# Import Libaries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
df = pd.read_csv('health care diabetes.csv')
```

In [3]:
```
df.head()
```

Out[3]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | DiabetesPedigreeFunction | A |
|---|---|---|---|---|---|---|---|---|
| **0** | 6 | 148 | 72 | 35 | 0 | 33.6 | 0.627 | |
| **1** | 1 | 85 | 66 | 29 | 0 | 26.6 | 0.351 | |
| **2** | 8 | 183 | 64 | 0 | 0 | 23.3 | 0.672 | |
| **3** | 1 | 89 | 66 | 23 | 94 | 28.1 | 0.167 | |
| **4** | 0 | 137 | 40 | 35 | 168 | 43.1 | 2.288 | |

In [4]:
```
df.shape
```

Out[4]:
```
(768, 9)
```

In [5]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [6]:
```
df.describe()
```

Out[6]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | DiabetesPe |
|---|---|---|---|---|---|---|---|
| **count** | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768.000000 | 768.000000 | |
| **mean** | 3.845052 | 120.894531 | 69.105469 | 20.536458 | 79.799479 | 31.992578 | |
| **std** | 3.369578 | 31.972618 | 19.355807 | 15.952218 | 115.244002 | 7.884160 | |
| **min** | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | |
| **25%** | 1.000000 | 99.000000 | 62.000000 | 0.000000 | 0.000000 | 27.300000 | |
| **50%** | 3.000000 | 117.000000 | 72.000000 | 23.000000 | 30.500000 | 32.000000 | |
| **75%** | 6.000000 | 140.250000 | 80.000000 | 32.000000 | 127.250000 | 36.600000 | |
| **max** | 17.000000 | 199.000000 | 122.000000 | 99.000000 | 846.000000 | 67.100000 | |

In [7]:
```
df.isnull().sum()
```

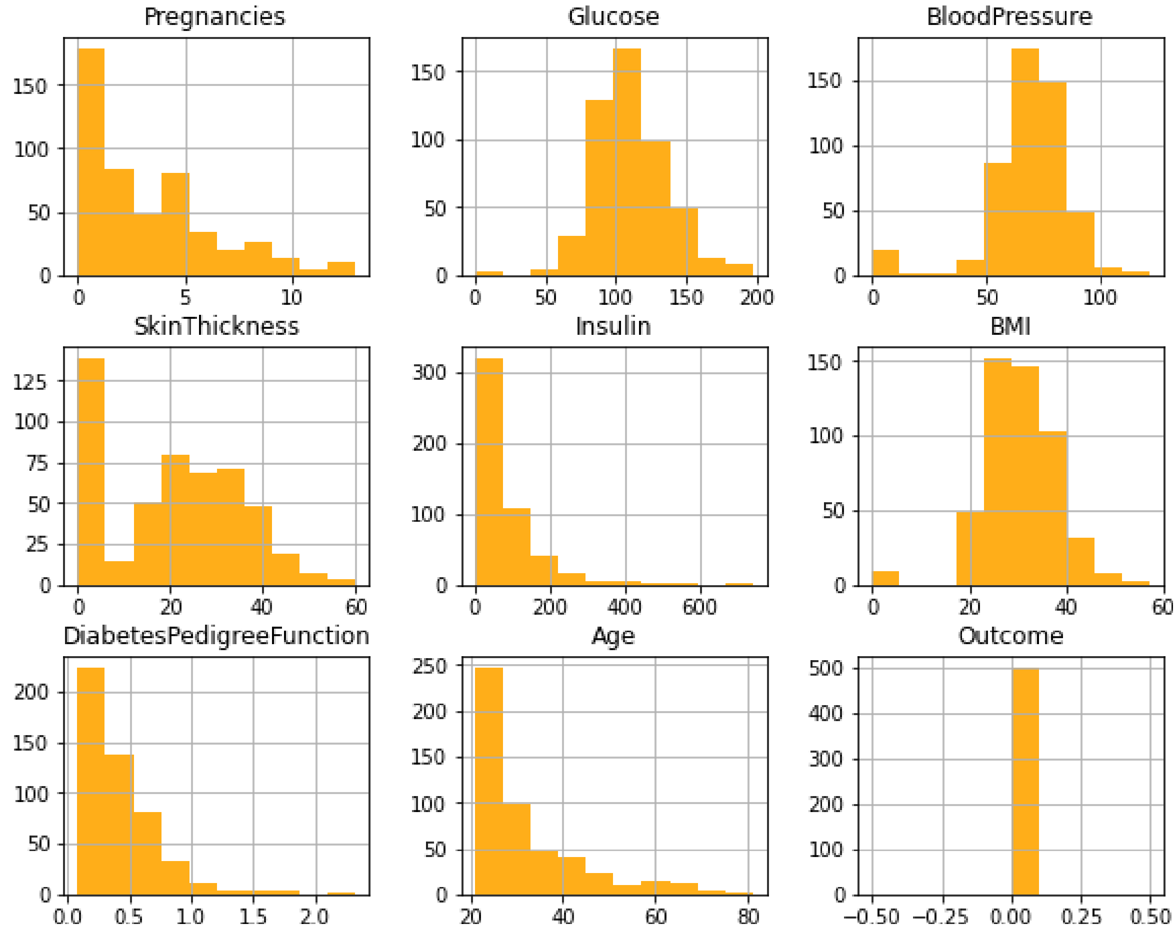
Out[7]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

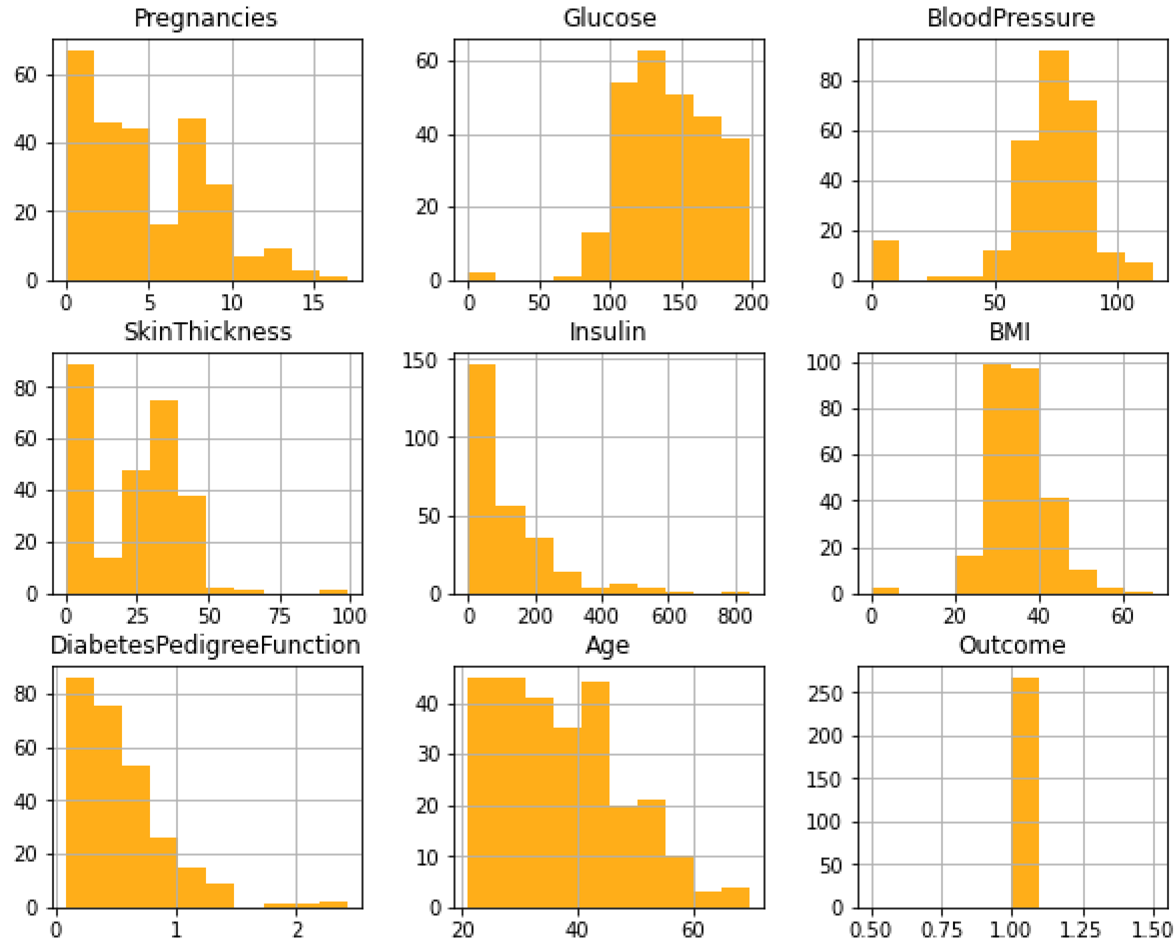
In [8]:
```
df.groupby('Outcome').size()
```

Out[8]:
```
Outcome
0    500
1    268
dtype: int64
```

In [9]:
```
def get_zeros_outcome_count(df,column_name):
    count = df[df[column_name] == 0].shape[0]
    print("Total No of zeros found in " + column_name + " : " + str(count))
    print(df[df[column_name] == 0].groupby('Outcome')['Age'].count())
```

In [10]:
```
df.groupby('Outcome').hist(figsize = (10, 8), color = 'Orange', alpha = 0.9)
plt.show()
```




# Observations:

From above histograms we can clearly analyze that Glucose, BloodPressure, SkinThickness, Insulin & BMI are having '0' which is not true for a alive person, so we will consider this values as missing values

In [11]:
```
get_zeros_outcome_count(df, 'Glucose')
```

