Project: Pima Indians Diabetes Medical Records - Using Data Analysis and Visual Tools to Predict Diabetes

BIOF 309

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What is our project question?

Are we able to determine which factors affect diabetes in Pima Indians population?

Context

Where did the data come from? National Institute of Diabetes and Digestive and Kidney Diseases.

Diabetes information:

What is diabetes?: If body does not produce or properly use insulin, it is released out through urination. This is called diabetes.

How many Americans have diabetes?

20.8 million children and adults (7% of population) (American Diabetes Association, 2007)

Pima Indian Diabetes (PID) dataset contains what?

768 records describing female patients of Pima Indian heritage which are 21 years old living in Phoenix, Arizona, USA (UCI-Machine-Learning Repository, 2007)

What do we want to do with this dataset?

To diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements

What are some contraints with working with this dataset?

Several constraints were placed on the selection of these instances from a larger database. All patients here are females at least 21 years old of Pima Indian heritage.

What medical predictors are included in this dataset?

Several medical predictor variables such as the number of pregnancies the patient has had, their BMI, insulin level, age, etc.

Is there a target variable?

Yes, one target variable, Outcome.

Reference:

kaggle datasets download -d uciml/pima-indians-diabetes-database https://www.kaggle.com/uciml/pima-indians-diabetes-database/downloads/pima-indians-diabetes-database.zip/1)
indians-diabetes-database/downloads/pima-indians-diabetes-database.zip/1)

Acknowledgements Smith, J.W., Everhart, J.E., Dickson, W.C., Knowler, W.C., & Johannes, R.S. (1988). Using the ADAP learning algorithm to forecast the onset of diabetes mellitus. In Proceedings of the Symposium on Computer Applications and Medical Care (pp. 261--265). IEEE Computer Society Press.

Inspiration:

Can you build a machine learning model to accurately predict whether or not the patients in the dataset have

```
In [1]: import pandas as pd
```

Read input data

Read the input CSV file as a pandas dataframe

```
In [9]: filename = "Desktop\diabetes.csv"
         df = pd.read csv(filename, sep=',', encoding='utf-8', header=0)
In [72]: # Assigning column names and mapping the meta information for each attribute
         cols = df.columns = ['n pregnant', 'glu conc', 'bp', 'tst', 'insulin', 'bmi',
         'dpf', 'age', 'diabetes?']
         metainfo = {'n_pregnant': 'Number of times pregnant',
                               'glu conc': 'Plasma glucose concentration a 2 hours in an
         oral glucose tolerance test',
                               'bp': 'Diastolic blood pressure (mm Hg)',
                               'tst': 'Triceps skin fold thickness (mm)'.
                               'insulin': '2-Hour serum insulin (mu U/ml)',
                               'bmi': 'Body mass index (weight in kg/(height in m)^2)',
                               'dpf': 'Diabetes pedigree function',
                               'age': 'Age (years)',
                               'diabetes?': 'Class variable (0 or 1)'}
         df.head()
```

Out[72]:

| | n_pregnant | glu_conc | bp | tst | insulin | bmi | dpf | age | diabetes? |
|---|------------|----------|----|-----|---------|------|-------|-----|-----------|
| 0 | 6 | 148 | 72 | 35 | 0 | 33.6 | 0.627 | 50 | 1 |
| 1 | 1 | 85 | 66 | 29 | 0 | 26.6 | 0.351 | 31 | 0 |
| 2 | 8 | 183 | 64 | 0 | 0 | 23.3 | 0.672 | 32 | 1 |
| 3 | 1 | 89 | 66 | 23 | 94 | 28.1 | 0.167 | 21 | 0 |
| 4 | 0 | 137 | 40 | 35 | 168 | 43.1 | 2.288 | 33 | 1 |

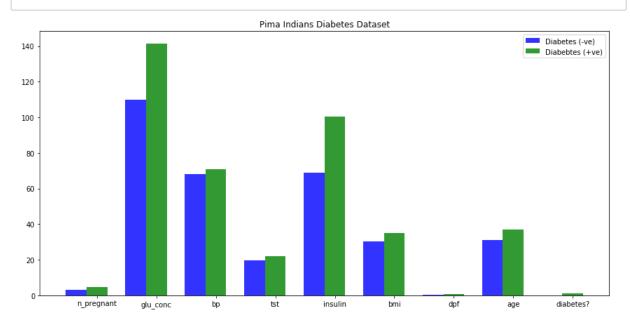
```
In [71]: # Describe the dataset
df_temp = df.drop(labels = 'diabetes?', axis=1)
df_temp.describe()
```

