Deliverable_2

Julian Abello Orozco

2023-10-08

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

Part 1: Data exploration and data wrangling

In this R Markdown document i will use a data set containing 22 variables that contains 253680 objects. With this dataset I will show how to apply data analysis, Knn, linear and miltilinear regression.

In order to start, it is necessary to load the data set 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 our data set we must inspect and analyze the information contained in this file. In the following image we can see the variables and brief information about their content.


Summary of the variables in the "diabetes_012_health_indicators_BRFSS2015.csv" dataset

Diabetes_012: 0 = no diabetes 1 = prediabetes 2 = diabetes
HighBP:0 = no high BP 1 = high BP
HighChol: 0 = no high cholesterol 1 = high cholesterol
CholCheck: 0 = no cholesterol check in 5 years 1 = yes cholesterol check in 5 years
BMI: Body Mass Index
Smoker: Have you smoked at least 100 cigarettes in your entire life? [Note: 5 packs = 100 cigarettes] 0 = no 1 = yes
Stroke: (Ever told) you had a stroke. 0 = no 1 = yes
HeartDiseaseorAttack: coronary heart disease (CHD) or myocardial infarction (MI) 0 = no 1 = yes **PhysActivity**: physical activity in past 30 days - not including job 0 = no 1 = yes
Fruits: Consume Fruit 1 or more times per day 0 = no 1 = yes
Veggies: Consume Vegetables 1 or more times per day 0 = no 1 = yes
HvyAlcoholConsump: (adult men >=14 drinks per week and adult women>=7 drinks per week) 0 = no 1 = yes **AnyHealthcare**: Have any kind of health care coverage, including health insurance, prepaid plans such as HMO, etc. 0 = no 1 = yes
NoDocbcCost: Was there a time in the past 12 months when you needed to see a doctor but could not because of cost? 0 = no 1 = yes
GenHlth: Would you say that in general your health is: scale 1-5 1 = excellent 2 = very good 3 = good 4 = fair 5 = poor
MentHlth: days of poor mental health scale 1-30 days
PhysHlth: physical illness or injury days in past 30 days scale 1-30
DiffWalk: Do you have serious difficulty walking or climbing stairs? 0 = no 1 = yes
Sex: 0 = female 1 = male
Age: 13-level age category (_AGEG5YR see codebook) 1 = 18-24 9 = 60-64 13 = 80 or older **Education**: Education level (EDUCA see codebook) scale 1-6 1 = Never attended school or only kindergarten 2 = elementary etc.
Income: Income scale (INCOME2 see codebook) scale 1-8 1 = less than $10,000 5 = less than $35,000 8 = $75,000 or more

Figure 1: Characteristics of the data set variables

later using the function `psych` we can extract a statistical analysis 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 are going to transform all the data that are not "= 0" in the variable Diabetes_012, then we will show in a small table how many data were classified as "0" or "1"" in this variable of our set of data

```
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 we will use the KNN predictive method, for this we will use 3 different variables to achieve the predictions. First, through a stratified sample, we will take approximately 1% of the data to train our models.

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

```
Conteo_ss_Diabetes
```

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

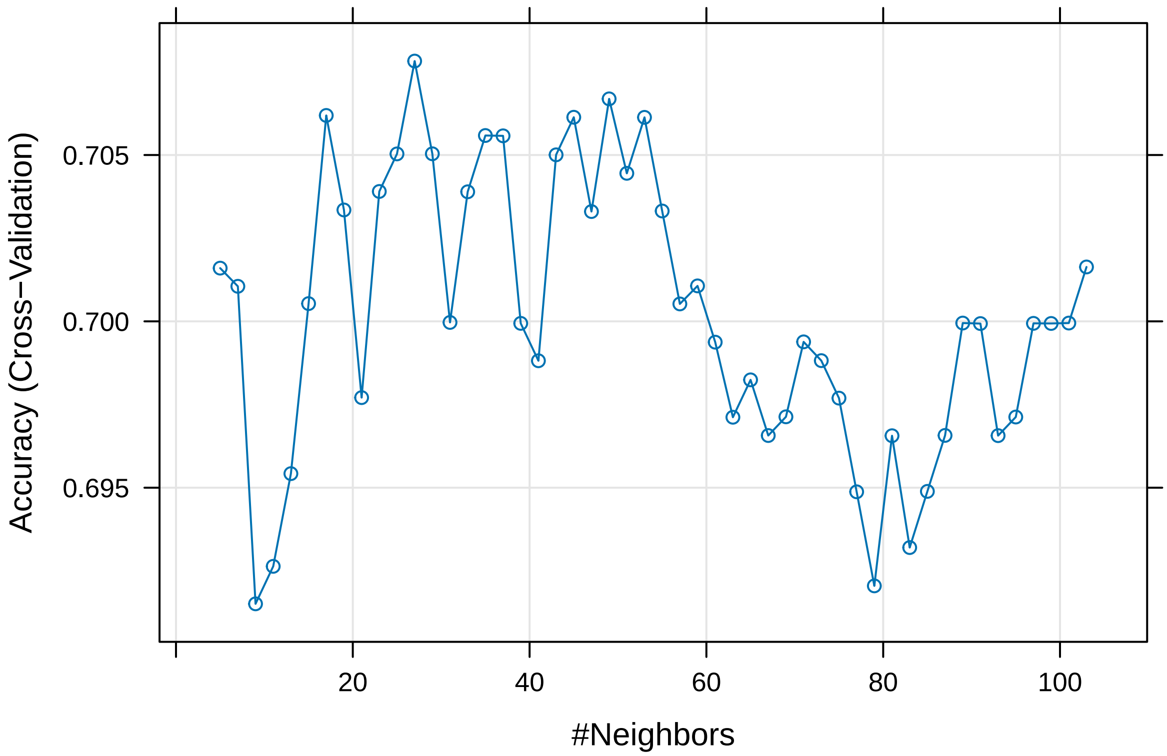
At this point we will find the appropriate number of "K" and we will train the Knn model to predict Diabetes