```
Total No of zeros found in Glucose : 5
Outcome
0    3
1    2
Name: Age, dtype: int64
```

In [12]:
```
get_zeros_outcome_count(df, 'BloodPressure')
```

```
Total No of zeros found in BloodPressure : 35
Outcome
0    19
1    16
Name: Age, dtype: int64
```

In [13]:
```
get_zeros_outcome_count(df, 'SkinThickness')
```

```
Total No of zeros found in SkinThickness : 227
Outcome
0    139
1     88
Name: Age, dtype: int64
```

In [14]:
```
get_zeros_outcome_count(df, 'Insulin')
```

```
Total No of zeros found in Insulin : 374
Outcome
0    236
1    138
Name: Age, dtype: int64
```

In [15]:
```
get_zeros_outcome_count(df, 'BMI')
```

```
Total No of zeros found in BMI : 11
Outcome
0    9
1    2
Name: Age, dtype: int64
```

# Observations:

After analyzing the above data so many 0s in Insulin & SkinThickness are found and removing the 0s or putting the mean values will not be a great idea. However we can remove the 0s from 'BMI', 'BloodPressure' & 'Glucose' as such values will not be present in alive person.

In [16]:
```
new_df = df[(df.BMI != 0) & (df.BloodPressure != 0) & (df.Glucose != 0)]
new_df.shape
```

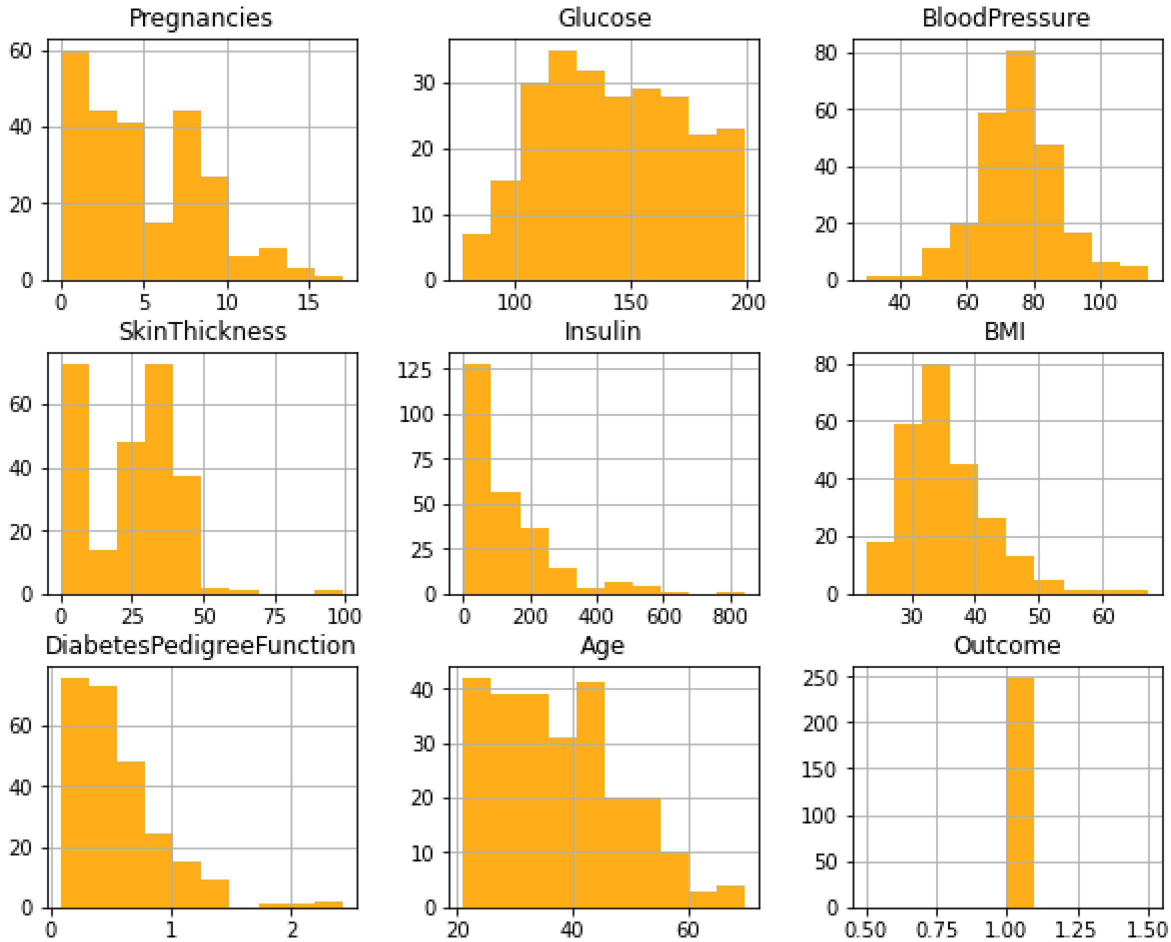
Out[16]:
```
(724, 9)
```

In [17]:
```
positive = new_df[new_df['Outcome'] == 1]
positive.head()
```

