Universidad Tecnológica de Bolívar

Programa de Ingeniería de Sistemas y Computación

Parcial 2do Corte

Prediction of Susceptibility to Suffer Diabetes

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INTELIGENCIA ARTIFICIAL (ISCO-A06A)

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Parcial 2do Corte | | Inteligencia Artificial ISCO-A06A

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[1]:
```
#Se vincula una cuenta de google drive para importar los dataset

# Mount your google drive in google colab
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

1 2. Data Understanding

Number of Instances: 614 (train), 5 (test)

Number of Attributes: 8 plus class

Columns Description:

1. Number of times pregnant
2. Plasma glucose concentration 2 hours in an oral glucose tolerance test
3. Diastolic blood pressure (mm Hg)
4. Triceps skin fold thickness (mm)
5. 2-Hour serum insulin (mu U/ml)
6. Body mass index (weight in kg/(height in m)^2)
7. Diabetes pedigree function
8. Age (years)
9. Class variable (0 or 1)

Class Distribution: (class value 1 is interpreted as "tested positive for diabetes")

[2]:
```
import pandas as pd
```

[3]:
```
#import train and test splits

df_train = pd.read_csv("/content/drive/MyDrive/parcial2/train_diabetes.csv")
df_test = pd.read_csv("/content/drive/MyDrive/parcial2/test_diabetes.csv")
```

[4]:
```
df_train.head()
```

[4]:
```
   p_id  no_times_pregnant  glucose_concentration  blood_pressure  \
0   316                  2                    112              68
```

```
1    25                 11                    143               94
2   710                  2                     93               64
3   658                  1                    120               80
4   542                  3                    128               72

   skin_fold_thickness  serum_insulin   bmi  diabetes pedigree  age  diabetes
0                   22             94  34.1              0.315   26         0
1                   33            146  36.6              0.254   51         1
2                   32            160  38.0              0.674   23         1
3                   48            200  38.9              1.162   41         0
4                   25            190  32.4              0.549   27         1
```

[5]:
```
#evaluating the equality of the data
df_train.info()

#There are not missing values
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 614 entries, 0 to 613
Data columns (total 10 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   p_id                    614 non-null    int64
 1   no_times_pregnant       614 non-null    int64
 2   glucose_concentration  614 non-null    int64
 3   blood_pressure          614 non-null    int64
 4   skin_fold_thickness     614 non-null    int64
 5   serum_insulin           614 non-null    int64
 6   bmi                     614 non-null    float64
 7   diabetes pedigree       614 non-null    float64
 8   age                     614 non-null    int64
 9   diabetes                614 non-null    int64
dtypes: float64(2), int64(8)
memory usage: 48.1 KB
```

[6]:
```
#We can also check the uniqueness of each column in the DataFrame

for col in df_train.columns:
  print(col + ": ", len(df_train[col].unique()))
```

```
p_id:  614
no_times_pregnant:  17
glucose_concentration:  127
blood_pressure:  44
skin_fold_thickness:  50
serum_insulin:  163
bmi:  237
diabetes pedigree:  439
```

```
age:  52
diabetes:  2
```

[7]:
```
#Check statistics of the data

df_train.describe()
```

[7]:
```
             p_id  no_times_pregnant  glucose_concentration  blood_pressure  \
count  614.000000         614.000000             614.000000      614.000000
mean   385.773616           3.853420             120.542345       68.765472
std    223.603024           3.358126              31.252286       19.914836
min      1.000000           0.000000               0.000000        0.000000
25%    191.250000           1.000000              99.000000       62.000000
50%    387.000000           3.000000             117.000000       72.000000
75%    572.750000           6.000000             139.000000       80.000000
max    768.000000          17.000000             197.000000      114.000000

       skin_fold_thickness  serum_insulin         bmi  diabetes pedigree  \
count           614.000000     614.000000  614.000000         614.000000
mean             20.244300      79.355049   31.909935           0.466342
std              15.886083     117.709950    8.007699           0.331090
min               0.000000       0.000000    0.000000           0.078000
25%               0.000000       0.000000   27.300000           0.240250
50%              23.000000      17.000000   32.000000           0.361000
75%              32.000000     126.000000   36.600000           0.613500
max              63.000000     846.000000   59.400000           2.420000

              age    diabetes
count  614.000000  614.000000
mean    33.325733    0.348534
std     11.929569    0.476895
min     21.000000    0.000000
25%     24.000000    0.000000
50%     29.000000    0.000000
75%     41.000000    1.000000
max     81.000000    1.000000
```

[8]:
```
df_train.dtypes
```

[8]:
```
p_id                       int64
no_times_pregnant          int64
glucose_concentration      int64
blood_pressure             int64
skin_fold_thickness        int64
serum_insulin              int64
bmi                      float64
diabetes pedigree        float64
age                        int64
```

