Exploring Predictive Markers for Diabetes Using Principal Component Analysis and Logistic Regression

```r
rm(list=ls())

library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(ggfortify)
library(factoextra)
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```r
library(moments)

knitr::purl("model.rmd", "model.R", documentation = 2)
```

```
##
##
## processing file: model.rmd

##   |                                                              |

## output file: model.R

## [1] "model.R"
```

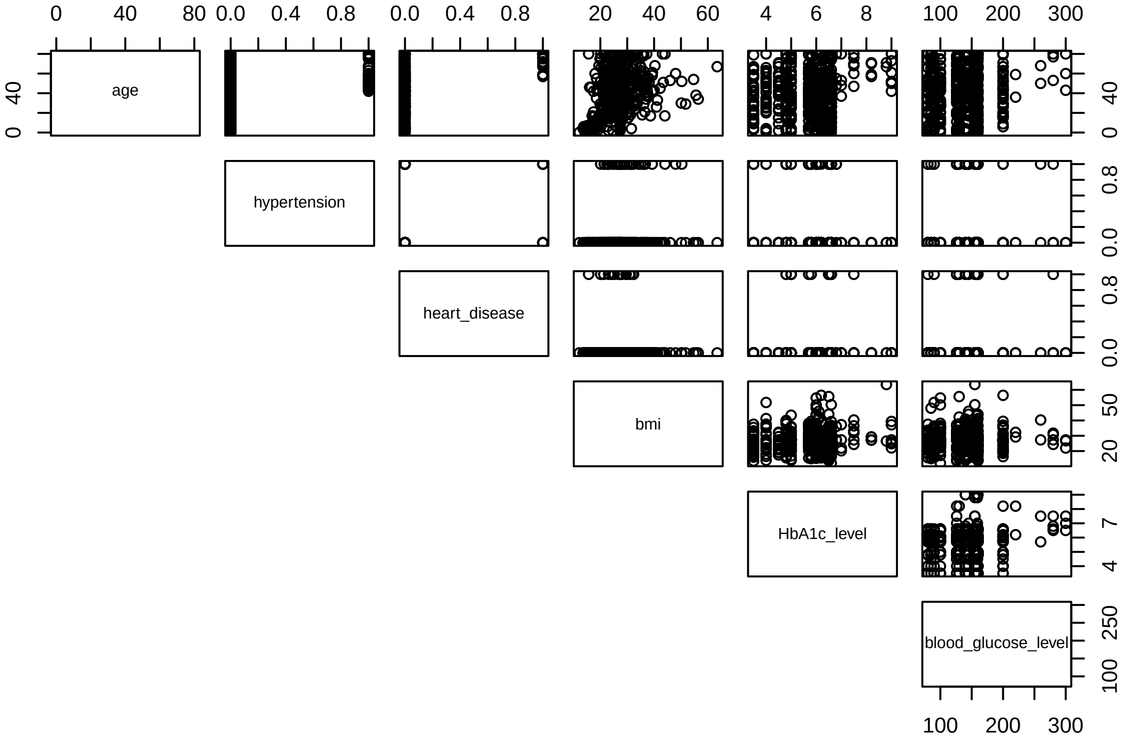
```r
diabetes <- read.csv("diabetes.csv", header=TRUE)
head(diabetes)
```

```
##   diabetes gender age hypertension heart_disease smoking_history   bmi
## 1        0 Female  80            0             1           never 25.19
## 2        0 Female  54            0             0         No Info 27.32
## 3        0   Male  28            0             0           never 27.32
## 4        0 Female  36            0             0         current 23.45
## 5        0   Male  76            1             1         current 20.14
## 6        0 Female  20            0             0           never 27.32
##   HbA1c_level blood_glucose_level
## 