

```
In [ ]: ## Navie Bayes
      ### check the patient have diabetic or not
```

```
In [122]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

```
In [29]: ### import data
data = pd.read_csv(r"C:\Users\shubham lokare\Downloads\archive (4)\Naive-Bayes-Classification-Data.csv")
```

```
In [30]: data
```

```
Out[30]:
```

| | glucose | bloodpressure | diabetes |
|-----|---------|---------------|----------|
| 0 | 40 | 85 | 0 |
| 1 | 40 | 92 | 0 |
| 2 | 45 | 63 | 1 |
| 3 | 45 | 80 | 0 |
| 4 | 40 | 73 | 1 |
| ... | ... | ... | ... |
| 990 | 45 | 87 | 0 |
| 991 | 40 | 83 | 0 |
| 992 | 40 | 83 | 0 |
| 993 | 40 | 60 | 1 |
| 994 | 45 | 82 | 0 |

995 rows × 3 columns

```
In [31]: data.head(10)
```

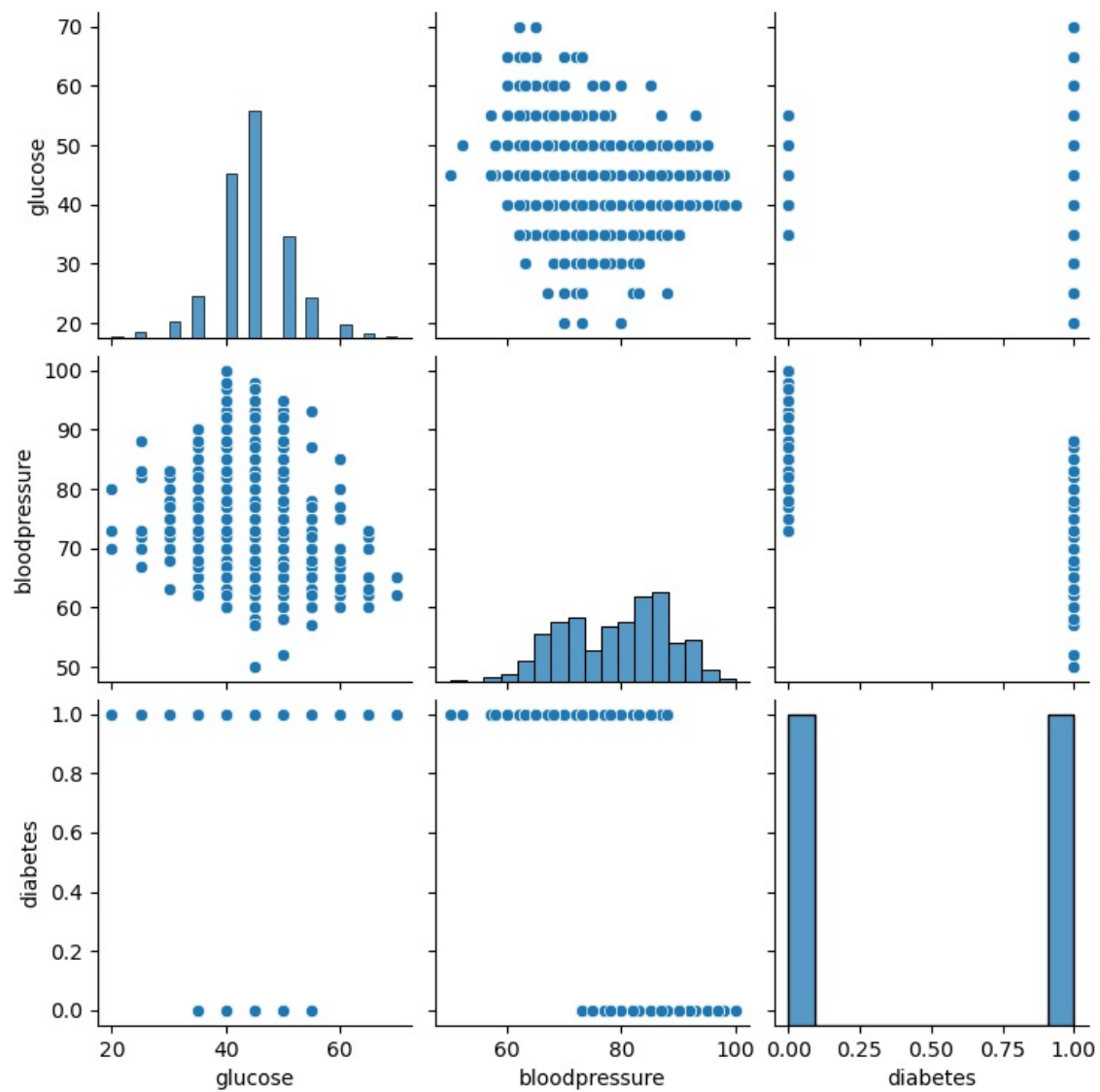
```
Out[31]:
```

| | glucose | bloodpressure | diabetes |
|---|---------|---------------|----------|
| 0 | 40 | 85 | 0 |
| 1 | 40 | 92 | 0 |
| 2 | 45 | 63 | 1 |
| 3 | 45 | 80 | 0 |
| 4 | 40 | 73 | 1 |
| 5 | 45 | 82 | 0 |
| 6 | 40 | 85 | 0 |
| 7 | 30 | 63 | 1 |
| 8 | 65 | 65 | 1 |
| 9 | 45 | 82 | 0 |