```
diabetes                           int64
dtype: object
```

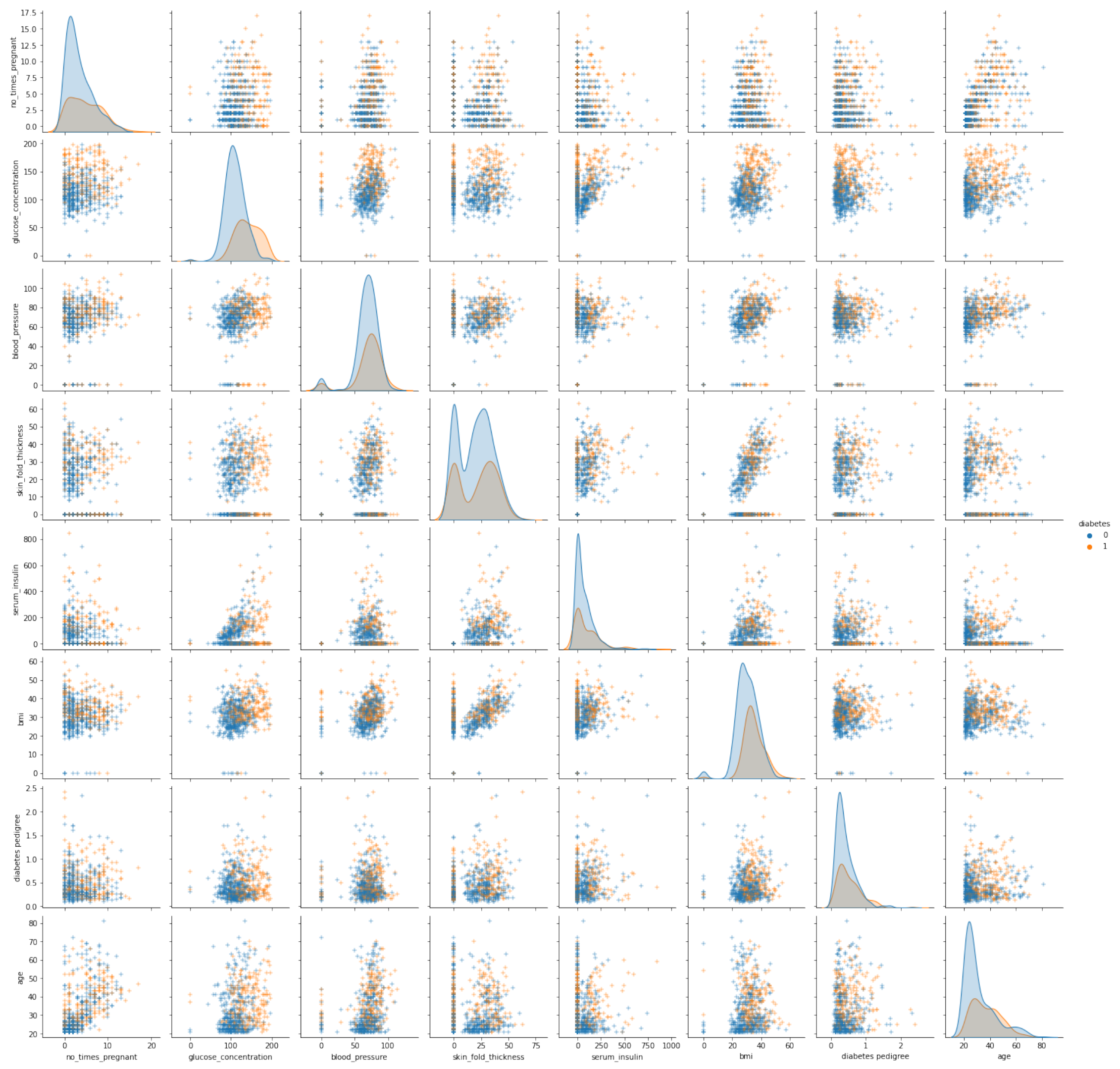
[9]:
```
#Classs distribution

