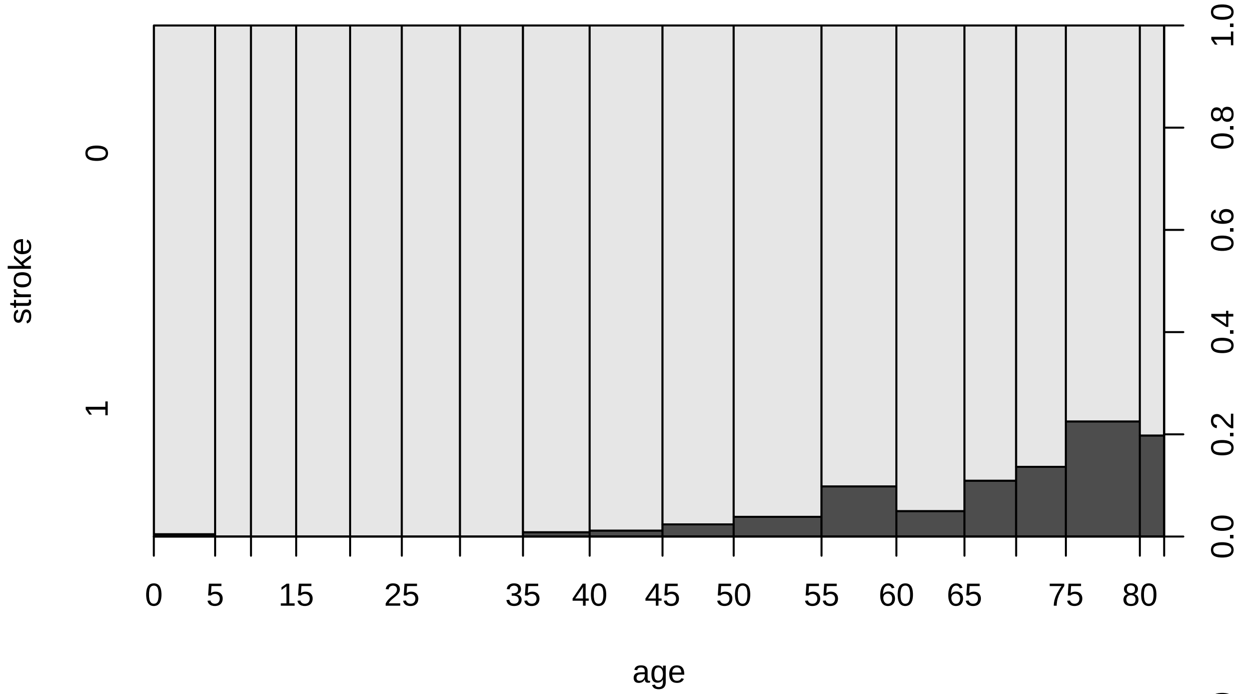
```
## Warning in abline(glm.stroke.binomial): only using the first two of 19
## regression coefficients
```