Out[71]:

| | n_pregnant | glu_conc | bp | tst | insulin | bmi | dpf | |
|-------|------------|------------|------------|------------|------------|------------|------------|-----|
| count | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768 |
| mean | 3.845052 | 120.894531 | 69.105469 | 20.536458 | 79.799479 | 31.992578 | 0.471876 | 33 |
| std | 3.369578 | 31.972618 | 19.355807 | 15.952218 | 115.244002 | 7.884160 | 0.331329 | 11 |
| min | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.078000 | 21 |
| 25% | 1.000000 | 99.000000 | 62.000000 | 0.000000 | 0.000000 | 27.300000 | 0.243750 | 24 |
| 50% | 3.000000 | 117.000000 | 72.000000 | 23.000000 | 30.500000 | 32.000000 | 0.372500 | 29 |
| 75% | 6.000000 | 140.250000 | 80.000000 | 32.000000 | 127.250000 | 36.600000 | 0.626250 | 41 |
| max | 17.000000 | 199.000000 | 122.000000 | 99.000000 | 846.000000 | 67.100000 | 2.420000 | 81 |
| | | | | | | | | |

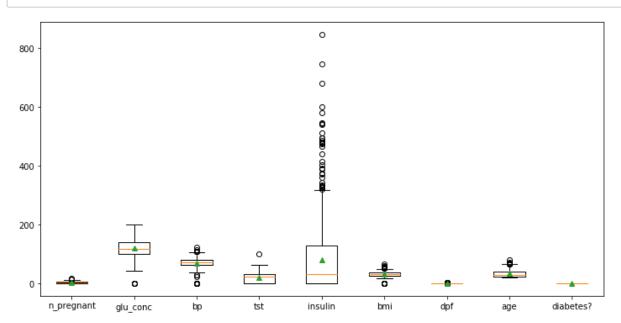
In [62]: import numpy as np import matplotlib.pyplot as plt def bar plot(df): plt.rcParams['figure.figsize'] = 12, 6 df_0 = df[df['diabetes?'] == 0] df_1 = df[df['diabetes?'] == 1] mean 0 = df 0.mean() $mean_1 = df_1.mean()$ list 0 = [] list 1 = [] for col in df.columns: list 0.append(mean 0[col]) list 1.append(mean 1[col]) index = np.arange(len(df.columns)) bar width = 0.35opacity = 0.8plt.bar(index, list 0, bar width, alpha=opacity, color='b', label='Diabetes (-ve)') plt.bar(index + bar_width, list_1, bar_width, alpha=opacity, color='g', label='Diabebtes (+ve)') plt.title('Pima Indians Diabetes Dataset') plt.xticks(index + bar_width, tuple(df.columns)) plt.legend() plt.tight_layout() plt.show()

In [63]: bar_plot(df)



```
In [64]: def box_plot(df, cols):
    plt.rcParams['figure.figsize'] = 12, 6
    data = np.array(df.values.tolist())
    plt.boxplot(data, labels=cols, showmeans=True)
    plt.show()
```

In [65]: box_plot(df, df.columns)



Normalize our data using pandas in a very simple and intuitive way i.e. (x-mean)/(max-min)

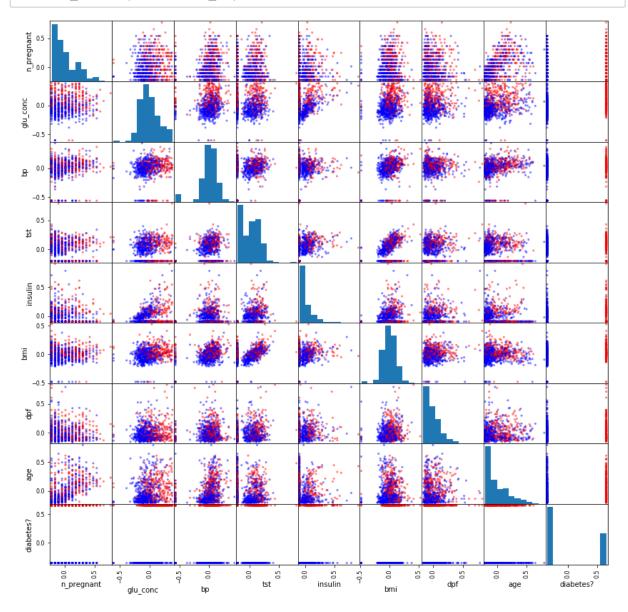
```
In [83]: def normalize(df):
    df_norm = (df - df.mean()) / (df.max() - df.min())
    return df_norm
    from pandas.plotting import scatter_matrix as pplotsm
    def scatter_matrix(df):
        plt.rcParams["figure.figsize"] = (14, 14)
        colors = list('r' if i >= 0.5 else 'b' for i in df['diabetes?'])
        pplotsm(df, color=colors)
        plt.show()
```

