Assignment_2

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KNN, Linear regression, and multilinear regression, In a diabetes_012 Dataset

Part 1: Data exploration and data wrangling

For this explainer document in R Markdown a dataset containing 22 variables and 253680 objects will be used. With this dataset it will be shown how to apply data analysis, Knn, linear and multilinear regression.

In order to start, it is necessary to load the dataset into the program as shown in the following section of the code.

```
folder <- dirname(rstudioapi::getSourceEditorContext()$path)

parentFolder <- dirname (folder)
data_set_dia <-
  read.csv(paste0(parentFolder,"/dataset/diabetes_012_health_indicators_BRFSS2015.csv"))
```

After loading the dataset, it is necessary to inspect and analyze the information contained in this file. In the following image you can see the variables and brief information about their content.

Figure 1: Characteristics of the dataset variables

Then, using the `psych` function, a statistical analysis can be made of the 22 variables contained in the dataset, which include the mean, standard deviation, minimum and maximum range, among others.

Finally, using the `mutate` function, we proceed to transform all the data that are not "= 0" into the variable Diabetes_012, then a small table shows how many data were classified as "0" or "1"" in this variable dataset.

```
test_diabetes<- data_set_dia %>% mutate(Diabetes_012 = ifelse(Diabetes_012!= "0", "1",Diabetes_012))
```

```
Conteo_Diabetes
```

```
##
##      0      1
## 213703  39977
```

Part 2: KNN

KNN DIABETES PREDICTION

First Prediction

In this part of the document the KNN predictive method will be used. This is why 3 different variables will be used to achieve the predictions. First, through a stratified sample, approximately 1% of the data will be taken to train the models.

```
ss_diabetes <- test_diabetes %>%
  group_by(Diabetes_012) %>%
  sample_n(1269, replace = TRUE) %>%
  ungroup()
```

```
Conteo_ss_Diabetes
```

