```
data shape: (1150, 20)
```

## data head

accuracy score accuracy of different models 0.4956521739130435 0.5652173913043478 0.5347826086956522 0.5043478260869565

cross validation 0.6243478260869566

best parameters

{'max\_depth': 20, 'max\_features': 10, 'min\_samples\_leaf': 20} 0.6521739130434783

accuracy of the model 0.6034782608695652

accuracy of gaussian cross validation 0.5947826086956522

[[500 39] [422 189]]

precision recall f1-score support

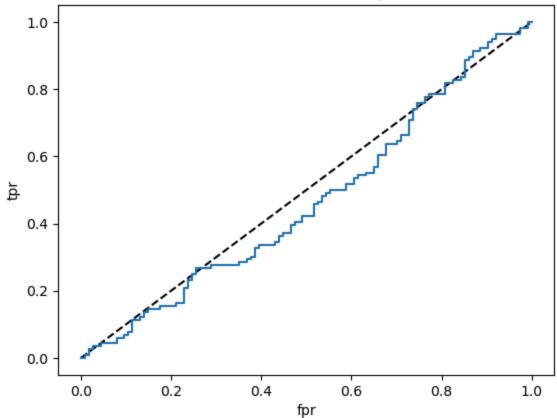
0 0.54 0.93 0.68 539

1 0.83 0.31 0.45 611

accuracy 0.60 1150 macro avg 0.69 0.62 0.57 1150 weighted avg 0.69 0.60 0.56 1150

area under the curve score, \((how reliable our model is\) 0.46748336358136716

## **ROC Curve Naive Bayes**



accuracy of cross val of pipeline 0.6182608695652174

optimal parameters for accuracy with pipeline model {'kn\_\_n\_neighbors': 23, 'pca\_\_n\_components': 14} 0.6617391304347826

accuracy of cross validation on gSearch2 0.6417391304347827

accuracy of cross validation on gSearch3 0.717391304347826

accuracy of cross validation on gSearch4 0.7278260869565217

## classification report

рі	recision	recall	f1-score	support	
0	0.54	0.93	0.68	539	
1	0.83	0.31	0.45	611	

accuracy	0.60 1150			
macro avg	0.69	0.62	0.57	1150
weighted avg	0.69	0.60	0.56	1150

classification report with updated parameters precision recall f1-score support

0 0.66 0.71 0.68 539 1 0.72 0.67 0.70 611

accuracy 0.69 1150 macro avg 0.69 0.69 0.69 1150 weighted avg 0.69 0.69 0.69 1150

Positive for disease