Accuracy and Confusion Matrix

In [1]:
```
import pandas as pd
import numpy as np
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report,roc_auc_score,confusion_matrix
```

In [2]:
```
from  sklearn.datasets import load_breast_cancer
```

In [3]:
```
Cancer = load_breast_cancer()
```

In [4]:
```
print(load_breast_cancer()['DESCR'])
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

    :Number of Instances: 569

    :Number of Attributes: 30 numeric, predictive attributes and the class

    :Attribute Information:
        - radius (mean of distances from center to points on the perimeter)
        - texture (standard deviation of gray-scale values)
        - perimeter
        - area
        - smoothness (local variation in radius lengths)
        - compactness (perimeter^2 / area - 1.0)
        - concavity (severity of concave portions of the contour)
        - concave points (number of concave portions of the contour)
        - symmetry
        - fractal dimension ("coastline approximation" - 1)

        The mean, standard error, and "worst" or largest (mean of the three
        worst/largest values) of these features were computed for each image,
        resulting in 30 features.  For instance, field 0 is Mean Radius, field
        10 is Radius SE, field 20 is Worst Radius.

        - class:
                - WDBC-Malignant
                - WDBC-Benign

    :Summary Statistics:

    ===================================== ====== ======
                                           Min    Max
    ===================================== ====== ======
    radius (mean):                        6.981  28.11
    texture (mean):                       9.71   39.28
```

```
    perimeter (mean):                     43.79  188.5
    area (mean):                          143.5  2501.0
    smoothness (mean):                    0.053  0.163
    compactness (mean):                   0.019  0.345
    concavity (mean):                     0.0    0.427
    concave points (mean):                0.0    0.201
    symmetry (mean):                      0.106  0.304
    fractal dimension (mean):             0.05   0.097
    radius (standard error):              0.112  2.873
    texture (standard error):             0.36   4.885
    perimeter (standard error):           0.757  21.98
    area (standard error):                6.802  542.2
    smoothness (standard error):          0.002  0.031
    compactness (standard error):         0.002  0.135
    concavity (standard error):           0.0    0.396
    concave points (standard error):      0.0    0.053
    symmetry (standard error):            0.008  0.079
    fractal dimension (standard error):   0.001  0.03
    radius (worst):                       7.93   36.04
    texture (worst):                      12.02  49.54
    perimeter (worst):                    50.41  251.2
    area (worst):                         185.2  4254.0
    smoothness (worst):                   0.071  0.223
    compactness (worst):                  0.027  1.058
    concavity (worst):                    0.0    1.252
    concave points (worst):               0.0    0.291
    symmetry (worst):                     0.156  0.664
    fractal dimension (worst):            0.055  0.208
    ===================================== ====== ======

    :Missing Attribute Values: None

    :Class Distribution: 212 - Malignant, 357 - Benign

    :Creator:  Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

    :Donor: Nick Street

    :Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2 (https://goo.gl/U2Uwz2)
```

```
Features are computed from a digitized image of a fine needle
aspirate (FNA) of a breast mass.  They describe
characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using
Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree.  Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. topic:: References

   - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
     for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
     Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
     San Jose, CA, 1993.
   - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
     prognosis via linear programming. Operations Research, 43(4), pages 570-577,
     July-August 1995.
   - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
     to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994)
     163-171.
```

In [5]:

```
y = Cancer.target
```

In [6]:
```
X = pd.DataFrame(Cancer.data, columns=Cancer.feature_names)
X.head()
```

Out[6]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst radius	worst texture	worst perimeter	worst area
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	...	25.38	17.33	184.60	2019.0
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	...	24.99	23.41	158.80	1956.0
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	...	23.57	25.53	152.50	1709.0
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	...	14.91	26.50	98.87	567.7
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	...	22.54	16.67	152.20	1575.0

5 rows × 30 columns

In [7]:
```
from sklearn.metrics import confusion_matrix,accuracy_score
```

In [8]:
```
clf = KNeighborsClassifier()
clf.fit(X,y)
```

Out[8]:
```
KNeighborsClassifier()
```

In [9]:
```
y
```

Out[9]:
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0,
       1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0,
       1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1,
       1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0,
       0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
       1, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0,
       1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
       1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0,
       0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0,
       0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0,
       1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 1,
       1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1,
       1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0,
       1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
       1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1,
       1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1])
```

In [14]:

```
print(accuracy_score(y,clf.predict(X))*100)

print(confusion_matrix(y,clf.predict(X)))
#94.72% -> Accurately classified
#5.28% -> Misclassified


```

```
94.72759226713534
[[191  21]
 [  9 348]]
```

In [15]:

```
(191+348)/X.shape[0]
```

Out[15]:

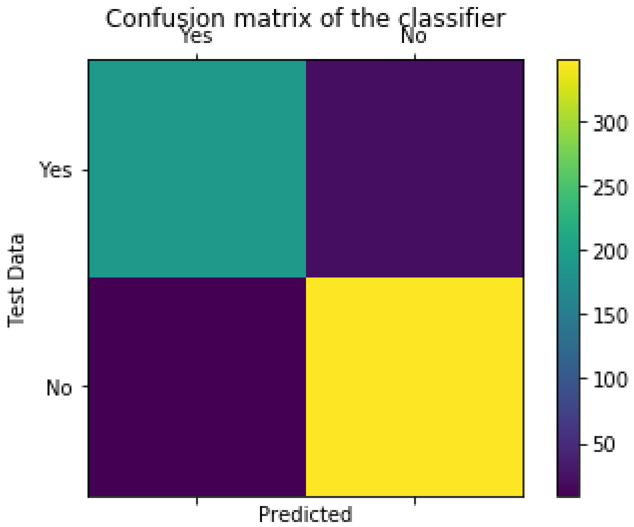
```
0.9472759226713533
```

In [16]:
```python
import matplotlib.pyplot as plt
plt.figure(figsize=(25, 25))
labels = ['Yes','No']
cm = confusion_matrix(y, clf.predict(X))
print(cm)
fig = plt.figure()
ax = fig.add_subplot(111)
cax = ax.matshow(cm)
plt.title('Confusion matrix of the classifier')
fig.colorbar(cax)
ax.set_xticklabels([''] + labels)
ax.set_yticklabels([''] + labels)
plt.xlabel('Predicted')
plt.ylabel('Test Data')
```

```
[[191  21]
 [  9 348]]
```

Out[16]:
```
Text(0,0.5,'Test Data')
```

```
<Figure size 1800x1800 with 0 Axes>
```



RoC_AUC

Roc - > Reciever Operator Char.

Auc - > Area Under the Curve

True Positivity rate(Sensitivity) = Tp/(Fn+Tp)

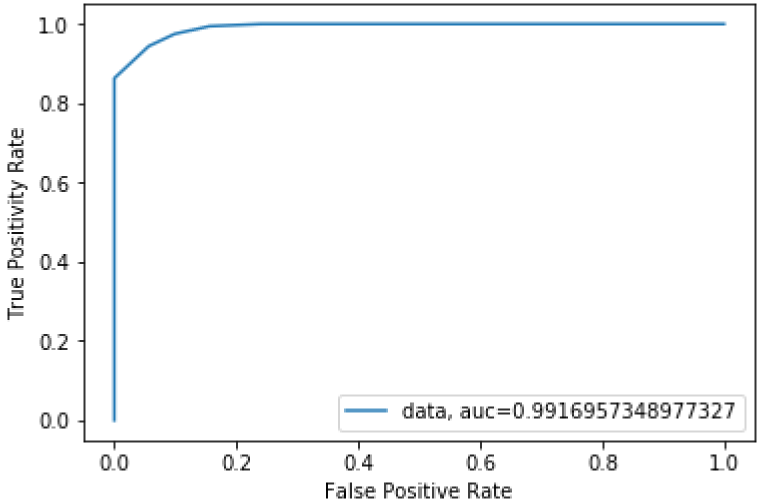
True Negative rate(Specifity) = Tn/(Fp+Tn)

False Positive rate = Fp/(Tn+Fp)

In [18]:
```
from sklearn import metrics
```

In [20]:
```
y_pred_proba = clf.predict_proba(X)[::,1]
fpr, tpr, _ = metrics.roc_curve(y,  y_pred_proba)
auc = metrics.roc_auc_score(y, y_pred_proba)
```

In [62]:
```
y_pred_proba = clf.predict_proba(X)[::,1]
fpr, tpr, _ = metrics.roc_curve(y,  y_pred_proba)
auc = metrics.roc_auc_score(y, y_pred_proba)
plt.plot(fpr,tpr,label="data, auc="+str(auc))
plt.legend(loc=4)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positivity Rate')
plt.show()
```



In [63]:
```
from sklearn.metrics import roc_auc_score
```

In [64]:
```
roc_auc_score(clf.predict(X),y)
```

Out[64]:
```
0.9490447154471544
```

Classification Report => Accuracy,Recall,Precision,F1 Score(Combination of precision and Recall)

In [65]:
```
from sklearn.metrics import classification_report
```

In [66]:
```
print(classification_report(clf.predict(X),y))
```

```
              precision    recall  f1-score   support

           0       0.90      0.95      0.93       200
           1       0.97      0.94      0.96       369

    accuracy                           0.95       569
   macro avg       0.94      0.95      0.94       569
weighted avg       0.95      0.95      0.95       569
```

In [ ]:
```

```

Precision

Precision = Tp/Tp+Fp

Ratio of correctly predicted positives to total predicted positives

What proportion of predicted positive values are actually positive

Model Effectiveness on the captured variation

Example :

Business use case is (We want to decrease credit limit - > Target[Whether to decrease limit or not])) and our priority is customer satisfaction so we want to avoid all cases where we decrease limit of a customer that can afford the higher limit.

Classification model: 1 -> Can decrease limit 0 -> Cannot decrease limit

False Positive Case -> We decrease cr limit of a person who can afford it (Predicted : 1 actual : 0)

Advantage of high precision:

To decrease FP cases we increase threshold : 0.9 :: Higher Threshold of positive classification == Higher precision value

Disadvantage of chasing a high precision with higher thresholds:

1.) Since we have a high threshold of prob for default to decrease the credit limit (i.e. 90%) we give higher credit limits to people with 80% chance of default that means we are giving riskier loans and hence there is a higher chance of losing money.

Recall

recall = Tp/(Tp+Fn)

Ratio of all correctly predicted positive values to all the positive values

What proportion of actual positives are predicted positives

Of how well your data is engineered and also a combination of how well you've selected your model on the basis of your data(Recall depends a lot on your data)

F-1 Score

Harmonic Mean of Precision and Recall

F1 = 2*(Precision X recall)/(Precision+recall)

Weighted Average of acc, Precision and Recall