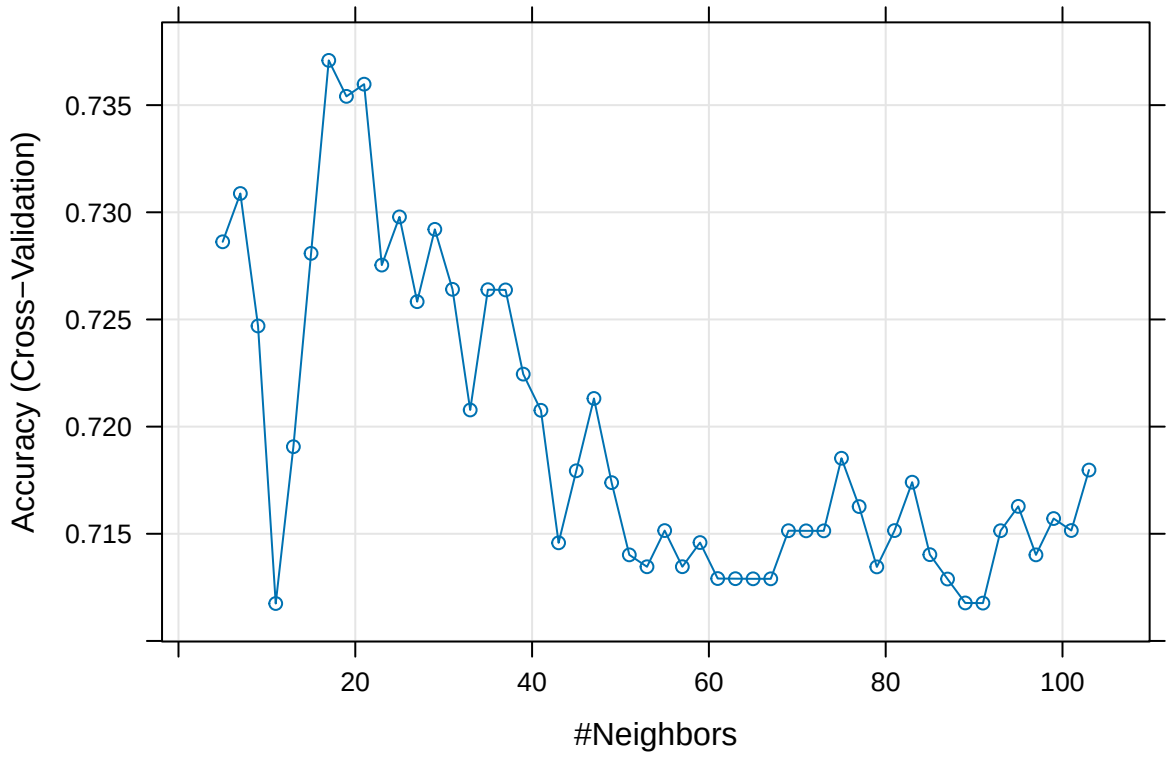
```
##
##    0    1
## 1269 1269
```

At this point the appropriate number of "K" is found and thus the Knn model will be trained to predict diabetes.

```
set.seed(123)
ss_diabetes_knn <- ss_diabetes %>%
  group_by(Diabetes_012) %>%
  sample_n(1269, replace = TRUE) %>%
  ungroup()


sample.index <- sample(1:nrow(ss_diabetes_knn)
                       ,nrow(ss_diabetes_knn)*0.7
                       ,replace = F)


predictors <- c("HighBP", "HighChol", "CholCheck", "BMI", "Smoker", "Stroke", "HeartDiseaseorAttack", "
train.data <- ss_diabetes_knn[sample.index, c(predictors, "Diabetes_012"), drop = FALSE]
test.data <- ss_diabetes_knn[-sample.index, c(predictors, "Diabetes_012"), drop = FALSE]


train.data$Diabetes_012 <- factor(train.data$Diabetes_012)
test.data$Diabetes_012 <- factor(test.data$Diabetes_012)
```

```
ctrl <- trainControl(method = "cv", p = 0.7)
knnFit <- train(Diabetes_012 ~ .
                , data = train.data
                , method = "knn", trControl = ctrl
```

```
                , preProcess = c("range") # c("center", "scale") for z-score
                , tuneLength = 50)

plot(knnFit)
```



