CI_Data_Analysis

February 27, 2020

1 Analysis of dataset

The objective of this dataset is to try to **define probability for a patient to have a disease** on their tooth supporting tissues from simple data that can be acquired remotely. It is to define the risk factors to develop such diseases.

1.1 Objectives:

1.1.1 Perform a detailed analysis on the dataset

1.1.2 Use 2 from the list and one from outside the list

• K Nearest Neighbors • Decision Trees • Generalized Linear Models • Support Vector Machines • Multilayer perceptrons ### Optimize the solutions for better predictibility of a model

Basic analysis of the dataset: 0. ID 2. Sex - Boolean (Woman 0, Man 1) 3. Age - Integer 4. BMI - Float 4. Smoking - Integer (Non smoker 0, Previous smoker 1, Smoker 2) 5. Pathologies - Integer (Yes, No, N/A) 6. Pregnant - Integer (Yes, No, N/A) 7. Food_Sugar - Integer (Never, Sometimes, Several times a day, Once a day, Several times a day) 8. Fat_Salty - Integer (Never, Sometimes, Several times a day, Once a day, Several times a day) 9. Soda - Integer (Never, Sometimes, Several times a day, Once a day, Several times a day) 10. Alcohol - Integer (Never, Sometimes, Several times a day, Once a day, Several times a day) 11. Frequence_Appoint_Dentist - Integer (Never, Once a year, 2-3 a year, Regularly) 12. Hygeine - Integer (0,1,2,3,4,5,6) 13. Gingivorrhagia - Integer (Absent, Corrélées (cycle, etc…), Provoked,Spontanées) 1 missing value 14. Stress_Daily - Integer (1-10) 4 missing values 15. PI - (0-3) 1 value missing *Label* 16. Diagnosis - Integer (Healthy, Periodontitis, Gingivitis) 49 values missing

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First meet with The Guy

- Deleting Y's sounded like an idea. We can use some of the data to train a model to see if it works well. Can have a strategy to implement this data
- For N/As in Pathologies - failed to extract that value from the patient
- We have a very accurate dataset, so making medians or means cannot be a good solution for missing vaues. Replacing missing values with outliers can be a good solution too. Consider this point when you're doing your analysis.

1.1.3 Mistakes spotted in the data set:

- BMI has an outlier - 937.5

1.2 General functions to be used

[0]:
```
#Imports

#Nimish
import pandas as pd
from pandas import read_csv
import matplotlib.pyplot as plt
import numpy as np
import warnings
warnings.filterwarnings('ignore')

#from sklearn.preprocessing import imputer as ip



#Ilya
import matplotlib.pyplot as plt
from sklearn import neighbors
from sklearn.model_selection import train_test_split, KFold, cross_val_score

#Reynaldo
import seaborn as sns
from scipy import stats
from sklearn.decomposition import PCA
from sklearn import preprocessing
from collections import Counter

#Whoever makes imports, write names xD
```

Code for converting dataset to numbers for readability. In order:

- convertSimple: converts the CSV file that is passed to a dataframe
- convertWithCategories: converts the dataframe so that all columns specified have their values converted to categories. Each category represents a number.
- convertDeleteNulls: converts the dataframe so that every row that has at least one column with a null value is deleted from the dataframe.
- deleteRowsWithOutlyingValues: deletes all aoutlying values
- getAllColumnsButID: returns an array of all the columns of a dataframe, except the ID.
- transformPCA: transforms a dataframe into a reduced dimentionality version, based on the number of components passed.

[0]:
```
def convertSimple(filename):
    data = pd.read_csv("{}.csv".format(filename))
    return data
```

[0]:
```
def convertWithCategories(data, columnNames):
    data_copy = data.copy()
    for column in columnNames:
      data_copy[column] = data_copy[column].astype('category')
      data_copy[column] = data_copy[column].cat.codes

    return data_copy
```

```
[0]: def convertDeleteNulls(data, columnNames):
         data_copy = data.copy()
         # Delete null values
         data_copy = data_copy.dropna(axis=0, subset=columnNames)

         return data_copy
```

```
[0]: def convertDeleteColumn(data, columnName):
         data_copy = data.copy()
         del data_copy[columnName]

         return data_copy
```

```
[0]: def deleteRowsWithOutlyingValues(dataframe, columns):
         data_copy = dataframe.copy()
         # For each column, first it computes the Z-score of each value in the␣
      ↪column, relative to the column mean and standard deviation.
         # Then is takes the absolute of Z-score because the direction does not␣
      ↪matter, only if it is below the threshold.
         # Finally, result of this condition is used to index the dataframe.
         return data_copy[(np.abs(stats.zscore(dataframe[columns])) < 3.5)]
```

```
[0]: def getAllColumnsButID(dataFrame):
         columns = []
         for col in dataFrame.columns:
             if col != 'ID':
                 columns.append(col)
         return columns
```

```
[0]: def transformPCA(dataframe, numberOfComponents):
         pca = PCA(n_components=numberOfComponents)
         pca.fit(dataframe)
         return pca.transform(dataframe)
```

Code for data visualization. In order:

- plotColumns: plots all the columns in the dataframe in a scatter plot with the x axis being the ID of the row.
- printNullColumns: prints all the columns that have at least one null value in any of the rows of the dataset.
- plotCorrelationHeatmap: plots a correlation heatmap etween the columns of a data frame, based on the columns that want to be analyzed.

[0]:
```python
def plotColumns(dataFrame):
    for column in dataFrame.columns:
      if column == "ID":
        continue
      number = len(Counter(dataFrame[column]).keys())
      print(number)
      plt.hist(dataFrame[column], bins=number, color='steelblue',␣
 ↪edgecolor='black', linewidth=1.0)
      plt.xlabel(column)
      plt.ylabel("Number of occurrences")
      plt.show()
```

[0]:
```python
def printNullColumns(dataframe):
    columns = dataframe.columns

    columnsNull = []

    for col in columns:
        for index, row in dataframe.iterrows():
            if pd.isna(row[col]):
                columnsNull.append(col)
                break
    print("Columns with null values: ", columnsNull)
```

[0]:
```python
def plotCorrelationHeatmap(dataframe, columnsToPlot):
    correlation = dataframe[columnsToPlot].corr()
    #set size of the plot
    plt.figure(figsize = (16,5))
    # plot the heatmap and annotation on it
    heatmap = sns.heatmap(correlation, xticklabels=correlation.columns,
                          yticklabels=correlation.columns, annot=True)
    return heatmap
```

1.3 Reynaldo's Code

1.3.1 Data visualization

First, we parse the data and we delete the rows with null values on the diagnosis column, as this is the label.

Afterwards, we parse the data to convert every specified row to a category, so that the string values are converted to numbers.

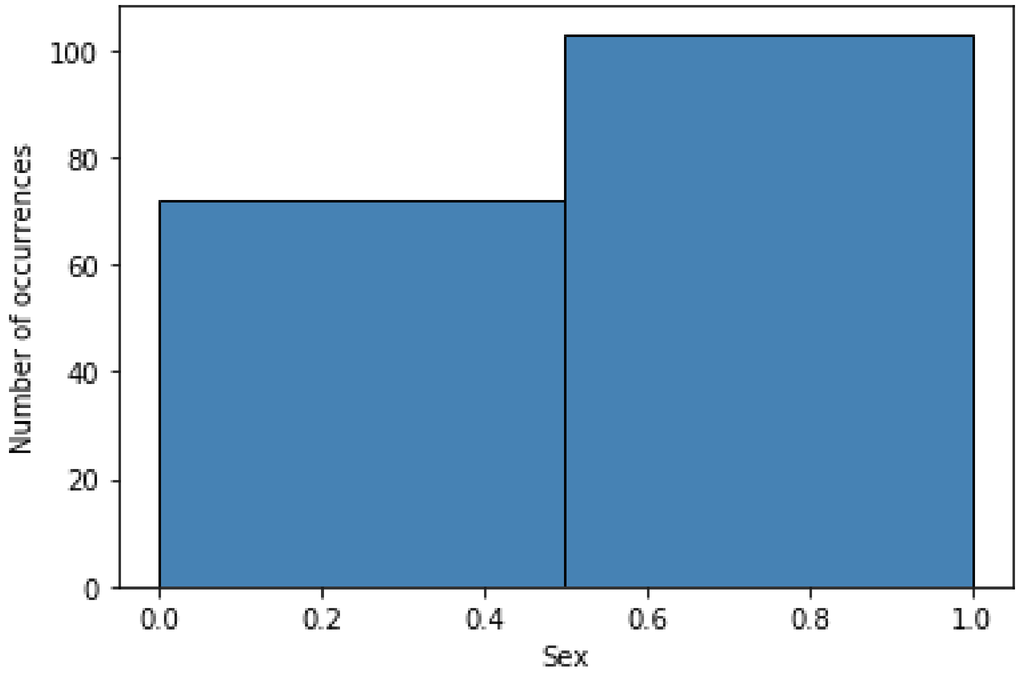
[0]:
```python
#Reynaldo's Code on data visualization

    data = convertSimple('/content/data')

    dataFiltered = convertDeleteNulls(data, ['Diagnosis'])
```

```
dataFilteredCat = convertWithCategories(dataFiltered, ['Sex', 'Smoking',␣
↪'Pathologies', 'Pregnant',
                                                     'Food_Sugar',␣
↪'Fat_Salty', 'Soda', 'Alcohol', 'Frequence_Appoint_Dentist',
                                                     'Hygiene_Dental',␣
↪'Stress_Daily', 'Gingivorrhagia', 'PI', 'Diagnosis'])
```