df_train['diabetes'].value_counts()
```

[9]:
```
0    400
1    214
Name: diabetes, dtype: int64
```

1.1 Visualize Data

[10]:
```
from matplotlib import pyplot as plt
import seaborn as sns
```

[12]:
```
tmp = df_train.drop('p_id', axis=1)
g = sns.pairplot(tmp, hue='diabetes', markers='+')
plt.show()
```



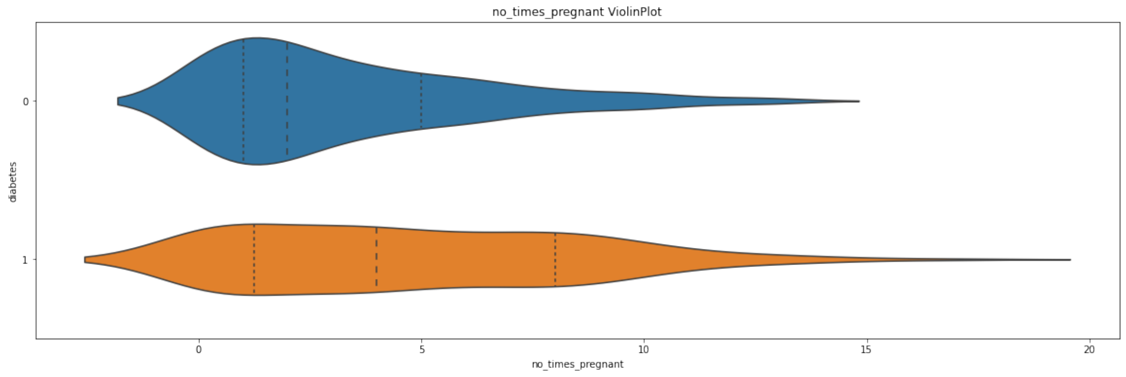
Assumption #2 “Y is distributed normally at each value of X” is true for this data

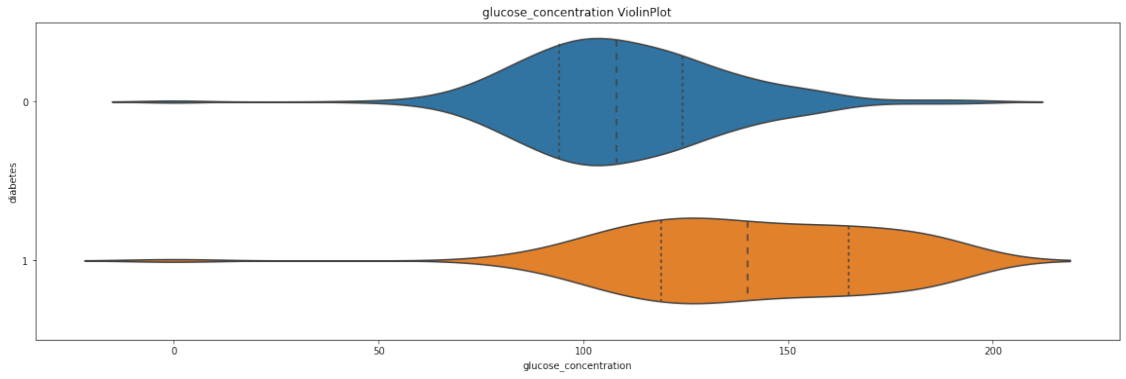
```
[13]: list(df_train.keys())
```

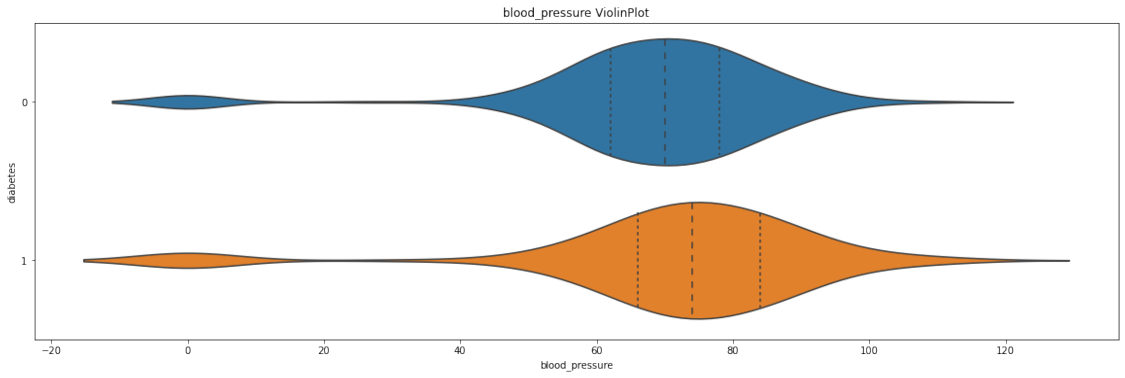
```
[13]: ['p_id',
       'no_times_pregnant',
       'glucose_concentration',
       'blood_pressure',
       'skin_fold_thickness',
       'serum_insulin',
       'bmi',
       'diabetes pedigree',
       'age',
       'diabetes']
```

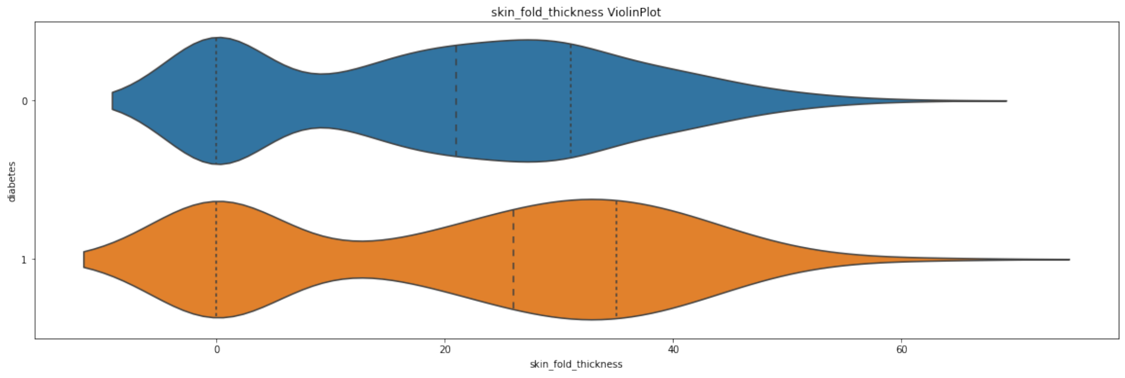
[14]:
```python
#Converts 0, 1 diabetes classes to str for better visualization
df_temp = df_train.copy()
df_temp['diabetes'] = df_temp['diabetes'].apply(str)
```

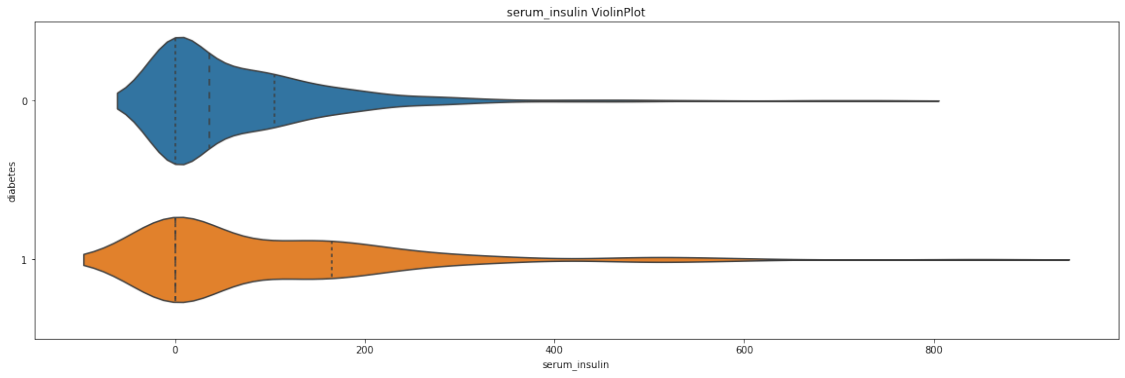
[15]:
```python
#Violin plot
X_col_names = list(df_train.keys())[1:-1]