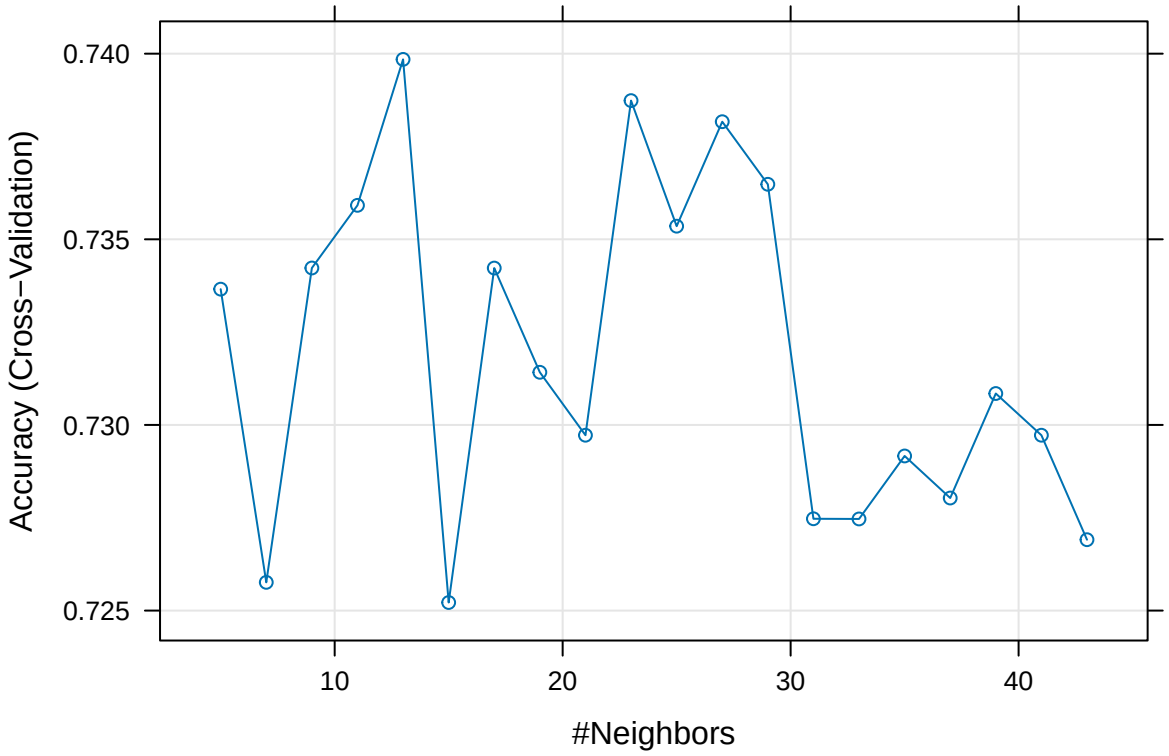

```
# Make predictions
knnPredict <- predict(knnFit, newdata = test.data)

# Creates the confusion matrix
confusionMatrix(data = knnPredict, reference = test.data$Diabetes_012)
```

```
## Confusion Matrix and Statistics
##
##            Reference
## Prediction   0   1
##          0 279 118
##          1  99 266
##
##                Accuracy : 0.7152
##                  95% CI : (0.6817, 0.747)
##     No Information Rate : 0.5039
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.4306
##
##  Mcnemar's Test P-Value : 0.2217
```

```
##
##             Sensitivity : 0.7381
##             Specificity : 0.6927
##          Pos Pred Value : 0.7028
##          Neg Pred Value : 0.7288
##              Prevalence : 0.4961
##          Detection Rate : 0.3661
##    Detection Prevalence : 0.5210
##       Balanced Accuracy : 0.7154
##
##        'Positive' Class : 0
##
```

Second Prediction

```
predictors_to_remove <- c("AnyHealthcare", "NoDocbcCost", "DiffWalk", "Education", "Income")
train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]


ctrl <- trainControl(method = "cv", number = 5)
knnFit2 <- train(Diabetes_012 ~ .
                 , data = train.data2
                 , method = "knn", trControl = ctrl
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 20)

plot(knnFit2)
```



