```
In [1]: import numpy as np
        import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns
        from sklearn.model selection import train test split
        from sklearn.metrics import accuracy score,classification report
        from sklearn.naive_bayes import GaussianNB
        df=pd.read csv('Naive-Bayes-Classification medical-Data.csv')
In [2]:
In [3]: df.head(5)
           glucose bloodpressure diabetes
Out[3]:
                40
                                        0
        0
                              85
        1
                40
                              92
                                        0
        2
                45
                              63
                                       1
        3
                45
                              80
                                        0
                40
         4
                              73
                                        1
In [4]: df.isnull().sum()
Out[4]: glucose
         bloodpressure
                         0
        diabetes
        dtype: int64
In [5]: df.shape
Out[5]: (995, 3)
In [6]: X=df.drop('diabetes',axis=1)
In [7]: X
```

Out[7]:		glucose	bloodpressure	
	0	40	85	
	1	40	92	
	2	45	63	
	3	45	80	
	4	40	73	
	•••			
	990	45	87	
	991	40	83	
	992	40	83	
	993	40	60	
	994	45	82	

995 rows × 2 columns

```
In [8]: y=df['diabetes']
In [9]: y
Out[9]: 0
               0
0
        1
         2
               1
         3
               0
         4
               1
        990
        991
        992
        993
               1
        994
        Name: diabetes, Length: 995, dtype: int64
```

In [10]: df.hist() Out[10]: array([[<Axes: title={'center': 'glucose'}>, <Axes: title={'center': 'bloodpressure'}>], [<Axes: title={'center': 'diabetes'}>, <Axes: >]], dtype=object) bloodpressure glucose 200 300 150 200 100 100 50 0 20 60 60 80 100 diabetes 400 200

0.75 1.00

-0.808303 1.000000

In [11]: df.corr()

0.00

0.25

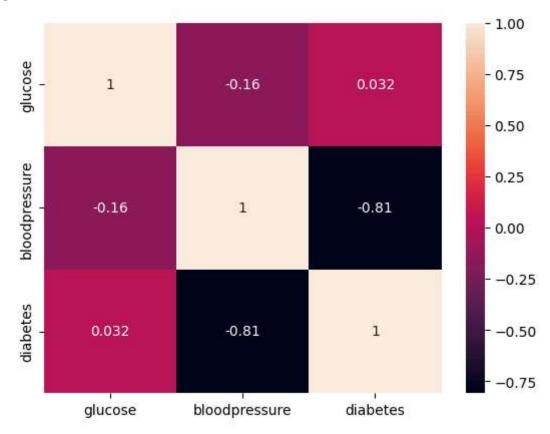
Out[11]:		glucose	bloodpressure	diabetes
	glucose	1.000000	-0.164553	0.031585
	bloodpressure	-0.164553	1.000000	-0.808303

diabetes 0.031585

0.50

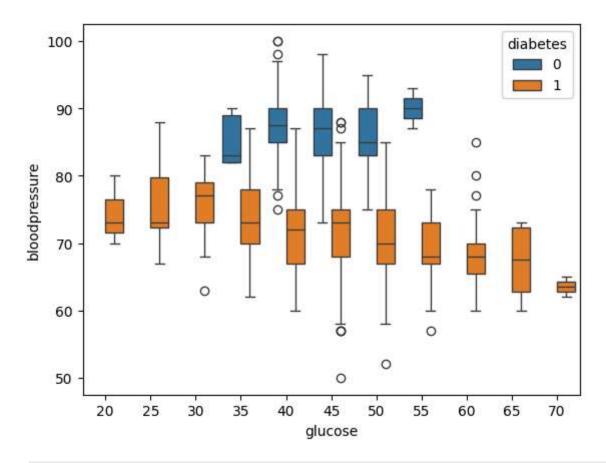
```
In [12]: sns.heatmap(df.corr(),annot=True)
```

Out[12]: <Axes: >



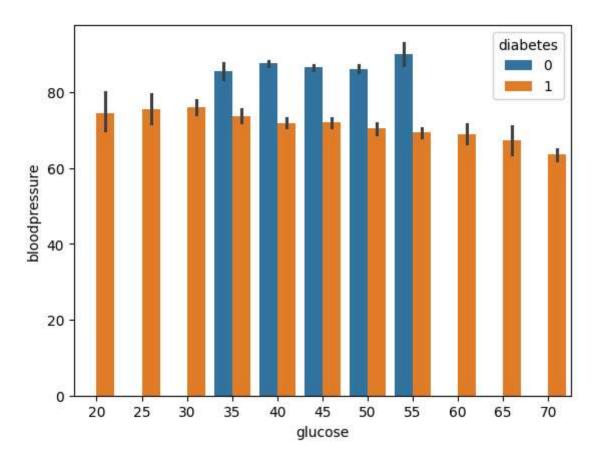
In [13]: sns.boxplot(x='glucose',y='bloodpressure',hue='diabetes',data=df)

Out[13]: <Axes: xlabel='glucose', ylabel='bloodpressure'>

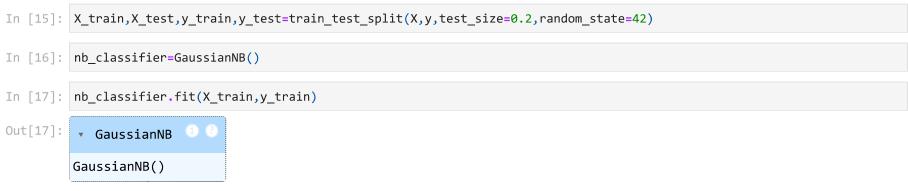


In [14]: sns.barplot(x='glucose',y='bloodpressure',hue='diabetes',data=df)

Out[14]: <Axes: xlabel='glucose', ylabel='bloodpressure'>



In [18]: y_pred=nb_classifier.predict(X_test)



```
In [19]: accuracy=accuracy_score(y_test,y_pred)
         print('Accuracy:',accuracy)
        Accuracy: 0.9296482412060302
In [20]: classification report=classification report(y test,y pred)
         print('Classification report:',classification report)
        Classification report:
                                                          recall f1-score
                                                                             support
                                             precision
                   0
                           0.92
                                     0.92
                                               0.92
                                                           93
                           0.93
                                     0.93
                   1
                                               0.93
                                                          106
                                               0.93
                                                          199
            accuracy
           macro avg
                           0.93
                                     0.93
                                               0.93
                                                          199
        weighted avg
                           0.93
                                     0.93
                                               0.93
                                                          199
In [21]: #Prediction
         y pred
Out[21]: array([1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 1,
                 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0,
                 0, 0, 1, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1,
                1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 1,
                0, 1, 0, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 1, 0,
                1, 0, 1, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1, 1, 1, 0,
                0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 1, 0, 0,
                1, 1, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 1, 0, 1, 0, 0, 1,
                0, 1, 1, 1, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0,
                0])
In [56]: sns.countplot(x=y pred, palette=['red', 'blue'])
         plt.title('Predicted Diabetes Class Distribution')
         plt.xlabel('Predicted Class')
         plt.ylabel('Count')
         plt.xticks([0, 1], ['No Diabetes', 'Diabetes'])
         plt.show()
```

C:\Users\KAUSHIK\AppData\Local\Temp\ipykernel_13152\2639116456.py:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `h ue` and set `legend=False` for the same effect.

sns.countplot(x=y_pred, palette=['red', 'blue'])

Predicted Diabetes Class Distribution