Out[17]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | DiabetesPedigreeFunction | A |
|---|---|---|---|---|---|---|---|---|
| **0** | 6 | 148 | 72 | 35 | 0 | 33.6 | 0.627 | |
| **2** | 8 | 183 | 64 | 0 | 0 | 23.3 | 0.672 | |
| **4** | 0 | 137 | 40 | 35 | 168 | 43.1 | 2.288 | |
| **6** | 3 | 78 | 50 | 32 | 88 | 31.0 | 0.248 | |
| **8** | 2 | 197 | 70 | 45 | 543 | 30.5 | 0.158 | |

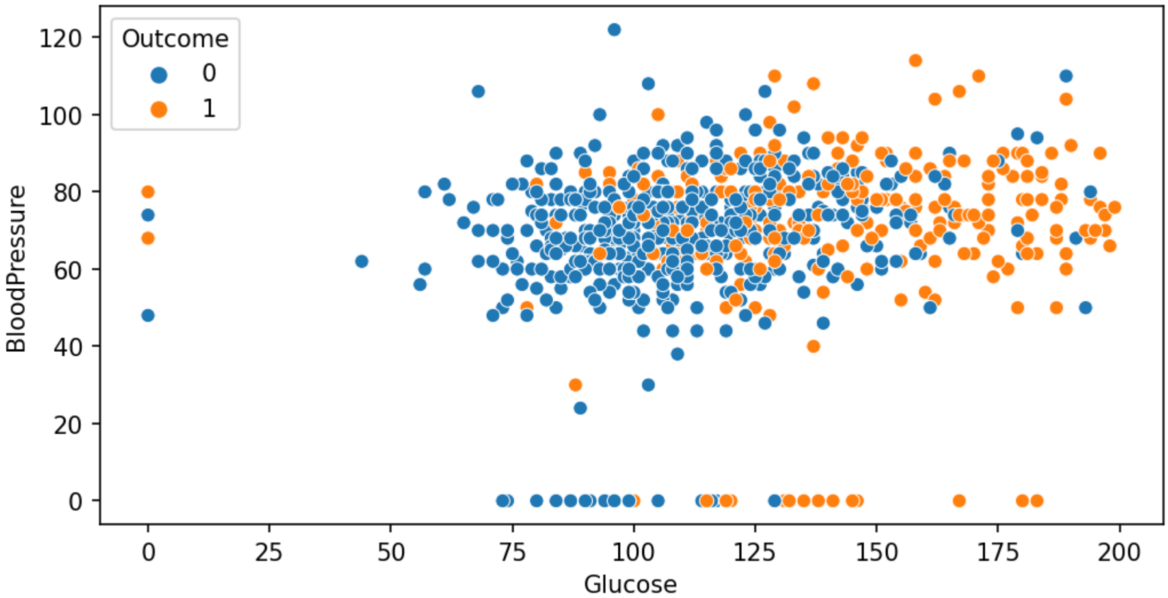
In [18]:
```
positive.groupby('Outcome').hist(figsize = (10,8), color = 'Orange', alpha = 0.9)
plt.show()
```



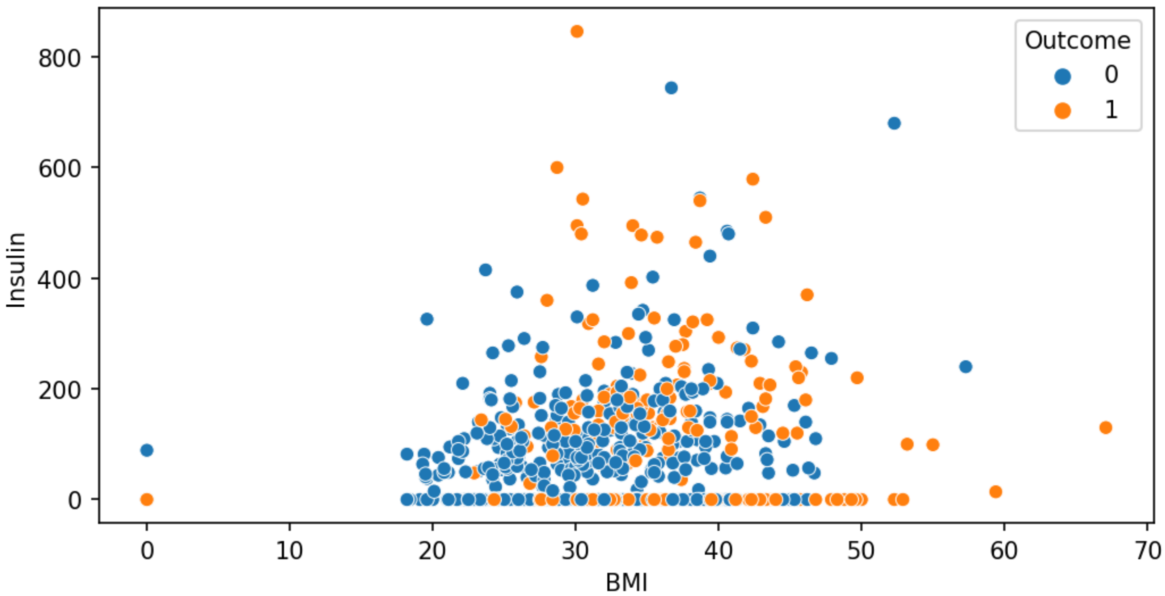

# Scatter plot

In [19]:
```
BloddPressure = positive["BloodPressure"]
BMI = positive["BMI"]
Glucose = positive["Glucose"]
Insulin = positive["Insulin"]
SkinThickness = positive["SkinThickness"]
```

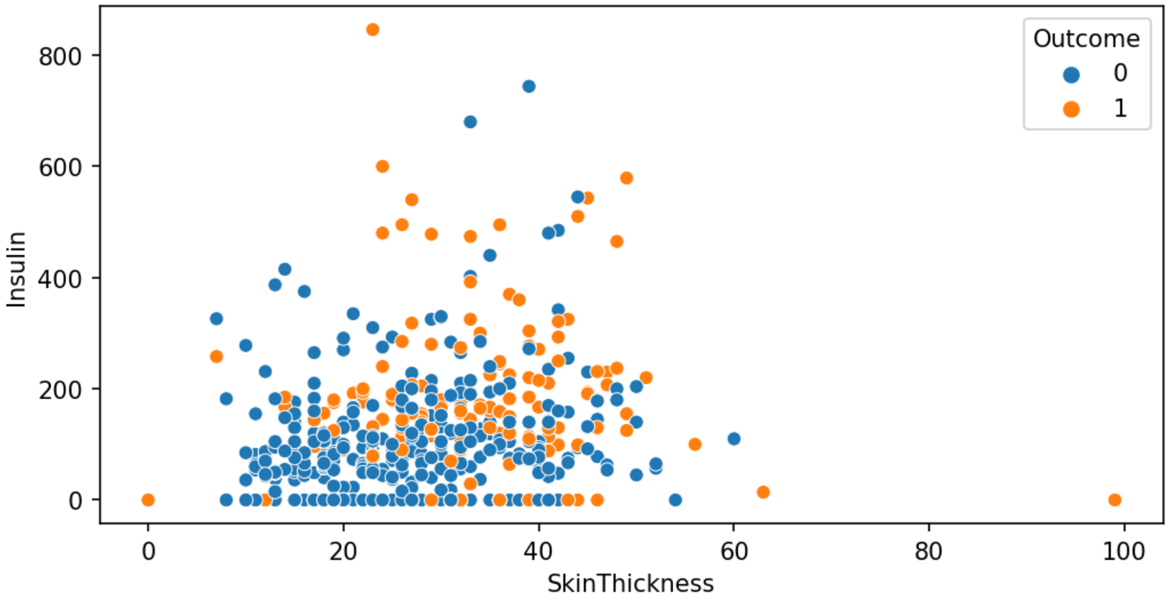
In [20]:
```
plt.figure(figsize = (8, 4), dpi = 150)
sns.scatterplot(x = "Glucose", y = "BloodPressure", hue = "Outcome", data = df)
plt.show()
```




In [21]:
```
plt.figure(figsize = (8, 4), dpi = 150)
sns.scatterplot(x = "BMI", y = "Insulin", hue = "Outcome", data = df)
plt.show()
```




In [22]:
```
plt.figure(figsize = (8, 4), dpi = 150)
sns.scatterplot(x = "SkinThickness", y = "Insulin", hue = "Outcome", data = df)
plt.show()
```



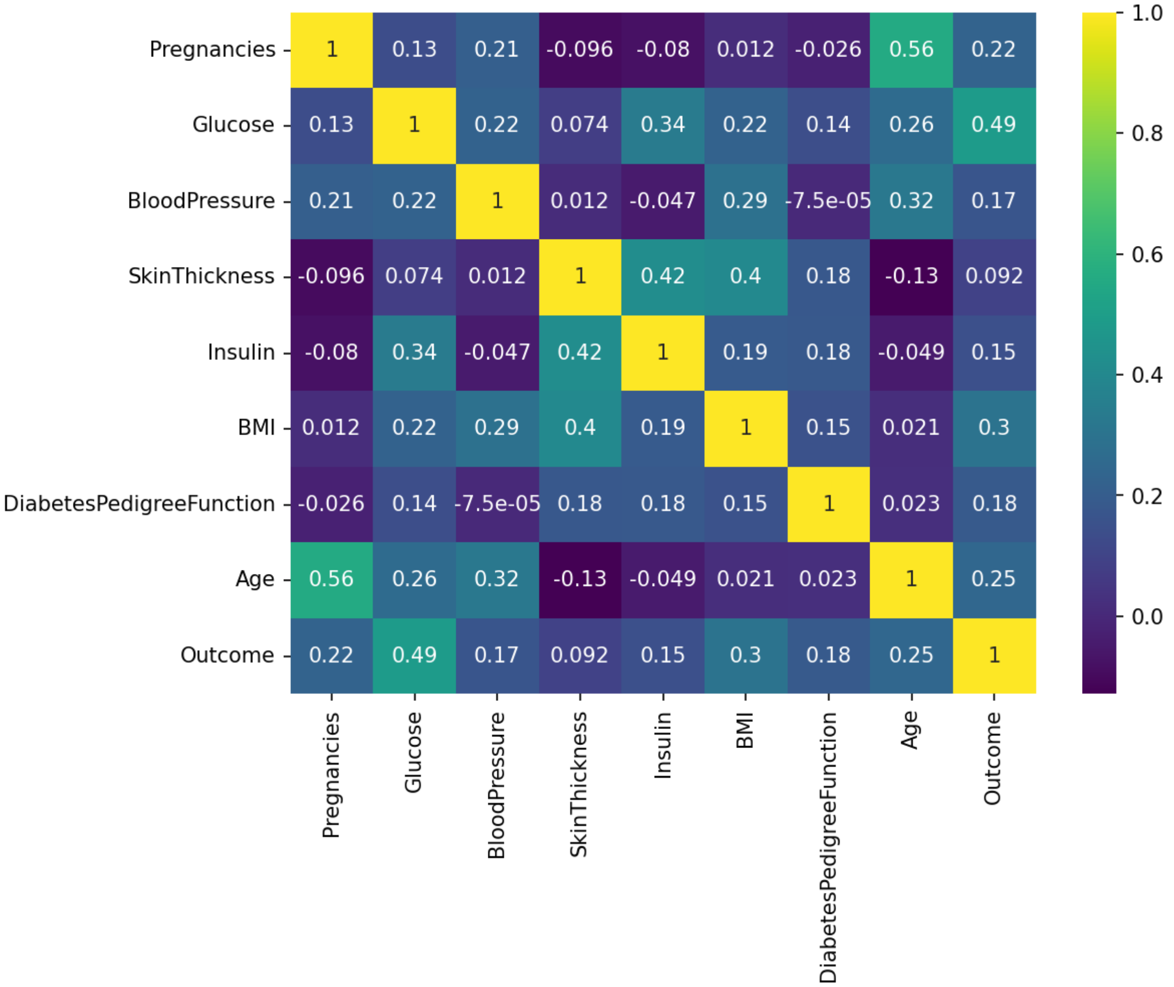