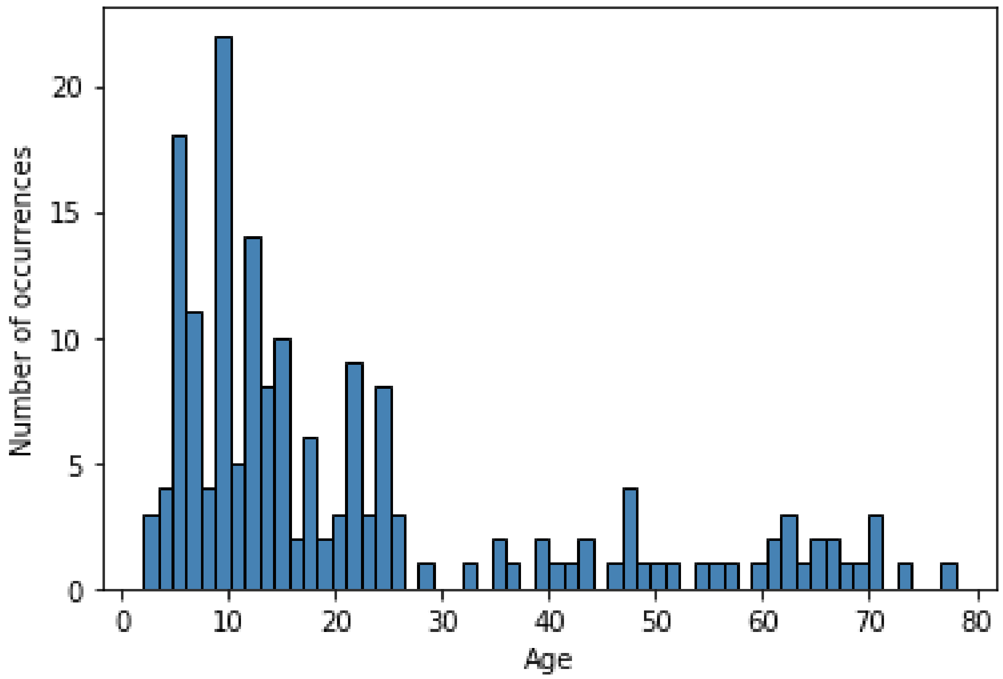
When the basic data conversion happens, we visualize the data creating a scatter plot of each column, with respect to the ID.