In [84]: normalized_df.head()

Out[84]:

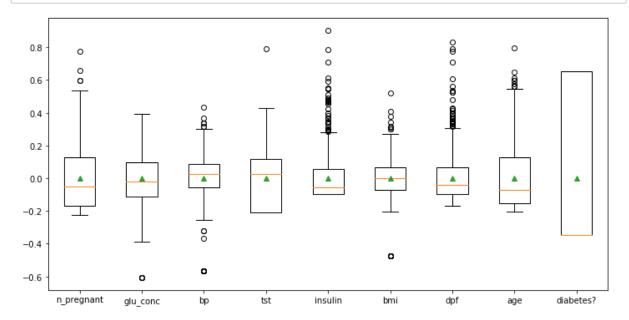
| | n_pregnant | glu_conc | bp | tst | insulin | bmi | dpf | age | diabe |
|---|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--------|
| 0 | 0.126762 | 0.136208 | 0.023726 | 0.146096 | -0.094326 | 0.023956 | 0.066236 | 0.279319 | 0.65 |
| 1 | -0.167356 | -0.180375 | -0.025455 | 0.085490 | -0.094326 | -0.080366 | -0.051612 | -0.037348 | -0.348 |
| 2 | 0.244409 | 0.312088 | -0.041848 | -0.207439 | -0.094326 | -0.129547 | 0.085450 | -0.020681 | 0.65 |
| 3 | -0.167356 | -0.160274 | -0.025455 | 0.024884 | 0.016785 | -0.058012 | -0.130178 | -0.204015 | -0.348 |
| 4 | -0.226180 | 0.080932 | -0.238569 | 0.146096 | 0.104256 | 0.165535 | 0.775458 | -0.004015 | 0.65 |
| | | | | | | | | | |

In [85]: normalized_df = normalize(df)
 scatter_matrix(normalized_df)



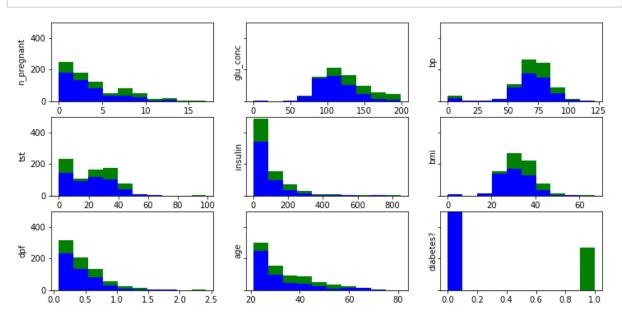
In []: #visualize the bivariate relationship between each variable using a scatter pl
 ot.
 #normalized data for plotting the scattered matrix was used
 #Both are overlapping with each other

In [66]: box_plot(normalized_df, df.columns)



```
In [67]: def stacked_histogram(df, cols):
    fig, axes = plt.subplots(3, 3, sharey=True) # Because I have 9 variables i
    n the dataset
    plt.rcParams['figure.figsize'] = 14, 14
    df_1 = df[df['diabetes?'] == 1]
    df_2 = df[df['diabetes?'] == 0]
    col_index = 0
    for row in axes:
        for col in row:
            col.hist([df_2[cols[col_index]], df_1[cols[col_index]]], bins=10,
    stacked=True, color=['b', 'g'])
            col.set_ylabel(cols[col_index])
            col_index += 1
            plt.show()
```

In [68]: stacked_histogram(df, df.columns)



In []: #Green bars shows the women with positive diabetes test and blue bars shows th e women with negative diabetes test.

#In glu_conc we see that diabetes are diagnosed to those women having high glu cose concentration levels.

#Similarly, bp (blood pressure diastolic) histogram shows that positive diabet es was found in women with high bp.

#Although there were samples where high bp women had a negative test but posit ive diabetes was found only with high bp.

#Insulin histogram shows that women with lower insulin levels have a positive diabetes test.