# Correlation Matrix

In [23]:
```
new_df.corr()
```

Out[23]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BM |
|---|---|---|---|---|---|---|
| **Pregnancies** | 1.000000 | 0.134915 | 0.209668 | -0.095683 | -0.080059 | 0.01234 |
| **Glucose** | 0.134915 | 1.000000 | 0.223331 | 0.074381 | 0.337896 | 0.22327 |
| **BloodPressure** | 0.209668 | 0.223331 | 1.000000 | 0.011777 | -0.046856 | 0.28740 |
| **SkinThickness** | -0.095683 | 0.074381 | 0.011777 | 1.000000 | 0.420874 | 0.40152 |
| **Insulin** | -0.080059 | 0.337896 | -0.046856 | 0.420874 | 1.000000 | 0.19183 |
| **BMI** | 0.012342 | 0.223276 | 0.287403 | 0.401528 | 0.191831 | 1.00000 |
| **DiabetesPedigreeFunction** | -0.025996 | 0.136630 | -0.000075 | 0.176253 | 0.182656 | 0.15485 |
| **Age** | 0.557066 | 0.263560 | 0.324897 | -0.128908 | -0.049412 | 0.02083 |
| **Outcome** | 0.224417 | 0.488384 | 0.166703 | 0.092030 | 0.145488 | 0.29937 |

In [24]:
```
plt.figure(figsize = (8, 6), dpi = 150)
sns.heatmap(new_df.corr(), annot = True, cmap = 'viridis')
plt.show()
```




# Build Model

In [25]:
```
from sklearn.model_selection import train_test_split
```

In [26]:
```
X = new_df.drop('Outcome', axis = 1)
y = new_df['Outcome']
```

In [27]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_st
```