1         6.6                 140
## 2         6.6                  80
## 3         5.7                 158
## 4         5.0                 155
## 5          4.8                   155
## 6          6.6                    85
```

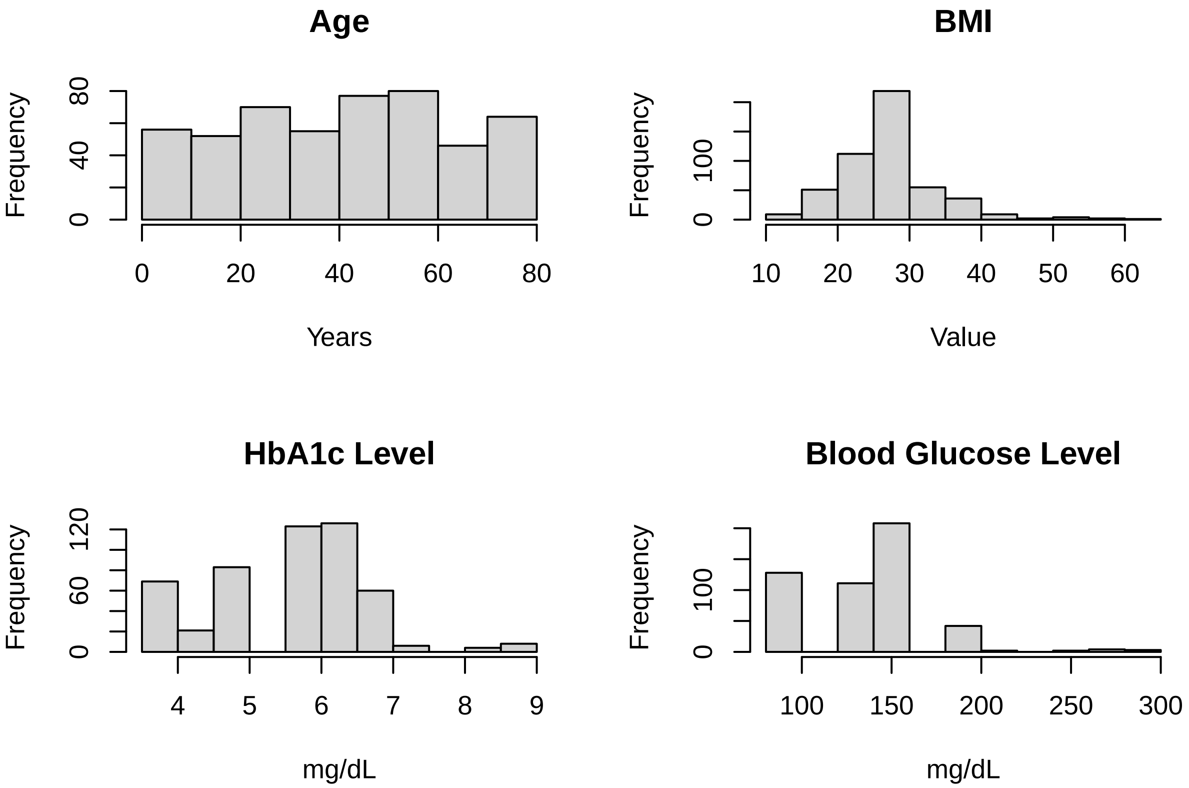
```
sapply(diabetes[c("age", "bmi", "HbA1c_level", "blood_glucose_level")], summary)
```

```
##               age      bmi HbA1c_level blood_glucose_level
## Min.      0.08000 12.15000      3.5000              80.000
## 1st Qu. 23.75000 23.10250      4.8000             100.000
## Median  42.00000 27.32000      5.8000             145.000
## Mean    41.65328 26.89078      5.6224             139.652
## 3rd Qu. 59.00000 28.93250      6.2000             159.000
## Max.    80.00000 63.48000      9.0000             300.000
```

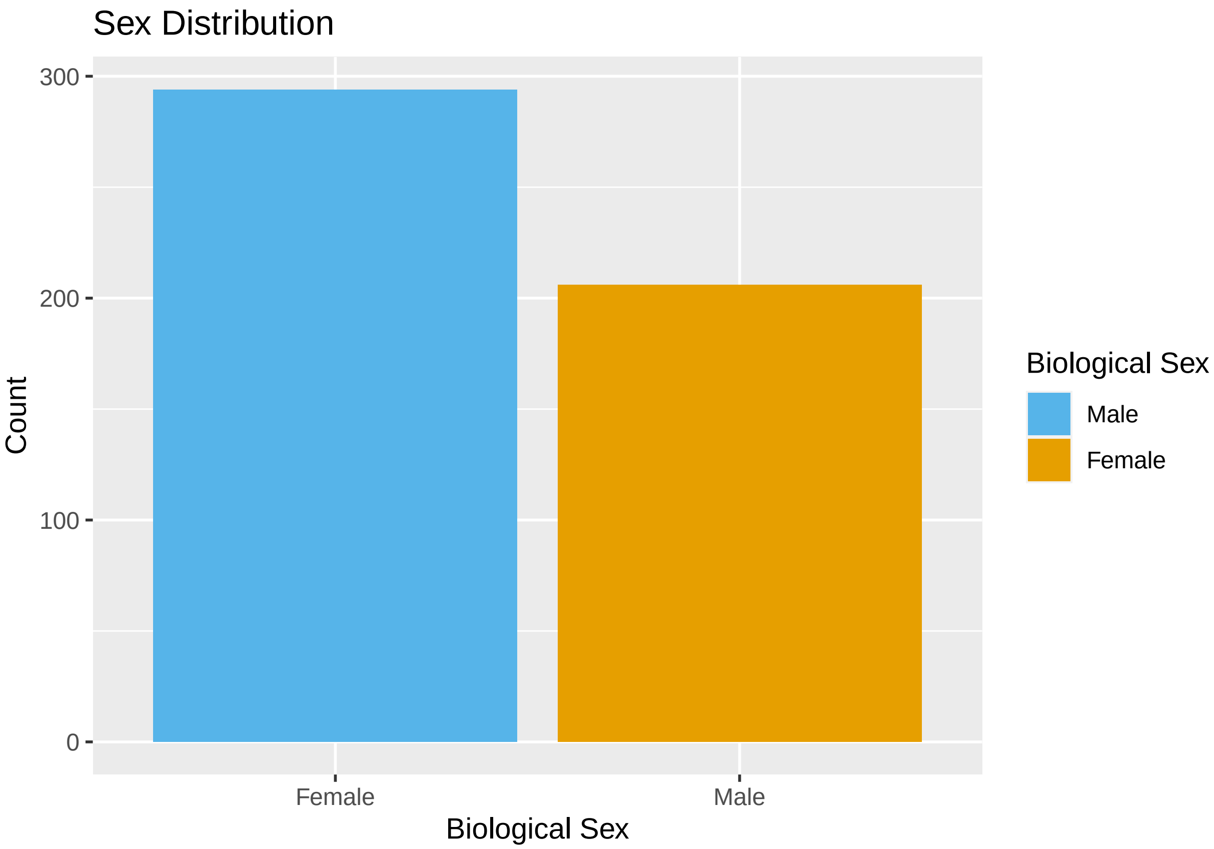
```
diabetes_numeric <- diabetes %>%
  select(c("age", "hypertension", "heart_disease", "bmi", "HbA1c_level", "blood_glucose_level"))

#Create a scatterplot matrix
pairs(diabetes_numeric, lower.panel = NULL)
```



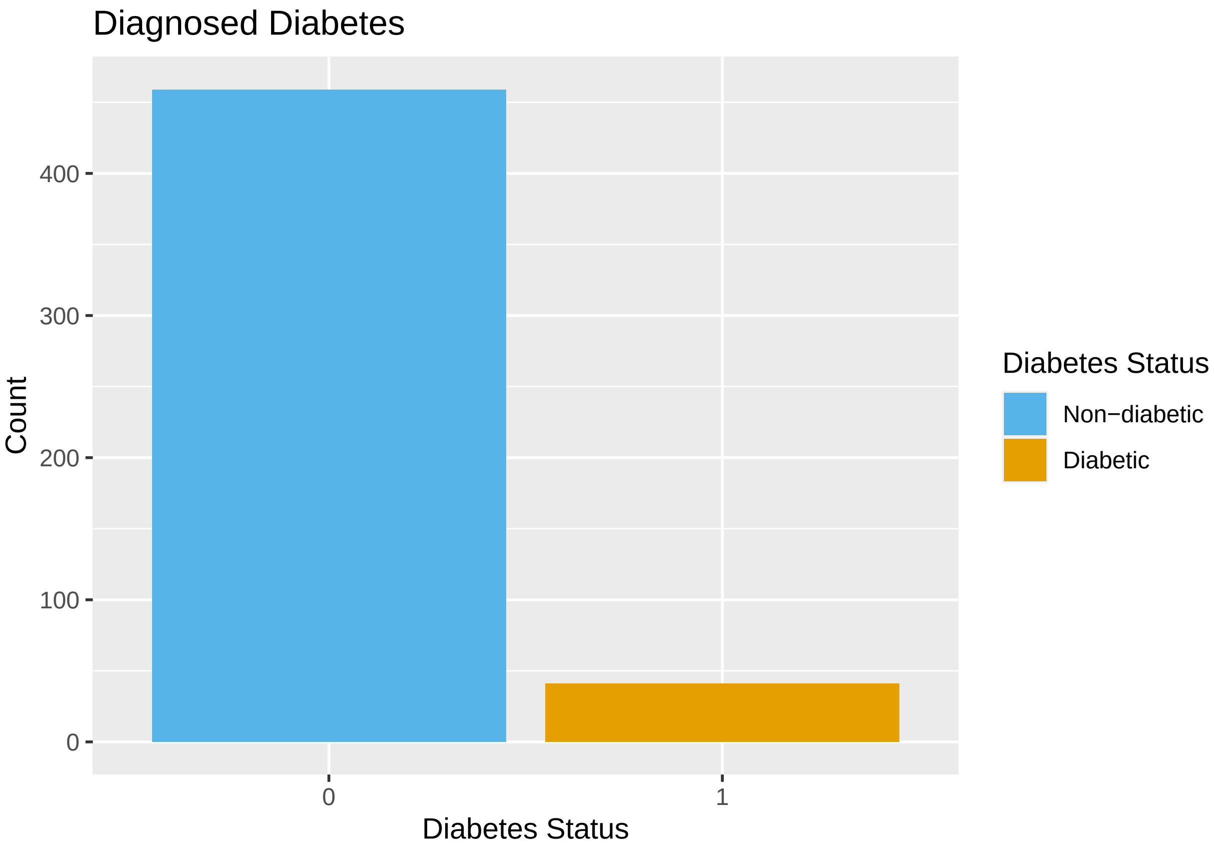
```
#Create histograms for all features
par(mfrow=c(2,2)) # Set up 2x2 grid of plots