```
In [123]: #### plot pairplot
sns.pairplot(data)
```

```
C:\Users\shubham lokare\anaconda3\Lib\site-packages\seaborn\axisgrid.py:118: UserWarning: The figure layout has
changed to tight
  self.figure.tight_layout(*args, **kwargs)
```

```
Out[123]: <seaborn.axisgrid.PairGrid at 0x229019aef10>
```



In [54]: ##### split data into input and output variable

```
X = pd.DataFrame(data.iloc[:, :2])
Y = pd.DataFrame(data.iloc[:, 2])
```

In [55]: ### input variable

```
X
```

```
Out[55]:
```

| | 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 [56]: ### target  
Y
```

```
Out[56]:
```

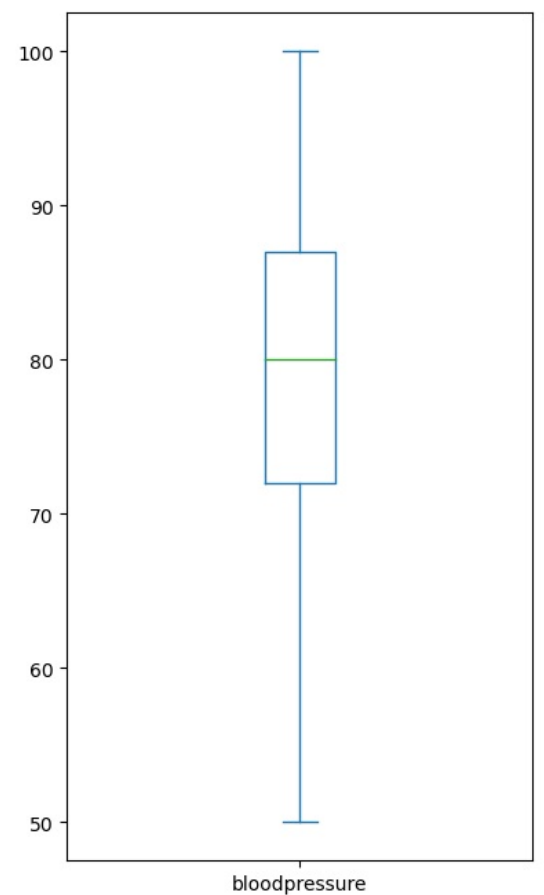
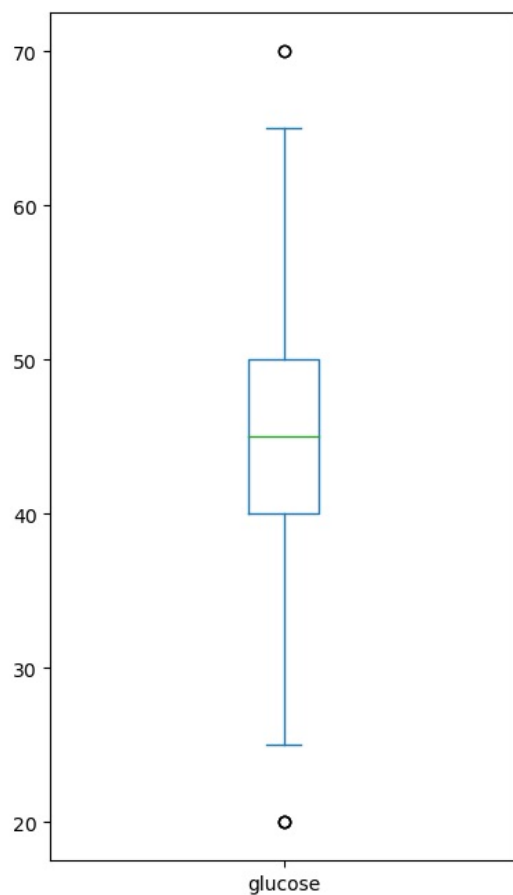
| | diabetes |
|-----|----------|
| 0 | 0 |
| 1 | 0 |
| 2 | 1 |
| 3 | 0 |
| 4 | 1 |
| ... | ... |
| 990 | 0 |
| 991 | 0 |
| 992 | 0 |
| 993 | 1 |
| 994 | 0 |