[0]:
```
plotColumns(dataFilteredCat)
```

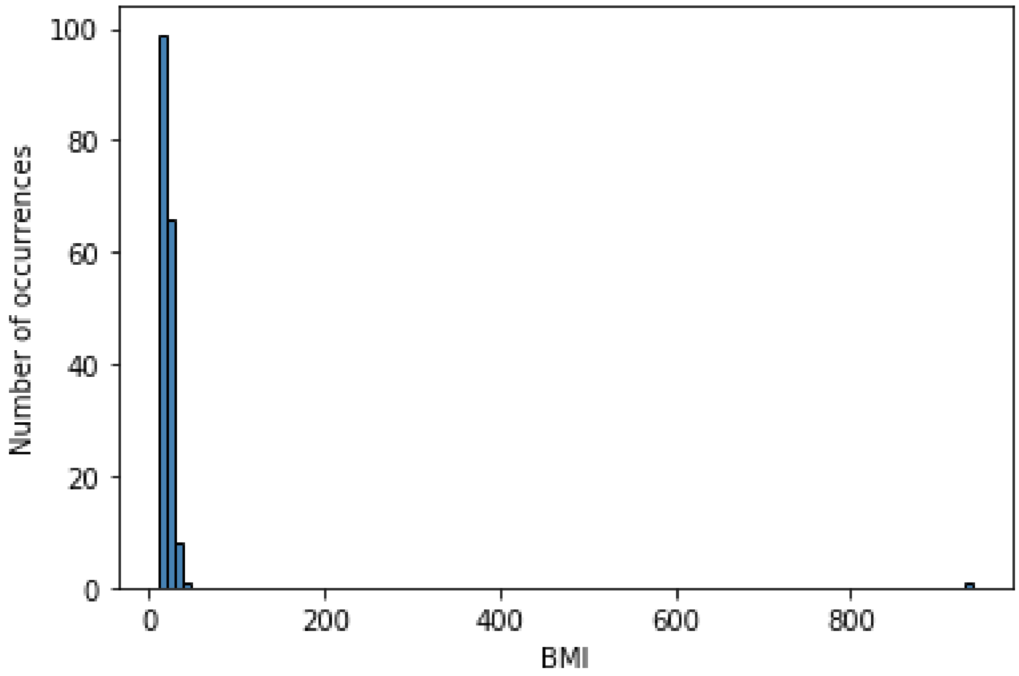
```
2
```



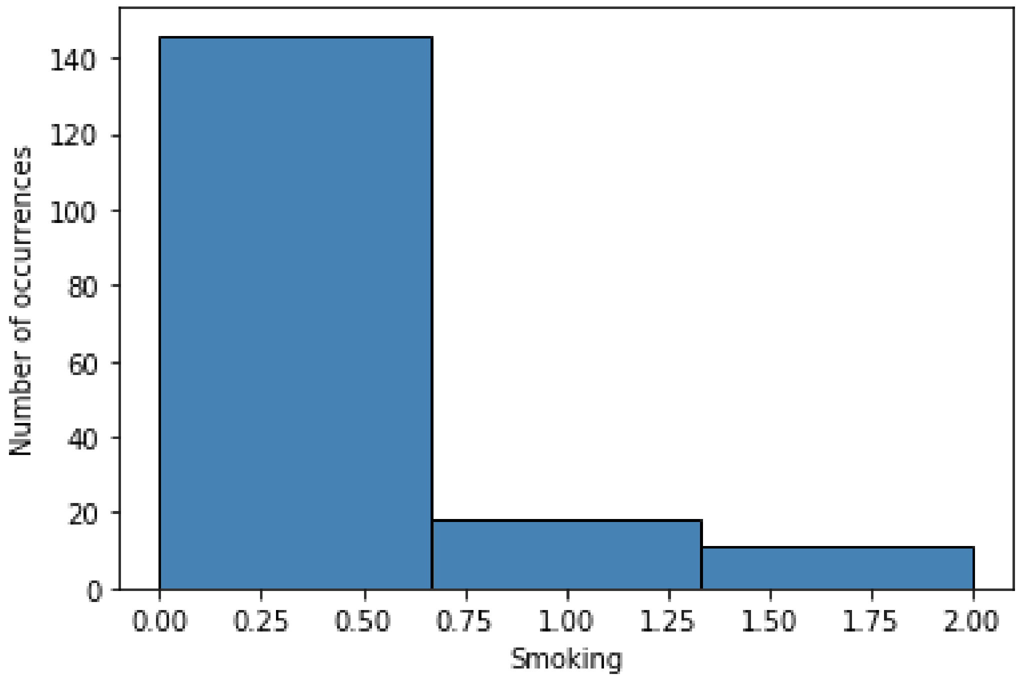
```
56
```


Number of occurrences
Age
0
5
10
15
20
0
10
20
30
40
50
60
70
80

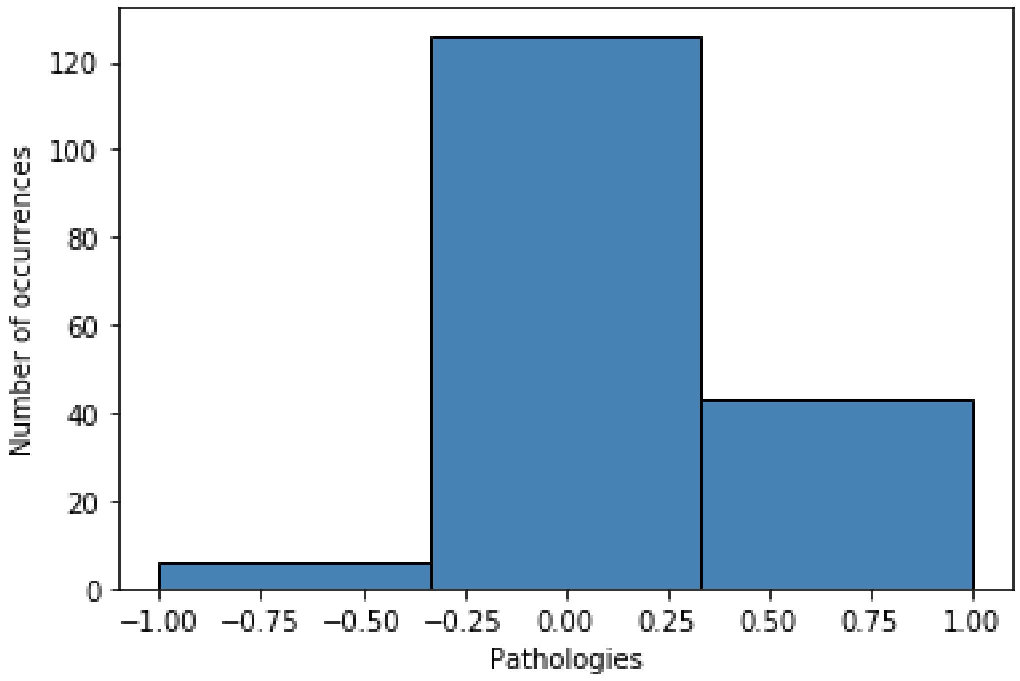
```
106
```


Number of occurrences
BMI
0
20
40
60
80
100
0
200
400
600
800

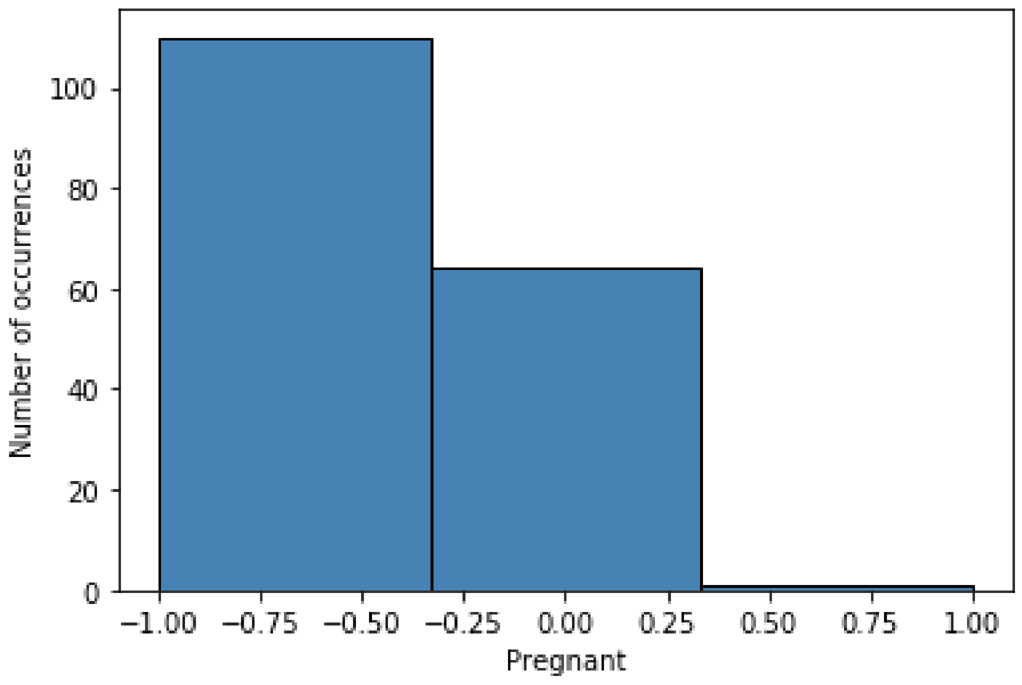
```
3
```


Number of occurrences
0
20
40
60
80
100
120
140
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00
Smoking

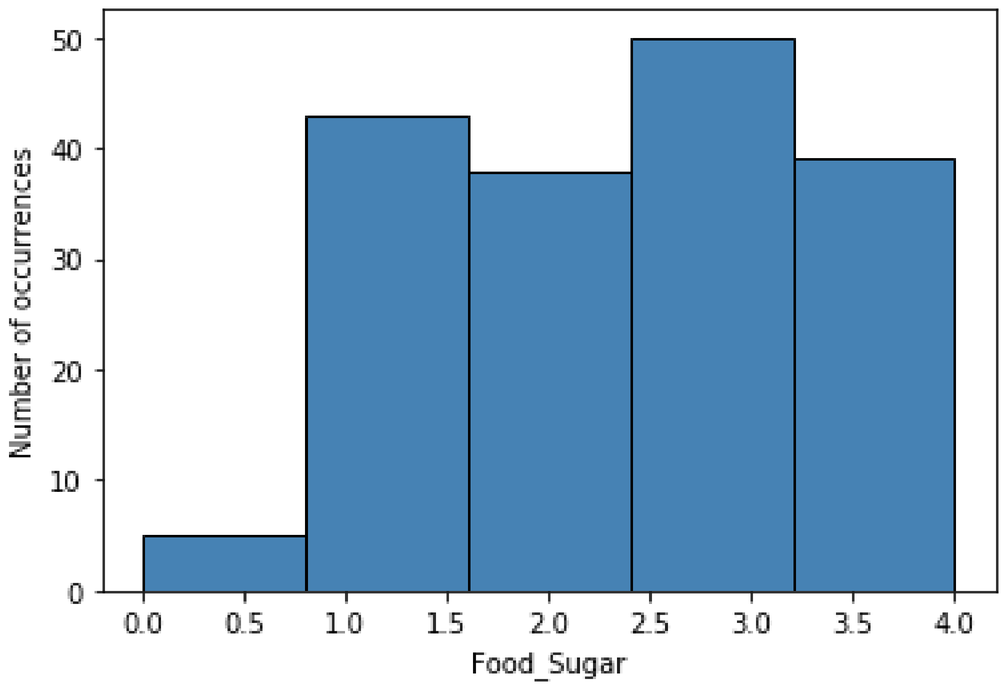
3


Number of occurrences
0
20
40
60
80
100
120
−1.00
−0.75
−0.50
−0.25
0.00
0.25
0.50
0.75
1.00
Pathologies

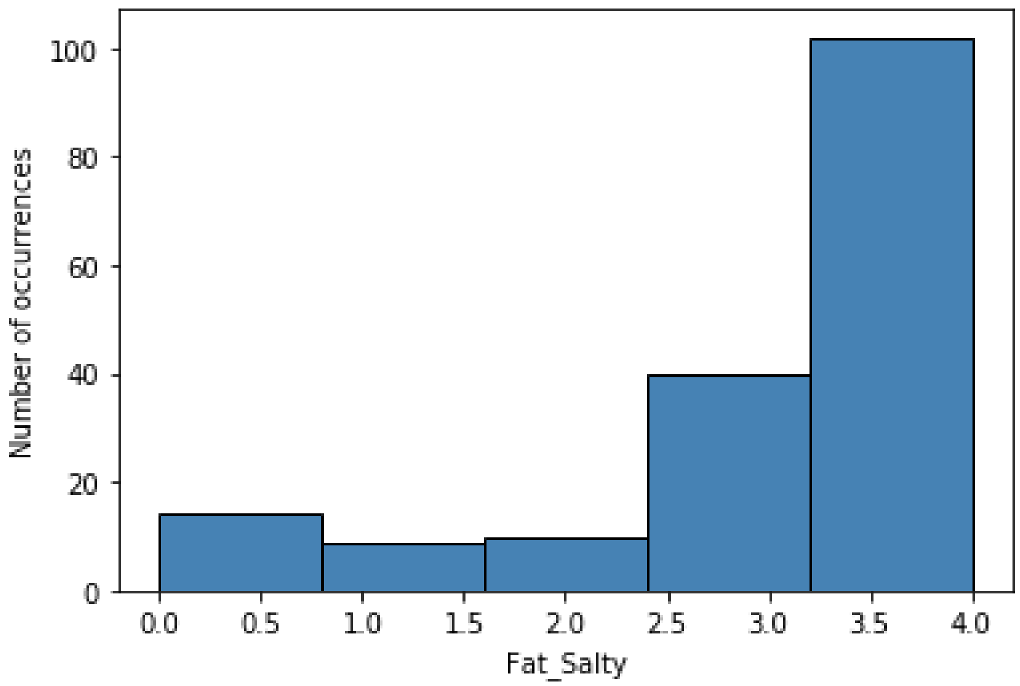
3


Number of occurrences
100
80
60
40
20
0
−1.00
−0.75
−0.50
−0.25
0.00
0.25
0.50
0.75
1.00
Pregnant