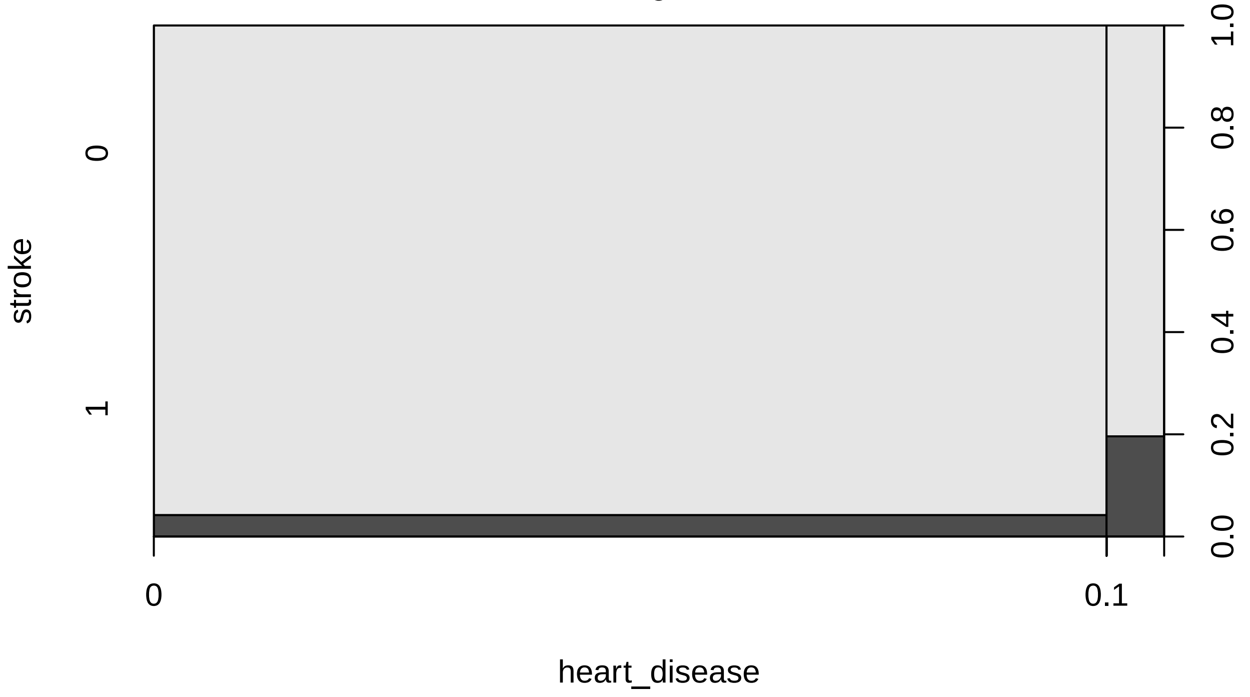


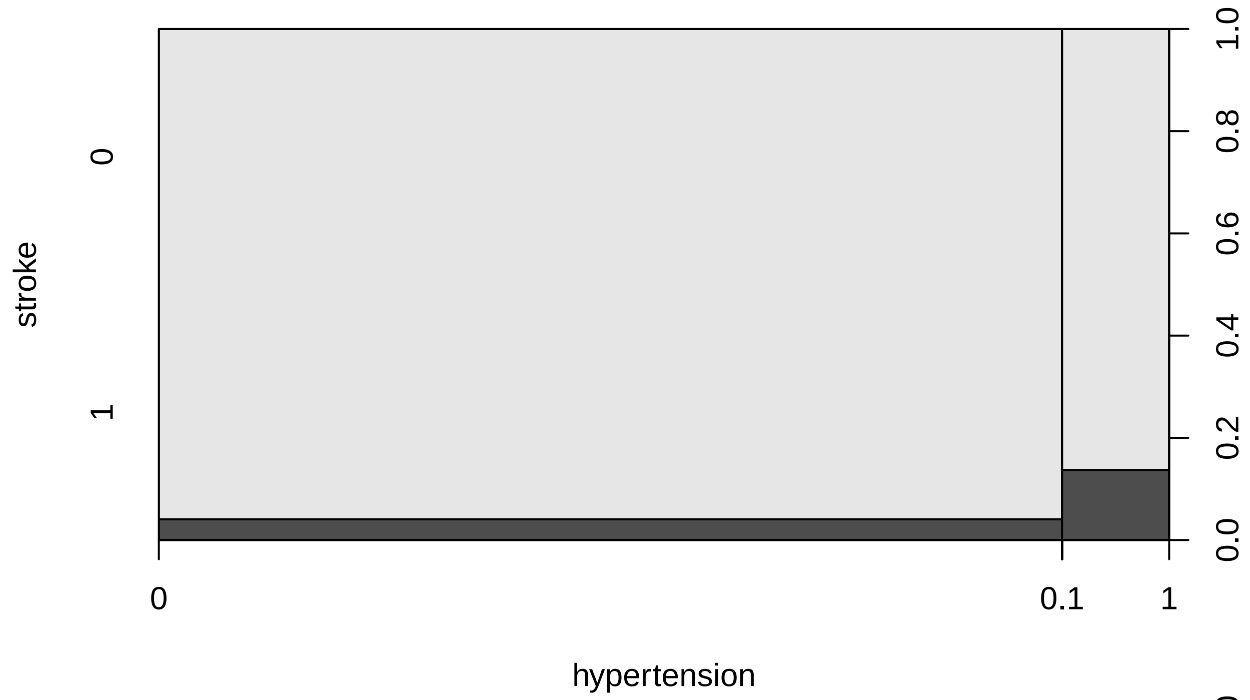
```
# First iteration with parameters chosen from intuitive domain knowledge and exploratory analysis of da
glm.stroke.binomial <- glm(stroke ~ age + heart_disease + hypertension + work_type + avg_glucose_level +
family = "binomial",
data = df_train_linear)
summary(glm.stroke.binomial)
```