995 rows × 1 columns

```
In [57]: # check missing values  
data.isna().sum()
```

```
Out[57]: glucose      0  
bloodpressure  0  
diabetes      0  
dtype: int64
```

```
In [58]: ### check outliers  
X.plot(kind = 'box' , subplots = True , figsize = (12,8))  
plt.subplots_adjust(wspace = 0.75)  
plt.show()
```



```
In [62]: ### use winsorizer method to remove the outliers
from feature_engine.outliers import Winsorizer

winsor = Winsorizer(capping_method= 'iqr' ,
                    tail= 'both' ,
                    fold = 1.5 ,
                    variables=list(X.columns))
```

```
In [63]: new_data = winsor.fit_transform(X)
```

```
In [64]: new_data
```

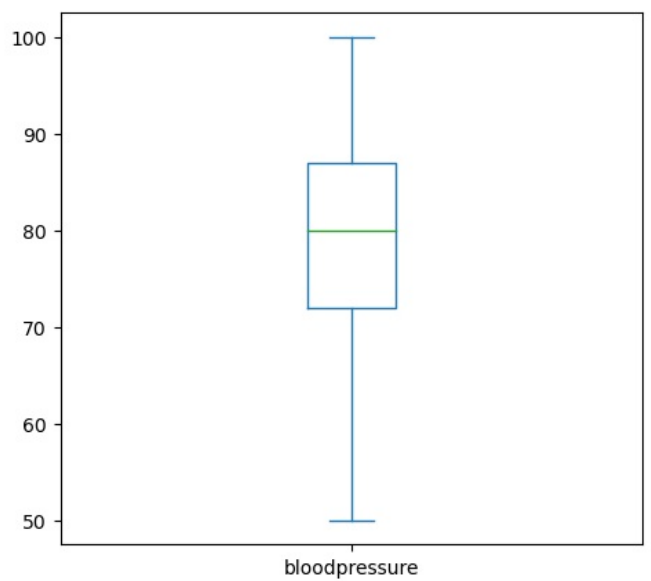
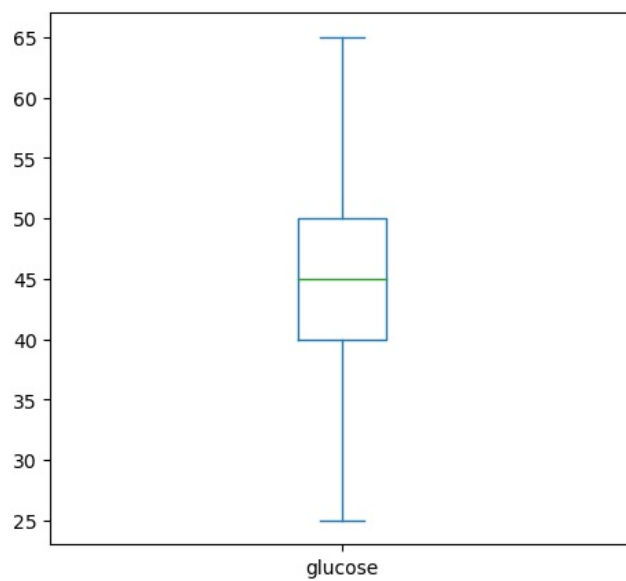
```
Out[64]:
```

| | 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 [65]: ### check the outliers are remove or not
new_data.plot(kind = 'box' , subplots = True , figsize = (12,5))
```