hist(diabetes$age, main="Age", xlab="Years")
hist(diabetes$bmi, main="BMI", xlab="Value")
hist(diabetes$HbA1c_level, main="HbA1c Level", xlab="mg/dL")
hist(diabetes$blood_glucose_level, main="Blood Glucose Level", xlab="mg/dL")
```



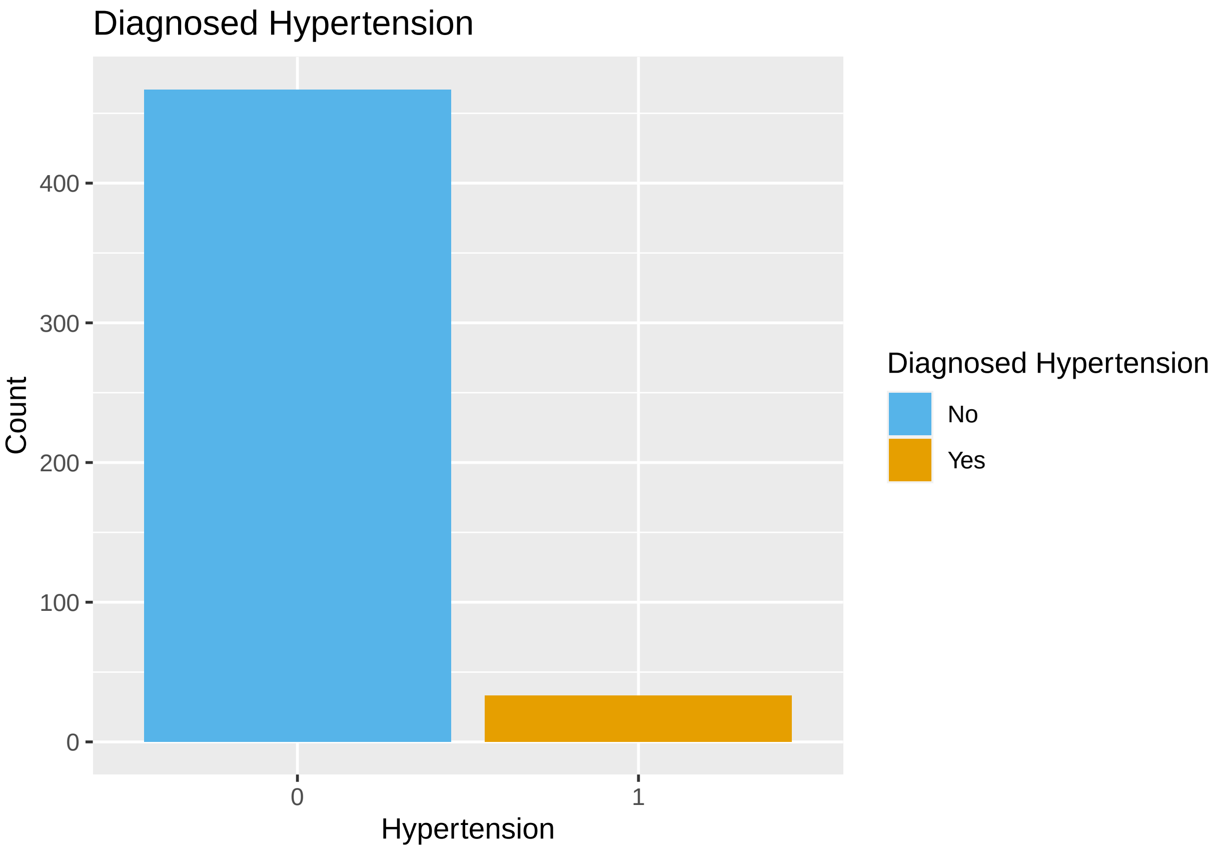
```r
#Create bar graphs of discrete and categorical features
ggplot(diabetes, aes(x = factor(gender), fill = factor(gender))) +
  geom_bar() +
  labs(title="Sex Distribution", x="Biological Sex", y="Count") +
  scale_fill_manual(name = "Biological Sex",
                    values = c("#56B4E9", "#E69F00", "#999999"),
                    labels = c("Male", "Female", "Unknown"))
```



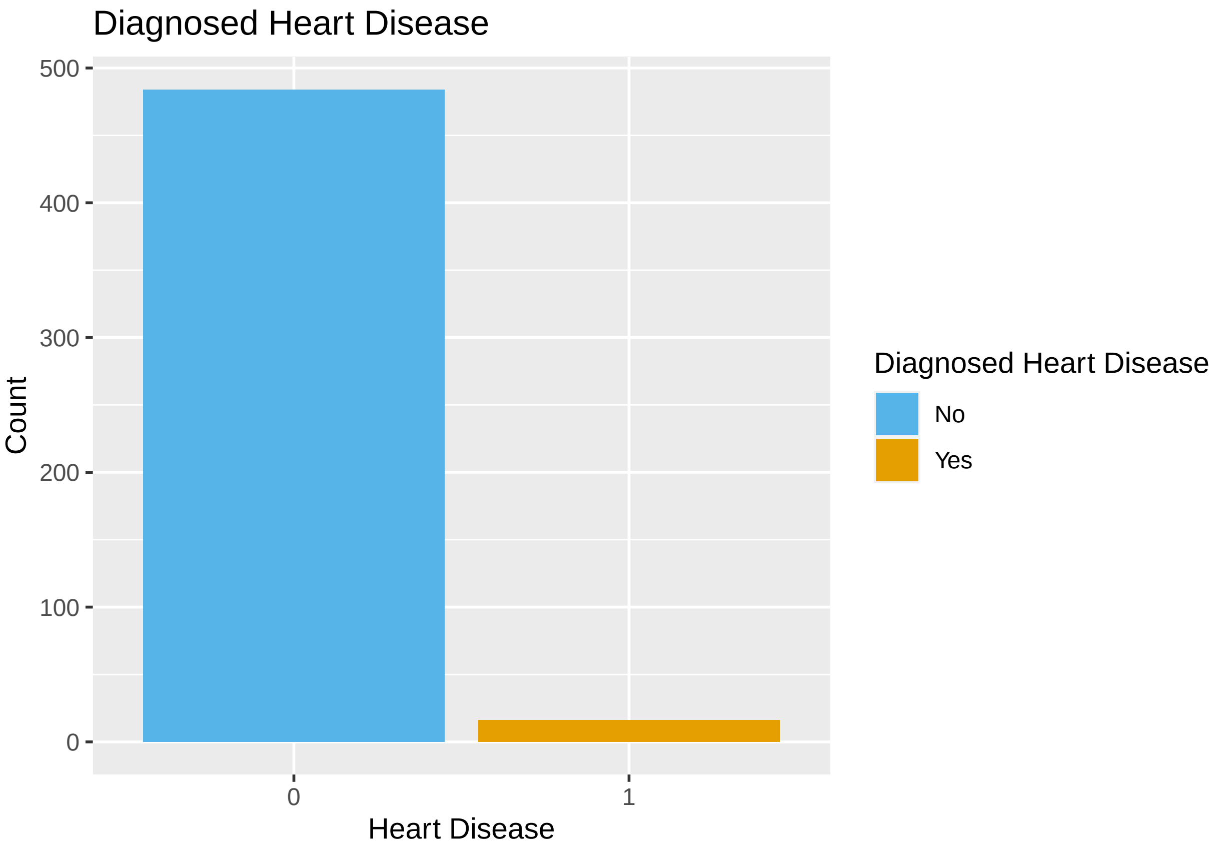
```r
ggplot(diabetes, aes(x = factor(diabetes), fill = factor(diabetes))) +
  geom_bar() +
  labs(title = "Diagnosed Diabetes", x = "Diabetes Status", y = "Count") +
  scale_fill_manual(name = "Diabetes Status",
                    values = c("#56B4E9", "#E69F00"),
                    labels = c("Non-diabetic", "Diabetic"))
```



```r
ggplot(diabetes, aes(x = factor(hypertension), fill = factor(hypertension))) +
  geom_bar() +
  labs(title = "Diagnosed Hypertension", x = "Hypertension", y = "Count") +