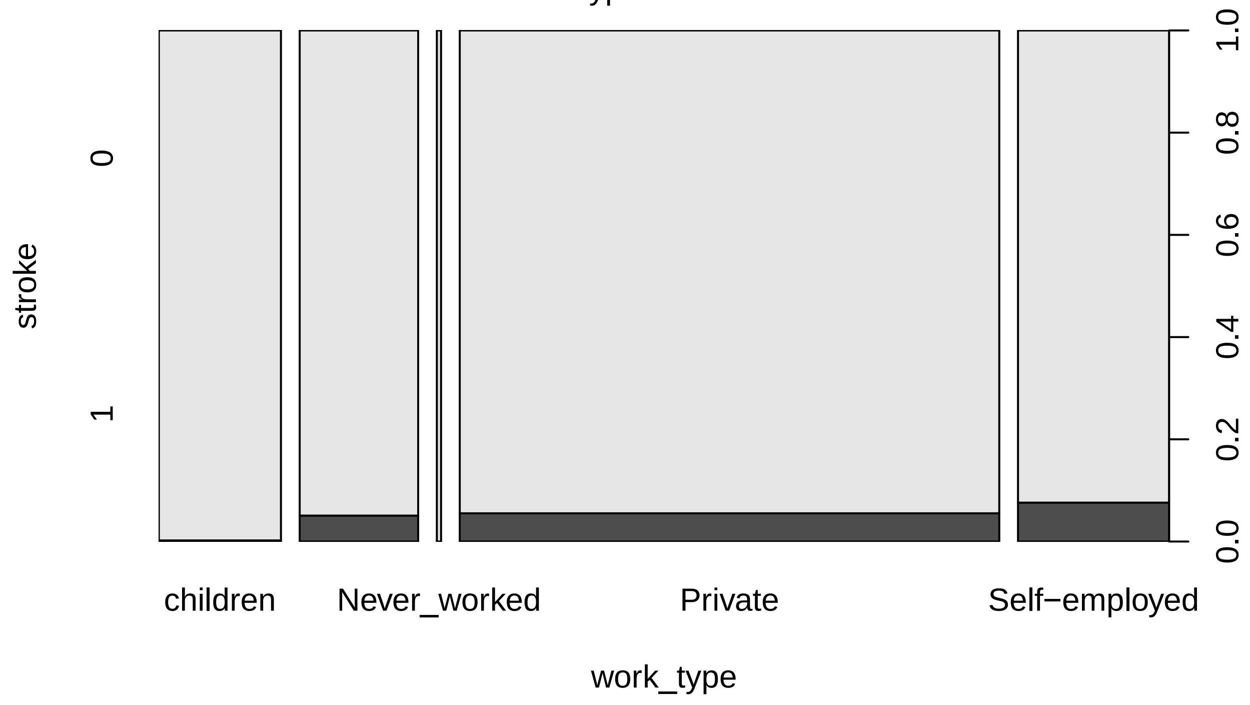
```
##
## Call:
## glm(formula = stroke ~ age + heart_disease + hypertension + work_type +
##     avg_glucose_level + smoking_status, family = "binomial",
##     data = df_train_linear)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.1696  -0.3241  -0.1595  -0.0771   3.6785
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -7.037953   1.036288  -6.792 1.11e-11 ***
## age                          0.078346   0.006958  11.260  < 2e-16 ***
## heart_disease                0.431469   0.213875   2.017   0.0437 *
## hypertension                 0.378996   0.189527   2.000   0.0455 *
## work_typeGovt_job           -1.003706   1.105068  -0.908   0.3637
## work_typeNever_worked      -10.077332 362.934034  -0.028   0.9778
## work_typePrivate            -0.818567   1.088363  -0.752   0.4520
## work_typeSelf-employed      -1.382649   1.112789  -1.243   0.2140
## avg_glucose_level            0.003936   0.001360   2.894   0.0038 **
## smoking_statusnever smoked  -0.186796   0.203452  -0.918   0.3586
## smoking_statussmokes         0.032194   0.256225   0.126   0.9000
## smoking_statusUnknown       -0.081986   0.243356  -0.337   0.7362
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1438.7  on 3576  degrees of freedom
## Residual deviance: 1117.5  on 3565  degrees of freedom
## AIC: 1141.5
##
## Number of Fisher Scoring iterations: 14
```