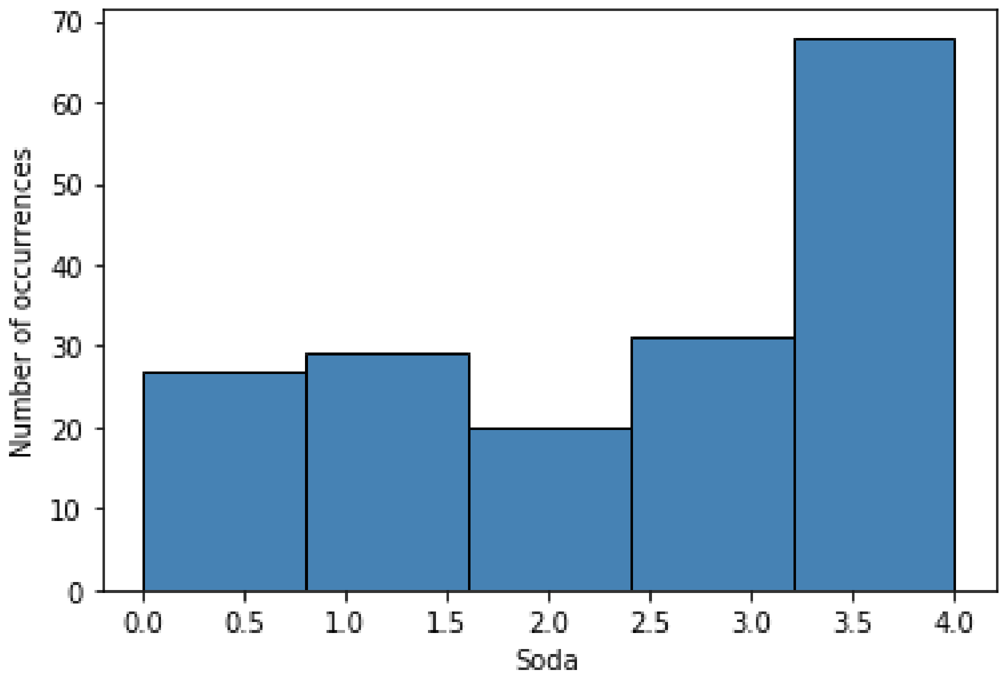
5


Number of occurrences
50
40
30
20
10
0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
Food_Sugar

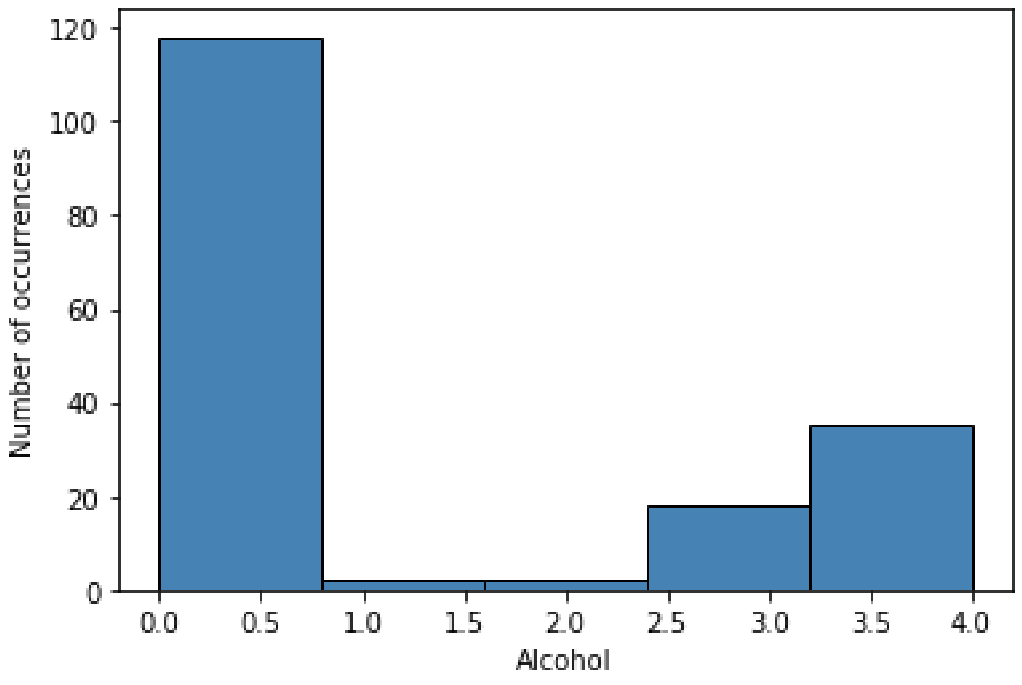
5


Number of occurrences
Fat_Salty
0
20
40
60
80
100
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

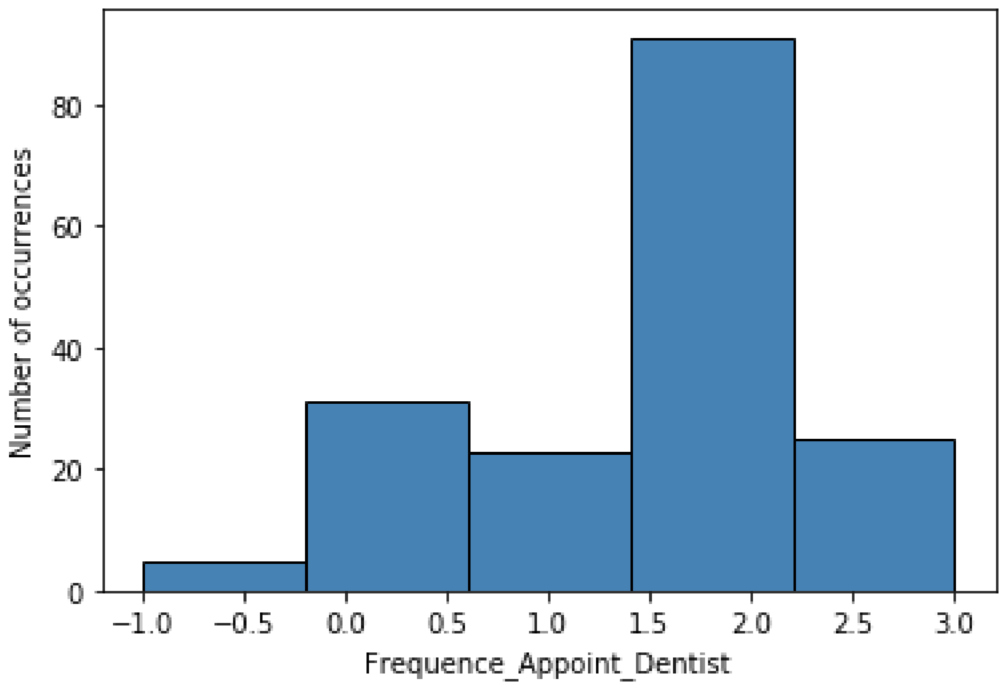
5


Number of occurrences
Soda
0
10
20
30
40
50
60
70
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

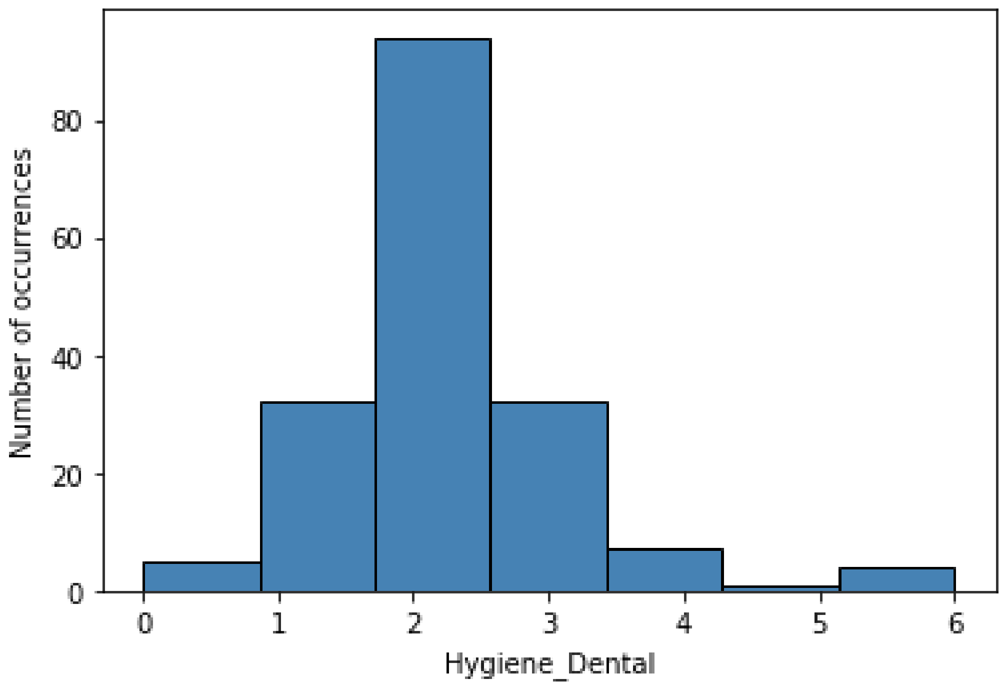
5


Number of occurrences
Alcohol
0
20
40
60
80
100
120
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