for col_name in range(len(X_col_names)):
  plt.figure(figsize=(20,6))
  sns.violinplot(x=X_col_names[col_name], y='diabetes', data=df_temp,␣
 ↪inner='quartile').set_title(X_col_names[col_name]+" ViolinPlot")
  plt.show()
```

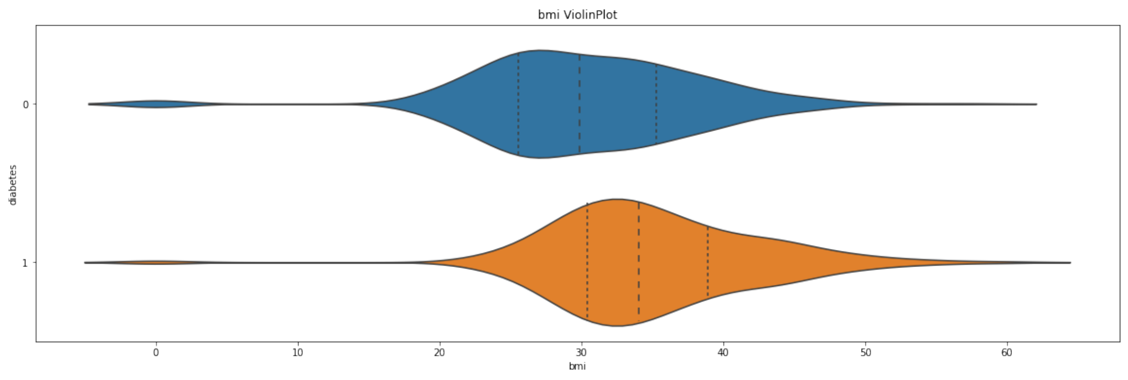


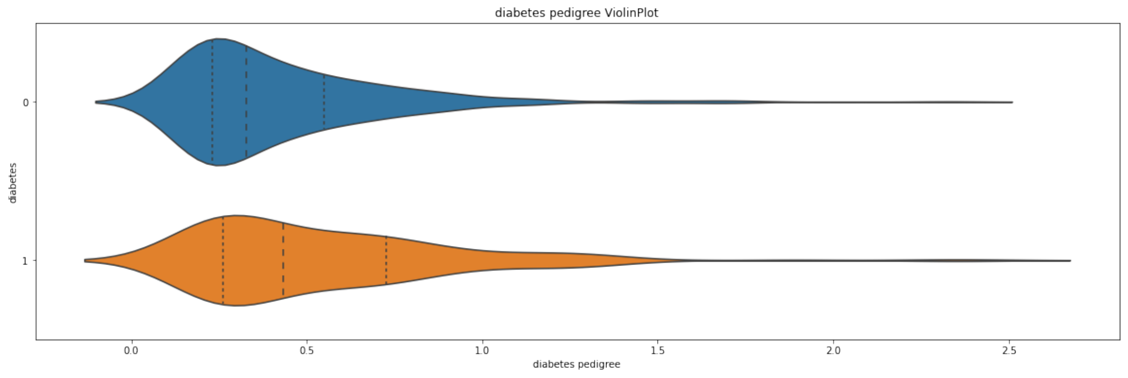


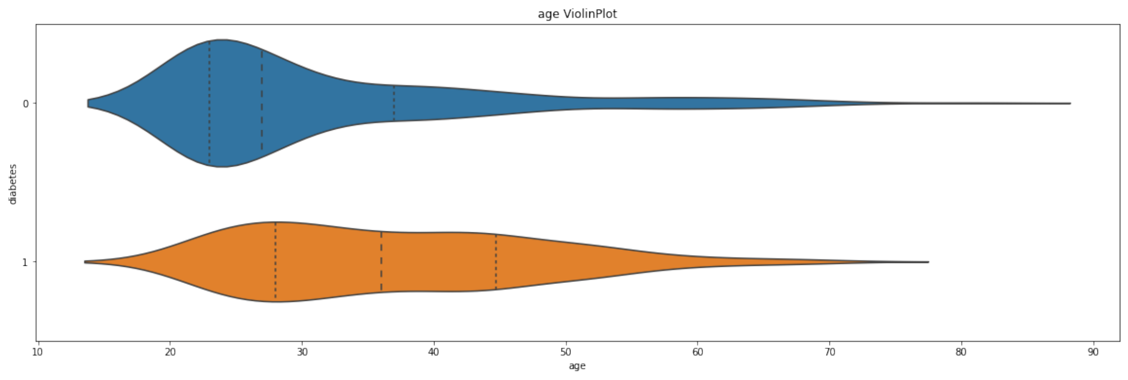

blood_pressure ViolinPlot
diabetes
0
1
−20
0
20
40
60
80
100
120
blood_pressure


skin_fold_thickness ViolinPlot
diabetes
0
1
0
20
40
60
skin_fold_thickness


serum_insulin ViolinPlot
diabetes
0
1
0
200
400
600
800
serum_insulin



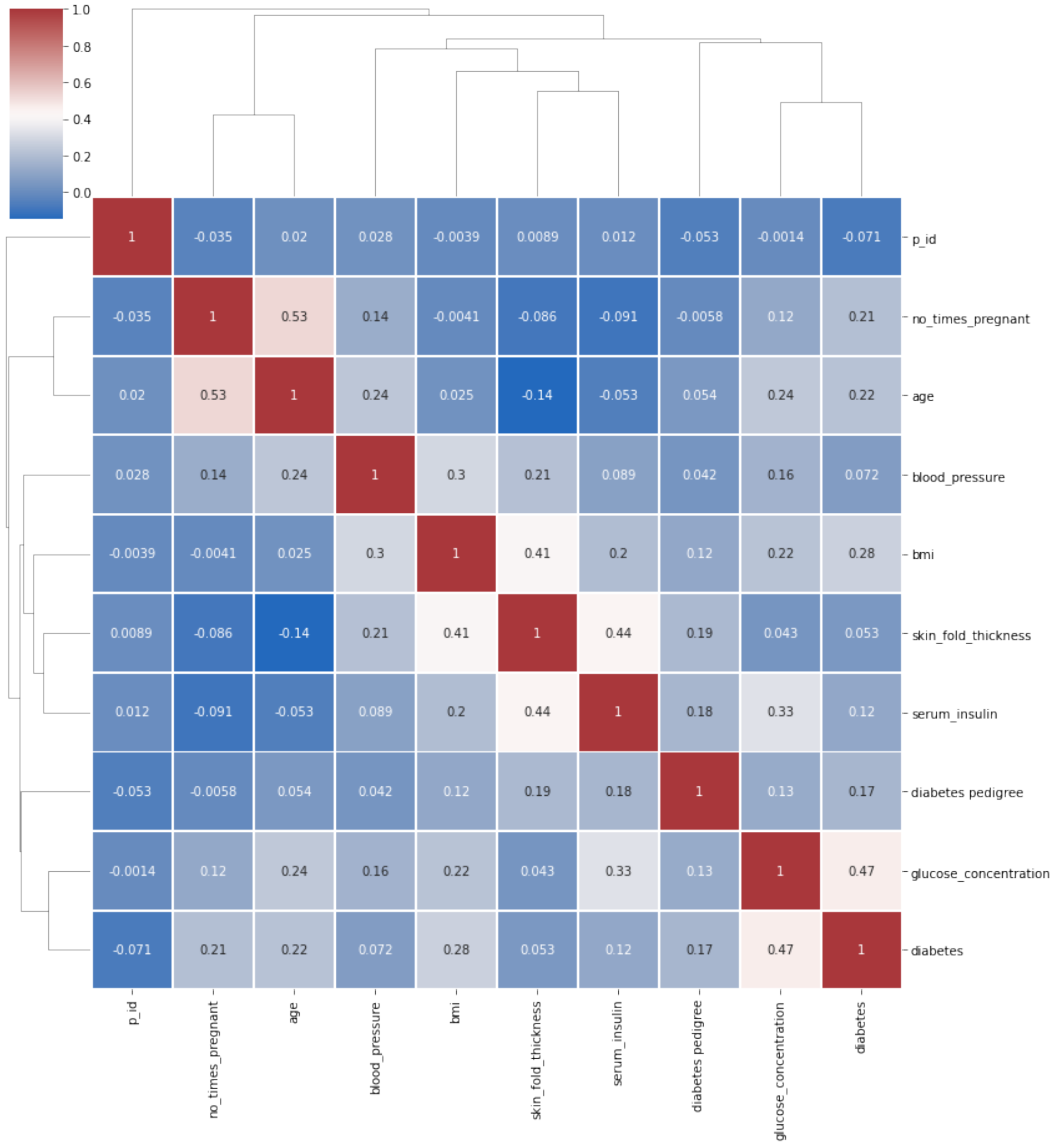




It does not seems that any attribute has a strong influence on the determination of diabetes class.

- **Assumption #3 "The variance of Y at every value of X is the same (homogeneity of variances)" seems to be true for this data**
- **Assumption #4 "The observations are independent" is true for this data**

[18]:
```
#Correlation between features

