Breast Cancer Detection *(Project)*

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```
#importing the essental libraries

import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
```

```
# Load The Data
from sklearn.datasets import load_breast_cancer
#loading the Breast cancer data in a variable
cancer = load_breast_cancer()
```

```
cancer
```

```
{'DESCR': '.. _breast_cancer_dataset:\n\nBreast cancer wisconsin (diagnostic) dataset\
 'data': array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
         1.189e-01],
        [2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
         8.902e-02],
        [1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
         8.758e-02],
        ...,
        [1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
         7.820e-02],
        [2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
         1.240e-01],
        [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
         7.039e-02]]),
 'data_module': 'sklearn.datasets.data',
 'feature_names': array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
        'mean smoothness', 'mean compactness', 'mean concavity',
        'mean concave points', 'mean symmetry', 'mean fractal dimension',
        'radius error', 'texture error', 'perimeter error', 'area error',
        'smoothness error', 'compactness error', 'concavity error',
        'concave points error', 'symmetry error',
        'fractal dimension error', 'worst radius', 'worst texture',
        'worst perimeter', 'worst area', 'worst smoothness',
        'worst compactness', 'worst concavity', 'worst concave points',
        'worst symmetry', 'worst fractal dimension'], dtype='<U23'),
 'filename': 'breast_cancer.csv',
 'frame': None,
 'target': array([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, 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, 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, 1, 0, 0, 0, 0, 0, 0, 1]),
 'target_names': array(['malignant', 'benign'], dtype='<U9')}
```

```
cancer.keys()
#Printing the keys of the Dictionary, to get enough details about the data.
```

```
dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_names', 'filen
```

```
print(cancer['DESCR'])
#Will basically gve you broad description of Breast Cancer Dataset
```

```
        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

    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.
```

```
print(cancer['target'])
#Printing the Target column, which is either 0=Malignenet or 1=Benign
```

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

```
print(cancer['target_names'])
#printing the Target names
```

```
['malignant' 'benign']
```

```
print(cancer['feature_names'])

#All the column names which are also known as features
```

```
['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
```

```
      'worst smoothness' 'worst compactness' 'worst concavity'
      'worst concave points' 'worst symmetry' 'worst fractal dimension']
```

```
cancer['data'].shape

#Shape of the Data which is 569 Rows and 30 Columns
```

```
    (569, 30)
```

```
df_cancer = pd.DataFrame(np.c_[cancer['data'], cancer['target']], columns= np.append(cancer

#Creating a Pandas DataFrame to deal with the data in a much easier way.
#While creating this DataFrame I added the additional column which is 'target' to the df_ca
```