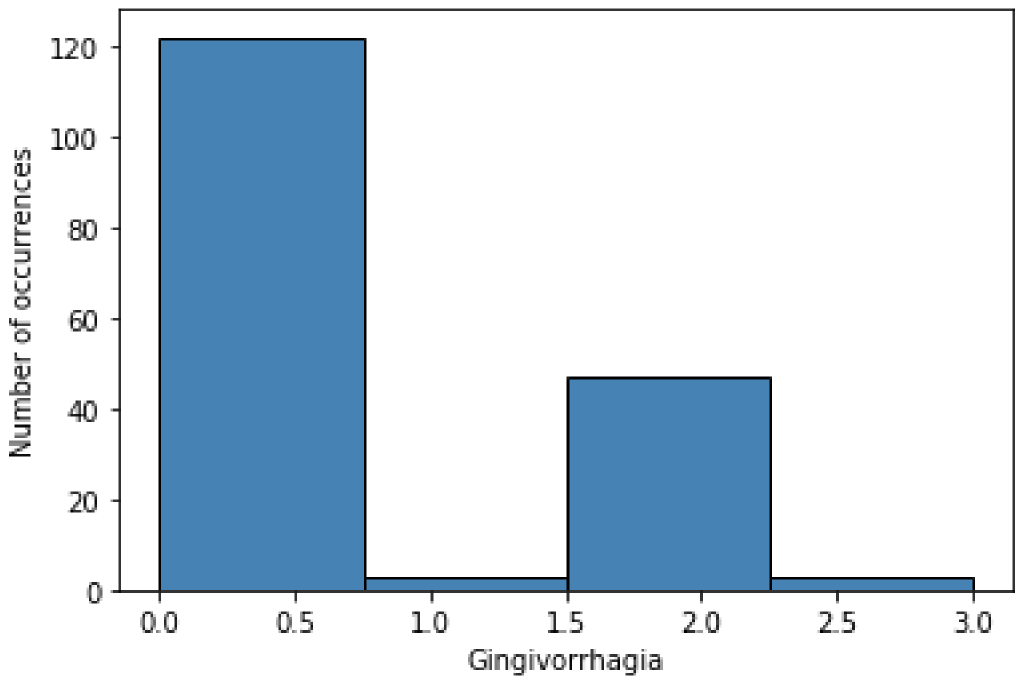
5


Number of occurrences
Frequence_Appoint_Dentist
0
20
40
60
80
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0

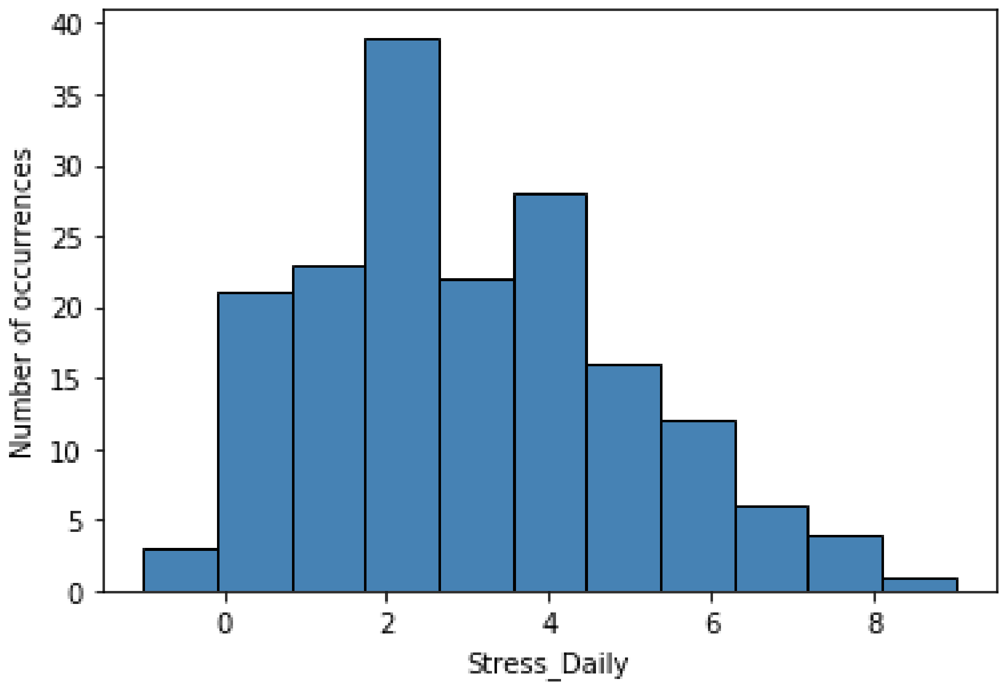
7


Number of occurrences
0
20
40
60
80
0
1
2
3
4
5
6
Hygiene_Dental

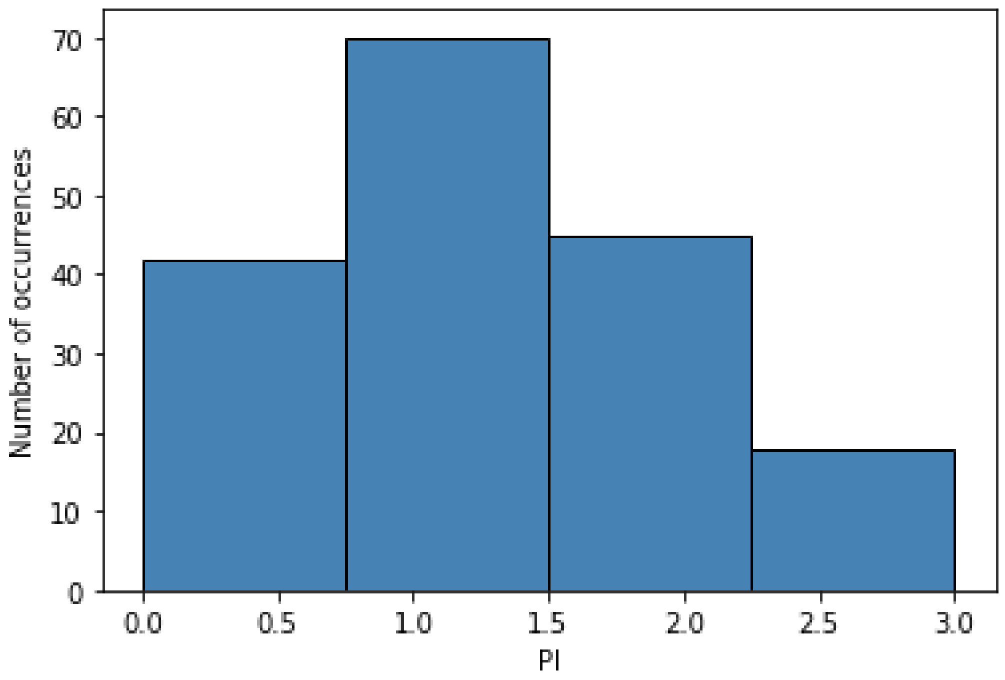
```
4
```


Number of occurrences
0
20
40
60
80
100
120
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Gingivorrhagia