sns.clustermap(df_train.corr(), cmap = "vlag", dendrogram_ratio = (0.1, 0.2),␣
↪annot = True, linewidths = .8, figsize = (12,13))
plt.show()
```



	p_id	no_times_pregnant	age	blood_pressure	bmi	skin_fold_thickness	serum_insulin	diabetes pedigree	glucose_concentration	diabetes
p_id	1	-0.035	0.02	0.028	-0.0039	0.0089	0.012	-0.053	-0.0014	-0.071
no_times_pregnant	-0.035	1	0.53	0.14	-0.0041	-0.086	-0.091	-0.0058	0.12	0.21
age	0.02	0.53	1	0.24	0.025	-0.14	-0.053	0.054	0.24	0.22
blood_pressure	0.028	0.14	0.24	1	0.3	0.21	0.089	0.042	0.16	0.072
bmi	-0.0039	-0.0041	0.025	0.3	1	0.41	0.2	0.12	0.22	0.28
skin_fold_thickness	0.0089	-0.086	-0.14	0.21	0.41	1	0.44	0.19	0.043	0.053
serum_insulin	0.012	-0.091	-0.053	0.089	0.2	0.44	1	0.18	0.33	0.12
diabetes pedigree	-0.053	-0.0058	0.054	0.042	0.12	0.19	0.18	1	0.13	0.17
glucose_concentration	-0.0014	0.12	0.24	0.16	0.22	0.043	0.33	0.13	1	0.47
diabetes	-0.071	0.21	0.22	0.072	0.28	0.053	0.12	0.17	0.47	1

2 3. Data Preparation

[20]:
```
#Check data types

df_train.dtypes
```

[20]:
```
p_id                          int64
no_times_pregnant             int64
glucose_concentration         int64
blood_pressure                int64
skin_fold_thickness           int64
serum_insulin                 int64
bmi                         float64
diabetes pedigree           float64
age                           int64
diabetes                      int64
dtype: object
```

[21]:
```
df_test.dtypes
```

[21]:
```
p_id                          int64
no_times_pregnant             int64
glucose_concentration         int64
blood_pressure                int64
skin_fold_thickness           int64
serum_insulin                 int64
bmi                         float64
diabetes pedigree           float64
age                           int64
dtype: object
```

Both dataframes has correct dtype for values. There are not missing values.

Dataset does not contain categorical features, son one-hot encoding is not necessary.

3 4. Modeling

Note: Cells commented must be ignored.

[39]:
```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import MinMaxScaler
```

[177]:
```
#Define independent and dependent variable:

X = df_train.drop(['diabetes', 'p_id'], axis=1)
y = df_train['diabetes']
```

3.1 Scaling Features

Scaling numeric features ensures that no particular feature has a disproportionate impact on the model's loss. Optimization algorithms also work better in practice with smaller numbers.

[194]:
```
X.describe()
```

[194]:
```
       no_times_pregnant  glucose_concentration  blood_pressure  \
count         614.000000             614.000000      614.000000
mean            3.853420             120.542345       68.765472
std             3.358126              31.252286       19.914836
min             0.000000               0.000000        0.000000
25%             1.000000              99.000000       62.000000
50%             3.000000             117.000000       72.000000
75%             6.000000             139.000000       80.000000
max            17.000000             197.000000      114.000000

       skin_fold_thickness  serum_insulin         bmi  diabetes pedigree  \
count           614.000000     614.000000  614.000000         614.000000
mean             20.244300      79.355049   31.909935           0.466342
std              15.886083     117.709950    8.007699           0.331090
min               0.000000       0.000000    0.000000           0.078000
25%               0.000000       0.000000   27.300000           0.240250
50%              23.000000      17.000000   32.000000           0.361000
75%              32.000000     126.000000   36.600000           0.613500
max              63.000000     846.000000   59.400000           2.420000

              age
count  614.000000
mean    33.325733
std     11.929569
min     21.000000
25%     24.000000
50%     29.000000
75%     41.000000
max     81.000000
```

3.2 Comparing

[195]:
```
# Scale to [0, 1]
max_ = X.max(axis=0)
min_ = X.min(axis=0)
X = (X - min_) / (max_ - min_)
```

[196]:
```
X.describe()
```

[196]:
```
       no_times_pregnant  glucose_concentration  blood_pressure  \
count         614.000000             614.000000      614.000000
```

```
mean          0.226672             0.611890        0.603206
std           0.197537             0.158641        0.174692
min           0.000000             0.000000        0.000000
25%           0.058824             0.502538        0.543860
50%           0.176471             0.593909        0.631579
75%           0.352941             0.705584        0.701754
max           1.000000             1.000000        1.000000

       skin_fold_thickness  serum_insulin         bmi  diabetes pedigree  \
count           614.000000     614.000000  614.000000         614.000000
mean              0.321338       0.093800    0.537204           0.165816
std               0.252160       0.139137    0.134810           0.141371
min               0.000000       0.000000    0.000000           0.000000
25%               0.000000       0.000000    0.459596           0.069278
50%               0.365079       0.020095    0.538721           0.120837
75%               0.507937       0.148936    0.616162           0.228651
max               1.000000       1.000000    1.000000           1.000000

              age
count  614.000000
mean     0.205429
std      0.198826
min      0.000000
25%      0.050000
50%      0.133333
75%      0.333333
max      1.000000
```

3.3 Import Dependencies

[214]:
```
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression, LinearRegression
from sklearn.ensemble import RandomForestRegressor, RandomForestClassifier