  scale_fill_manual(name = "Diagnosed Hypertension",
                    values = c("#56B4E9", "#E69F00"),
                    labels = c("No", "Yes"))
```



```
ggplot(diabetes, aes(x = factor(heart_disease), fill = factor(heart_disease))) +
  geom_bar() +
  labs(title = "Diagnosed Heart Disease", x = "Heart Disease", y = "Count") +
  scale_fill_manual(name = "Diagnosed Heart Disease",
                    values = c("#56B4E9", "#E69F00"),
                    labels = c("No", "Yes"))
```



```
#Test the skewness in diabetes data
age_skew <- skewness(diabetes$age)
cat("Skewness of age:", age_skew, "\n")
```

```
## Skewness of age: -0.01478161
```

```
cat("Absolute skewness of age:", abs(age_skew), "\n")
```

```
## Absolute skewness of age: 0.01478161
```

```
bmi_skew <- skewness(diabetes$bmi)
cat("Skewness of bmi:", bmi_skew, "\n")
```

```
## Skewness of bmi: 1.208401
```

```
cat("Absolute skewness of bmi:", abs(bmi_skew), "\n")
```

```
## Absolute skewness of bmi: 1.208401
```

```
hba1c_skew <- skewness(diabetes$HbA1c_level)
cat("Skewness of HbA1c level:", hba1c_skew, "\n")
```

```
## Skewness of HbA1c level: -0.08341524
```

```