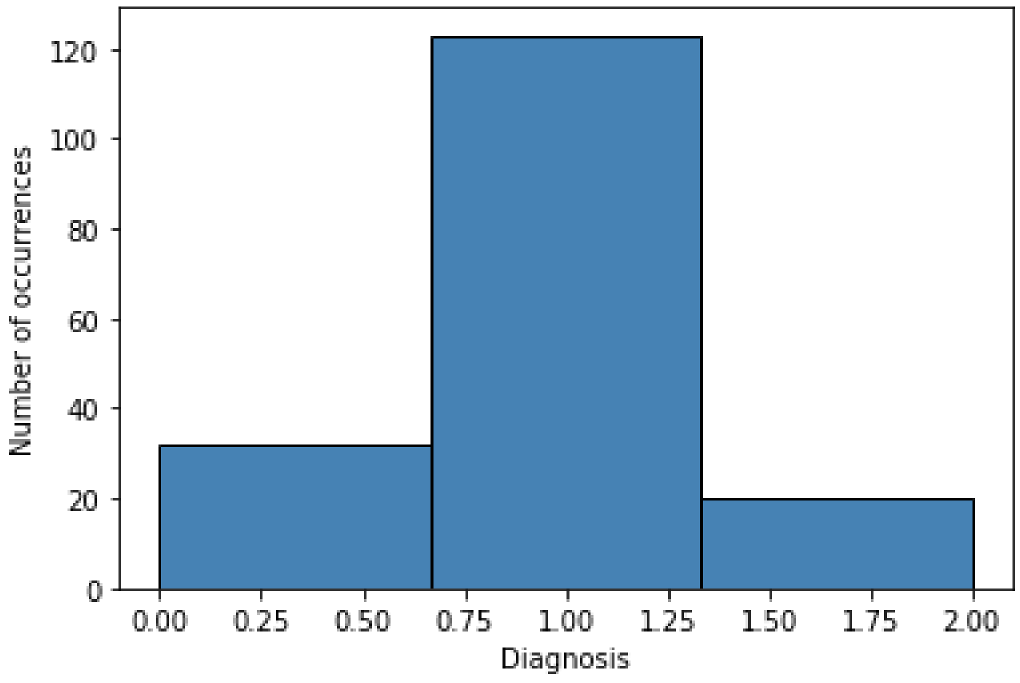
```
11
```


Number of occurrences
Stress_Daily

4


Number of occurrences
PI

3



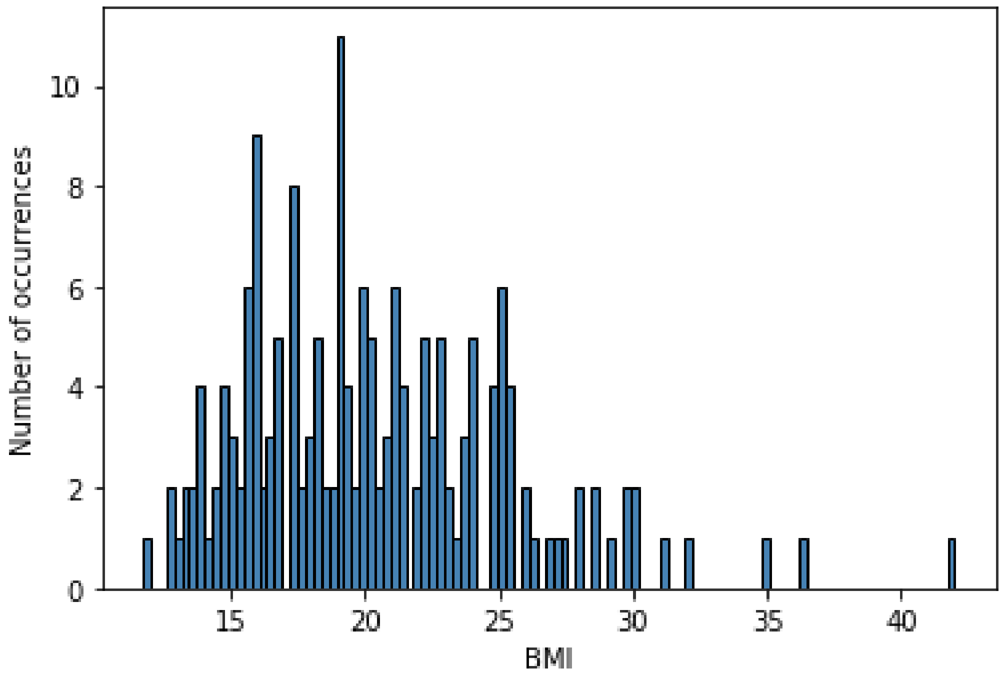
It's visible that the categorization went smoothily, as all the plots consists on clear lines on integer values. However, it can be seen in the BMI column that there is an error, with a value being way outside of the range. This can be explained by human error on inputing the value. To deal with that value, we decided to just remove it from the dataframe, as there is no clear way to replace that value for another one.

This removal was performed using a function that removes all outlying values from the dataframe in the columns specified. The functions searches for the Z-value of each row with regards f the column being analyzed and deletes every row that returns an absolute value of more than 3.5 in said Z-value, as it is recommended here.

Note: Z-value represents, for a specific value, how many standard deviations it is from the mean.

```
[0]: dataFilteredCatNoOutlier = deleteRowsWithOutlyingValues(dataFilteredCat,␣
      ↪['BMI'])
     plotColumns(dataFilteredCatNoOutlier[['ID','BMI']])
```

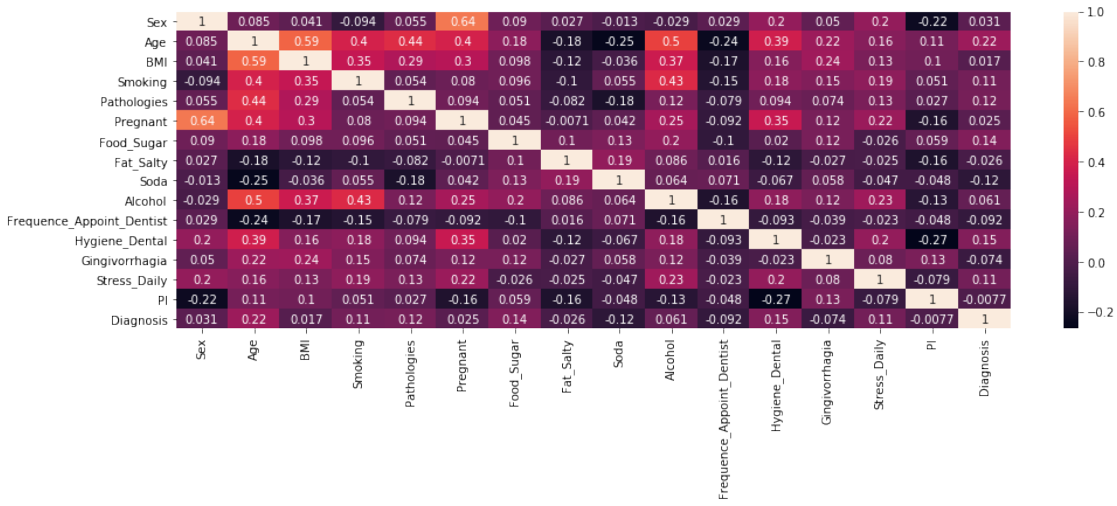
```
105
```



Now that we have eliminated the outlying value, we perform a correlation analysis between the variables. This will allow us to see what are the features that influence more the final diagnosis and will also allow us to see if there are variables that are very alike, so that they can be later merged or eliminated.

```
[0]:     plotCorrelationHeatmap(
             dataFilteredCatNoOutlier, getAllColumnsButID(dataFilteredCatNoOutlier))
```

```
[0]: <matplotlib.axes._subplots.AxesSubplot at 0x7f5881080898>
```



	Sex	Age	BMI	Smoking	Pathologies	Pregnant	Food_Sugar	Fat_Salty	Soda	Alcohol	Frequence_Appoint_Dentist	Hygiene_Dental	Gingivorrhagia	Stress_Daily	PI	Diagnosis
Sex	1	0.085	0.041	-0.094	0.055	0.64	0.09	0.027	-0.013	-0.029	0.029	0.2	0.05	0.2	-0.22	0.031
Age	0.085	1	0.59	0.4	0.44	0.4	0.18	-0.18	-0.25	0.5	-0.24	0.39	0.22	0.16	0.11	0.22
BMI	0.041	0.59	1	0.35	0.29	0.3	0.098	-0.12	-0.036	0.37	-0.17	0.16	0.24	0.13	0.1	0.017
Smoking	-0.094	0.4	0.35	1	0.054	0.08	0.096	-0.1	0.055	0.43	-0.15	0.18	0.15	0.19	0.051	0.11
Pathologies	0.055	0.44	0.29	0.054	1	0.094	0.051	-0.082	-0.18	0.12	-0.079	0.094	0.074	0.13	0.027	0.12
Pregnant	0.64	0.4	0.3	0.08	0.094	1	0.045	-0.0071	0.042	0.25	-0.092	0.35	0.12	0.22	-0.16	0.025
Food_Sugar	0.09	0.18	0.098	0.096	0.051	0.045	1	0.1	0.13	0.2	-0.1	0.02	0.12	-0.026	0.059	0.14
Fat_Salty	0.027	-0.18	-0.12	-0.1	-0.082	-0.0071	0.1	1	0.19	0.086	0.016	-0.12	-0.027	-0.025	-0.16	-0.026
Soda	-0.013	-0.25	-0.036	0.055	-0.18	0.042	0.13	0.19	1	0.064	0.071	-0.067	0.058	-0.047	-0.048	-0.12
Alcohol	-0.029	0.5	0.37	0.43	0.12	0.25	0.2	0.086	0.064	1	-0.16	0.18	0.12	0.23	-0.13	0.061
Frequence_Appoint_Dentist	0.029	-0.24	-0.17	-0.15	-0.079	-0.092	-0.1	0.016	0.071	-0.16	1	-0.093	-0.039	-0.023	-0.048	-0.092
Hygiene_Dental	0.2	0.39	0.16	0.18	0.094	0.35	0.02	-0.12	-0.067	0.18	-0.093	1	-0.023	0.2	-0.27	0.15
Gingivorrhagia	0.05	0.22	0.24	0.15	0.074	0.12	0.12	-0.027	0.058	0.12	-0.039	-0.023	1	0.08	0.13	-0.074
Stress_Daily	0.2	0.16	0.13	0.19	0.13	0.22	-0.026	-0.025	-0.047	0.23	-0.023	0.2	0.08	1	-0.079	0.11
PI	-0.22	0.11	0.1	0.051	0.027	-0.16	0.059	-0.16	-0.048	-0.13	-0.048	-0.27	0.13	-0.079	1	-0.0077
Diagnosis	0.031	0.22	0.017	0.11	0.12	0.025	0.14	-0.026	-0.12	0.061	-0.092	0.15	-0.074	0.11	-0.0077	1

It can be seen that, for the diagnosis label, there are some variables that have a correlation close to 0, which means they do not influence the outcome. These are:

1. PI with a score of -0.0077
2. BMI with a score of 0.017
3. Pregnancy with a score of 0.025
4. Fat_Salty with a score of -0.026
5. Sex with a score of 0.031

There are others, but we decided to consider these 5 due to them having an absolute value that can be rounded to a value lower than 0.1.

Another thing that can be pointed out is that there are highly correlated variables:

1. Sex and pregnancy are highly correlated.
2. Age and: BMI, pathologies, smoking, pregnancy and alcohol
3. Alcohol and smoking

There are other somehow correlated values, but we decided to focus on these due to them having an arbitrary absolute value of 0.4 or more.

This information can be useful in performing a PCA analysis.