from sklearn.model_selection import cross_val_score

from sklearn.metrics import mean_squared_error, mean_squared_log_error,␣
 ↪accuracy_score
```

[256]:
```
linreg_pipeline = Pipeline(steps=[('model', LinearRegression())])
```

[257]:
```
logreg_pipeline = Pipeline(steps=[('model',␣
 ↪LogisticRegression(solver='liblinear'))])
```

[278]:
```
rf_pipeline = Pipeline(steps=[('model', RandomForestClassifier(n_estimators=200,␣
 ↪random_state=64))])
```

4 5. Evaluating Models (k-Fold Cross Validation)

4.1 Mean Squared Error (MSE)

Linear Regression

[270]:
```
# Multiply by -1 since sklearn calculates *negative* MSE
scores = -1 * cross_val_score(linreg_pipeline, X, y,
                              cv=10,
                              scoring='neg_mean_squared_error')

print("MSE scores:\n", scores)
print("\n Average MSE score (across experiments):")
print(scores.mean())
```

```
MSE scores:
 [0.1582769  0.15118501 0.13235929 0.17008284 0.17367299 0.16595435
 0.17022733 0.161198   0.18887061 0.18736717]

 Average MSE score (across experiments):
0.16591944838299763
```

Logistic Regresion

[260]:
```
# Multiply by -1 since sklearn calculates *negative* MSE
scores = -1 * cross_val_score(logreg_pipeline, X, y,
                              cv=10,
                              scoring='neg_mean_squared_log_error')

print("MLSE scores:\n", scores)
print("\n Average MLSE score (across experiments):")
print(scores.mean())
```

```
MLSE scores:
 [0.10074015 0.10074015 0.08524166 0.12398787 0.12602046 0.08663907
 0.14177302 0.11814418 0.13389674 0.10239163]

 Average MLSE score (across experiments):
0.11195749369807266
```

Random Forest for classification

[261]:
```
# Multiply by -1 since sklearn calculates *negative* MSE
scores = -1 * cross_val_score(rf_pipeline, X, y,
                              cv=10,
                              scoring='neg_mean_squared_log_error')

print("MLSE scores:\n", scores)
print("\n Average MLSE score (across experiments):")
print(scores.mean())
```

```
MLSE scores:
 [0.11623863 0.12398787 0.07749242 0.10074015 0.10239163 0.09451535
 0.10239163 0.09451535 0.12602046 0.11814418]

 Average MLSE score (across experiments):
0.10564376688904713
```

The problem addressed is of the classification type. Therefore, a linear regression is not the right approach. To solve classification problems, models such as Logistic Regression or Random Forest for Classification are used. We will now compare the last two with the metrics corresponding to classification problems.

4.2 Accuracy

Logistic Regresion

[275]:
```
scores = cross_val_score(logreg_pipeline, X, y,
                              cv=10,
                              scoring='accuracy')

print("Accuracy scores:\n", scores)
print("\n Average Accuracy score (across experiments):")
print(scores.mean())
```

```
Accuracy scores:
 [0.79032258 0.79032258 0.82258065 0.74193548 0.73770492 0.81967213
 0.70491803 0.75409836 0.72131148 0.78688525]

 Average Accuracy score (across experiments):
0.7669751454257007
```

Random Forest for classification

[279]:
```
scores = cross_val_score(rf_pipeline, X, y,
                              cv=10,
                              scoring='accuracy')

print("Accuracy scores:\n", scores)
print("\n Average Accuracy score (across experiments):")
print(scores.mean())
```

```
Accuracy scores:
 [0.74193548 0.74193548 0.83870968 0.80645161 0.7704918  0.80327869
 0.78688525 0.83606557 0.73770492 0.78688525]

 Average Accuracy score (across experiments):
0.7850343733474352
```

4.3 Logaritmic Loss

Logistic Regression

```
[264]: scores = -1 * cross_val_score(logreg_pipeline, X, y,
                                     cv=10,
                                     scoring='neg_log_loss')

       print("Logarithmic Loss scores:\n", scores)
       print("\n Average Logarithmic Loss score (across experiments):")
       print(scores.mean())
```

```
Logarithmic Loss scores:
 [0.53029444 0.49533375 0.48809391 0.52422738 0.55542863 0.44782837
 0.52346336 0.50469808 0.60778733 0.4723959 ]

 Average Logarithmic Loss score (across experiments):
0.5149551168821109
```

Random Forest for classification

```
[265]: scores = -1 * cross_val_score(rf_pipeline, X, y,
                                     cv=10,
                                     scoring='neg_log_loss')

       print("Logarithmic Loss scores:\n", scores)
       print("\n Average Logarithmic Loss score (across experiments):")
       print(scores.mean())
```

```
Logarithmic Loss scores:
 [0.53152699 0.51647937 0.44047989 0.45198319 0.49193008 0.4644009
 0.46463281 0.40011293 0.52648169 0.4149656 ]

 Average Logarithmic Loss score (across experiments):
0.47029934461234896
```

4.4 F1 Score

Logistic Regression

```
[266]: scores = cross_val_score(logreg_pipeline, X, y,
                                cv=10,
                                scoring='f1')

       print("F1 scores:\n", scores)
       print("\n Average F1 score (across experiments):")
       print(scores.mean())
```

```
F1 scores:
 [0.62857143 0.60606061 0.7027027  0.55555556 0.5        0.73170732
 0.4        0.57142857 0.51428571 0.60606061]

 Average F1 score (across experiments):
0.5816372501738356
```

Random Forest for classification

[267]:
```
scores = cross_val_score(rf_pipeline, X, y,
                              cv=10,
                              scoring='f1')

print("F1 scores:\n", scores)
print("\n Average F1 score (across experiments):")
print(scores.mean())
```

```
F1 scores:
 [0.63414634 0.52941176 0.73684211 0.66666667 0.66666667 0.72727273
 0.62857143 0.7        0.6        0.59459459]

 Average F1 score (across experiments):
0.6484172295204538
```

Random forest outperform logistic regresion with default hyperparameters.

5 6. Fitting and Evaluating Models with df_test

[305]:
```
from sklearn.metrics import confusion_matrix
```

[295]:
```
X_full = df_train.drop(['diabetes', 'p_id'], axis=1)
y_full = df_train['diabetes']