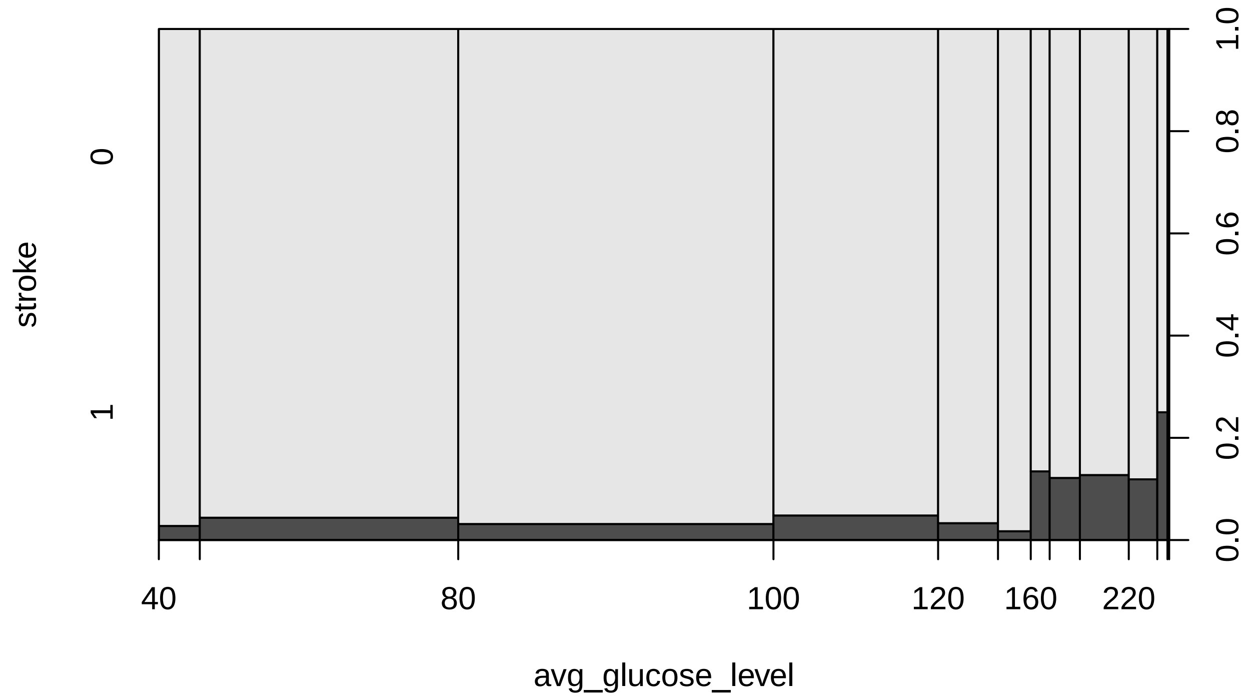
```
plot(stroke ~ age + heart_disease + hypertension + work_type + avg_glucose_level + smoking_status, data
```


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
5
15
25
35
40
45
50
55
60
65
75
80
age