```
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)
```

These lines of code are related to training and evaluating a machine learning model using the caret library in R, specifically a k-Nearest Neighbors (KNN) model.

```
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)
```



This code in R performs prediction of a pre-trained K-Nearest Neighbors (KNN) model on new data (test set) and creates a confusion matrix to evaluate the performance of the model on the test data.

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

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

This part of the code uses the `confusionMatrix()` function to calculate a confusion matrix and various metrics to evaluate the performance of the KNN model on the predictions made on the test set.

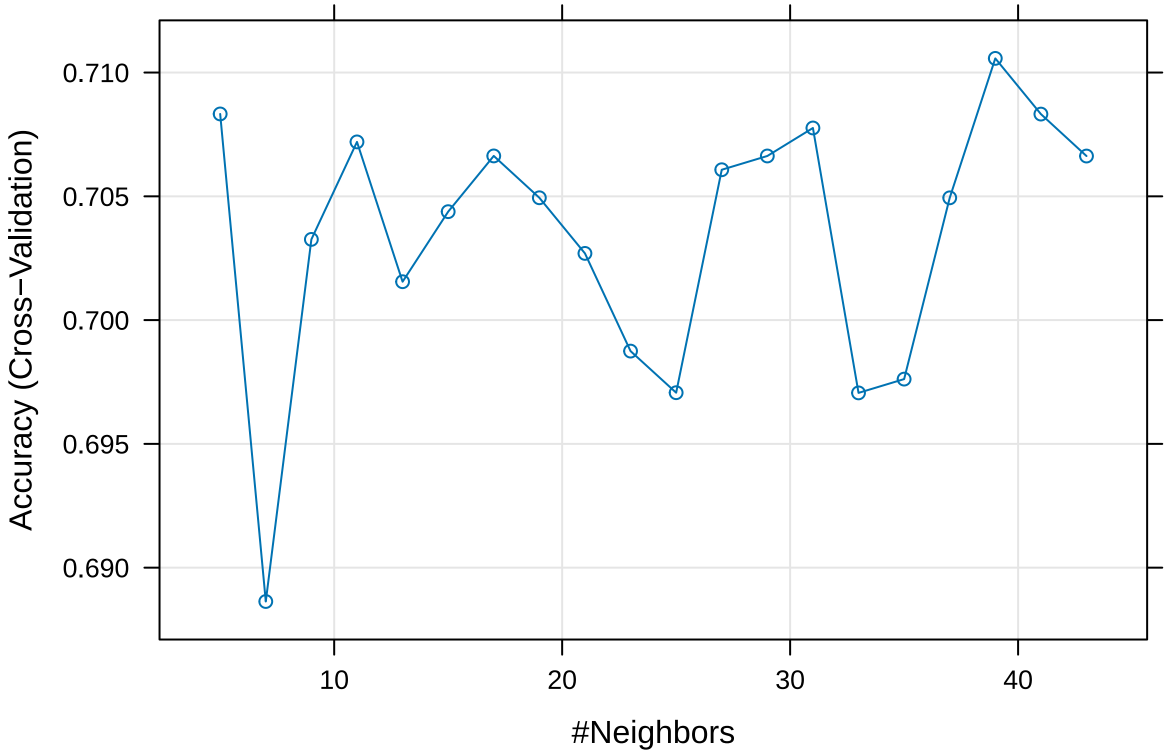
```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction    0   1
##            0 281 121
##            1  97 263
##
##                Accuracy : 0.7139
```