# Scale to [0, 1]
max_ = df_train.drop(['diabetes', 'p_id'], axis=1).max(axis=0)
min_ = df_train.drop(['diabetes', 'p_id'], axis=1).min(axis=0)
X_full = (X_full - min_) / (max_ - min_)

#split data into train and validation sets
X_train, X_valid, y_train, y_valid = train_test_split(X_full, y_full,␣
 ↪test_size=0.3, random_state=64)
```

[296]:
```
print(X_train.shape, X_valid.shape, y_train.shape, y_valid.shape)
```

```
(429, 8) (185, 8) (429,) (185,)
```

[301]:
```
X_test = df_test.drop('p_id', axis=1)
X_test
```

[301]:
```
   no_times_pregnant  glucose_concentration  blood_pressure  \
0                  2                    112              68   
1                 11                    143              94   
2                  2                     93              64   
3                  1                    120              80   
4                  3                    128              72   

   skin_fold_thickness  serum_insulin   bmi  diabetes pedigree  age  
0                   22             94  34.1              0.315   26  
1                   33            146  36.6              0.254   51  
2                   32            160  38.0              0.674   23  
3                   48            200  38.9              1.162   41  
4                   25            190  32.4              0.549   27  
```

[302]:
```
# Scale to [0, 1]
max_ = df_train.drop(['diabetes', 'p_id'], axis=1).max(axis=0)
min_ = df_train.drop(['diabetes', 'p_id'], axis=1).min(axis=0)
X_test = (X_test - min_) / (max_ - min_)
```

[312]:
```
#Function to compute accuracy and confusion matrix for a given inputs and target

def predict_and_plot(inputs, targets, model, name=''):
    preds = model.predict(inputs)

    accuracy = accuracy_score(targets, preds)
    print("Accuracy: {:.2f}%".format(accuracy * 100))

    cf = confusion_matrix(targets, preds, normalize='true')
    plt.figure()
    sns.heatmap(cf, annot=True)
    plt.xlabel('Prediction')
    plt.ylabel('Target')
    plt.title('{} Confusion Matrix'.format(name));
```

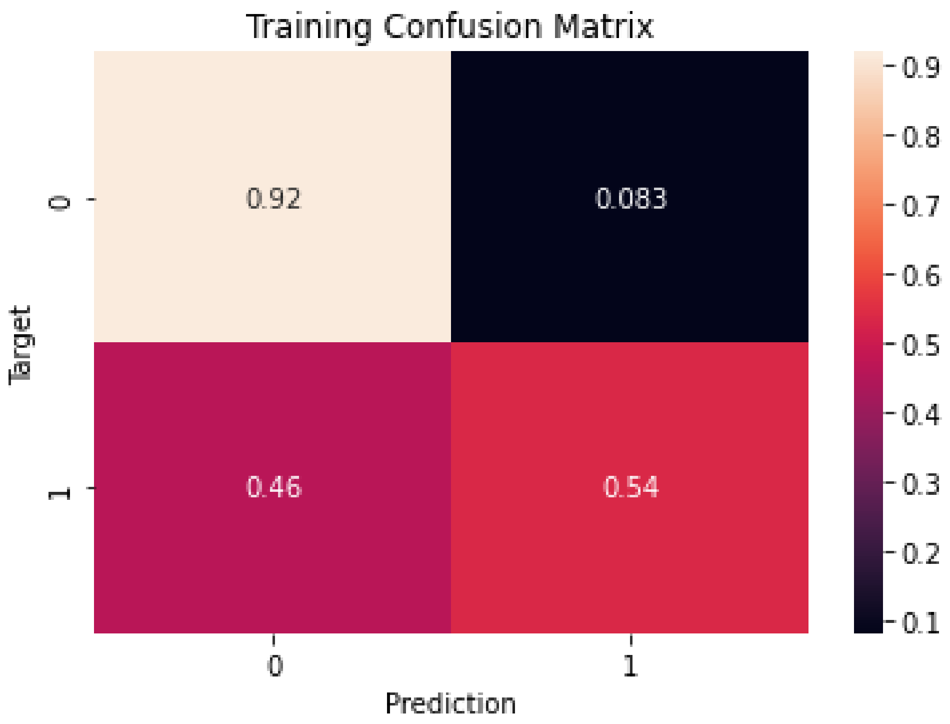
5.1 Logistic Regression

[324]:
```
#Fitting
logreg_model = LogisticRegression()
logreg_model.fit(X_train, y_train)
```

[324]:
```
LogisticRegression()
```

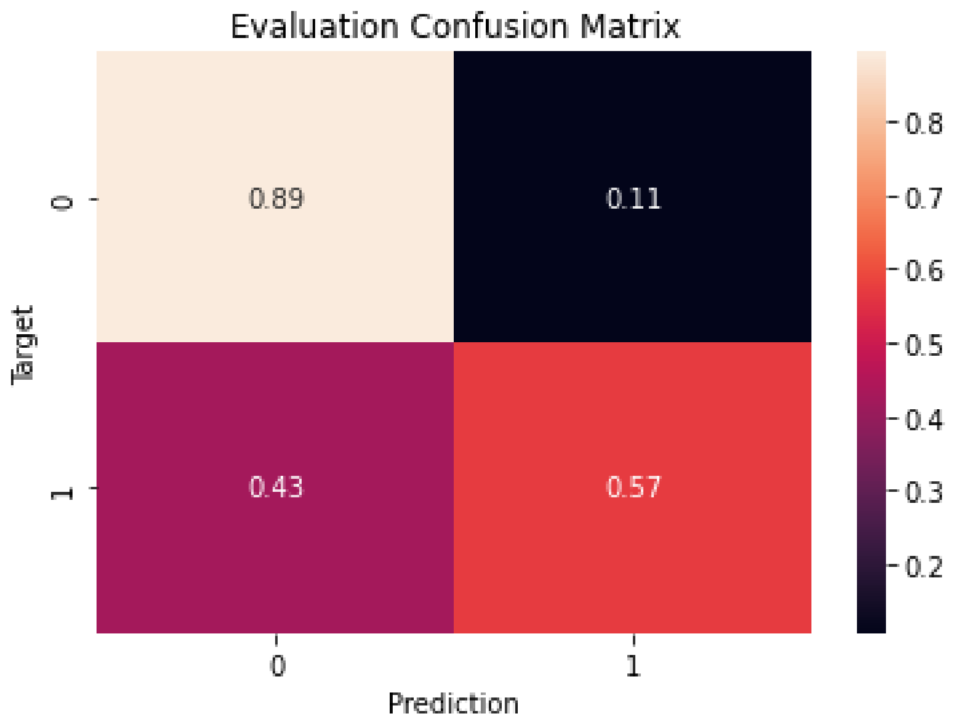
[325]:
```
#Predictions and Evaluation (Training set)
predict_and_plot(X_train, y_train, logreg_model, 'Training')
```