```
df_cancer.head()
```

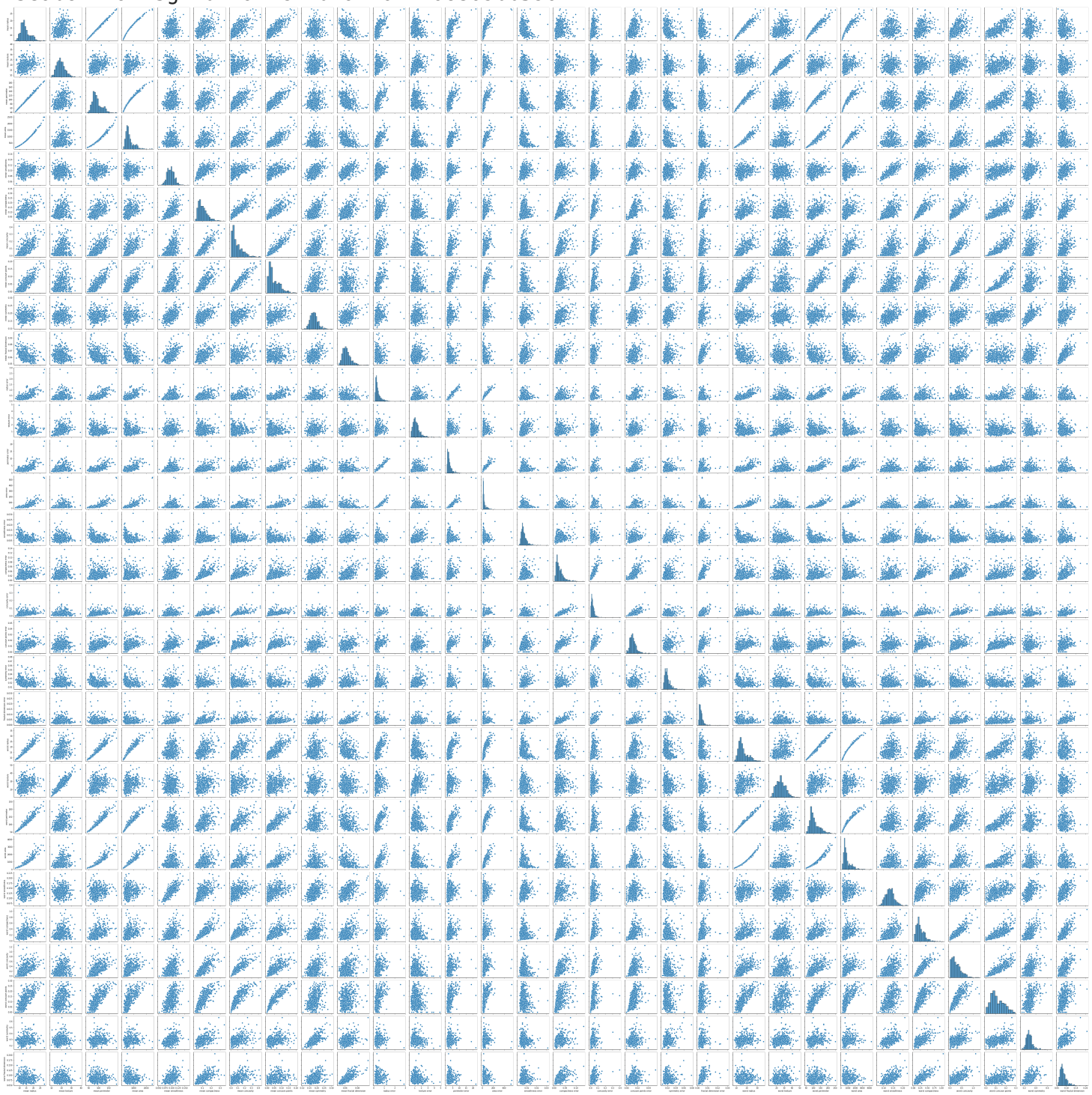
	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	m symme
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1

5 rows × 31 columns

Visualising the data

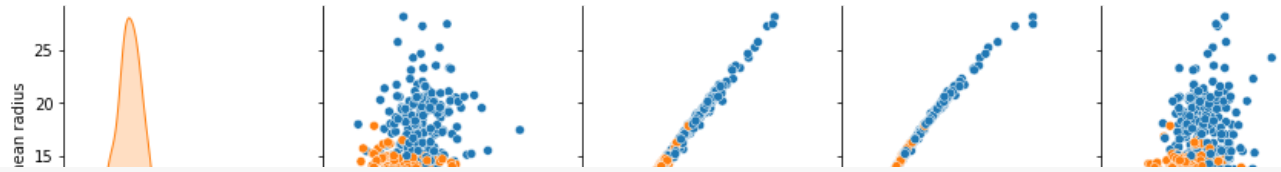
```
sns.pairplot(df_cancer , vars =['mean radius','mean texture', 'mean perimeter', 'mean area'
 'mean smoothness', 'mean compactness' ,'mean concavity',
 'mean concave points', 'mean symmetry', 'mean fractal dimension',
 'radius error', 'texture error', 'perimeter error', 'area error',
 'smoothness error', 'compactness error', 'concavity error',
 'concave points error', 'symmetry error', 'fractal dimension error',
 'worst radius', 'worst texture', 'worst perimeter', 'worst area',
 'worst smoothness', 'worst compactness', 'worst concavity',
 'worst concave points', 'worst symmetry', 'worst fractal dimension'])
```

<seaborn.axisgrid.PairGrid at 0x7f06809bb590>



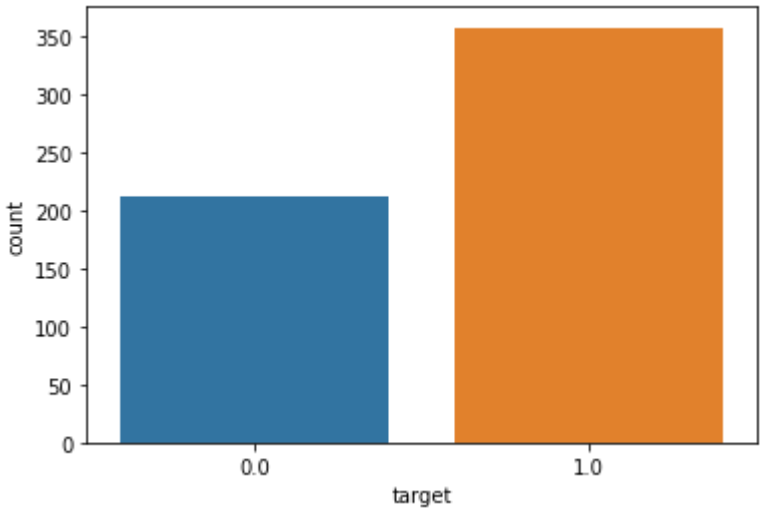
```
#in above plotting we are not able to differentiate much,so we use 'hue' on target column, w
sns.pairplot(df_cancer, hue = 'target', vars = ['mean radius', 'mean texture', 'mean perime
 'mean smoothness'])