```
Out[65]: glucose          Axes(0.125,0.11;0.352273x0.77)
bloodpressure Axes(0.547727,0.11;0.352273x0.77)
dtype: object
```



```
In [66]: ### make the data into scale
from sklearn.preprocessing import StandardScaler

scale = StandardScaler()

scale_data = scale.fit_transform(new_data)
```

```
In [67]: clean_data = pd.DataFrame(scale_data)
```

```
In [68]: clean_data
```

```
Out[68]:
```

| | 0 | 1 |
|-----|-----------|-----------|
| 0 | -0.651307 | 0.622899 |
| 1 | -0.651307 | 1.372724 |
| 2 | 0.103997 | -1.733695 |
| 3 | 0.103997 | 0.087309 |
| 4 | -0.651307 | -0.662516 |
| ... | ... | ... |
| 990 | 0.103997 | 0.837134 |
| 991 | -0.651307 | 0.408663 |
| 992 | -0.651307 | 0.408663 |
| 993 | -0.651307 | -2.055049 |
| 994 | 0.103997 | 0.301545 |

995 rows × 2 columns

```
In [69]: clean_data.describe()
```

```
Out[69]:
```

| | 0 | 1 |
|-------|---------------|---------------|
| count | 9.950000e+02 | 9.950000e+02 |
| mean | -2.303015e-16 | 3.034982e-17 |
| std | 1.000503e+00 | 1.000503e+00 |
| min | -2.917216e+00 | -3.126227e+00 |
| 25% | -6.513066e-01 | -7.696339e-01 |
| 50% | 1.039965e-01 | 8.730915e-02 |
| 75% | 8.592996e-01 | 8.371343e-01 |
| max | 3.125209e+00 | 2.229667e+00 |

```
In [70]: #### apply model navies bayes
```

```
from sklearn.model_selection import train_test_split
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score ,classification_report
```

In [71]: *### train and test data*

```
X_train ,X_test , Y_train ,Y_test =train_test_split(clean_data , Y , test_size = 0.2 , random_state =0)
```

In [72]: *## train data*

```
X_train
```

```
Out[72]:
```

| | 0 | 1 |
|-----|-----------|-----------|
| 864 | 0.103997 | -0.662516 |
| 874 | 0.103997 | -2.055049 |
| 878 | -0.651307 | 0.837134 |
| 113 | 1.614603 | -2.055049 |
| 608 | 0.103997 | -0.662516 |
| ... | ... | ... |
| 835 | -0.651307 | -1.519459 |
| 192 | 0.103997 | 0.622899 |
| 629 | -0.651307 | 0.408663 |
| 559 | 0.859300 | 1.158488 |
| 684 | 0.859300 | -0.448280 |

796 rows × 2 columns

In [73]: *#### test data*

```
Y_test
```

```
Out[73]:
```

| | diabetes |
|-----|----------|
| 420 | 1 |
| 985 | 1 |
| 31 | 1 |
| 692 | 1 |
| 553 | 0 |
| ... | ... |
| 769 | 1 |
| 958 | 1 |
| 382 | 1 |
| 271 | 0 |
| 643 | 1 |

199 rows × 1 columns

In [75]: *### apply gaussianNB model*

```
model = GaussianNB()
model.fit(X_train ,Y_train)
```

C:\Users\shubham lokare\anaconda3\Lib\site-packages\sklearn\utils\validation.py:1184: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples,), for example using ravel().
y = column_or_1d(y, warn=True)

```
Out[75]:
```

▼ GaussianNB
 GaussianNB()

In [76]: `predict = model.predict(X_test)`

In [77]: `print(predict)`