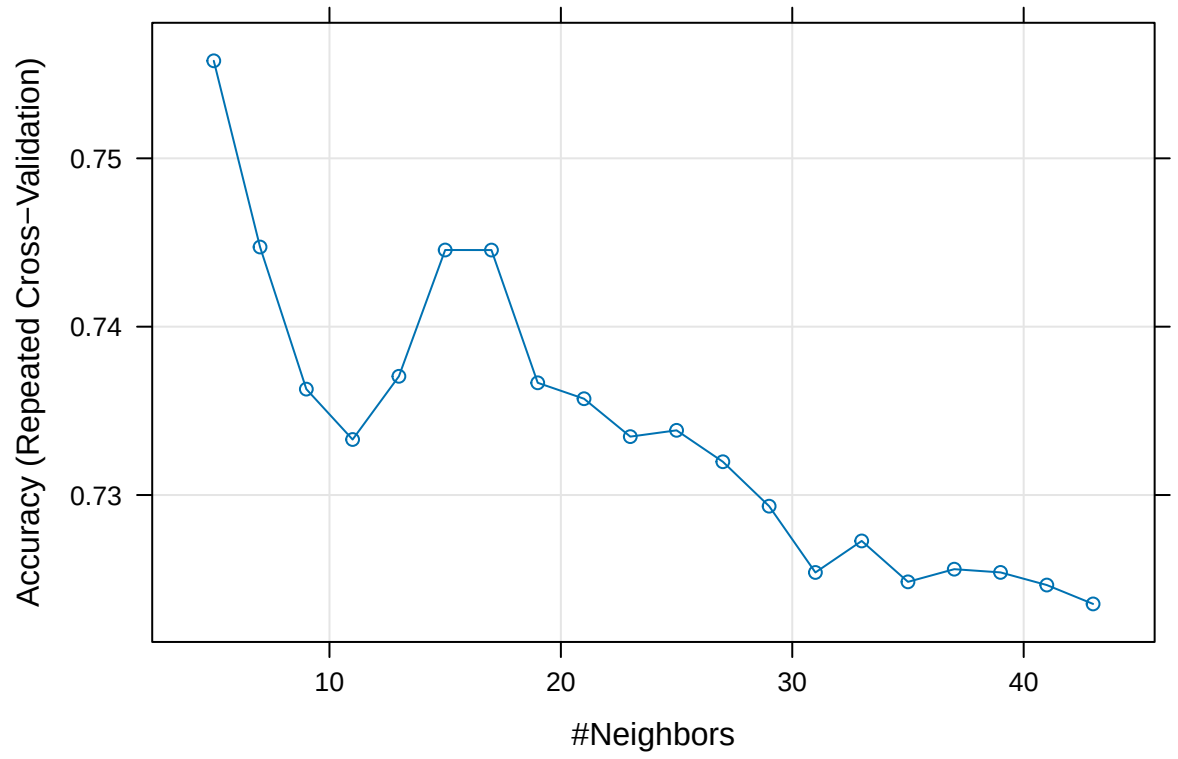

```r
# Make predictions
knnPredict2 <- predict(knnFit2, newdata = test.data2)

# Creates the confusion matrix
confusionMatrix(data = knnPredict2, reference = test.data2$Diabetes_012)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 265  92
##          1 113 292
##
##                Accuracy : 0.731
##                  95% CI : (0.698, 0.7622)
##     No Information Rate : 0.5039
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.4617
##
##  Mcnemar's Test P-Value : 0.1625
##
##             Sensitivity : 0.7011
##             Specificity : 0.7604
##          Pos Pred Value : 0.7423
##          Neg Pred Value : 0.7210
```

```
##              Prevalence : 0.4961
##          Detection Rate : 0.3478
##    Detection Prevalence : 0.4685
##       Balanced Accuracy : 0.7307
##
##        'Positive' Class : 0
##
```

Third Prediction

```
predictors_to_remove2 <- c("ChoclCheck", "MentHlth","PhysHlth", "Fruits", "Veggies")
train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove2)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove2)]

ctrl2 <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
knnFit3 <- train(Diabetes_012 ~ .
                 , data = train.data3
                 , method = "knn", trControl = ctrl2
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 20)

plot(knnFit3)
```




```
knnPredict3 <- predict(knnFit3, newdata = test.data3)

# Creates the confusion matrix
```

```r
confusionMatrix(data = knnPredict3, reference = test.data3$Diabetes_012)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 276  90
##          1 102 294
##
##                Accuracy : 0.748
##                  95% CI : (0.7156, 0.7785)
##     No Information Rate : 0.5039
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.4959
##
##  Mcnemar's Test P-Value : 0.4273
##
##             Sensitivity : 0.7302
##             Specificity : 0.7656
##          Pos Pred Value : 0.7541
##          Neg Pred Value : 0.7424
##              Prevalence : 0.4961
##          Detection Rate : 0.3622
##    Detection Prevalence : 0.4803
##       Balanced Accuracy : 0.7479
##
##        'Positive' Class : 0
##
```