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
0.1
heart_disease

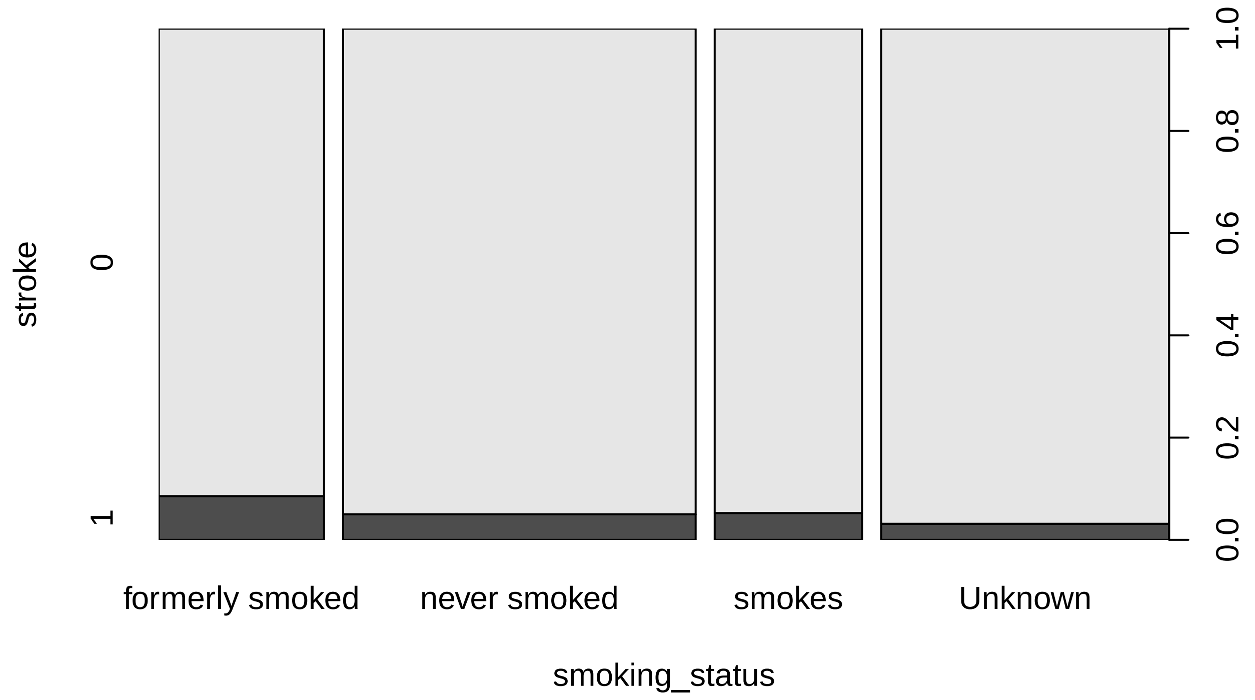

stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
0
0.1
1
hypertension


stroke
0
1
1.0
0.8
0.6
0.4
0.2
0.0
children
Never_worked
Private
Self−employed
work_type



```r
abline(glm.stroke.binomial)
```

```
## Warning in abline(glm.stroke.binomial): only using the first two of 12
## regression coefficients
```