In [28]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_repor
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier

from sklearn.model_selection import KFold, cross_val_score
```

In [29]:
```
LR_model = LogisticRegression(solver = 'liblinear')
LR_model.fit(X_train, y_train)
```

Out[29]:
```
▾ LogisticRegression
LogisticRegression(solver='liblinear')
```

In [30]:
```
print("LogisticRegression Score :{}".format(LR_model.score(X_train,y_train)))
```

```
y_pred = LR_model.predict(X_test)
scores = (accuracy_score(y_test, y_pred))

print("\nLogisticRegression Accuracy Score :{}".format(scores))
```

```
LogisticRegression Score :0.7651122625215889

LogisticRegression Accuracy Score :0.7862068965517242
```

In [31]:
```
accuracyScores = []
modelScores = []
models = []
names = []
#Store algorithm into array to get score and accuracy
models.append(('LR', LogisticRegression(solver='liblinear')))
models.append(('SVC', SVC()))
models.append(('KNN', KNeighborsClassifier()))
models.append(('DT', DecisionTreeClassifier()))
models.append(('GNB', GaussianNB()))
models.append(('RF', RandomForestClassifier()))
models.append(('GB', GradientBoostingClassifier()))
```

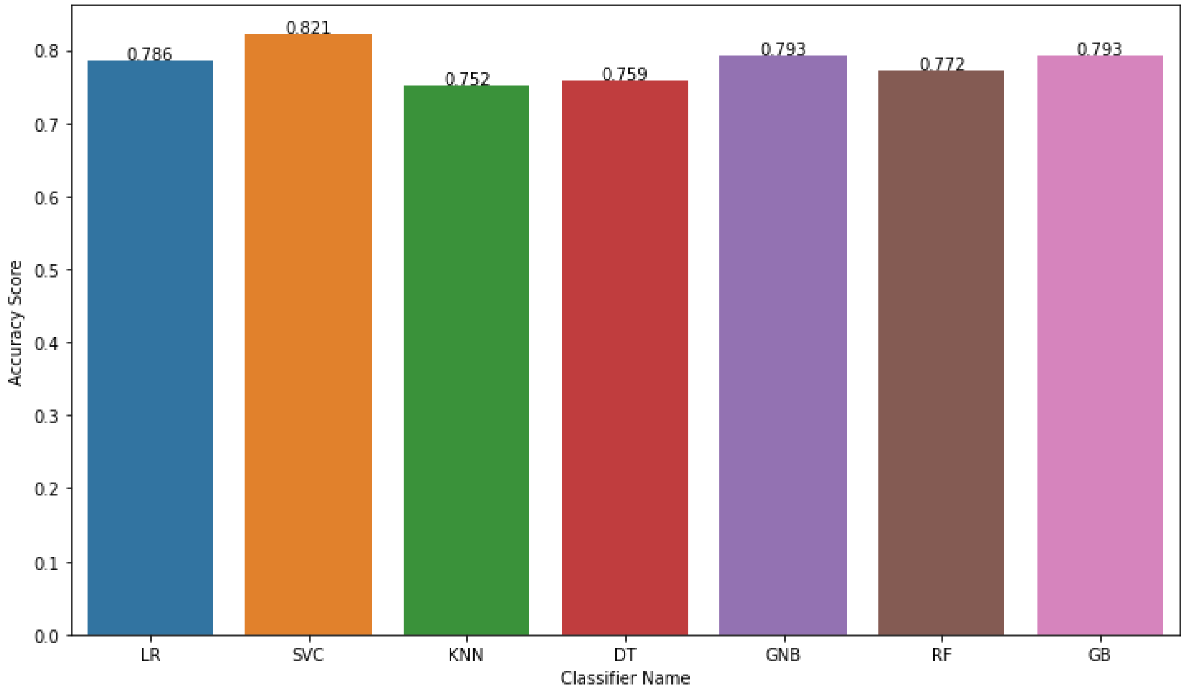
In [32]:
```
for name, model in models:
    model.fit(X_train, y_train)
    modelScores.append(model.score(X_train,y_train))
    y_pred = model.predict(X_test)
    accuracyScores.append(accuracy_score(y_test, y_pred))
    names.append(name)

tr_split_data = pd.DataFrame({'Name': names, 'Score': modelScores,'Accuracy Score'
print(tr_split_data)
```

```
C:\Users\prabh\anaconda3\envs\Simplilearn\lib\site-packages\sklearn\neighbors\_cla
ssification.py:237: FutureWarning: Unlike other reduction functions (e.g. `skew`,
`kurtosis`), the default behavior of `mode` typically preserves the axis it acts a
long. In SciPy 1.11.0, this behavior will change: the default value of `keepdims`
will become False, the `axis` over which the statistic is taken will be eliminate
d, and the value None will no longer be accepted. Set `keepdims` to True or False
to avoid this warning.
  mode, _ = stats.mode(_y[neigh_ind, k], axis=1)
C:\Users\prabh\anaconda3\envs\Simplilearn\lib\site-packages\sklearn\neighbors\_cla
ssification.py:237: FutureWarning: Unlike other reduction functions (e.g. `skew`,
`kurtosis`), the default behavior of `mode` typically preserves the axis it acts a
long. In SciPy 1.11.0, this behavior will change: the default value of `keepdims`
will become False, the `axis` over which the statistic is taken will be eliminate
d, and the value None will no longer be accepted. Set `keepdims` to True or False
to avoid this warning.
  mode, _ = stats.mode(_y[neigh_ind, k], axis=1)
  Name     Score  Accuracy Score
0   LR  0.765112        0.786207
1  SVC  0.749568        0.820690
2  KNN  0.784111        0.751724
3   DT  1.000000        0.758621
4  GNB  0.744387        0.793103
5   RF  1.000000        0.772414
6   GB  0.937824        0.793103
```

In [33]:
```
plt.figure(figsize = (6,3))
plt.subplots(figsize=(12,7))


axis = sns.barplot(x = 'Name', y = 'Accuracy Score', data = tr_split_data)
axis.set(xlabel='Classifier Name', ylabel='Accuracy Score')
for p in axis.patches:
```

```
    height = p.get_height()
    axis.text(p.get_x() + p.get_width()/2, height + 0.002, '{:1.3f}'.format(height

plt.show()
```

```
<Figure size 432x216 with 0 Axes>
```




In [34]:
```
cm = confusion_matrix(y,LR_model.predict(X))
cm
```

Out[34]:
```
array([[422,  53],
       [114, 135]], dtype=int64)
```

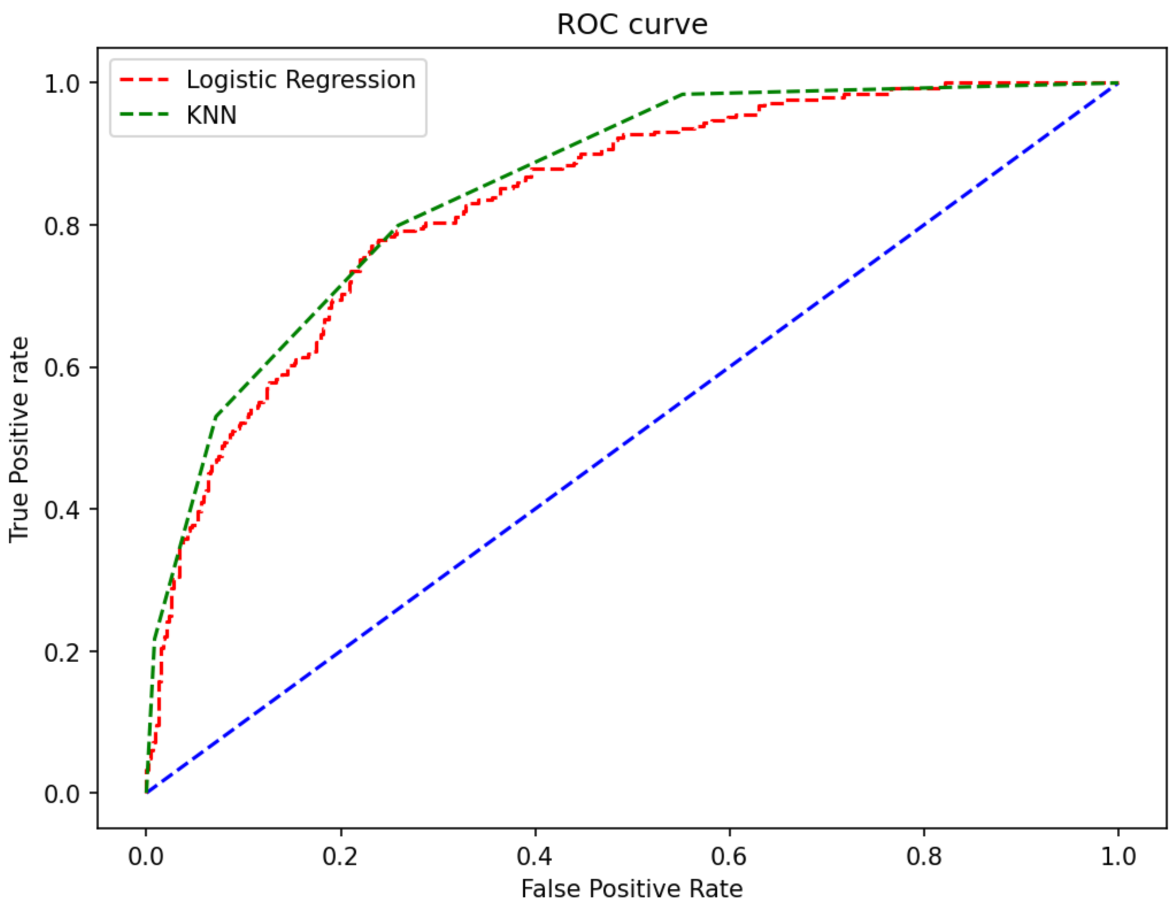
In [35]:
```
print(classification_report(y,LR_model.predict(X)))
```