cat("Absolute skewness of HbA1c level:", abs(hba1c_skew), "\n")
```

```
## Absolute skewness of HbA1c level: 0.08341524
```

```
glucose_skew <- skewness(diabetes$blood_glucose_level)
cat("Skewness of blood glucose level:", glucose_skew, "\n")
```

```
## Skewness of blood glucose level: 0.7202705
```

```
cat("Absolute skewness of blood glucose level:", abs(glucose_skew), "\n")
```

```
## Absolute skewness of blood glucose level: 0.7202705
```

```
knitr::purl("model.rmd", "model.R", documentation = 2)
```

```
## [1] "model.R"
```

```
data_select <- diabetes %>% select(age, bmi, HbA1c_level, blood_glucose_level)

data_scale <- scale(data_select)

#Create PCA model
pca_model <- prcomp(data_scale, scale. = TRUE)
pca_model
```

```
## Standard deviations (1, .., p=4):
## [1] 1.1860099 1.0077506 0.9517091 0.8197981
##
## Rotation (n x k) = (4 x 4):
##                            PC1        PC2         PC3         PC4
## age                 -0.6465562  0.2382414 -0.07648468  0.72066375
## bmi                 -0.6076987  0.4054814 -0.02835388 -0.68226330
## HbA1c_level         -0.3491517 -0.5545748  0.75368930 -0.04992315
## blood_glucose_level -0.3012649 -0.6864930 -0.65214921 -0.11255318
```