```
Accuracy: 78.32%
```



[326]:
```
#Predictions and Evaluation (Evaluation set)
predict_and_plot(X_valid, y_valid, logreg_model, 'Evaluation')
```

```
Accuracy: 78.38%
```



[327]:
```
#Predictions on df_test
logreg_model.predict(X_test)
```

[327]:
```
array([0, 1, 0, 0, 0])
```

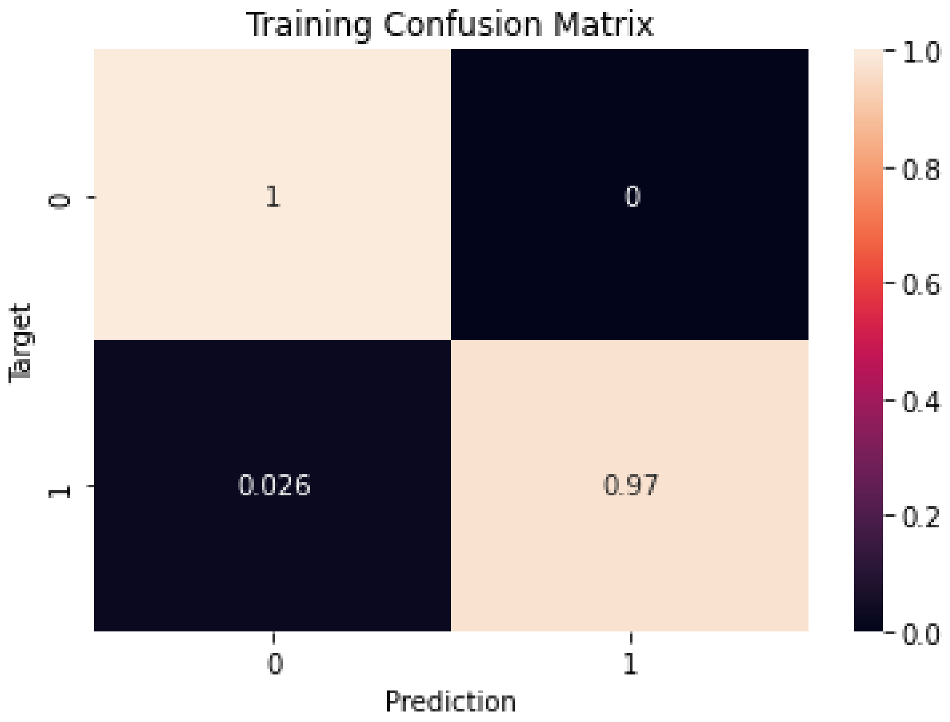
5.2 RandomForest Classifier

[373]:
```
#Fitting
rf_model = RandomForestClassifier(n_estimators=10, random_state=64)
rf_model.fit(X_train, y_train)
```

[373]:
```
RandomForestClassifier(n_estimators=10, random_state=64)
```

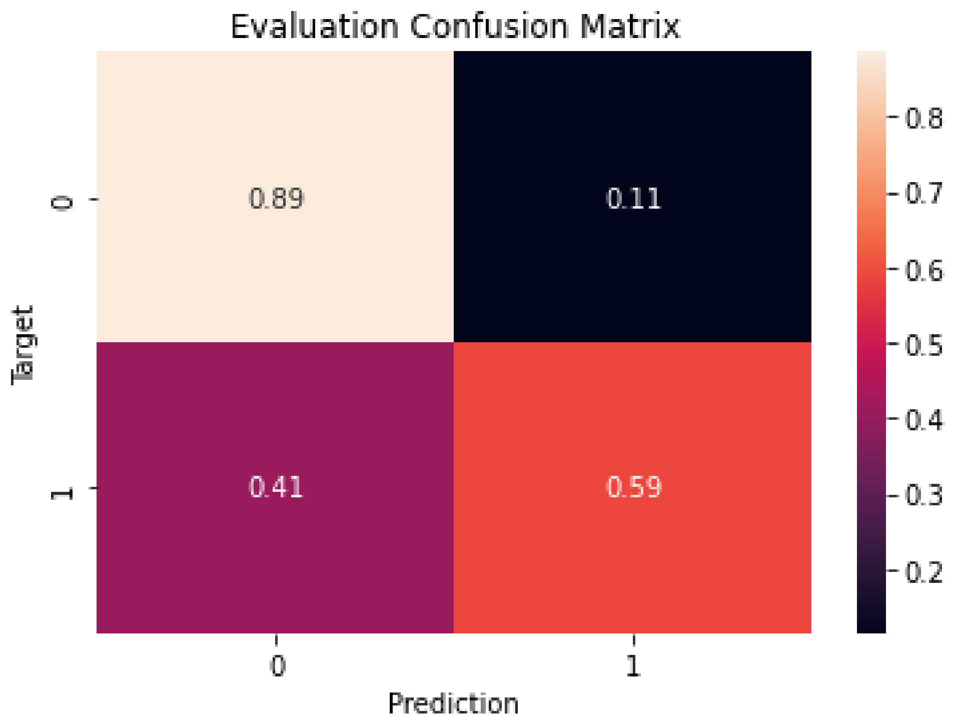
[374]:
```
#Predictions and Evaluation (Training set)
predict_and_plot(X_train, y_train, rf_model, 'Training')
```

```
Accuracy: 99.07%
```



[375]:
```
#Predictions and Evaluation (Evaluation set)
predict_and_plot(X_valid, y_valid, rf_model, 'Evaluation')
```

```
Accuracy: 78.38%
```



```
[376]: #Predictions on df_test
       rf_model.predict(X_test)

[376]: array([0, 1, 0, 0, 1])
```

6 7. Conclusion

None of the trained models exceeded an accuracy of 80%. This may be due to the small size of the dataset. It is also necessary to have knowledge of the hyperparameters of each model to choose the ones that improve the performance for the problem.