```
              precision    recall  f1-score   support

           0       0.79      0.89      0.83       475
           1       0.72      0.54      0.62       249

    accuracy                           0.77       724
   macro avg       0.75      0.72      0.73       724
weighted avg       0.76      0.77      0.76       724
```

In [36]:
```
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score
```

In [37]:
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve) - LR, KNN
# predict probabilities for LR
plt.figure(figsize = (8, 6), dpi = 150)
probs_LR = LR_model.predict_proba(X)

# predict probabilities for KNN - where models[2] is KNN
model_KNN = KNeighborsClassifier(n_neighbors=4)
model_KNN.fit(X_train, y_train)
probs_KNN = model_KNN.predict_proba(X)

# Sklearn has a very potent method roc_curve() which computes the ROC for your cla:
# It returns the FPR, TPR, and threshold values: calculate roc curve
fpr, tpr, thresholds = roc_curve(y, probs_LR[:, 1],pos_label=1)
fpr1, tpr1, thresholds1 = roc_curve(y, probs_KNN[:, 1],pos_label=1)
```

```
# roc curve for tpr = fpr
random_probs = [0 for i in range(len(y))]
p_fpr, p_tpr, _ = roc_curve(y, random_probs, pos_label=1)

# plot no skill
plt.plot(p_fpr, p_tpr, linestyle='--',color='blue')
plt.plot(fpr, tpr, linestyle='--',color='red', label='Logistic Regression')
plt.plot(fpr1, tpr1, linestyle='--',color='green', label='KNN')

# plot the roc curve for the model
plt.title('ROC curve')
# x label
plt.xlabel('False Positive Rate')
# y label
plt.ylabel('True Positive rate')
#plt.plot(fpr, tpr, marker='.')
plt.legend(loc='best')
plt.show();

# keep probabilities for the positive outcome only
#The AUC score can be computed using the roc_auc_score() method of sklearn: calcul

auc_LR = roc_auc_score(y, probs_LR[:, 1])
auc_KNN = roc_auc_score(y, probs_KNN[:, 1])
print('AUC LR: %.5f' % auc_LR, 'AUC KNN: %.5f' % auc_KNN)
```




```
AUC LR: 0.83528 AUC KNN: 0.85476
```

In [38]:

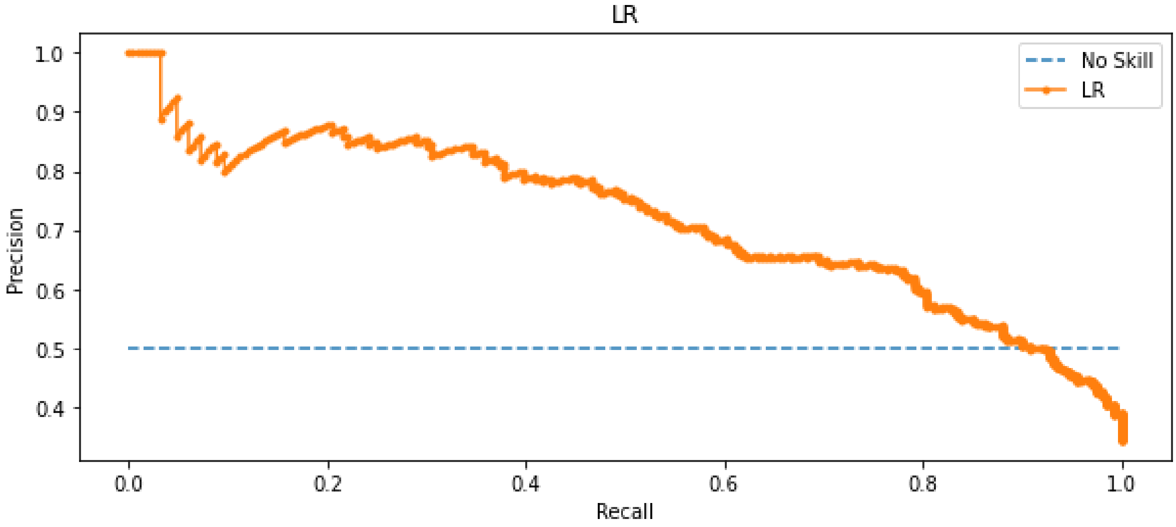
```
def generate_graph(recall, precision,name):
    # plot no skill
    # plot the precision-recall curve for the model
    plt.figure()
    plt.subplots(figsize=(10,4))
    plt.plot([0, 1], [0.5, 0.5], linestyle='--',label='No Skill')
    plt.plot(recall, precision, marker='.',label=name)
```

```
    plt.xlabel('Recall')
    plt.ylabel('Precision')
    plt.title(name)
    plt.legend(loc='best')
    plt.show()
```