```
#PC1 is made up mostly of age, bmi. PC2 is made up mostly of A1c, blood glucose. PC3 is made up mostly
summary(pca_model)
```

```
## Importance of components:
##                           PC1    PC2    PC3    PC4
## Standard deviation     1.1860 1.0078 0.9517 0.8198
## Proportion of Variance 0.3517 0.2539 0.2264 0.1680
## Cumulative Proportion  0.3517 0.6056 0.8320 1.0000
```

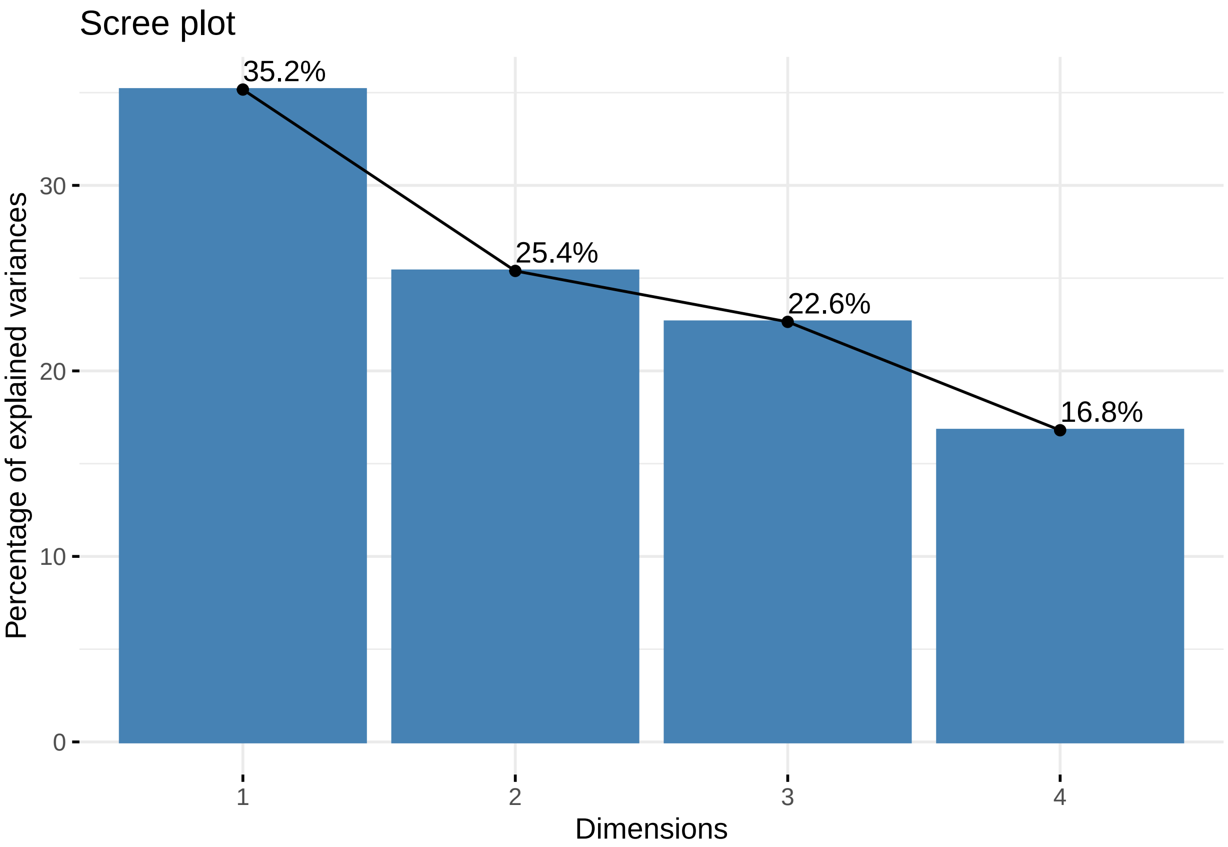
```
pca_var <- get_pca_var(pca_model)
#Contribution % of features to their respective PC
pca_var$contrib[,1]
```

```
##                 age                 bmi         HbA1c_level blood_glucose_level
##           41.803487           36.929771           12.190691            9.076051
```

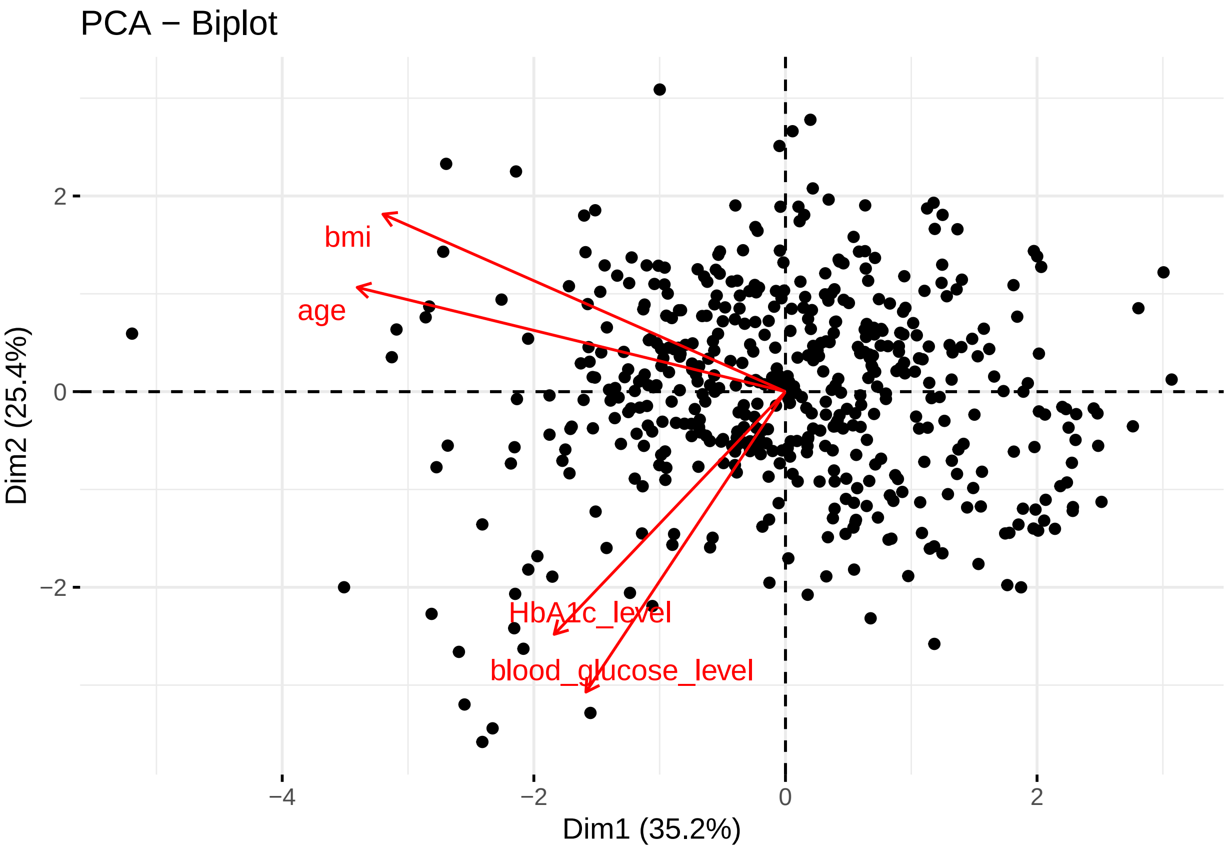
```
pca_var$contrib[,2]
```

```
##                 age                 bmi         HbA1c_level blood_glucose_level
##            5.675898           16.441513           30.755322           47.127268
```

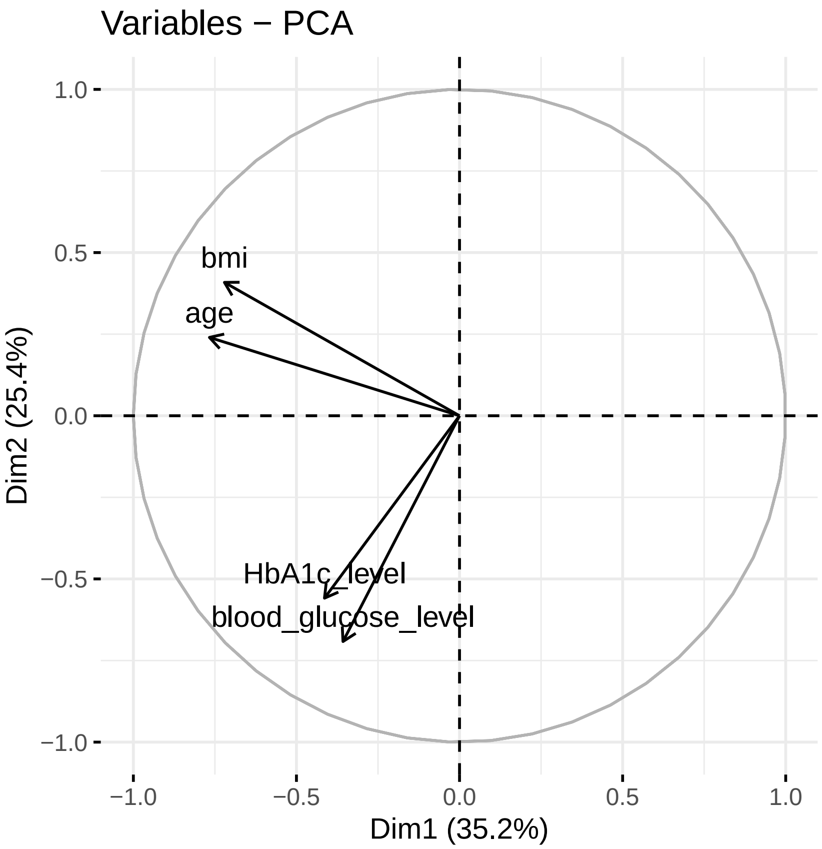
```
fviz_eig(pca_model, addlabels = TRUE)
```



```r
pca_scores <- as.data.frame(pca_model$x)

pca_scores$outcome <- diabetes$outcome

#PCA biplot