#blue points are malignent case which are severe cases or life threatning cases.
#orange points are not very severe or life threatning
```

```
<seaborn.axisgrid.PairGrid at 0x7f06694b87d0>
```



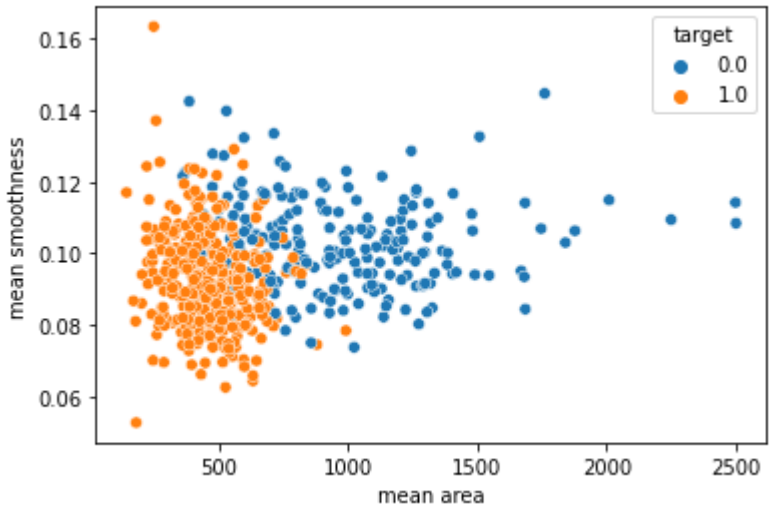