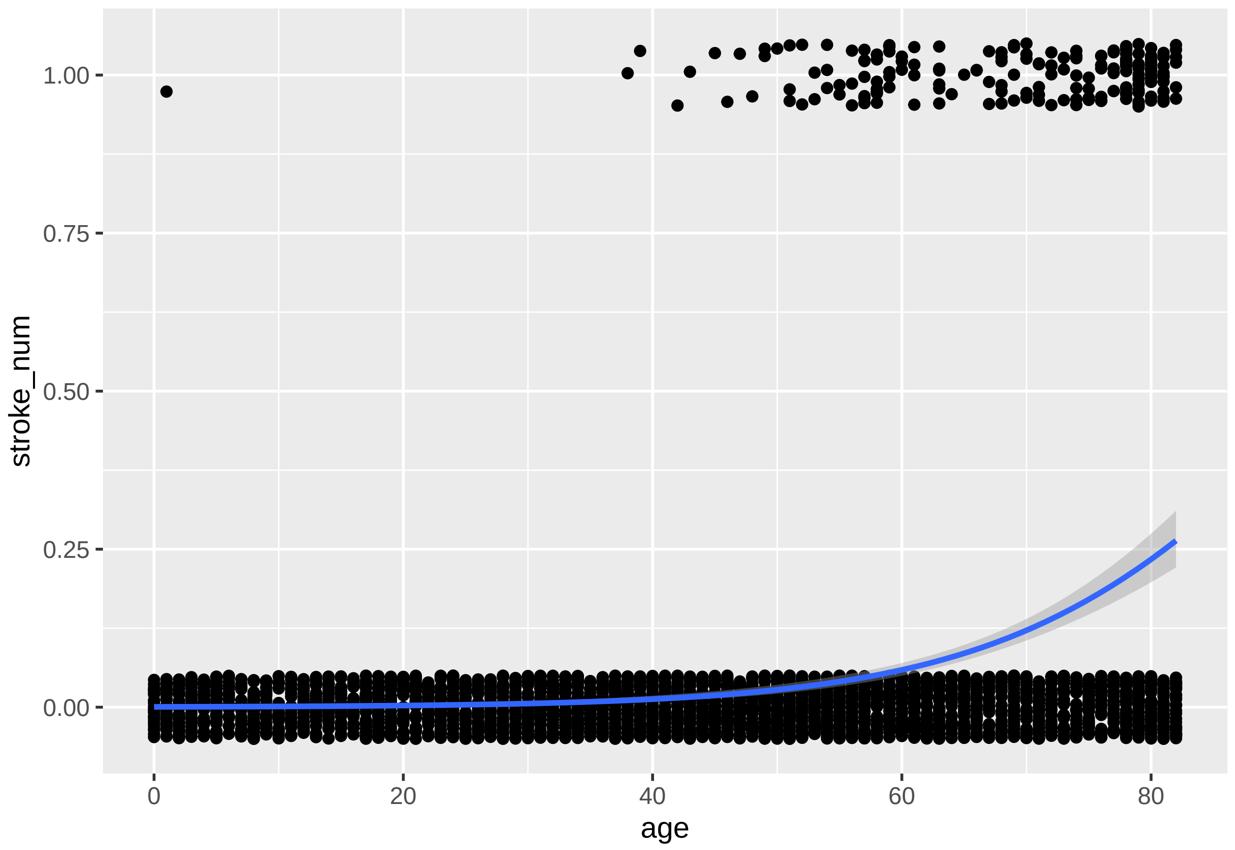


```r
# second iteration only keeping statistically relevant parameters from previous model
glm.stroke.binomial.2 <- glm(stroke_num ~ age + heart_disease + hypertension + avg_glucose_level,
family = "binomial",
data = df_train_linear)
summary(glm.stroke.binomial.2)
```

```
##
## Call:
## glm(formula = stroke_num ~ age + heart_disease + hypertension +
##     avg_glucose_level, family = "binomial", data = df_train_linear)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.1183  -0.3237  -0.1671  -0.0764   3.8413
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -7.739236   0.443953 -17.433   <2e-16 ***
## age                0.072374   0.006312  11.467   <2e-16 ***
## heart_disease      0.465121   0.211312   2.201   0.0277 *
## hypertension       0.362843   0.187103   1.939   0.0525 .
## avg_glucose_level  0.004117   0.001351   3.048   0.0023 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1438.7  on 3576  degrees of freedom
## Residual deviance: 1127.6  on 3572  degrees of freedom
## AIC: 1137.6
##
## Number of Fisher Scoring iterations: 7
```

```r
# plot(stroke ~ age + heart_disease + hypertension + avg_glucose_level, data = df_train_linear)
# abline(glm.stroke.binomial.2)

pred <- predict(glm.stroke.binomial.2)
# pred

ggplot(data = df_train_linear, aes(x = age, y = stroke_num)) +
  geom_jitter(width = 0, height = 0.05) +
  geom_smooth(method = "glm", method.args = list(family = "binomial"))
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
# Evaluating model fit using fitted()

# fitted(glm.stroke.binomial.2)
fitted.glm.stroke.binomial.2 <- ifelse(fitted(glm.stroke.binomial.2) < 0.2, yes = 0, no = 1)
head(fitted.glm.stroke.binomial.2)
```

```
## 1 2 3 4 5 6
## 0 1 0 1 1 1
```

```
obs.fitted.comp <- data.frame(obs = df_train_linear$stroke_num, fitted = fitted.glm.stroke.binomial.2)

table(obs = obs.fitted.comp$obs, fit = obs.fitted.comp$fitted)
```

```
##    fit
## obs    0    1
##   0 3235  160
##   1  130   52
```

```
table(obs = obs.fitted.comp$obs, fit = obs.fitted.comp$fitted) %>%
  prop.table() %>%
  round(digits = 2)
```

```
##    fit
## obs    0    1
##   0 0.90 0.04
##   1 0.04 0.01
```

```
# Evaluating model fit using predict
```

```r
# predict(glm.stroke.binomial.2, df_test_linear, type = "response")

# predicted(glm.stroke.binomial.2)
predicted.glm.stroke.binomial.2 <- ifelse(predict(glm.stroke.binomial.2, df_test_linear, type = "respons
head(predicted.glm.stroke.binomial.2)
```

```
## 1 2 3 4 5 6
## 0 0 0 0 0 0
```

```r
obs.predicted.comp <- data.frame(obs = df_test_linear$stroke_num, predicted = predicted.glm.stroke.bino

table(obs = obs.predicted.comp$obs, fit = obs.predicted.comp$predicted)
```

```
##    fit
## obs    0    1
##   0 1412   54
##   1   54   13
```

```r
table(obs = obs.predicted.comp$obs, fit = obs.predicted.comp$predicted) %>%
  prop.table() %>%
  round(digits = 2)
```

```
##    fit
## obs    0    1
##   0 0.92 0.04
##   1 0.04 0.01
```