fviz_pca_biplot(pca_model, geom = c("point", "text"), label = "var", col.var = "red", repel = TRUE)
```



```
fviz_pca_var(pca_model)
```



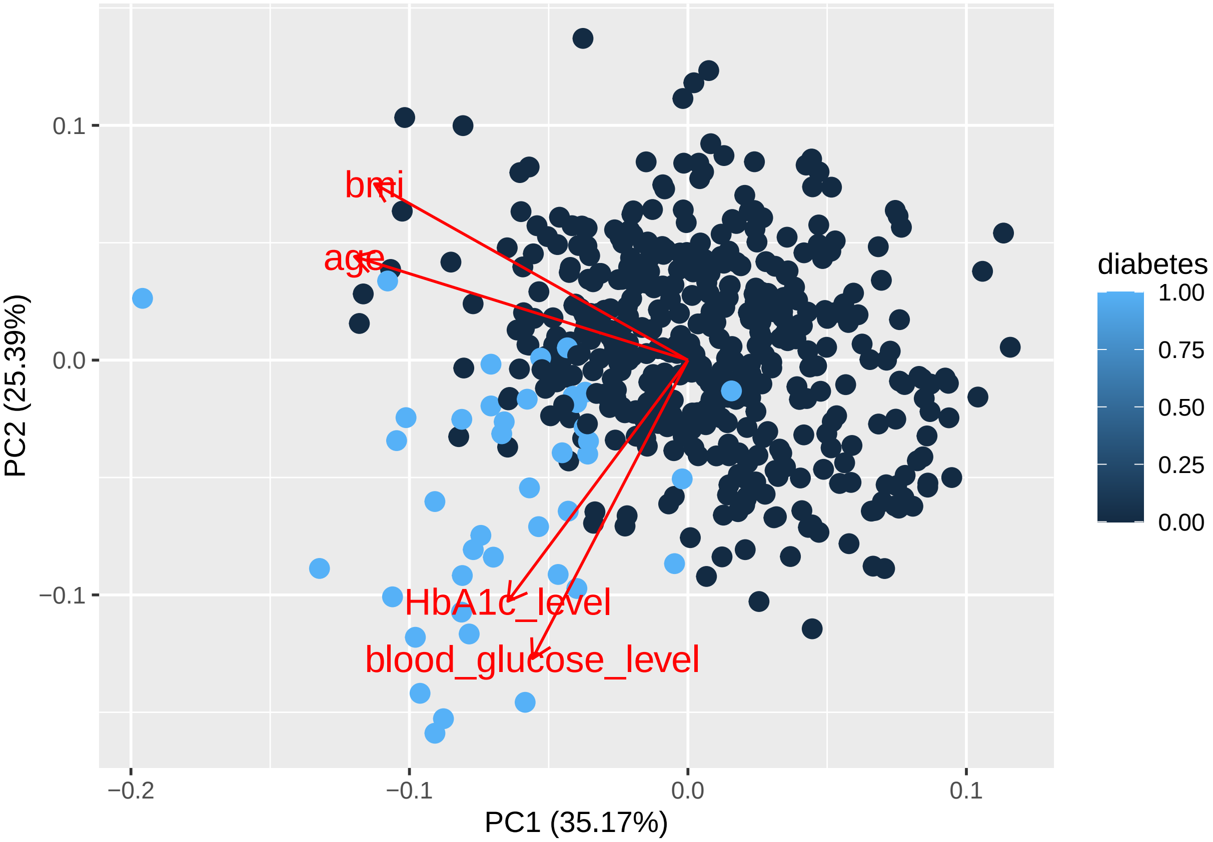
```r
knitr::purl("model.rmd", "model.R", documentation = 2)
```

```
## [1] "model.R"
```

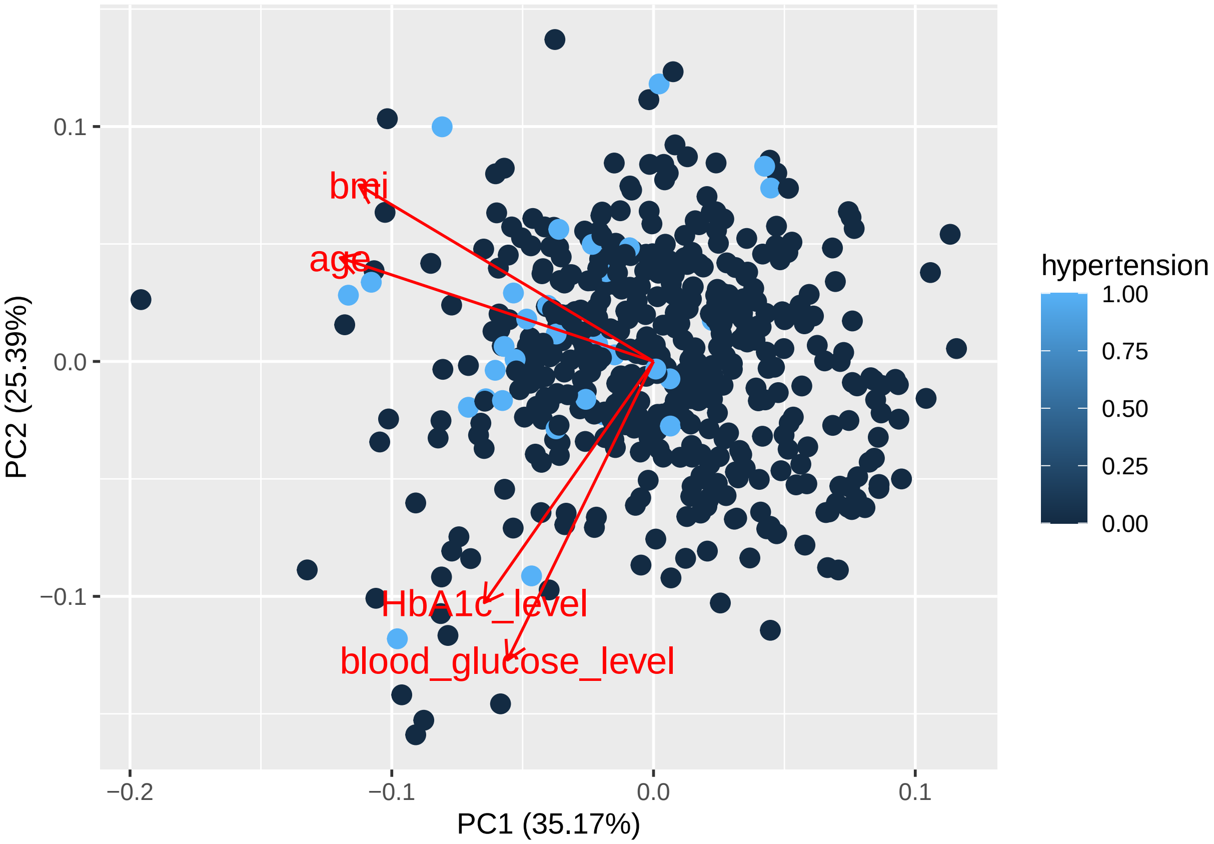
```r
#Create logistic regression model with outcome as response and first 2 principal components as predicto
model <- glm(diabetes~pca_scores$PC1 + pca_scores$PC2 + pca_scores$PC3 + pca_scores$PC4, data = diabete

summary(model)
```

```
##
## Call:
## glm(formula = diabetes ~ pca_scores$PC1 + pca_scores$PC2 + pca_scores$PC3 +
##     pca_scores$PC4, family = binomial, data = diabetes)
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -6.75904    0.99410  -6.799 1.05e-11 ***
## pca_scores$PC1 -2.93566    0.51983  -5.647 1.63e-08 ***
## pca_scores$PC2 -3.43703    0.68916  -4.987 6.12e-07 ***
## pca_scores$PC3  2.23192    0.69052   3.232  0.00123 **
## pca_scores$PC4  0.02427    0.30519   0.080  0.93661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 283.627  on 499  degrees of freedom
## Residual deviance:  85.997  on 495  degrees of freedom
## AIC: 95.997
##
## Number of Fisher Scoring iterations: 9
```