```
#will simply tell you how many Malignent and Benign cases we have.
#Malignent= 200~ and Benign = 350~ approx.
sns.countplot(df_cancer['target'])
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass
  FutureWarning
<matplotlib.axes._subplots.AxesSubplot at 0x7f0664a1c7d0>
```



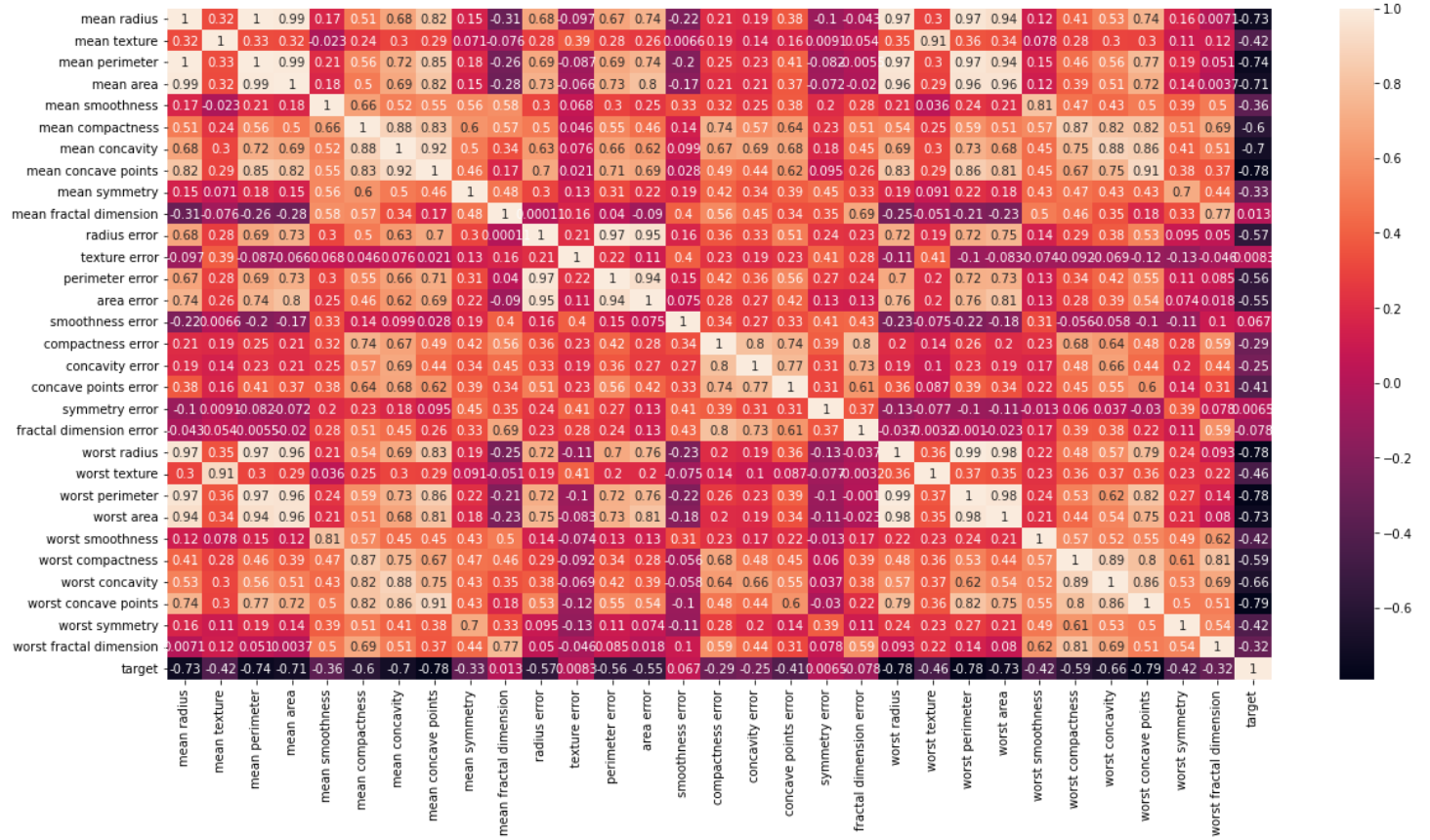