KNN HeartDiseaseorAttack Prediction

First Prediction

```r
set.seed(123)
ss_heartDiseaseorAttack <- ss_diabetes %>%
  group_by(HeartDiseaseorAttack) %>%
  sample_n(1269, replace = TRUE) %>%
  ungroup()

predictors <- c("Diabetes_012","HighBP", "HighChol", "CholCheck", "BMI", "Smoker", "Stroke",  "PhysActi

# Original data
train.data <- ss_heartDiseaseorAttack[sample.index, c(predictors, "HeartDiseaseorAttack"), drop = FALSE]
test.data <- ss_heartDiseaseorAttack[-sample.index, c(predictors, "HeartDiseaseorAttack"), drop = FALSE]

train.data$HeartDiseaseorAttack <- factor(train.data$HeartDiseaseorAttack)
test.data$HeartDiseaseorAttack <- factor(test.data$HeartDiseaseorAttack)

# Train the k-NN model
ctrl <- trainControl(method = "cv", p = 0.7)
knnFit <- train(HeartDiseaseorAttack ~ .
                , data = train.data
                , method = "knn", trControl = ctrl
```

```
                , preProcess = c("range") # c("center", "scale") for z-score
                , tuneLength = 50)

# Make predictions
knnPredict <- predict(knnFit, newdata = test.data)

# Creates the confusion matrix
# Original data
train.data <- ss_heartDiseaseorAttack[sample.index, c(predictors, "HeartDiseaseorAttack"), drop = FALSE]
test.data <- ss_heartDiseaseorAttack[-sample.index, c(predictors, "HeartDiseaseorAttack"), drop = FALSE]

train.data$HeartDiseaseorAttack <- factor(train.data$HeartDiseaseorAttack)
test.data$HeartDiseaseorAttack <- factor(test.data$HeartDiseaseorAttack)

# Train the k-NN model
ctrl <- trainControl(method = "cv", p = 0.7)
knnFit <- train(HeartDiseaseorAttack ~ .
                , data = train.data
                , method = "knn", trControl = ctrl
                , preProcess = c("range") # c("center", "scale") for z-score
                , tuneLength = 50)

# Make predictions
knnPredict <- predict(knnFit, newdata = test.data)

# Creates the confusion matrix
confusionMatrix(data = knnPredict, reference = test.data$HeartDiseaseorAttack)
```

Second Prediction

```
### second model

predictors_to_remove <- c("AnyHealthcare", "NoDocbcCost", "DiffWalk", "Education", "Income")
train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]

# Train the k-NN model
ctrl <- trainControl(method = "cv", number = 5)
knnFit2 <- train(HeartDiseaseorAttack ~ .
                 , data = train.data2
                 , method = "knn", trControl = ctrl
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 50)


# Make predictions
knnPredict2 <- predict(knnFit2, newdata = test.data2)

# Creates the confusion matrix
confusionMatrix(data = knnPredict2, reference = test.data2$HeartDiseaseorAttack)
```

Third Prediction

```
### Third Model

predictors_to_remove2 <- c("ChoclCheck", "MentHlth","HvyAlcoholConsump", "Fruits", "Veggies")
train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove2)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove2)]

# Train the k-NN model
ctrl2 <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
knnFit3 <- train(HeartDiseaseorAttack ~ .
                 , data = train.data3
                 , method = "knn", trControl = ctrl2
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 50)


# Make predictions
knnPredict3 <- predict(knnFit3, newdata = test.data3)

# Creates the confusion matrix
confusionMatrix(data = knnPredict3, reference = test.data3$HeartDiseaseorAttack)
```