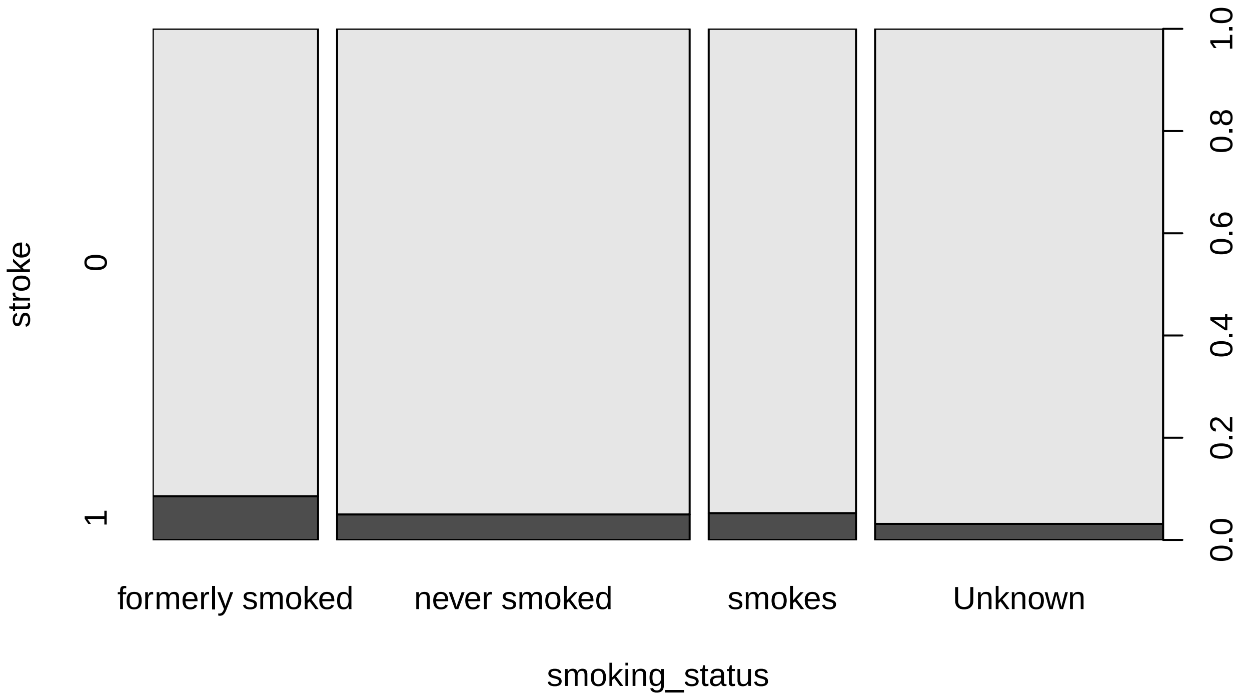
7 Generalised Additive Model

```r
library(mgcv)

gam.stroke <- gam(stroke ~ smoking_status + s(bmi),
family = "binomial",
data = df_train_linear)
summary(gam.stroke)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## stroke ~ smoking_status + s(bmi)
##
## Parametric coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  -2.6671     0.1636 -16.302  < 2e-16 ***
## smoking_statusnever smoked  -0.5438     0.1924  -2.827  0.00470 **
## smoking_statussmokes        -0.5377     0.2398  -2.243  0.02492 *
## smoking_statusUnknown       -0.7270     0.2298  -3.164  0.00155 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##          edf Ref.df Chi.sq  p-value
## s(bmi) 4.745  5.588  26.22 0.000161 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0132   Deviance explained =  4.5%
## UBRE = -0.61102  Scale est. = 1         n = 3577
```

```
plot(stroke ~ smoking_status, data = df_train_linear)
abline(gam.stroke)
```

```
## Warning in abline(gam.stroke): only using the first two of 13 regression
## coefficients
```