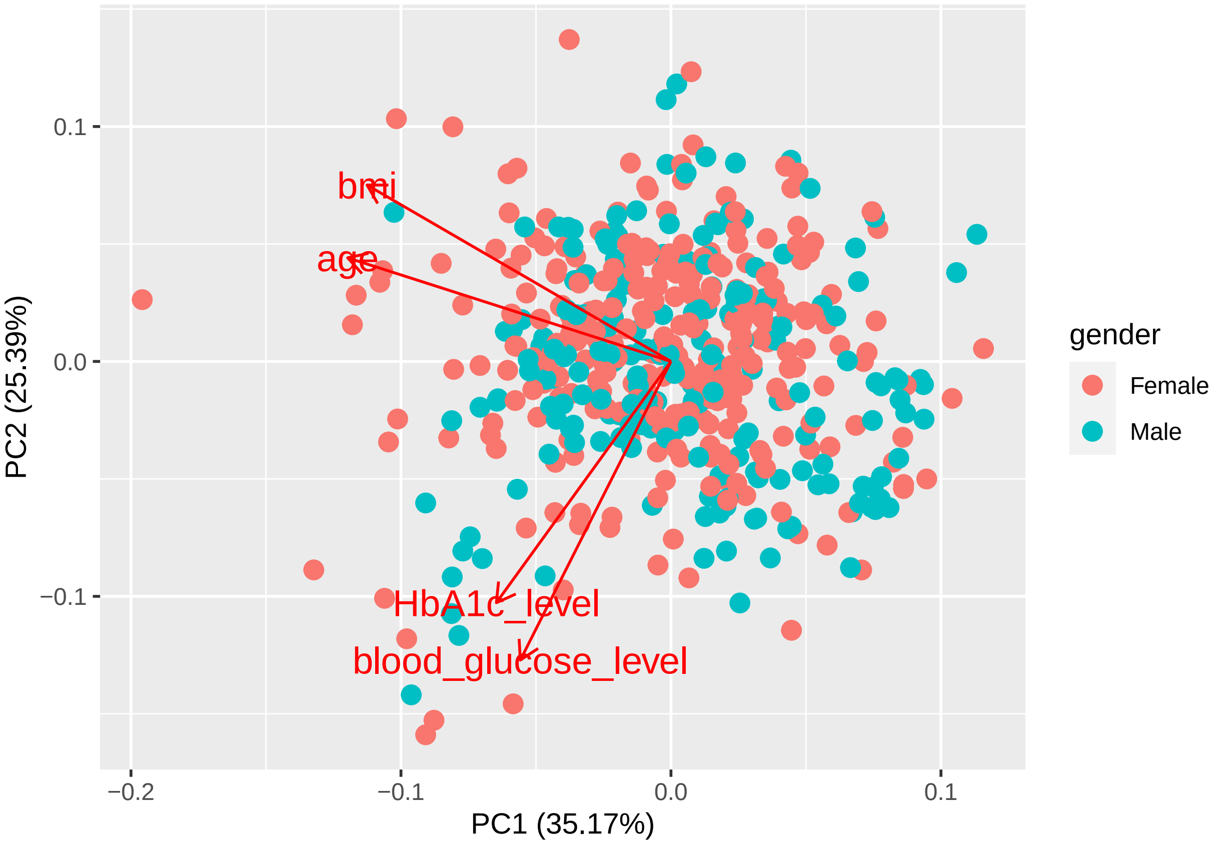
```
#Create scatterplots similar to biplot with relationship to discrete/categorical features
autoplot(
  pca_model, #The PCA model object
  data = diabetes, #The dataset being plotted
  colour = 'diabetes', #The variable being used to color the points
  loadings=TRUE, #Indicates that the plot should also show the loadings
  size = 3, #The size of the points
  loadings.label = TRUE, #Indicates that the plot should label the loadings
  loadings.label.size=5 #The size of the loading labels
  )
```



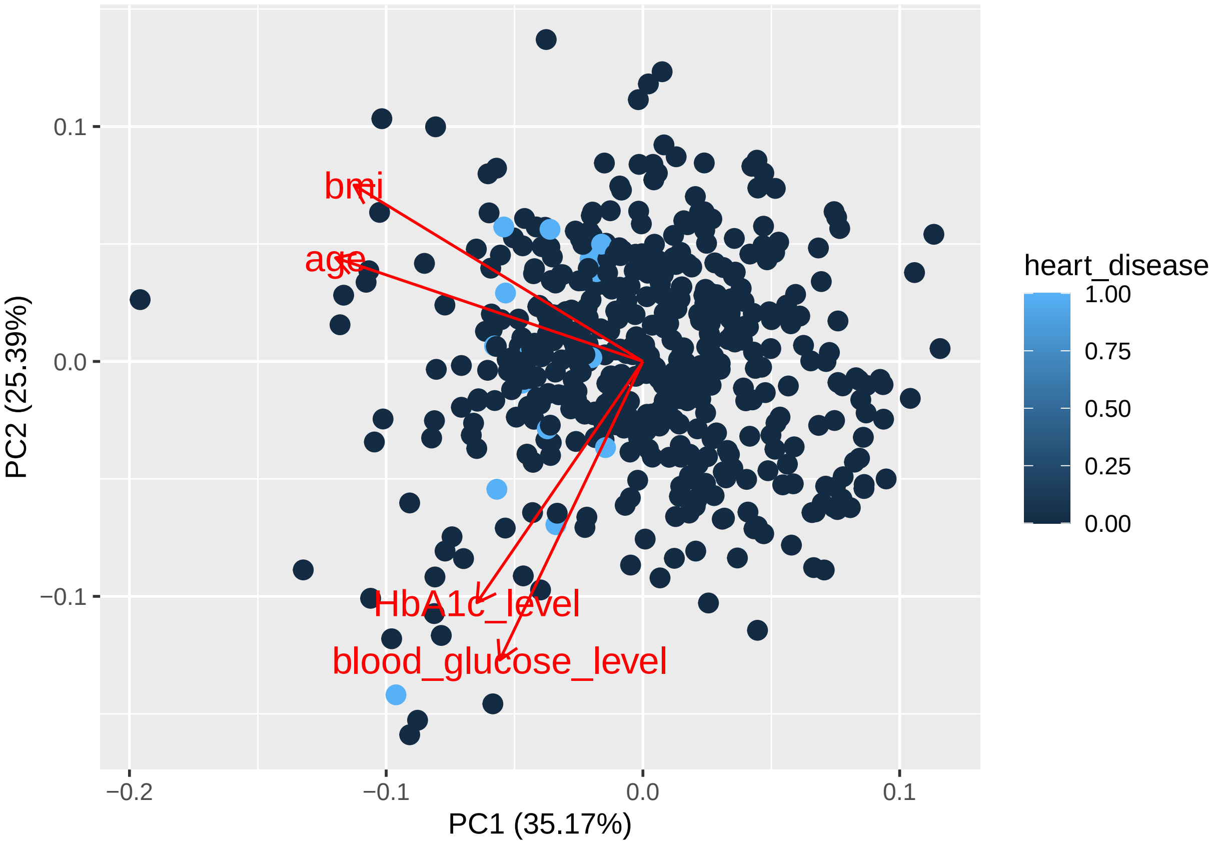
```
autoplot(
  pca_model,
  data = diabetes,
  colour = 'hypertension',
  loadings=TRUE,
  size = 3,
  loadings.label = TRUE,
  loadings.label.size=5
  )
```



```
autoplot(
  pca_model,
  data = diabetes,
  colour = 'gender',
  loadings=TRUE,
  size = 3,
  loadings.label = TRUE,
  loadings.label.size=5
  )
```



```
autoplot(
  pca_model,
  data = diabetes,
  colour = 'heart_disease',
  loadings=TRUE,
  size = 3,
  loadings.label = TRUE,
  loadings.label.size=5
  )
```



```
knitr::purl("model.rmd", "model.R", documentation = 2)
```

```
## [1] "model.R"
```