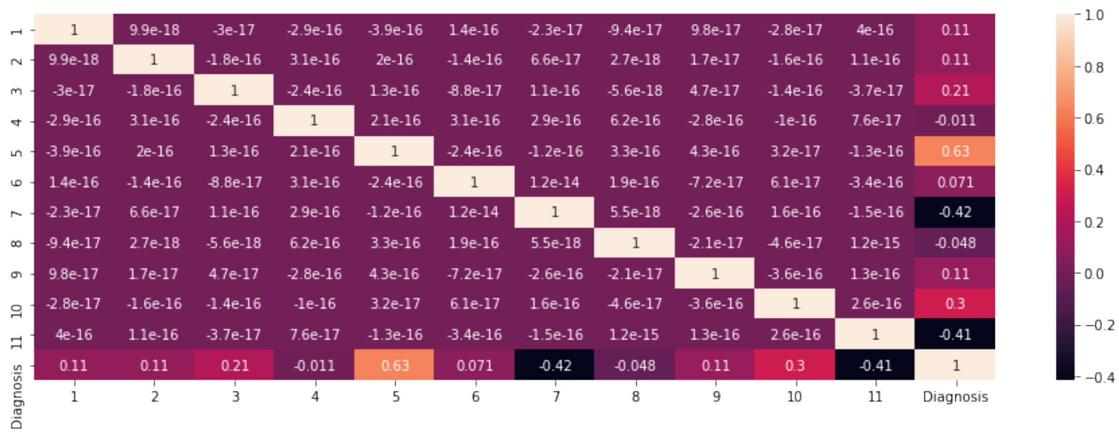
It also needs to be considered that these correlation, which uses the pearson method, only measures linear correlation. This means that this score is not a guarantee that the variables are not correlated, however it gives a good indication on what can be filtered out so that the data is of better quality to train the models.

Now, we can perform a PCA conversion based on the information we have. First, we can create a PCA based on all information and afterwards a PCA based on the reduced feature dataframe.

For both, we first need to separate the features from the label, perform the PCA on the features and then reunite the new components with the corresponding label to reperform the correlation analysis.

[0]:
```python
ids = pd.DataFrame(dataFilteredCatNoOutlier['ID'])
y_label = pd.DataFrame(dataFilteredCatNoOutlier['Diagnosis'])

x_label = dataFilteredCatNoOutlier.drop(['ID', 'Diagnosis'], axis=1)

#We normalize the data, so that PCA gets better results
x_label = dataFilteredCatNoOutlier.values #returns a numpy array
min_max_scaler = preprocessing.MinMaxScaler()
x_label_scaled = min_max_scaler.fit_transform(x_label)
x_label_scaled = pd.DataFrame(x_label_scaled)

x_label_scaled = pd.DataFrame(transformPCA(x_label_scaled, 11))

resulting_pca_all = pd.DataFrame(np.hstack([ids, x_label_scaled, y_label]))
resulting_pca_all = resulting_pca_all.rename(columns={0:'ID', 12:'Diagnosis'})

plotCorrelationHeatmap(
      resulting_pca_all, [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 'Diagnosis'])
```

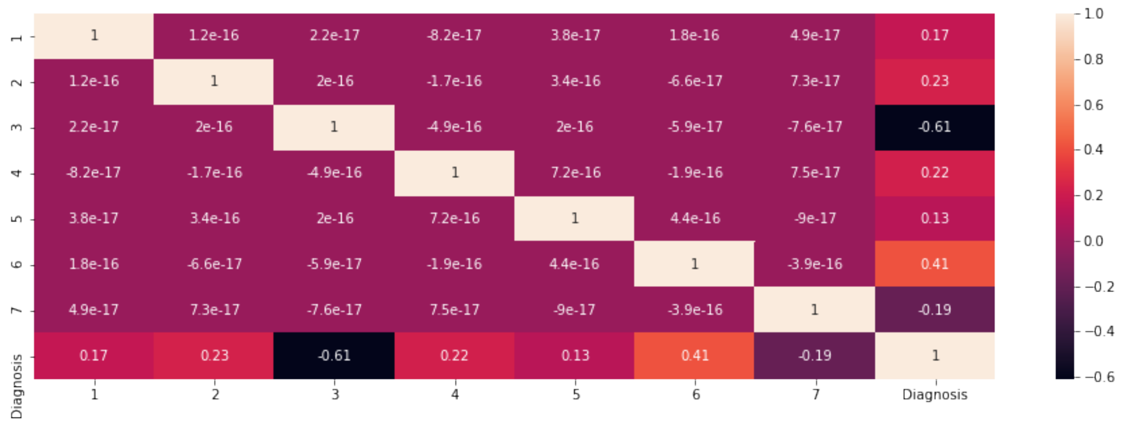
```
[0]: <matplotlib.axes._subplots.AxesSubplot at 0x7f588110ca58>
```



```
[0]:  dataDeletedColumns = dataFilteredCatNoOutlier.copy()
      dataDeletedColumns = convertDeleteColumn(dataDeletedColumns, 'PI')
      dataDeletedColumns = convertDeleteColumn(dataDeletedColumns, 'BMI')
      dataDeletedColumns = convertDeleteColumn(dataDeletedColumns, 'Pregnant')
      dataDeletedColumns = convertDeleteColumn(dataDeletedColumns, 'Fat_Salty')
      dataDeletedColumns = convertDeleteColumn(dataDeletedColumns, 'Sex')

      ids = pd.DataFrame(dataDeletedColumns['ID'])
      y_label = pd.DataFrame(dataDeletedColumns['Diagnosis'])

      x_label = dataDeletedColumns.drop(['ID', 'Diagnosis'], axis=1)
      #We normalize the data, so that PCA gets better results
      x_label = dataDeletedColumns.values
      min_max_scaler = preprocessing.MinMaxScaler()
      x_label_scaled = min_max_scaler.fit_transform(x_label)
      x_label_scaled = pd.DataFrame(x_label_scaled)

      x_label_scaled = pd.DataFrame(transformPCA(x_label_scaled, 7))

      resulting_pca_deleted = pd.DataFrame(np.hstack([ids, x_label_scaled,␣
     ↪y_label]))

      resulting_pca_deleted = resulting_pca_deleted.rename(columns={0:'ID', 8:
     ↪'Diagnosis'})
```

```
plotCorrelationHeatmap(
      resulting_pca_deleted, [1, 2, 3, 4, 5, 6, 7, 'Diagnosis'])
```

```
[0]: <matplotlib.axes._subplots.AxesSubplot at 0x7f587e0bfc50>
```



	1	2	3	4	5	6	7	Diagnosis
1	1	1.2e-16	2.2e-17	-8.2e-17	3.8e-17	1.8e-16	4.9e-17	0.17
2	1.2e-16	1	2e-16	-1.7e-16	3.4e-16	-6.6e-17	7.3e-17	0.23
3	2.2e-17	2e-16	1	-4.9e-16	2e-16	-5.9e-17	-7.6e-17	-0.61
4	-8.2e-17	-1.7e-16	-4.9e-16	1	7.2e-16	-1.9e-16	7.5e-17	0.22
5	3.8e-17	3.4e-16	2e-16	7.2e-16	1	4.4e-16	-9e-17	0.13
6	1.8e-16	-6.6e-17	-5.9e-17	-1.9e-16	4.4e-16	1	-3.9e-16	0.41
7	4.9e-17	7.3e-17	-7.6e-17	7.5e-17	-9e-17	-3.9e-16	1	-0.19
Diagnosis	0.17	0.23	-0.61	0.22	0.13	0.41	-0.19	1

As we can see, it makes a difference of 13% In accuracy if we consider pregnant column (and remove all the NAs)