```
[1 1 1 0 0 0 1 1 0 1 0 0 1 1 1 1 0 1 1 0 0 0 0 1 1 1 0 0 0 1 1 0 0 0 1 0
 1 1 1 1 1 0 0 0 1 0 1 0 0 0 0 1 0 0 0 0 1 1 0 1 0 1 0 1 0 0 1 1 1 0 1 0 1
 0 1 1 1 0 1 0 1 1 1 0 1 0 0 1 0 0 1 0 0 0 1 0 1 0 0 1 0 0 0 0 1 1 0 0
 1 1 0 1 1 0 0 0 1 1 0 1 1 1 0 0 1 1 0 1 1 1 1 0 0 1 1 0 0 1 1 1 1 0 1 0 0
 0 1 1 0 1 1 1 0 1 1 1 1 0 1 0 0 1 0 1 1 1 0 0 0 1 0 0 0 0 1 1 1 1 0 1 1 0
 0 1 1 1 1 0 1 0 1 1 0 1 0 1]
```

In [79]: *## check accuracy*

```
print('test accuracy :' , accuracy_score(Y_test , predict))
```

```
test accuracy : 0.9095477386934674
```

```
In [80]: ### classification reopr  
score =classification_report(Y_test , predict)
```

```
In [81]: print(score)
```

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 0.87 | 0.93 | 0.90 | 88 |
| 1 | 0.94 | 0.89 | 0.92 | 111 |
| accuracy | | | 0.91 | 199 |
| macro avg | 0.91 | 0.91 | 0.91 | 199 |
| weighted avg | 0.91 | 0.91 | 0.91 | 199 |

```
In [82]: ### cross check the model  
pd.crosstab(Y_test.diabetes, predict)
```

```
Out[82]:   col_0  0   1  
diabetes  
0      82   6  
1      12  99
```

```
In [83]: ### also check confusion metrics  
from sklearn.metrics import confusion_matrix
```

```
In [84]: conf = confusion_matrix(Y_test , predict)
```

```
In [85]: conf
```

```
Out[85]: array([[82,  6],  
               [12, 99]], dtype=int64)
```

```
In [87]: print("True Positive :" , conf[1,1])  
True Positive : 99
```

```
In [89]: print("Flase Positive:" ,conf[1,0])  
Flase Positive: 12
```

```
In [90]: print("False negative :" , conf[0,1])  
False negative : 6
```

```
In [91]: print("True negitive :" , conf[0 ,0])  
True negative : 82
```

```
In [115]: ### hyperparameter tuning  
from sklearn.model_selection import GridSearchCV  
gnb = GaussianNB()
```

```
In [116]: param_grid = {  
    'priors': [None], # Example values for priors  
    'var_smoothing': [1e-9, 1e-8, 1e-7] # Example values for var_smoothing  
}
```

```
In [117]: grid = GridSearchCV(gnb , param_grid , scoring='accuracy' , cv =8 ,verbose=1)  
grid.fit(X_train , Y_train)
```

```
Fitting 8 folds for each of 3 candidates, totalling 24 fits
```

```
C:\Users\shubham lokare\anaconda3\Lib\site-packages\sklearn\utils\validation.py:1184: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
```

```
y = column_or_1d(y, warn=True)
```

```
C:\Users\shubham lokare\anaconda3\Lib\site-packages\sklearn\utils\validation.py:1184: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
```

```
y = column_or_1d(y, warn=True)
```

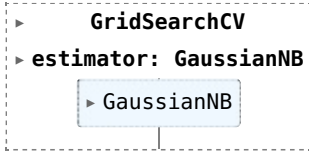
```
C:\Users\shubham lokare\anaconda3\Lib\site-packages\sklearn\utils\validation.py:1184: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
```

```
y = column_or_1d(y, warn=True)
```

```
C:\Users\shubham lokare\anaconda3\Lib\site-packages\sklearn\utils\validation.py:1184: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
```

[illegible]

Out[117]:



In [118... grid.best_params_

Out[118]: {'priors': None, 'var_smoothing': 1e-09}

In [119... predict = grid.predict(X_test)

In [120... predict

Out[120]: array([1, 1, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0, 0,
0, 0, 1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0,
0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, 1, 0,
0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 0, 1, 0, 0,
1, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0,
0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 1, 1,
1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 0, 1, 1,
1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0,
0, 1, 1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0,
1], dtype=int64)

In [121... print("test Accureacy :", accuracy_score(Y_test , predict))

test Accureacy : 0.9095477386934674

In []:

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