```
#plotting a scatter plot diagram for mean area anf mean smoothness, you can plot any featur
sns.scatterplot(x='mean area',y='mean smoothness',hue='target',data =df_cancer)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f0664890350>
```




```
#here we made a heatmap figure of correlation of all the columns
plt.figure(figsize =(20,10))
sns.heatmap(df_cancer.corr(), annot =True)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f06648e0450>
```



SPLITTING THE DATASET

```
x = df_cancer.drop(['target'],axis =1)
#train test split
```

```
x
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	sym
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	
...	...	...	...	...	...	...	...	...	

```
y= df_cancer['target']
y
```

```
0      0.0
1      0.0
2      0.0
3      0.0
4      0.0
      ...
564    0.0
565    0.0
566    0.0
567    0.0
568    1.0
Name: target, Length: 569, dtype: float64
```

```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=5)
```

```
x_train
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	sym

```
y_train
```

```
306    1.0
410    1.0
197    0.0
376    1.0
244    0.0
      ...
8      0.0
73     0.0
400    0.0
118    0.0
206    1.0
Name: target, Length: 455, dtype: float64
```

```
y_test
```

```
28     0.0
163    1.0
123    1.0
361    1.0
549    1.0
      ...
414    0.0
515    1.0
186    0.0
3      0.0
261    0.0
Name: target, Length: 114, dtype: float64
```

TRAINING THE MODEL USING LOGISTIC REGRESSION

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report , confusion_matrix
```

```
logistic_model = LogisticRegression(random_state = 0)
logistic_model.fit(x_train, y_train)
```

```
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:818: Converge
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
LogisticRegression(random_state=0)
```

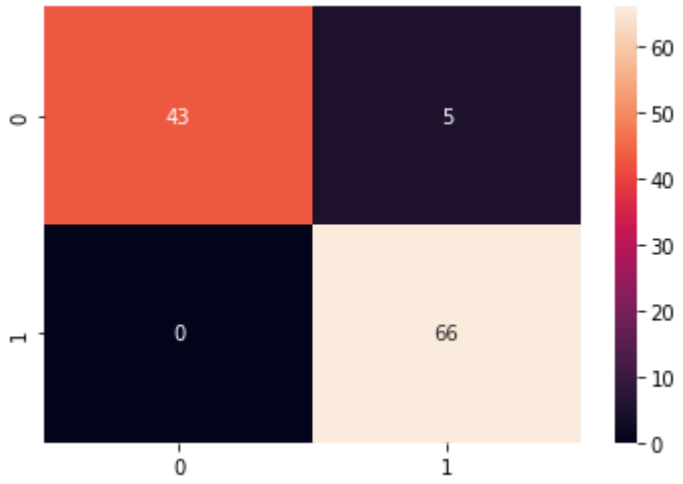
```
y_predict =logistic_model.predict(x_test)
y_predict
```

```
array([0., 1., 1., 1., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 0., 1., 0., 0., 0., 0., 0.,
       1., 1., 0., 1., 1., 0., 1., 1., 1., 0., 1., 1., 0., 0., 1., 0., 1.,
       1., 1., 1., 1., 0., 0., 0., 1., 0., 0., 0., 1., 1., 1., 1., 1., 1.,
       1., 0., 1., 0., 1., 1., 1., 1., 0., 1., 0., 1., 0., 1., 0., 0., 0.,
       1., 0., 1., 0., 0., 0., 0., 1., 1., 0., 0., 1., 1., 1., 1., 1., 0.,
       1., 1., 0., 0., 1., 0., 1., 0., 1., 0., 1., 0.])
```

```
cm = confusion_matrix(y_test,y_predict)
```

```
sns.heatmap(cm ,annot=True)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f0663a8d490>
```




```
print(classification_report(y_test,y_predict))
```

```
              precision    recall  f1-score   support

         0.0       1.00      0.90      0.95        48
         1.0       0.93      1.00      0.96        66

    accuracy                           0.96       114
   macro avg       0.96      0.95      0.95       114
weighted avg       0.96      0.96      0.96       114
```

The accuracy we recieved is 96% or 95.8% for exact accuracy.