1.4 Dataframes to be used ahead

```
[0]:  # We end up with the following sets of data:

      # Data without null values on diagnosis, all relevant features converted to␣
    ↪categories, no outlier value in BMI
      print(dataFilteredCatNoOutlier)

      # Same as before, but without columns that, according to the correlation␣
    ↪study, seem to not influence the diagnosis
      print(dataDeletedColumns)

      # PCA done to all variables (so, PCA to the first dataset)
      print(resulting_pca_all)

      # PCA done to relevant variables (so, PCA to the second dataset)
      print(resulting_pca_deleted)
```

```
     ID  Sex  Age   BMI  …  Gingivorrhagia  Stress_Daily  PI  Diagnosis
0     1    1   56  26.9  …               0             4   1          0
1     2    1   61  21.2  …               0             4   1          2
2     3    1    8  14.7  …               0             3   1          1
3     4    0   22  21.1  …               0             1   0          1
4     5    1   23  19.1  …               0             4   0          1
..   …   …   …    …   …              …           …  ..        …
```

```
211  222    1   78  29.1  …              1             5   3          2
213  230    0   18  21.9  …              0             4   0          1
215  232    0   15  25.2  …              0             2   1          1
216  233    1   12  15.2  …              0             6   0          1
217  234    1   18  19.2  …              0            -1   0          1

[174 rows x 17 columns]
      ID  Age  Smoking  …  Gingivorrhagia  Stress_Daily  Diagnosis
0      1   56        1  …               0             4          0
1      2   61        1  …               0             4          2
2      3    8        0  …               0             3          1
3      4   22        0  …               0             1          1
4      5   23        0  …               0             4          1
..   …  …       …  …             …           …         …
211  222   78        1  …               1             5          2
213  230   18        0  …               0             4          1
215  232   15        0  …               0             2          1
216  233   12        0  …               0             6          1
217  234   18        0  …               0            -1          1

[174 rows x 12 columns]
        ID         1         2  …        10        11  Diagnosis
0      1.0  0.713320  0.278014  … -0.142313 -0.065457        0.0
1      2.0  1.011341  0.632104  …  0.526679 -0.226030        2.0
2      3.0  0.358891 -0.424921  … -0.069818 -0.172468        1.0
3      4.0 -0.274951  0.581475  … -0.125525 -0.022397        1.0
4      5.0  0.706854  0.095418  …  0.230889 -0.151533        1.0
..     …        …        …  …       …        …        …
169  222.0  0.907462  0.709892  …  0.345312 -0.116383        2.0
170  230.0 -0.168831  0.712684  …  0.172761  0.579968        1.0
171  232.0 -0.663394  0.046946  … -0.193069  0.253888        1.0
172  233.0  0.291425 -0.615028  … -0.086564  0.164135        1.0
173  234.0  0.223844 -0.613540  … -0.212626  0.423592        1.0

[174 rows x 13 columns]
        ID         1         2  …         6         7  Diagnosis
0      1.0  0.555497  0.636056  … -0.205755  0.235184        0.0
1      2.0  1.079077 -0.201345  …  0.666830 -0.123247        2.0
2      3.0 -0.162163 -0.216071  …  0.480505  0.561617        1.0
3      4.0  0.339510 -0.182685  …  0.050004 -0.069164        1.0
4      5.0  0.443376  0.530394  … -0.079144 -0.437269        1.0
..     …        …        …  …       …        …        …
169  222.0  1.050940  0.375344  … -0.117108 -0.460072        2.0
170  230.0  0.519756 -0.419882  …  0.025087 -0.227108        1.0
171  232.0 -0.345992 -0.398801  … -0.132261  0.123390        1.0
172  233.0 -0.382437  0.083096  … -0.120873 -0.196603        1.0
173  234.0 -0.447981  0.069139  … -0.290034 -0.121834        1.0
```

```
[174 rows x 9 columns]
```

As we can see, the dataset is highly cut down if we clear the rows which have a high impact on the model. Lets try How it goes with SVM Secondly, if I try removing the pregnant columnn as a whole, it lets us 161 values, so we use dataset_nulls_deleted_removed_pregnant to illustrate that data

```
[0]: # Creating a list for simply importing the 4 dataframes together, anywhere we␣
     ↪want.

     four_dataframes =␣
     ↪[dataFilteredCatNoOutlier,dataDeletedColumns,resulting_pca_all,resulting_pca_deleted]
```

1.5 Nimish's code

SVM Kernels: linear, polynomial, rbf, sigmoid

```
[0]: #Nimish's code for SVM using the four datasets mentioned above
     #Putting each of them through available kernels of SVM and finding the score of␣
     ↪each.
     def svm_scores(dataframes_array,kernel_name='linear'):
         from sklearn import svm
         for data in dataframes_array:
             i = data.copy()
             clf = svm.SVC(kernel=kernel_name)
             y = i[['Diagnosis']]
             x = i.drop(['ID','Diagnosis'],axis=1)
             LVOOfolds = KFold(n_splits=x.shape[0]-1)
             tenKfolds = KFold(n_splits=10)
             scores = cross_val_score(clf, x, y_label.to_numpy().ravel(),␣
     ↪cv=LVOOfolds)
             scores2 = cross_val_score(clf, x, y.to_numpy().ravel(), cv=tenKfolds)
             print('LVOOCV : ')
             print("Accuracy: %0.2f" % (scores.mean()))
             print('10 folds : ')
             print("Accuracy: %0.2f" % (scores2.mean()))

     #Nimish's code for SVM using the four datasets mentioned above
     #Putting each of them through available kernels of SVM and finding the score of␣
     ↪each.
     def deprecated_svm_scores(dataframes_array,kernel_name='linear'):
         from sklearn import svm
         for i in dataframes_array:
             clf = svm.SVC(kernel=kernel_name)
             y = i[['Diagnosis']]
             X = i.drop('Diagnosis',axis=1)
             clf.fit(X,y)
             print(clf.kernel,clf.score(X,y))
```

[0]:
```
svm_scores(four_dataframes)
print("---")
svm_scores(four_dataframes,"rbf")
print("---")
svm_scores(four_dataframes,"poly")
print("---")
svm_scores(four_dataframes,"sigmoid")
print("---")
```

```
LVOOCV :
Accuracy: 0.74
10 folds :
Accuracy: 0.74
LVOOCV :
Accuracy: 0.76
10 folds :
Accuracy: 0.76
LVOOCV :
Accuracy: 0.98
10 folds :
Accuracy: 0.98
LVOOCV :
Accuracy: 0.89
10 folds :
Accuracy: 0.86
---
LVOOCV :
Accuracy: 0.78
10 folds :
Accuracy: 0.79
LVOOCV :
Accuracy: 0.79
10 folds :
Accuracy: 0.79
LVOOCV :
Accuracy: 0.91
10 folds :
Accuracy: 0.90
LVOOCV :
Accuracy: 0.86
10 folds :
Accuracy: 0.84
---
LVOOCV :
Accuracy: 0.79
10 folds :
Accuracy: 0.78
```

```
LVOOCV :
Accuracy: 0.79
10 folds :
Accuracy: 0.79
LVOOCV :
Accuracy: 0.90
10 folds :
Accuracy: 0.89
LVOOCV :
Accuracy: 0.84
10 folds :
Accuracy: 0.82
---
LVOOCV :
Accuracy: 0.71
10 folds :
Accuracy: 0.71
LVOOCV :
Accuracy: 0.71
10 folds :
Accuracy: 0.71
LVOOCV :
Accuracy: 0.98
10 folds :
Accuracy: 0.98
LVOOCV :
Accuracy: 0.87
10 folds :
Accuracy: 0.88
---
```

As per the above observation, for SVM's linear kernel on Dataframe "PCA done to all variables (so, PCA to the first dataset)" gets us a 98% Accuracy, which is incredible.

1.6 Ilya's Code

We use KNN as a benchmark classifier with the different sub-datasets we have extracted from the original data source.

[0]:
```
def applyKNN(dataFrame, columnsToUse, numberOfNeighbours):

    # load the data
    dataFeatures = pd.DataFrame(dataFrame, columns=columnsToUse)
    dataTarget = pd.DataFrame(dataFrame, columns=['Diagnosis'])

    # splitting
    # X_train, X_test, y_train, y_test = train_test_split(
    #     dataFeatures, dataTarget, test_size=0.20)
    # modelling
    knn = neighbors.KNeighborsClassifier(n_neighbors=numberOfNeighbours)
    # knn.fit(X_train, y_train.to_numpy().ravel())
    # predictions = knn.predict(X_test)

    # scores
    # train_score = knn.score(X_train, y_train)
    # test_score = knn.score(X_test, y_test)
    # print('Train Acc: %.3f' % train_score)
    # print('Test Acc: %.3f' % test_score)

    #CV
    LVOOfolds = KFold(n_splits=dataFeatures.shape[0]-1)
    tenKfolds = KFold(n_splits=10)
    scores = cross_val_score(knn, dataFeatures, dataTarget.to_numpy().ravel(),␣
 ↪cv=LVOOfolds)
    scores2 = cross_val_score(knn, dataFeatures, dataTarget.to_numpy().ravel(),␣
 ↪cv=tenKfolds)
    print('LVOOCV : ')
    print("Accuracy: %0.2f" % (scores.mean()))
    print('10 folds : ')
    print("Accuracy: %0.2f" % (scores2.mean()))

    #The line / model
    # plt.scatter(y_test, predictions)
    # plt.xlabel("True Values")
    # plt.ylabel("Predictions")
    # plt.show()
```

[0]:
```
# #All the dataset with converted NAN's values into numeric values
# dataFrame = convertWithCategories('data')
# columnsToUse = getAllColumnsButID(dataFrame)
# result = applyKNN(dataFrame, columnsToUse, 6)

# #All rows containing nulls are deleted (58 lines)
# dataFrame = convertDeleteNulls('data')
# columnsToUse = getAllColumnsButID(dataFrame)
# result = applyKNN(dataFrame, columnsToUse, 6)

# #All rows deleted after deleting the pregnant column
# dataFrame = convertDeleteNullsNoPregnant('data')
# columnsToUse = getAllColumnsButID(dataFrame)
# result = applyKNN(dataFrame, columnsToUse, 6)


for i in four_dataframes:
```

```
applyKNN(i, getAllColumnsButID(i), 6)
```

```
LVOOCV :
Accuracy: 0.79
10 folds :
Accuracy: 0.78
LVOOCV :
Accuracy: 0.77
10 folds :
Accuracy: 0.77
LVOOCV :
Accuracy: 0.97
10 folds :
Accuracy: 0.97
LVOOCV :
Accuracy: 0.99
10 folds :
Accuracy: 0.99
```

[0]:

```

```