```
##                  95% CI : (0.6804, 0.7458)
##     No Information Rate : 0.5039
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.4281
##
##  Mcnemar's Test P-Value : 0.1193
##
##             Sensitivity : 0.7434
##             Specificity : 0.6849
##          Pos Pred Value : 0.6990
##          Neg Pred Value : 0.7306
##              Prevalence : 0.4961
##          Detection Rate : 0.3688
##    Detection Prevalence : 0.5276
##       Balanced Accuracy : 0.7141
##
##        'Positive' Class : 0
##
```

Second Prediction

In this process, a vector called **predictors_to_remove** is created to specify the variables for removal from the dataset. Subsequently, a new dataset named **train.data2** is generated by excluding the columns listed in **predictors_to_remove** from the original dataset **train.data**. This exclusion is achieved using the **%in%** operator. The training control is configured, employing 5-fold cross-validation (CV) for evaluating the model's performance. Finally, a graphical representation is produced to visualize the K hyperparameter tuning process applied to the trained K-Nearest Neighbors (KNN) model. The x-axis displays the tested K values, while the y-axis illustrates a performance metric (e.g., precision, root mean square error, etc.) for each K value.

```r
predictors_to_remove <- c("NoDocbcCost", "PhysHlth", "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)
```

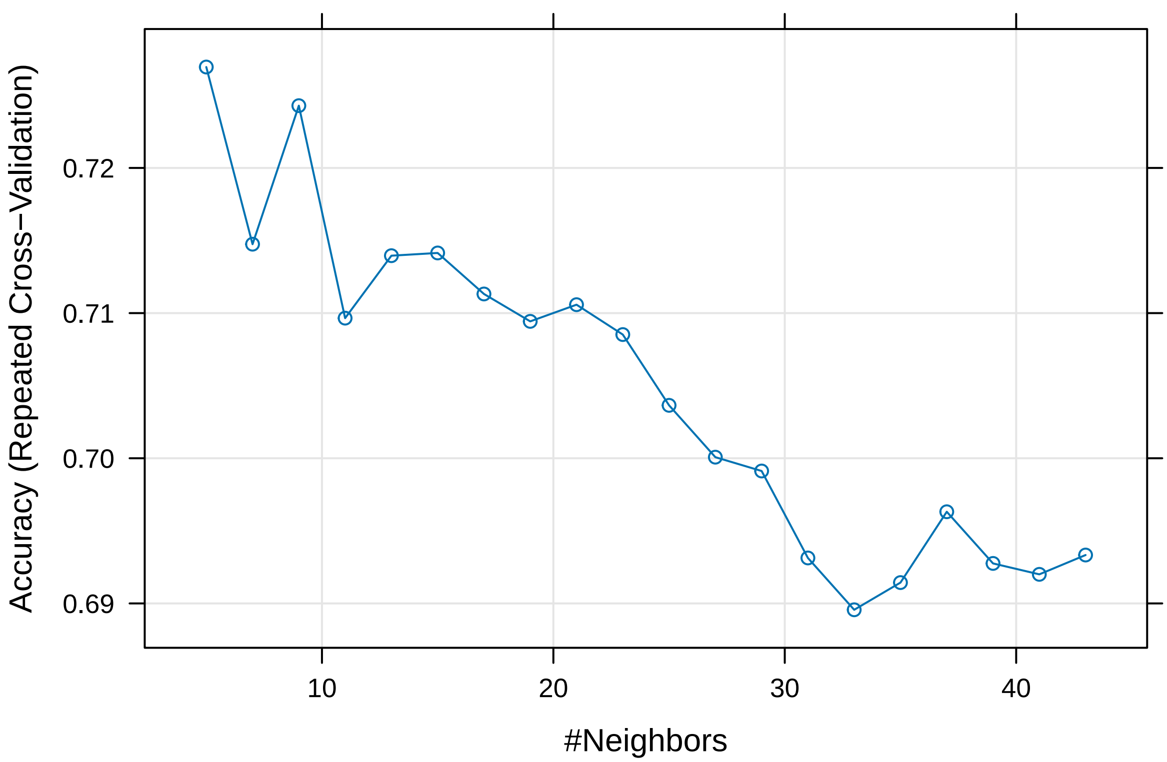
```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   0   1
##            0 269 110
##            1 109 274
##
##                 Accuracy : 0.7126
##                   95% CI : (0.679, 0.7445)
##      No Information Rate : 0.5039
##      P-Value [Acc > NIR] : <2e-16
##
##                    Kappa : 0.4252
##
##   Mcnemar's Test P-Value : 1
##
##              Sensitivity : 0.7116
##              Specificity : 0.7135
##           Pos Pred Value : 0.7098
##           Neg Pred Value : 0.7154
```

```
##               Prevalence : 0.4961
##           Detection Rate : 0.3530
##     Detection Prevalence : 0.4974
##        Balanced Accuracy : 0.7126
##
##         'Positive' Class : 0
##
```

Third Prediction

Finally, the process is carried out again but this time only using K. Testing the performance of the model by using 3 repeated 10-fold cross-validations.