Using KNeighborsClassifier Method of neighbors class to use Nearest Neighbor algorithm

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report , confusion_matrix
```

```
knn_model = KNeighborsClassifier(n_neighbors = 5, metric = 'minkowski', p = 2)
knn_model.fit(x_train, y_train)
```

```
KNeighborsClassifier()
```

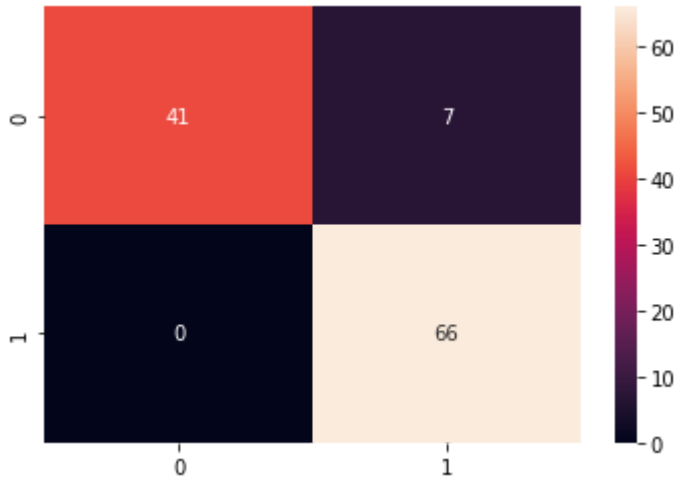
```
y_predict =knn_model.predict(x_test)
y_predict
```

```
array([0., 1., 1., 1., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 0., 0., 1., 0., 0., 0., 1., 0.,
       1., 1., 0., 1., 1., 0., 1., 1., 1., 0., 1., 1., 0., 0., 1., 0., 1.,
       1., 1., 1., 1., 0., 1., 0., 1., 0., 0., 0., 1., 1., 1., 1., 1., 1.,
       1., 0., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 0., 1., 0., 0., 0.,
       1., 0., 1., 0., 0., 0., 0., 1., 1., 0., 0., 1., 1., 1., 1., 1., 0.,
       1., 1., 0., 0., 1., 0., 1., 0., 1., 0., 1., 0.])
```

```
cm = confusion_matrix(y_test,y_predict)
```

```
sns.heatmap(cm ,annot=True)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f0663807690>
```




```
from sklearn import metrics
print("Train set Accuracy: ", metrics.accuracy_score(y_train, knn_model.predict(x_train)))
print("Test set Accuracy: ", metrics.accuracy_score(y_test, y_predict))
```

```
Train set Accuracy:  0.945054945054945
Test set Accuracy:  0.9385964912280702
```

```
print(classification_report(y_test,y_predict))
```

```
              precision    recall  f1-score   support

         0.0       1.00      0.85      0.92        48
         1.0       0.90      1.00      0.95        66

    accuracy                           0.94       114
   macro avg       0.95      0.93      0.94       114
weighted avg       0.94      0.94      0.94       114
```

Trying for a random k value for example 9