8 Neural Network Yves

9 Support Vector Machine (Larissa)

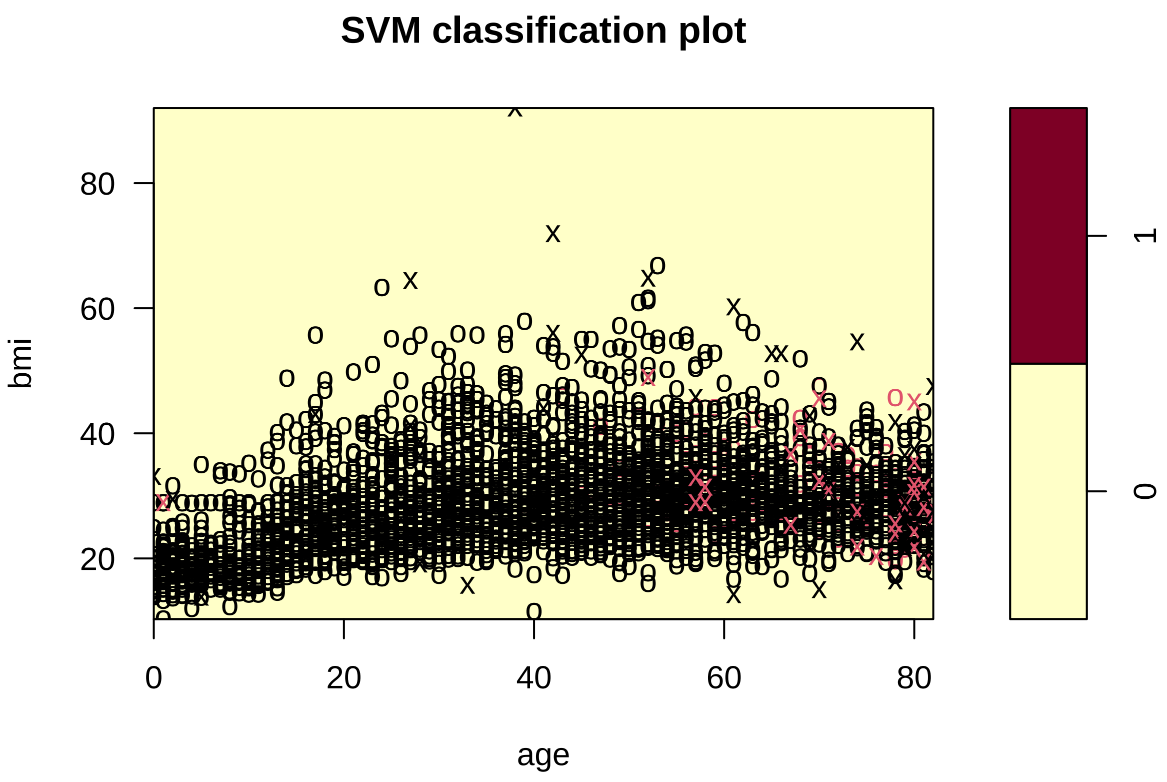
Stroke Data Classification using a Support Vector Machine.

```
ytrain = df_train$stroke
ytest = df_test$stroke
```

```
svm_model <- svm(stroke ~. , data = df_train, type = "C-classification", kernel = "radial", cost = "5")
summary(svm_model)
```

```
##
## Call:
## svm(formula = stroke ~ ., data = df_train, type = "C-classification",
##     kernel = "radial", cost = "5")
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  radial
##        cost:  5
##
## Number of Support Vectors:  95
##
##  ( 31 64 )
##
##
## Number of Classes:  2
##
## Levels:
##  0 1
```

```
plot(svm_model, data = df_train, bmi ~ age, slice = list(avg_glucose_level = 3))
```



```
#svm_training_prediction <- predict(svm_model, newdata = df_train)
#svm_training_error <- mean(svm_training_prediction != ytrain)
#draw_confusion_matrix(confusionMatrix(svm_training_prediction,df_train$stroke), "Stroke", "No Stroke")
#svm_training_error
#confusionMatrix(svm_training_prediction,df_train$stroke)
```

```
#svm_prediction <- predict(svm_model, newdata = df_test)
#svm_test_error <- mean(svm_prediction != ytest)
#draw_confusion_matrix(confusionMatrix(svm_prediction,df_test$stroke), "Stroke", "No Stroke")
#svm_test_error
```

10 OPTIONAL solve an optimisation problem