```
predictors_to_remove2 <- c("Veggies", "MentHlth","HvyAlcoholConsump", "Fruits", "CholCheck")
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)
```



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

# Creates the confusion matrix
confusionMatrix(data = knnPredict3, reference = test.data3$Diabetes_012)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 288 120
##          1  90 264
##
##                Accuracy : 0.7244
##                  95% CI : (0.6912, 0.7559)
##     No Information Rate : 0.5039
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.4491
##
##  Mcnemar's Test P-Value : 0.04537
##
##             Sensitivity : 0.7619
##             Specificity : 0.6875
##          Pos Pred Value : 0.7059
##          Neg Pred Value : 0.7458
##              Prevalence : 0.4961
##          Detection Rate : 0.3780
##    Detection Prevalence : 0.5354
##       Balanced Accuracy : 0.7247
##
##        'Positive' Class : 0
##
```

The K-Nearest Neighbors (KNN) predictive method is applied to three different sets of variables for diabetes prediction. Firstly, a stratified sample comprising approximately 1% of the data is created for model training. The appropriate value of "K" is determined, and a KNN model is trained to predict diabetes. The model's performance is evaluated using cross-validation with a graphical representation of the K hyperparameter tuning process. In the second prediction, a vector of variables to remove is defined, resulting in a modified dataset used to train a KNN model, followed by model evaluation. Lastly, the process is repeated using different variables and a repeated 10-fold cross-validation for model assessment. Confusion matrices are generated to evaluate the performance of each model.

KNN HeartDiseaseorAttack Prediction

Subsequently, each step is performed again but this time to predict the HeartDiseaseorAttack variable.

First Prediction

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

```r
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

```r
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

```
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

And finally the knn process is repeated again to predict the sex

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]
```

```r
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)


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

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

Second Prediction

```r
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
predictors_to_remove2 <- c("CholCheck", "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)
```

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

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

Part 3: Linear regression model BM

First Prediction

```r
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
```

```r
# 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

```r
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)

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

```
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

This code section refers to a linear regression analysis applied to the response variable "MentHlth" using the dataset "data_estratificada2.

First Prediction

```
### Linear regression model MentHlth

set.seed(123)
data_estratificada2 <- data[sample(nrow(data), 1269), ]

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

### ENTRENAMIENTO
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)
```

- `set.seed(123)`: Sets a random seed to ensure reproducibility of results.
- `data_estratificada3 <- data[sample(nrow(data), 1269), ]`: Creates a stratified random sample from the original "data" dataset. This involves randomly selecting 1269 rows from the original dataset.
- `predictors <- colnames(data_estratificada2)[-17]`: Defines the predictor variables for the linear regression model. The variable "PhysHlth" is excluded from the list of predictor variables.
- `sample.index <- sample(1:nrow(data_estratificada3), nrow(data_estratificada3) * 0.7, replace = FALSE)`: Selects a random sample index corresponding to 70% of the stratified dataset, which will be used as the training set.
- `train.data <- data_estratificada2[sample.index, c(predictors, "PhysHlth"), drop = FALSE]` and `test.data <- data_estratificada2[-sample.index, c(predictors, "PhysHlth"), drop = FALSE]`: Divides the stratified dataset into two sets: a training set (train.data) and a testing set (test.data). Both sets include columns of predictor variables and the "PhysHlth" column.
- `ins_model <- lm(PhysHlth ~ ., data = train.data)`: Fits a linear regression model using the "lm()" function. The "MentHlth" variable is used as the response variable, and all other variables are used as predictors. A summary of the model is then displayed using "summary(ins_model)".
- `train.control <- trainControl(method = "cv", number = 10)`: Configures the training control to perform a 10-fold cross-validation.
- `model <- train(PhysHlth ~ ., data = train.data, method = "lm", trControl = train.control)`: Trains a linear regression model using the "train()" function from the "caret" library. A 10-fold cross-validation is used, and a summary of the model is displayed.

Second Prediction

```
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

```
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)]
```

```r
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

```r
#### Linear regression model PhysHlth
set.seed(123)
data_estratificada3 <- data[sample(nrow(data), 1269), ]

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

```r
predictors_to_remove <- c("Sex", "DiffWalk", "Diabetes_012", "CholCheck", "Income")

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

```
predictors_to_remove <- c("Fruits", "HeartDiseaseorAttack", "BMI", "Veggies", "Fruits")

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)
```