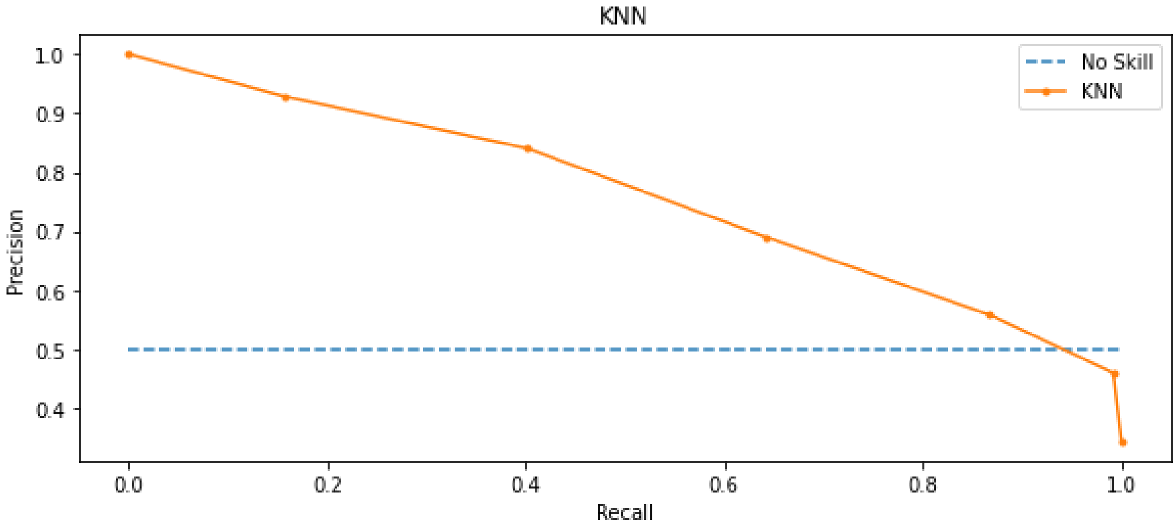
In [39]:

```
#Store algorithm into array to get score and accuracy
p_r_Models = []
p_r_Models.append(('LR', LogisticRegression(solver='liblinear')))
p_r_Models.append(('KNN', KNeighborsClassifier()))
p_r_Models.append(('DT', DecisionTreeClassifier()))
p_r_Models.append(('GNB', GaussianNB()))
p_r_Models.append(('RF', RandomForestClassifier()))
p_r_Models.append(('GB', GradientBoostingClassifier()))


#Precision Recall Curve for All classifier
for name, model in p_r_Models:
    from sklearn.metrics import precision_recall_curve
    from sklearn.metrics import f1_score
    from sklearn.metrics import auc
    from sklearn.metrics import average_precision_score
    print("\n====================------- Precision Recall Curve for {} ---------====

    model.fit(X_train, y_train)
    # predict probabilities
    probs = model.predict_proba(X)
    # keep probabilities for the positive outcome only
    probs = probs[:, 1]
    # predict class values
    yhat = model.predict(X)

    # calculate precision-recall curve
    precision, recall, thresholds = precision_recall_curve(y, probs)

    # calculate F1 score, # calculate precision-recall AUC
    f1, auc = f1_score(y, yhat), auc(recall, precision)

    # calculate average precision score
    ap = average_precision_score(y, probs)
    generate_graph(recall, precision,name)
    print(str(name) + " calculated value : " + 'F1 Score =%.3f, Area Under the Cur
    print("The above precision-recall curve plot is showing the precision/recall fo
```

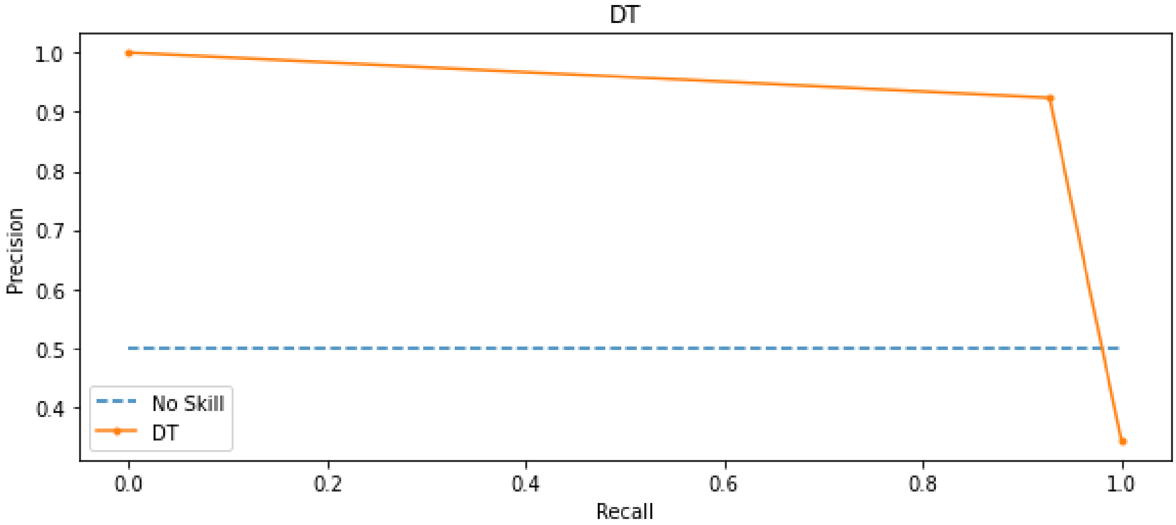
```
=========================------- Precision Recall Curve for LR ---------=========================
===

<Figure size 432x288 with 0 Axes>
```



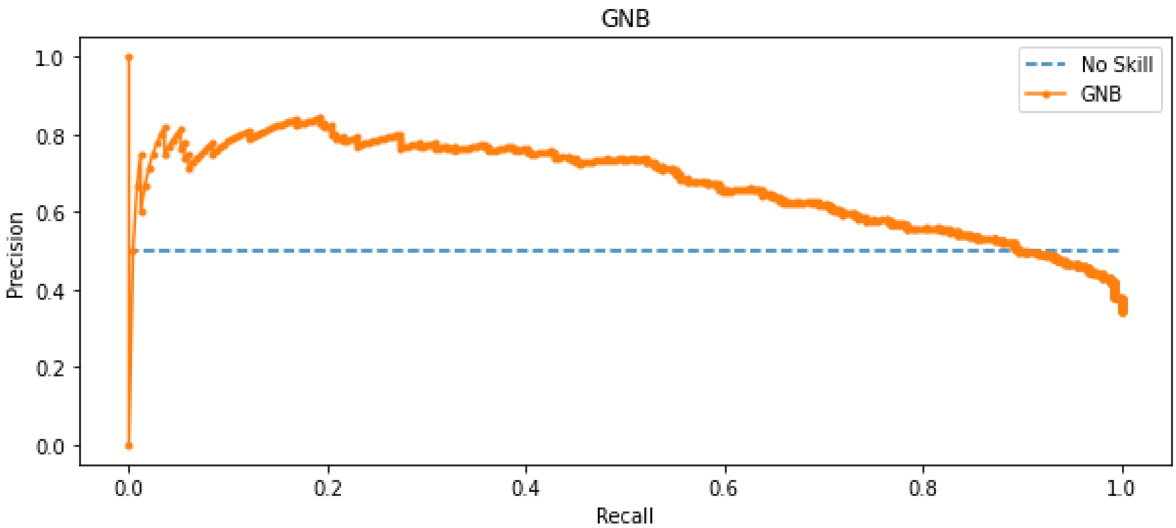

```
LR calculated value : F1 Score =0.618, Area Under the Curve=0.721, Average Precisi
on=0.722

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a LR model (orange) compared to a no skill model (blue).

========================------- Precision Recall Curve for KNN ----------===============
====

C:\Users\prabh\anaconda3\envs\Simplilearn\lib\site-packages\sklearn\neighbors\_cla
ssification.py:237: FutureWarning: Unlike other reduction functions (e.g. `skew`,
`kurtosis`), the default behavior of `mode` typically preserves the axis it acts a
long. In SciPy 1.11.0, this behavior will change: the default value of `keepdims`
will become False, the `axis` over which the statistic is taken will be eliminate
d, and the value None will no longer be accepted. Set `keepdims` to True or False
to avoid this warning.
  mode, _ = stats.mode(_y[neigh_ind, k], axis=1)
<Figure size 432x288 with 0 Axes>
```