```
k = 9

neigh6 = KNeighborsClassifier(n_neighbors = k).fit(x_train,y_train)
```

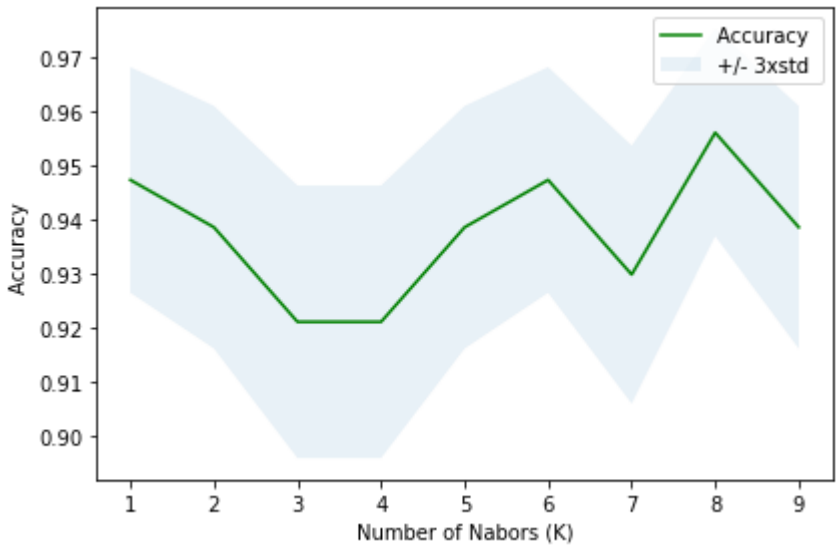
```
yhat6 = neigh6.predict(x_test)

print("Train set Accuracy: ", metrics.accuracy_score(y_train, neigh6.predict(x_train)))
print("Test set Accuracy: ", metrics.accuracy_score(y_test, yhat6))
```

```
Train set Accuracy:  0.9384615384615385
Test set Accuracy:  0.9385964912280702
```

```
Ks = 10
mean_acc = np.zeros((Ks-1))
std_acc = np.zeros((Ks-1))
ConfustionMx = [];
for n in range(1,Ks):

    #Train Model and Predict
    neigh = KNeighborsClassifier(n_neighbors = n).fit(x_train,y_train)
    yhat=neigh.predict(x_test)
    mean_acc[n-1] = metrics.accuracy_score(y_test, yhat)


    std_acc[n-1]=np.std(yhat==y_test)/np.sqrt(yhat.shape[0])

mean_acc
```

```
array([0.94736842, 0.93859649, 0.92105263, 0.92105263, 0.93859649,
       0.94736842, 0.92982456, 0.95614035, 0.93859649])
```

```
plt.plot(range(1,Ks),mean_acc,'g')
plt.fill_between(range(1,Ks),mean_acc - 1 * std_acc,mean_acc + 1 * std_acc, alpha=0.10)
plt.legend(('Accuracy ', '+/- 3xstd'))
plt.ylabel('Accuracy ')
plt.xlabel('Number of Nabors (K)')
plt.tight_layout()
plt.show()
```




```
print( "The best accuracy was with", mean_acc.max(), "with k=", mean_acc.argmax()+1)
```

```
The best accuracy was with 0.956140350877193 with k= 8
```

```
k = 8
```

```
neigh6 = KNeighborsClassifier(n_neighbors = k).fit(x_train,y_train)

yhat6 = neigh6.predict(x_test)

print("Train set Accuracy: ", metrics.accuracy_score(y_train, neigh6.predict(x_train)))
print("Test set Accuracy: ", metrics.accuracy_score(y_test, yhat6))
```

```
Train set Accuracy:  0.9318681318681319
Test set Accuracy:  0.956140350877193
```

Now that we have the value of k, we can try to improve the accuracy for our model

```
knn_model = KNeighborsClassifier(n_neighbors = 8, metric = 'minkowski', p = 2)
knn_model.fit(x_train, y_train)
```

```
KNeighborsClassifier(n_neighbors=8)
```

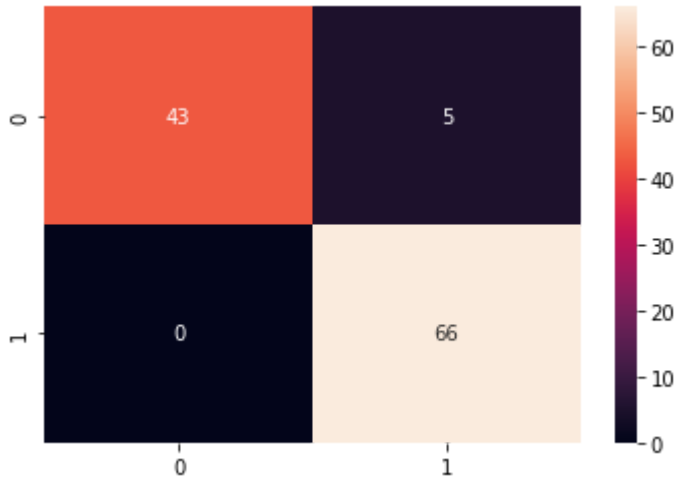
```
y_predict =knn_model.predict(x_test)
y_predict
```

```
array([0., 1., 1., 1., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 1., 1., 1.,
       1., 1., 1., 0., 1., 1., 1., 1., 1., 0., 0., 1., 0., 0., 0., 1., 0.,
       1., 1., 0., 1., 1., 0., 1., 1., 1., 0., 1., 1., 0., 0., 1., 0., 1.,
       1., 1., 1., 1., 0., 0., 0., 1., 0., 0., 0., 1., 1., 1., 1., 1., 1.,
       1., 0., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 0., 1., 0., 0., 0.,
       1., 0., 1., 0., 0., 0., 0., 1., 1., 0., 0., 1., 1., 1., 1., 1., 0.,
       1., 1., 0., 0., 1., 0., 1., 0., 1., 0., 1., 0.])
```

```
cm = confusion_matrix(y_test,y_predict)
```

```
sns.heatmap(cm ,annot=True)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f0664016a50>
```




```
from sklearn import metrics
print("Train set Accuracy: ", metrics.accuracy_score(y_train, neigh.predict(x_train)))
print("Test set Accuracy: ", metrics.accuracy_score(y_test, yhat))
```

```
Train set Accuracy:  0.9384615384615385
```

```
Test set Accuracy:  0.9385964912280702
```

```
print(classification_report(y_test,y_predict))
```

```
                precision    recall  f1-score   support

           0.0       1.00      0.90      0.95        48
           1.0       0.93      1.00      0.96        66

      accuracy                           0.96       114
     macro avg       0.96      0.95      0.95       114
  weighted avg       0.96      0.96      0.96       114
```

As we can see the Test set accuracy for the model has increased from 94% to 96% when taken the best value for nearest neighbours

TRAINING THE MODEL USING SVM

```
from sklearn.svm import SVC
from sklearn.metrics import classification_report , confusion_matrix
```

```
from sklearn.svm import SVC
svm_model = SVC(kernel = 'linear', random_state = 0)
svm_model.fit(x_train, y_train)
```

```
SVC(kernel='linear', random_state=0)
```

```
y_predict =svm_model.predict(x_test)
```

```
y_predict
```

```
array([0., 1., 1., 1., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 1., 1., 1.,
       1., 1., 1., 0., 1., 1., 1., 1., 1., 0., 0., 1., 0., 0., 0., 1., 0.,
       1., 1., 0., 1., 1., 0., 1., 1., 1., 0., 1., 1., 0., 0., 1., 0., 1.,
       1., 1., 1., 1., 0., 0., 0., 1., 0., 0., 0., 1., 1., 1., 1., 1., 1.,
       1., 0., 1., 0., 1., 1., 1., 1., 0., 1., 0., 0., 0., 1., 0., 0., 0.,
       1., 0., 1., 0., 0., 0., 0., 1., 1., 0., 0., 1., 1., 1., 1., 1., 0.,
       1., 1., 0., 0., 0., 0., 1., 0., 1., 0., 0., 0.])
```

```
cm = confusion_matrix(y_test,y_predict)
sns.heatmap(cm ,annot=True)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f06635fee10>
```

CALCULATING F1 SCORE

```
from sklearn.metrics import f1_score
f1_score(y_test, yhat, average='weighted')
```

```
0.9377278780169241
```