KNN Find Sex Prediction

First Prediction

```
###KNN Models and Experiments to Find Sex ##########################################################################


## selection of 1500 samples of each factor of the dataset#
set.seed(123)
ss_sex <- ss_diabetes %>%
  group_by(Sex) %>%
  sample_n(1269, replace = TRUE) %>%
  ungroup()

predictors <- c("Diabetes_012","HighBP", "HighChol", "CholCheck", "BMI", "Smoker", "Stroke", "HeartDisea

# Original data
train.data <- ss_sex[sample.index, c(predictors, "Sex"), drop = FALSE]
test.data <- ss_sex[-sample.index, c(predictors, "Sex"), drop = FALSE]

train.data$Sex <- factor(train.data$Sex)
test.data$Sex <- factor(test.data$Sex)

# Train the k-NN model
ctrl <- trainControl(method = "cv", p = 0.7)
knnFit <- train(Sex ~ .
                , data = train.data
                , method = "knn", trControl = ctrl
                , preProcess = c("range") # c("center", "scale") for z-score
                , tuneLength = 50)
```

```r
# Make predictions
knnPredict <- predict(knnFit, newdata = test.data)

# Creates the confusion matrix
confusionMatrix(data = knnPredict, reference = test.data$Sex)
```

Second Prediction

```r
# second model

predictors_to_remove <- c("AnyHealthcare", "NoDocbcCost", "DiffWalk", "Age", "PhysActivity")
train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]

# Train the k-NN model
ctrl <- trainControl(method = "cv", number = 5)
knnFit2 <- train(Sex ~ .
                 , data = train.data2
                 , method = "knn", trControl = ctrl
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 50)

#Make predictions
knnPredict2 <- predict(knnFit2, newdata = test.data2)

# Creates the confusion matrix
  confusionMatrix(data = knnPredict2, reference = test.data2$Sex)
```

Third Prediction

```r
### Third Model

predictors_to_remove2 <- c("ChoclCheck", "MentHlth","HvyAlcoholConsump", "Fruits", "Veggies")
train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove2)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove2)]

# Train the k-NN model
ctrl2 <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
knnFit3 <- train(Sex ~ .
                 , data = train.data3
                 , method = "knn", trControl = ctrl2
                 , preProcess = c("range") # c("center", "scale") for z-score
                 , tuneLength = 50)


#Make predictions
knnPredict3 <- predict(knnFit3, newdata = test.data3)

# Creates the confusion matrix
confusionMatrix(data = knnPredict3, reference = test.data3$Sex)
```

Analysis: From what was explained above, it can be analyzed that models in general should be trained and evaluated using cross-validation since this allows selecting a good number of neighbors ('K') and also allows

evaluating the performance of the model. Additionally, it can be observed that the elimination of certain predictor variables affects the performance of the model, both in terms of precision and generalization. On the other hand, it can be said that the confusion matrix and the evaluation measures provide information about the quality of the model predictions (true positives, true negatives, false positives and false negatives). As a summary, it could be analyzed that these experiments with KNN together with the manipulation of predictor variables allow us to understand how different attributes influence the prediction of the target variables and how the appropriate choice of variables can improve the performance of any model.

Part 3: Linear regression model BMI

First Prediction

```
### Linear regression model BMI
folder <- dirname(rstudioapi :: getSourceEditorContext()$path)

parentFolder <- dirname (folder)
data <-
  read.csv(paste0(parentFolder,"/dataset/diabetes_012_health_indicators_BRFSS2015.csv"))

data$Diabetes_012 <- ifelse(data$Diabetes_012 == 0, 0, 1)

set.seed(1)
data_estratificada2 <- data[sample(nrow(data), 3000), ]

predictors <- colnames(data_estratificada2)[-5]
sample.index <- sample(1:nrow(data_estratificada2),
                       nrow(data_estratificada2) * 0.7,
                       replace = FALSE)


train.data <- data_estratificada2[sample.index, c(predictors, "BMI"), drop = FALSE]
test.data <- data_estratificada2[-sample.index, c(predictors, "BMI"), drop = FALSE]

ins_model <- lm(BMI ~ ., data = train.data)

summary(ins_model)
```

```
##
## Call:
## lm(formula = BMI ~ ., data = train.data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.218  -3.753  -0.727   2.651  59.718
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          29.700892   1.248923  23.781  < 2e-16 ***
## Diabetes_012          2.282214   0.396631   5.754 1.00e-08 ***
## HighBP                2.821500   0.297689   9.478  < 2e-16 ***
## HighChol              0.566150   0.283749   1.995 0.046146 *
## CholCheck             0.859487   0.677266   1.269 0.204564
## Smoker               -0.522257   0.272625  -1.916 0.055546 .
## Stroke               -0.813064   0.708187  -1.148 0.251063
```

```
## HeartDiseaseorAttack -1.095276   0.483551  -2.265 0.023611 *
## PhysActivity         -0.974136   0.338502  -2.878 0.004046 **
## Fruits               -0.722677   0.287499  -2.514 0.012023 *
## Veggies              -0.537476   0.351942  -1.527 0.126870
## HvyAlcoholConsump    -0.945193   0.597458  -1.582 0.113796
## AnyHealthcare         0.162150   0.612766   0.265 0.791329
## NoDocbcCost          -0.528085   0.505369  -1.045 0.296168
## GenHlth               0.621751   0.163830   3.795 0.000152 ***
## MentHlth              0.006135   0.019977   0.307 0.758794
## PhysHlth             -0.049331   0.019188  -2.571 0.010210 *
## DiffWalk              2.097624   0.436809   4.802 1.68e-06 ***
## Sex                  -0.023210   0.274379  -0.085 0.932593
## Age                  -0.414443   0.048185  -8.601  < 2e-16 ***
## Education             0.065025   0.152360   0.427 0.669579
## Income               -0.113682   0.076249  -1.491 0.136132
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.968 on 2078 degrees of freedom
## Multiple R-squared:  0.157,  Adjusted R-squared:  0.1485
## F-statistic: 18.43 on 21 and 2078 DF,  p-value: < 2.2e-16
```

```
# Train the model
train.control <- trainControl(method = "cv", number = 10 )
model <- train(BMI ~ ., data = train.data, method = "lm",
               trControl = train.control)

# Summarize the results
print(model)
```

```
## Linear Regression
##
## 2100 samples
##   21 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 1891, 1891, 1890, 1889, 1889, 1891, ...
## Resampling results:
##
##   RMSE      Rsquared   MAE
##   5.984649  0.1486856  4.319634
##
## Tuning parameter 'intercept' was held constant at a value of TRUE
```

Second Prediction

```
#### Second

predictors_to_remove <- c("AnyHealthcare", "CholCheck", "MentHlth", "Education", "Sex")

train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]

ins_model <- lm(BMI ~ ., data = train.data2)
```

```r
summary(ins_model)

# Train the model
train.control <- trainControl(method = "cv", number = 5)
model <- train(BMI ~ ., data = train.data2, method = "lm",
               trControl = train.control)

# Summarize the results
print(model)
```

Third Prediction

```r
#### Third
predictors_to_remove <- c("Income", "Stroke", "NoDocbcCost", "Veggies", "HvyAlcoholConsump")

train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove)]

ins_model <- lm(BMI ~ ., data = train.data3)

summary(ins_model)

# Train the model
train.control <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
model <- train(BMI ~ ., data = train.data3, method = "lm",
               trControl = train.control)
# Summarize the results
print(model)
```

Linear regression model MentHlth

First Prediction

```r
### Linear regression model MentHlth

set.seed(1)
data_estratificada2 <- data[sample(nrow(data), 3000), ]

predictors <- colnames(data_estratificada2)[-16]
sample.index <- sample(1:nrow(data_estratificada2),
                       nrow(data_estratificada2) * 0.7,
                       replace = FALSE)

### TRAINING
train.data <- data_estratificada2[sample.index, c(predictors, "MentHlth"), drop = FALSE]
test.data <- data_estratificada2[-sample.index, c(predictors, "MentHlth"), drop = FALSE]

ins_model <- lm(MentHlth ~ ., data = train.data)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "cv", number = 10 )
model <- train(MentHlth ~ ., data = train.data, method = "lm",
```

```
               trControl = train.control)

# Summarize the results
print(model)
```

Second Prediction

```
### Second

predictors_to_remove <- c("BMI", "HeartDiseaseorAttack", "Stroke", "PhysActivity", "CholCheck")

train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]

ins_model <- lm(MentHlth ~ ., data = train.data2)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "cv", number = 5)
model <- train(MentHlth ~ ., data = train.data2, method = "lm",
               trControl = train.control)

# Summarize the results
print(model)
```

Third Prediction

```
#### Third
predictors_to_remove <- c("Diabetes_012", "HighBP", "HighChol", "Veggies", "Education")

train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove)]

ins_model <- lm(MentHlth ~ ., data = train.data3)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
model <- train(MentHlth ~ ., data = train.data3, method = "lm",
               trControl = train.control)
# Summarize the results
print(model)
```

Linear regression model PhysHlth

First Prediction

```
#### Linear regression model PhysHlth
set.seed(1)
data_estratificada3 <- data[sample(nrow(data), 3000), ]

predictors <- colnames(data_estratificada2)[-17]
sample.index <- sample(1:nrow(data_estratificada3),
```

```
                      nrow(data_estratificada3) * 0.7,
                      replace = FALSE)

train.data <- data_estratificada2[sample.index, c(predictors, "PhysHlth"), drop = FALSE]
test.data <- data_estratificada2[-sample.index, c(predictors, "PhysHlth"), drop = FALSE]

ins_model <- lm(PhysHlth ~ ., data = train.data)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "cv", number = 10 )
model <- train(PhysHlth ~ ., data = train.data, method = "lm",
               trControl = train.control)
# Summarize the results
print(model)
```

Second Prediction

```
### Second

predictors_to_remove <- c("Sex", "Diabetes_012", "Education", "CholCheck", "Smoker")

train.data2 <- train.data[, !(names(train.data) %in% predictors_to_remove)]
test.data2 <- test.data[, !(names(test.data) %in% predictors_to_remove)]

ins_model <- lm(PhysHlth ~ ., data = train.data2)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "cv", number = 5)
model <- train(PhysHlth ~ ., data = train.data2, method = "lm",
               trControl = train.control)
# Summarize the results
print(model)
```

Third Prediction

```
#### Third

predictors_to_remove <- c("BMI", "HeartDiseaseorAttack", "PhysActivity", "Veggies", "Stroke")

train.data3 <- train.data2[, !(names(train.data2) %in% predictors_to_remove)]
test.data3 <- test.data2[, !(names(test.data2) %in% predictors_to_remove)]

ins_model <- lm(PhysHlth ~ ., data = train.data3)
summary(ins_model)

# Train the model
train.control <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
model <- train(PhysHlth ~ ., data = train.data3, method = "lm",
               trControl = train.control)
# Summarize the results
print(model)
```

Analysis: Through what was explained above, it can be analyzed that cross validation is used in all predictions to evaluate the performance of the model. Likewise, the use of a systematic approach is observed in order to test different combinations of predictor variables and thus evaluate how they affect the model. Additionally, it is understood that the interpretation of the coefficients and their significance is crucial to understand the relationship between the predictor variables and the target variables. Thanks to all this, it is concluded that this approach helps to understand in detail how different variables affect linear regression models. Likewise, it is understood that the elimination of certain variables can help simplify the model and, in some cases, improve its interpretation. Finally, it is observed that it is essential to consider both the quality of the fit and the practical interpretation of the results when selecting predictor variables. As a summary, it is identified that in this part of the document a systematic and structured approach is followed in order to evaluate linear regression models, taking into account different combinations of predictor variables and thus being able to see their impact on the resulting models. This is essential to understand the relationship between variables, and thus be able to make informed decisions when building predictive models.