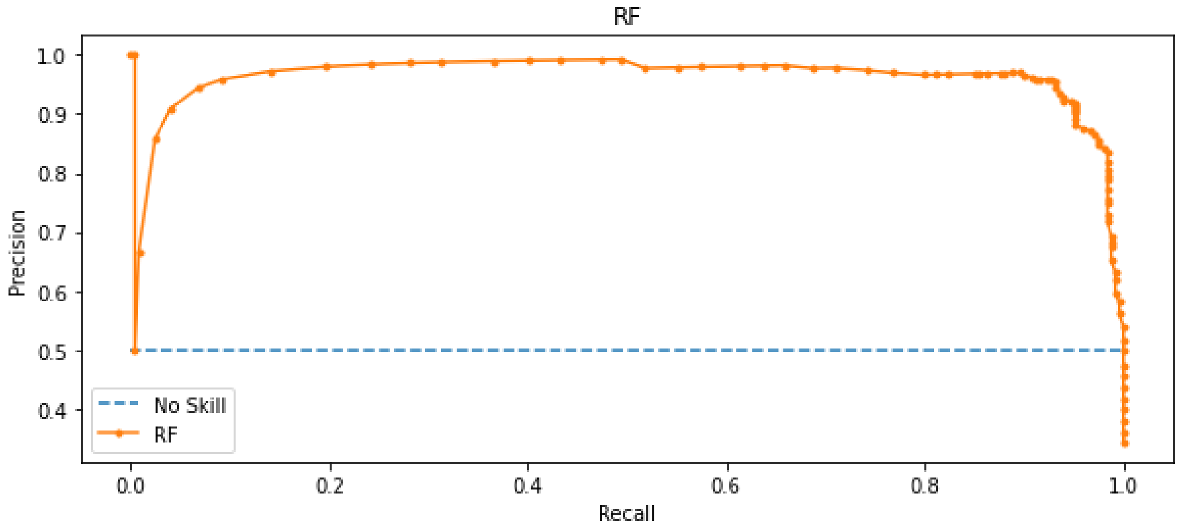

```
KNN calculated value : F1 Score =0.665, Area Under the Curve=0.759, Average Precis
ion=0.703

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a KNN model (orange) compared to a no skill model (blue).

========================------- Precision Recall Curve for DT ---------================
===

<Figure size 432x288 with 0 Axes>
```



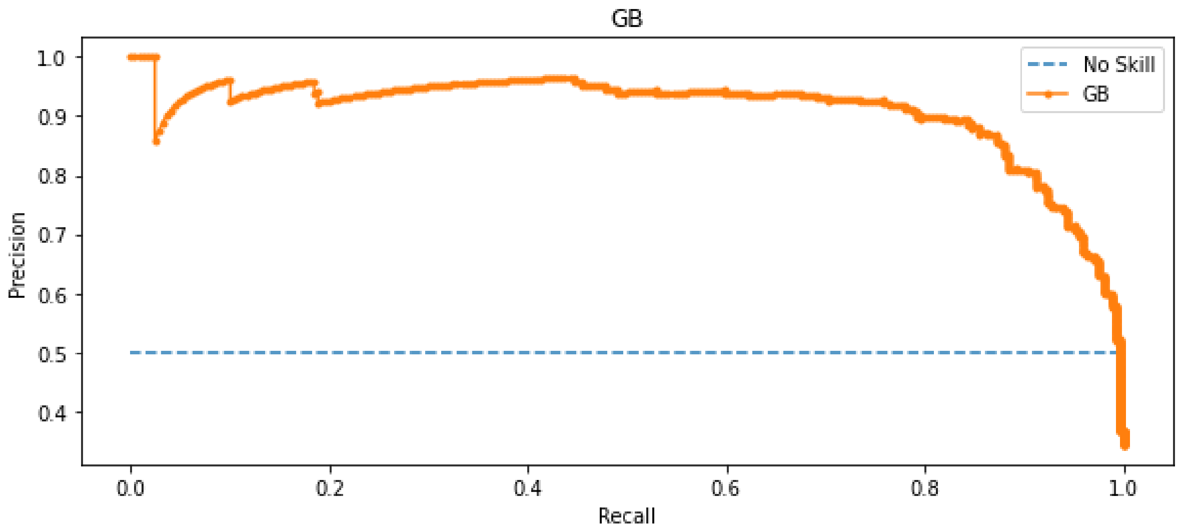

```
DT calculated value : F1 Score =0.926, Area Under the Curve=0.938, Average Precisi
on=0.882

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a DT model (orange) compared to a no skill model (blue).

======================------- Precision Recall Curve for GNB ---------======================
====

<Figure size 432x288 with 0 Axes>
```




```
GNB calculated value : F1 Score =0.628, Area Under the Curve=0.675, Average Precis
ion=0.678

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a GNB model (orange) compared to a no skill model (blue).

======================------- Precision Recall Curve for RF ---------======================
===

<Figure size 432x288 with 0 Axes>
```




```
RF calculated value : F1 Score =0.934, Area Under the Curve=0.959, Average Precisi
on=0.963

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a RF model (orange) compared to a no skill model (blue).

========================------- Precision Recall Curve for GB ---------================
===

<Figure size 432x288 with 0 Axes>
```



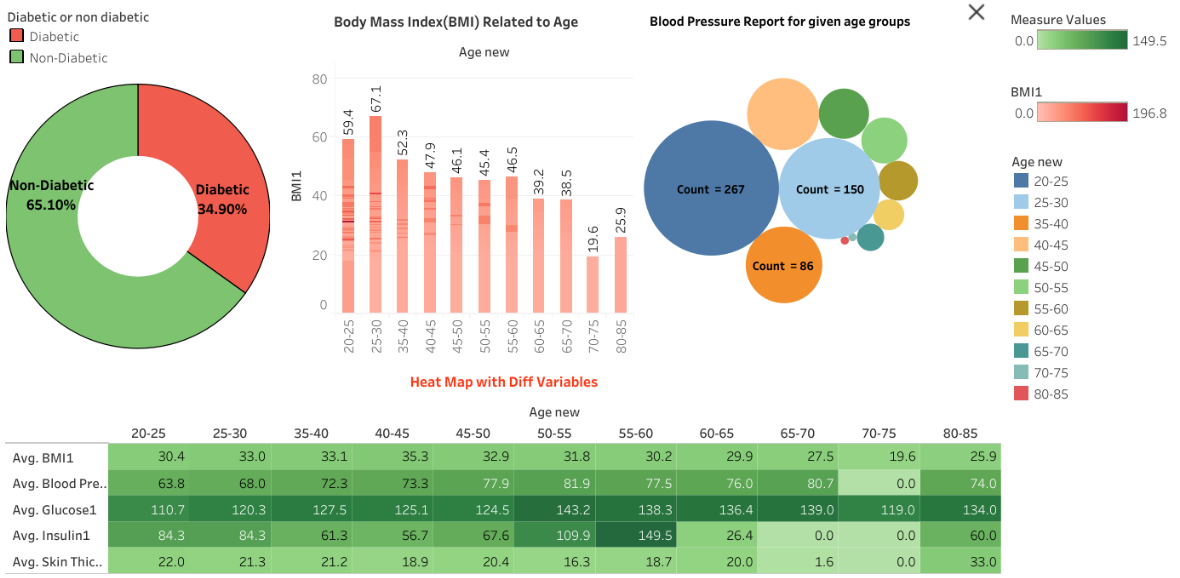

```
GB calculated value : F1 Score =0.862, Area Under the Curve=0.910, Average Precisi
on=0.910

The above precision-recall curve plot is showing the precision/recall for each thr
eshold for a GB model (orange) compared to a no skill model (blue).
```

# Dashboard in Tableau

In [40]:
```
from IPython import display
```

In [41]:
```
display.Image(r"C:\Users\prabh\Simplilearn\Data Science Capstone Project\Tableau Da
```

Out[41]:




# Dashboard

https://public.tableau.com/authoring/Capstone_Project_Healthcare_16783653500920/Dashboard

In [ ]: