CASE STUDY: BREAST CANCER CLASSIFICATION

STEP #1: PROBLEM STATEMENT

- Predicting if the cancer diagnosis is benign or malignant based on several observations/features
- 30 features are used, examples:
 - 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)
- Datasets are linearly separable using all 30 input features
- Number of Instances: 569
- Class Distribution: 212 Malignant, 357 Benign
- · Target class:
 - Malignant
 - Benign

https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic)

STEP #2: IMPORTING DATA

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In [1]:
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```
# import libraries
import pandas as pd # Import Pandas for data manipulation using dataframes
import numpy as np # Import Numpy for data statistical analysis
import matplotlib.pyplot as plt # Import matplotlib for data visualisation
import seaborn as sns # Statistical data visualization
# %matplotlib inline
```

```
In [2]:
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```
# Import Cancer data drom the Sklearn library
from sklearn.datasets import load_breast_cancer
cancer = load_breast_cancer()
```

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In [3]:
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```
cancer
Out[3]:
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I. 440E-01],
           [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
           7.039e-0211),
 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,
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          0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0,
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          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,
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          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, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1]),
 'target names': array(['malignant', 'benign'], dtype='<U9'),
 'DESCR': 'Breast Cancer Wisconsin (Diagnostic)
Database\n======\n\nNotes\n----\nData Set
Characteristics:\n :Number of Instances: 569\n\n :Number of Attributes: 30 numeric, predictiv
e attributes and the class\n\n :Attribute Information:\n - radius (mean of distances from
center to points on the perimeter) \  - texture (standard deviation of gray-scale values) \  \n
- perimeter\n - area\n - smoothness (local variation in radius lengths)\n - cc
mpactness (perimeter^2 / area - 1.0)\n - concavity (severity of concave portions of the
contour)\n - concave points (number of concave portions of the contour)\n - symmetry
\n - fractal dimension ("coastline approximation" - 1)\n\n The mean, standard error,
and "worst" or largest (mean of the three\n largest values) of these features were computed
for each image,\n resulting in 30 features. For instance, field 3 is Mean Radius, field\n
13 is Radius SE, field 23 is Worst Radius.\n\n - class:\n
                                                                                                      - WDBC-Malignant\n
=\n
                                                                         6.981 28.11\n texture (mean):
====== ====\n
                      radius (mean):
9.71 39.28\n perimeter (mean):
143.5 2501.0\n smoothness (mean):
                                                                        43.79 188.5\n
                                                                                               area (mean):
                                                                        0.053 0.163\n compactness (mean):
0.019 0.345\n concavity (mean):
                                                                       0.0 0.427\n concave points (mean):
                                                                        0.106 0.304\n fractal dimension (mean):
0.0
        0.201\n symmetry (mean):
0.05 0.097\n radius (standard error): 0.112 2.873\n texture (standard error): 0.36 4.885\n perimeter (standard error): 0.757 21.98\n area (standard error): 6.802 542.2\n smoothness (standard error): 0.002 0.031\n compactness (standard error)
or): 0.002 0.135\n concavity (standard error): 0.0 0.396\n concave points (standard error): 0.0 0.053\n symmetry (standard error): 0.008 0.079\n
fractal dimension (standard error): 0.001 0.03\n radius (worst):
                                                                                                                        7.93
                                                          12.02 49.54\n perimeter (worst):
36.04\n texture (worst):
                                                                        185.2 4254.0\n smoothness (worst):
50.41 251.2\n area (worst):
0.071 0.223\n
                                                                        0.027 1.058\n
                      compactness (worst):
                                                                                               concavity (worst):
                                                                      0.0 0.291\n symmetry (worst):
        1.252\n concave points (worst):
                                                                      0.055 0.208\n
0.156 0.664\n fractal dimension (worst):
:Class Distribution: 212 - Malignant, 357 - Benign\n\n :Creator: Dr. William H. Wolberg, W.
Nick Street, Olvi L. Mangasarian\n\n :Donor: Nick Street\n\n :Date: November, 1995\n\nThis is
a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.\nttps://goo.gl/U2Uwz2\nFeatures
are computed from a digitized image of a fine needle\naspirate (FNA) of a breast mass. They
{\tt describe} \verb| ncharacteristics of the cell nuclei present in the image. \verb| nnSeparating plane described a | {\tt describe} | {\tt nnSeparating plane described} | {\tt describe} | {\tt nnSeparating plane described} | {\tt nnSeparatin
bove was obtained using\nMultisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision
Tree\nConstruction Via Linear Programming." Proceedings of the 4th\nMidwest Artificial
Intelligence and Cognitive Science Society, \npp. 97-101, 1992], a classification method which uses
linear\nprogramming to construct a decision tree. Relevant features\nwere selected using an
exhaustive search in the space of 1-4\n and 1-3 separating planes.\n mThe actual linear pr
ogram used to obtain the separating plane\nin the 3-dimensional space is that described in:\n[K. P
. Bennett and O. L. Mangasarian: "Robust Linear\nProgramming Discrimination of Two Linearly
Inseparable Sets", \nOptimization Methods and Software 1, 1992, 23-34].\nThis database is also av
ailable through the UW CS ftp server:\n\nftp ftp.cs.wisc.edu\ncd math-prog/cpo-dataset/machine-lea
rn/WDBC/\n\nReferences\n-----\n - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear fe
ature extraction \n for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on \n
Electronic Imaging, Caionae and Machaeleau, volume 1005 pages 061 070 \n
```

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- O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and \n
                                                                                              pro
gnosis via linear programming. Operations Research, 43(4), pages 570-577, \n July-August
1995.\n - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques\n
                                                                                              to
diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994) \n 163-171.\n',
 'feature_names': array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
        \hbox{\tt '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')}
In [4]:
cancer.keys()
Out[4]:
dict_keys(['data', 'target', 'target_names', 'DESCR', 'feature_names'])
In [5]:
print(cancer['DESCR'])
Breast Cancer Wisconsin (Diagnostic) Database
______
Notes
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)
        - fractal dimension ("coastline approximation" - 1)
       The mean, standard error, and "worst" or largest (mean of the three
       largest values) of these features were computed for each image,
        resulting in 30 features. For instance, field 3 is Mean Radius, field
       13 is Radius SE, field 23 is Worst Radius.
        - class:
                - WDBC-Malignant
                - WDBC-Benign
    :Summary Statistics:
    Min
   radius (mean):
                                         6.981 28.11
                                         9.71
    texture (mean):
                                         43.79 188.5
   perimeter (mean):
                                         143.5 2501.0
   area (mean):
                                        0.053 0.163
   smoothness (mean):
   compactness (mean):
                                        0.019 0.345
                                              0.427
                                        0.0
   concavity (mean):
   concave points (mean):
                                         0.0
                                                0.201
                                         0.106 0.304
    symmetry (mean):
```

0.05 0.097

0.112 2.873

fractal dimension (mean):

radius (standard error):

Electionic imaging: Science and rechnology, volume 1900, pages out-o/0,\n

San Jose, CA,

texture (standard error): 0.36 4.885 0.757 21.98 perimeter (standard error): 6.802 542.2 0.002 0.031 area (standard error): smoothness (standard error): 0.002 0.135 compactness (standard error): 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 radius (worst): 7.93 12.02 49.54 texture (worst): perimeter (worst): 50.41 251.2 area (worst): 185.2 4254.0 0.071 0.223 0.027 1.058 smoothness (worst): compactness (worst): 1.252 concavity (worst): 0.0 concave points (worst): 0.0 0.291 symmetry (worst): 0.156 0.664 0.055 0.208 fractal dimension (worst):

: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 $\verb|cd| math-prog/cpo-dataset/machine-learn/WDBC/|$

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 [6]:

```
['malignant' 'benign']
In [7]:
print(cancer['target'])
1 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 0 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 1 \;\; 1 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\; 0 \;\;
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     1 1 1 1 1 1 1 0 0 0 0 0 0 1]
In [8]:
print(cancer['feature names'])
 ['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']
In [9]:
print(cancer['data'])
 [[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]]
In [10]:
cancer['data'].shape
Out[10]:
 (569, 30)
In [11]:
df_cancer = pd.DataFrame(np.c_[cancer['data'], cancer['target']], columns = np.append(cancer['featu
 re names'], ['target']))
In [12]:
df cancer.head()
Out[12]:
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	worst texture	
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	 17.33	184
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	 23.41	158
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	 25.53	152
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	 26.50	98.
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	 16.67	152

5 rows × 31 columns

In [13]:

df_cancer.tail()

Out[13]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	 worst texture	ŗ
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	0.05623	 26.40	1
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	0.05533	 38.25	1
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	0.05648	 34.12	1
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	0.07016	 39.42	1
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	0.05884	 30.37	5

5 rows × 31 columns

```
In [14]:
```

```
x = np.array([1,2,3])
x.shape
```

Out[14]:

(3,)

In [15]:

```
Example = np.c_[np.array([1,2,3]), np.array([4,5,6])]
Example.shape
```

Out[15]:

(3, 2)

STEP #3: VISUALIZING THE DATA

```
In [16]:
```

```
sns.pairplot(df_cancer, hue = 'target', vars = ['mean radius', 'mean texture', 'mean area', 'mean p
erimeter', 'mean smoothness'] )
```

Out[16]:

<seaborn.axisgrid.PairGrid at 0x1c93d061b00>



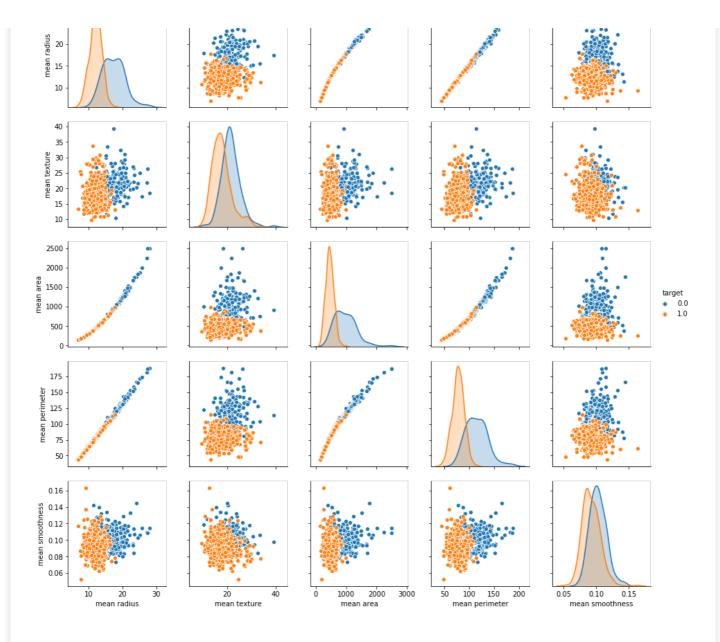










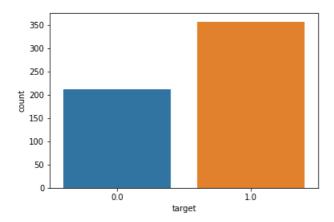


In [17]:

sns.countplot(df_cancer['target'], label = "Count")

Out[17]:

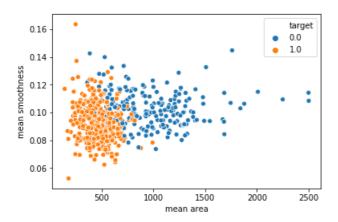
<matplotlib.axes._subplots.AxesSubplot at 0x1c93eebdeb8>



In [18]:

```
sns.scatterplot(x = 'mean area', y = 'mean smoothness', hue = 'target', data = df_cancer)
```

Out[18]:



In [19]:

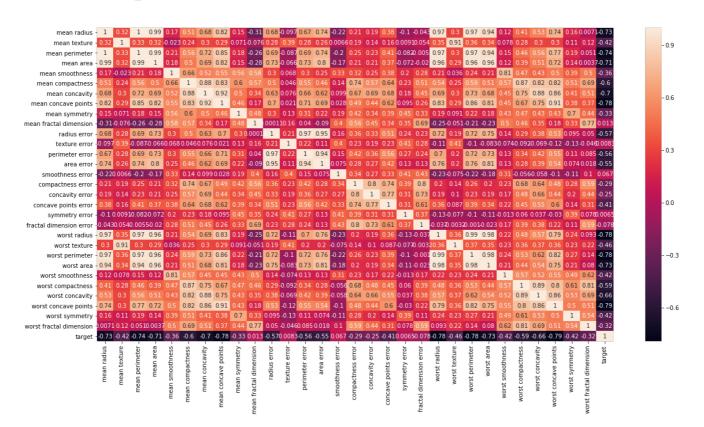
```
#sns.lmplot('mean area', 'mean smoothness', hue ='target', data = df_cancer_all, fit_reg=False)
```

In [20]:

```
# Let's check the correlation between the variables
# Strong correlation between the mean radius and mean perimeter, mean area and mean primeter
plt.figure(figsize=(20,10))
sns.heatmap(df_cancer.corr(), annot=True)
```

Out[20]:

<matplotlib.axes._subplots.AxesSubplot at 0x1c93f754940>



STEP #4: MODEL TRAINING (FINDING A PROBLEM SOLUTION)

In [21]:

In [22]:

Х

Out[22]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension		worst radius	t
0	17.990	10.38	122.80	1001.0	0.11840	0.27760	0.300100	0.147100	0.2419	0.07871		25.380	1
1	20.570	17.77	132.90	1326.0	0.08474	0.07864	0.086900	0.070170	0.1812	0.05667		24.990	2
2	19.690	21.25	130.00	1203.0	0.10960	0.15990	0.197400	0.127900	0.2069	0.05999		23.570	2
3	11.420	20.38	77.58	386.1	0.14250	0.28390	0.241400	0.105200	0.2597	0.09744		14.910	2
4	20.290	14.34	135.10	1297.0	0.10030	0.13280	0.198000	0.104300	0.1809	0.05883		22.540	1
5	12.450	15.70	82.57	477.1	0.12780	0.17000	0.157800	0.080890	0.2087	0.07613		15.470	2
6	18.250	19.98	119.60	1040.0	0.09463	0.10900	0.112700	0.074000	0.1794	0.05742		22.880	2
7	13.710	20.83	90.20	577.9	0.11890	0.16450	0.093660	0.059850	0.2196	0.07451		17.060	2
8	13.000	21.82	87.50	519.8	0.12730	0.19320	0.185900	0.093530	0.2350	0.07389		15.490	3
9	12.460	24.04	83.97	475.9	0.11860	0.23960	0.227300	0.085430	0.2030	0.08243		15.090	4
10	16.020	23.24	102.70	797.8	0.08206	0.06669	0.032990	0.033230	0.1528	0.05697		19.190	3
11	15.780	17.89	103.60	781.0	0.09710	0.12920	0.099540	0.066060	0.1842	0.06082		20.420	2
12	19.170	24.80	132.40	1123.0	0.09740	0.24580	0.206500	0.111800	0.2397	0.07800		20.960	2
13	15.850	23.95	103.70	782.7	0.08401	0.10020	0.099380	0.053640	0.1847	0.05338		16.840	2
14	13.730	22.61	93.60	578.3	0.11310	0.22930	0.212800	0.080250	0.2069	0.07682		15.030	3
15	14.540	27.54	96.73	658.8	0.11390	0.15950	0.163900	0.073640	0.2303	0.07077		17.460	3
16	14.680	20.13	94.74	684.5	0.09867	0.07200	0.073950	0.052590	0.1586	0.05922		19.070	3
17	16.130	20.68	108.10	798.8	0.11700	0.20220	0.172200	0.102800	0.2164	0.07356		20.960	3
18	19.810	22.15	130.00	1260.0	0.09831	0.10270	0.147900	0.094980	0.1582	0.05395		27.320	3
19	13.540	14.36	87.46	566.3	0.09779	0.08129	0.066640	0.047810	0.1885	0.05766		15.110	1
20	13.080	15.71	85.63	520.0	0.10750	0.12700	0.045680	0.031100	0.1967	0.06811		14.500	2
21	9.504	12.44	60.34	273.9	0.10240	0.06492	0.029560	0.020760	0.1815	0.06905		10.230	1
22	15.340	14.26	102.50	704.4	0.10730	0.21350	0.207700	0.097560	0.2521	0.07032		18.070	1
23	21.160	23.04	137.20	1404.0	0.09428	0.10220	0.109700	0.086320	0.1769	0.05278		29.170	3
24	16.650	21.38	110.00	904.6	0.11210	0.14570	0.152500	0.091700	0.1995	0.06330		26.460	3
25	17.140	16.40	116.00	912.7	0.11860	0.22760	0.222900	0.140100	0.3040	0.07413		22.250	2
26	14.580	21.53	97.41	644.8	0.10540	0.18680	0.142500	0.087830	0.2252	0.06924		17.620	3
27	18.610	20.25	122.10	1094.0	0.09440	0.10660	0.149000	0.077310	0.1697	0.05699		21.310	2
28	15.300	25.27	102.40	732.4	0.10820	0.16970	0.168300	0.087510	0.1926	0.06540		20.270	3
29	17.570	15.05	115.00	955.1	0.09847	0.11570	0.098750	0.079530	0.1739	0.06149		20.010	1
													Ī.,
		25.44	48.34	170.4	0.08668	0.11990	0.092520	0.013640	0.2037	0.07751			3
	11.540		74.65	402.9	0.09984	0.11200	0.067370	0.025940		0.06782		12.260	H
	14.470		95.81	656.4	0.08837	0.12300	0.100900	0.038900		0.06341		16.220	-
	14.740		94.70	668.6	0.08275	0.07214	0.041050	0.030270		0.05680	ļ	16.510	H
	13.210		84.88	538.4	0.08671	0.06877	0.029870	0.032750		0.05781		14.370	_
	13.870		89.77	584.8	0.09578	0.10180	0.036880	0.023690		0.06688		15.050	-

545	13.620 mean	23.23 mean	87.19 mean	573.2 mean	0.09246 mean	0.06747 mean	0.029740 mean	0.0 2443 6	mean	0.058 mean		15.350 worst	
546	1 a dia9	textore	βēr∛mheter	32 ár@a	9m964Aness	0ol 1 p2∕ctness	0 0101√10y	6.005495 points	ยิ่งใหม่คือจetry	0.06201	:::	14d459	₽
547	10.260	16.58	65.85	320.8	0.08877	0.08066	0.043580	0.024380	0.1669	0.06714		10.830	2
548	9.683	19.34	61.05	285.7	0.08491	0.05030	0.023370	0.009615	0.1580	0.06235		10.930	2
549	10.820	24.21	68.89	361.6	0.08192	0.06602	0.015480	0.008160	0.1976	0.06328		13.030	3
550	10.860	21.48	68.51	360.5	0.07431	0.04227	0.000000	0.000000	0.1661	0.05948		11.660	2
551	11.130	22.44	71.49	378.4	0.09566	0.08194	0.048240	0.022570	0.2030	0.06552		12.020	2
552	12.770	29.43	81.35	507.9	0.08276	0.04234	0.019970	0.014990	0.1539	0.05637		13.870	3
553	9.333	21.94	59.01	264.0	0.09240	0.05605	0.039960	0.012820	0.1692	0.06576		9.845	2
554	12.880	28.92	82.50	514.3	0.08123	0.05824	0.061950	0.023430	0.1566	0.05708		13.890	3
555	10.290	27.61	65.67	321.4	0.09030	0.07658	0.059990	0.027380	0.1593	0.06127		10.840	3
556	10.160	19.59	64.73	311.7	0.10030	0.07504	0.005025	0.011160	0.1791	0.06331		10.650	2
557	9.423	27.88	59.26	271.3	0.08123	0.04971	0.000000	0.000000	0.1742	0.06059		10.490	3
558	14.590	22.68	96.39	657.1	0.08473	0.13300	0.102900	0.037360	0.1454	0.06147		15.480	2
559	11.510	23.93	74.52	403.5	0.09261	0.10210	0.111200	0.041050	0.1388	0.06570		12.480	3
560	14.050	27.15	91.38	600.4	0.09929	0.11260	0.044620	0.043040	0.1537	0.06171		15.300	3
561	11.200	29.37	70.67	386.0	0.07449	0.03558	0.000000	0.000000	0.1060	0.05502		11.920	3
562	15.220	30.62	103.40	716.9	0.10480	0.20870	0.255000	0.094290	0.2128	0.07152		17.520	4
563	20.920	25.09	143.00	1347.0	0.10990	0.22360	0.317400	0.147400	0.2149	0.06879		24.290	2
564	21.560	22.39	142.00	1479.0	0.11100	0.11590	0.243900	0.138900	0.1726	0.05623		25.450	2
565	20.130	28.25	131.20	1261.0	0.09780	0.10340	0.144000	0.097910	0.1752	0.05533		23.690	3
566	16.600	28.08	108.30	858.1	0.08455	0.10230	0.092510	0.053020	0.1590	0.05648		18.980	3
567	20.600	29.33	140.10	1265.0	0.11780	0.27700	0.351400	0.152000	0.2397	0.07016		25.740	3
568	7.760	24.54	47.92	181.0	0.05263	0.04362	0.000000	0.000000	0.1587	0.05884		9.456	3

569 rows × 30 columns

```
In [23]:
```

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

Out[23]:

```
0.0
     0.0
1
2
      0.0
      0.0
      0.0
4
5
     0.0
     0.0
7
      0.0
8
      0.0
9
      0.0
10
      0.0
      0.0
11
12
      0.0
13
      0.0
      0.0
14
      0.0
15
16
      0.0
17
      0.0
```

18

19

20

21

22

23

24

0.0

1.0

1.0

1.0

0.0

0.0

0.0

```
25
      0.0
26
      0.0
27
      0.0
28
     0.0
29
     0.0
     . . .
539
      1.0
    1.0
540
541
     1.0
542
     1.0
    1.0
543
544
      1.0
545
      1.0
546
     1.0
547
     1.0
548
    1.0
     1.0
549
550
      1.0
     1.0
551
552
     1.0
553
    1.0
554
    1.0
555
      1.0
556
      1.0
557
     1.0
558
    1.0
559
     1.0
    1.0
560
561
      1.0
     0.0
562
563
     0.0
564
    0.0
565
     0.0
566
      0.0
567
      0.0
568
    1.0
Name: target, Length: 569, dtype: float64
In [24]:
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20, random_state=5)
In [25]:
X_train.shape
Out[25]:
(455, 30)
In [26]:
X_test.shape
Out[26]:
(114, 30)
In [27]:
y train.shape
Out[27]:
(455,)
In [28]:
y_test.shape
```

```
Out[28]: (114,)
```

In [29]:

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

svc_model = SVC()
svc_model.fit(X_train, y_train)
```

Out[29]:

```
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
  decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
  max_iter=-1, probability=False, random_state=None, shrinking=True,
  tol=0.001, verbose=False)
```

STEP #5: EVALUATING THE MODEL

In [30]:

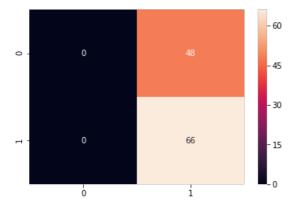
```
y_predict = svc_model.predict(X_test)
cm = confusion_matrix(y_test, y_predict)
```

In [31]:

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

Out[31]:

<matplotlib.axes. subplots.AxesSubplot at 0x1c93face2b0>



In [32]:

 $\verb|print(classification_report(y_test, y_predict))|\\$

support	f1-score	recall	precision	
48	0.00	0.00	0.00	0.0
66	0.73	1.00	0.58	1.0
114	0.42	0.58	0.34	avg / total

C:\Users\Dr. Ryan\Anaconda3\lib\site-packages\sklearn\metrics\classification.py:1135: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples.

'precision', 'predicted', average, warn_for)

STEP #6: IMPROVING THE MODEL

In [33]:

```
min_train = X_train.min()
min_train
```

Out[33]:

mean radius	6.981000
mean texture	9.710000
mean perimeter	43.790000
mean area	143.500000
mean smoothness	0.052630
mean compactness	0.019380
mean concavity	0.000000
mean concave points	0.000000
mean symmetry	0.106000
mean fractal dimension	0.049960
radius error	0.111500
texture error	0.362100
perimeter error	0.757000
area error	6.802000
smoothness error	0.001713
compactness error	0.002252
concavity error	0.000000
concave points error	0.000000
symmetry error	0.007882
fractal dimension error	0.000950
worst radius	7.930000
worst texture	12.020000
worst perimeter	50.410000
worst area	185.200000
worst smoothness	0.071170
worst compactness	0.027290
worst concavity	0.000000
worst concave points	0.000000
worst symmetry	0.156500
worst fractal dimension	0.055040
dtype: float64	

In [34]:

```
range_train = (X_train - min_train).max()
range_train
```

Out[34]:

mean radius	21.129000
mean texture	29.570000
mean perimeter	144.710000
mean area	2355.500000
mean smoothness	0.110770
mean compactness	0.326020
mean concavity	0.426800
mean concave points	0.201200
mean symmetry	0.198000
mean fractal dimension	0.045790
radius error	2.761500
texture error	4.522900
perimeter error	21.223000
area error	518.798000
smoothness error	0.029417
compactness error	0.133148
concavity error	0.396000
concave points error	0.052790
symmetry error	0.071068
fractal dimension error	0.028890
worst radius	25.190000
worst texture	37.520000
worst perimeter	170.390000
worst area	3246.800000
worst smoothness	0.129430
worst compactness	1.030710
worst concavity	1.105000

worst concave points 0.291000
worst symmetry 0.420900
worst fractal dimension 0.152460

dtype: float64

In [35]:

X_train_scaled = (X_train - min_train)/range_train

In [36]:

X_train_scaled

Out[36]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	
306	0.294335	0.206628	0.278350	0.167183	0.293220	0.101620	0.003423	0.016208	0.288889	0.196113	 0.2
410	0.207251	0.265810	0.198328	0.108809	0.324546	0.103521	0.065206	0.104374	0.273232	0.200262	 0.2
197	0.525297	0.410213	0.508673	0.373806	0.190304	0.205632	0.258435	0.287177	0.358586	0.075126	 0.4
376	0.169861	0.355428	0.182157	0.082700	0.343956	0.449727	0.534208	0.295278	0.569697	0.754313	 0.1
244	0.587770	0.466351	0.589524	0.429421	0.452018	0.418441	0.480084	0.441650	0.463636	0.219262	 0.5
299	0.167022	0.452486	0.159353	0.080959	0.441184	0.149040	0.058458	0.093191	0.320707	0.340686	 0.1
312	0.273510	0.123774	0.266049	0.153089	0.318769	0.184345	0.094939	0.126640	0.273232	0.249836	 0.2
331	0.283923	0.326006	0.281459	0.157291	0.389636	0.285627	0.166518	0.146620	0.354040	0.337192	 0.2
317	0.531923	0.309773	0.517656	0.375080	0.404712	0.283173	0.264761	0.395129	0.377273	0.145883	 0.5
341	0.124237	0.241123	0.123350	0.058162	0.290512	0.223606	0.197329	0.113917	0.492929	0.464949	 0.1
156	0.506366	0.373013	0.508673	0.348206	0.531462	0.451261	0.434630	0.523857	0.460101	0.255514	 0.4
71	0.090255	0.166723	0.103656	0.042666	0.408053	0.410159	0.201640	0.142744	0.425253	0.870059	 0.0
218	0.606702	0.400744	0.593670	0.461261	0.371942	0.341145	0.298032	0.431958	0.522222	0.127757	 0.7
344	0.223816	0.194116	0.215880	0.117512	0.563059	0.163886	0.093861	0.161531	0.479293	0.329766	 0.2
247	0.279663	0.148799	0.284431	0.156527	0.315699	0.353414	0.321931	0.197813	0.270707	0.308583	 0.2
212	1.000000	0.296246	1.000000	1.000000	0.555836	0.405558	0.750000	0.792744	0.296970	0.115527	 3.0
559	0.214350	0.480893	0.212356	0.110380	0.360928	0.253727	0.260544	0.204026	0.165657	0.343743	 0.1
176	0.138341	0.282381	0.143805	0.067459	0.400469	0.337464	0.306232	0.184692	0.307576	0.681371	 0.1
422	0.219083	0.213392	0.218851	0.112375	0.507087	0.298816	0.166284	0.223509	0.417172	0.289146	 0.1
248	0.173648	0.524518	0.167369	0.086394	0.396678	0.162444	0.055740	0.080268	0.422727	0.291112	 0.1
232	0.200625	0.815015	0.186580	0.103290	0.227228	0.050181	0.011638	0.031978	0.396465	0.181699	 0.1
444	0.522931	0.241461	0.509364	0.359372	0.332581	0.318447	0.255389	0.310835	0.333333	0.171216	 0.4
383	0.255999	0.262766	0.254647	0.135598	0.465559	0.338384	0.138051	0.143141	0.363131	0.347674	 0.2
279	0.325098	0.184985	0.312349	0.188453	0.383949	0.176370	0.104944	0.184443	0.530303	0.187159	 0.2
494	0.292442	0.366250	0.278281	0.167778	0.187054	0.102356	0.042174	0.062425	0.329798	0.194802	 0.2
316	0.246060	0.147785	0.231221	0.134961	0.223075	0.039077	0.026312	0.025104	0.309596	0.142608	 0.1
523	0.318472	0.303348	0.310552	0.181490	0.420060	0.268757	0.126172	0.188022	0.330303	0.403363	 0.2
90	0.361541	0.483936	0.350909	0.220420	0.335019	0.204527	0.072680	0.146968	0.315657	0.189998	 0.3
469	0.219556	0.286439	0.225209	0.112630	0.585628	0.395436	0.238988	0.276541	0.453030	0.493339	 0.2
373	0.646457	0.258370	0.628913	0.505837	0.377629	0.270597	0.357779	0.444384	0.258081	0.105263	 0.6
539	0.033603	0.531958	0.031442	0.011420	0.307394	0.308325	0.216776	0.067793	0.493434	0.601660	 0.0

110	0.132330 mean	0.246195 mean	0.129293 mean	0.062280 mean	0.461045 mean	0.198331 mean	0.101546 mean	0.0 %&&a n	0.264646 mean	0.451 m/e5an		0.1
5	0. 25%609	0.202570	perfinerer	0.143688			ପରୀବିତ୍ୟ ି ଅନ୍ତ	6.905aye points	ย ง ร์กำลจิจสรา	0.571522 dimension	:::	0.2
144	0.178380	0.177883	0.169097	0.089917	0.228401	0.098184	0.052741	•	0.171212	0.151125		0.1
103	0.137015	0.327697	0.139313	0.065719	0.432157	0.237992	0.144189	0.150547	0.446970	0.289583		0.1
210	0.643618	0.420358	0.628222	0.486733	0.345491	0.354027	0.384255	0.475199	0.356061	0.006115		0.6
446	0.509679	0.619547	0.507981	0.355806	0.427372	0.343599	0.397844	0.412177	0.329798	0.200917		0.5
41	0.187846	0.393642	0.194251	0.096625	0.632572	0.314153	0.244611	0.281759	0.421717	0.409260		0.1
362	0.273510	0.308759	0.263147	0.149904	0.398393	0.184467	0.062980	0.088519	0.353030	0.259227		0.2
377	0.306640	0.625634	0.290927	0.177712	0.203485	0.085516	0.029780	0.055517	0.182323	0.167504		0.2
254	0.590137	0.325330	0.571557	0.435364	0.459240	0.304951	0.323102	0.426988	0.361616	0.142171		0.7
146	0.228075	0.232330	0.243245	0.122479	0.509795	0.461996	0.388707	0.368539	0.817172	0.518672		0.2
86	0.354915	0.397362	0.348697	0.214264	0.377449	0.245660	0.282099	0.245427	0.512626	0.139769		6.0
542	0.367220	0.531282	0.351807	0.222925	0.271915	0.161831	0.096181	0.150447	0.393939	0.149378		0.3
431	0.256472	0.269530	0.260383	0.137678	0.476393	0.344212	0.181373	0.139115	0.379293	0.459926		0.1
65	0.369114	0.481231	0.370465	0.222798	0.582920	0.394209	0.296860	0.448757	0.451010	0.362088		6.0
205	0.385205	0.235712	0.380001	0.243303	0.326171	0.234648	0.176898	0.202734	0.269697	0.216204		0.3
44	0.292915	0.409199	0.287679	0.164721	0.401824	0.261702	0.193510	0.261034	0.346465	0.257917		6.0
27	0.550381	0.356442	0.541151	0.403524	0.377088	0.267530	0.349110	0.384245	0.321717	0.153527		0.5
80	0.211510	0.380791	0.207449	0.109531	0.519726	0.227716	0.107568	0.110984	0.394949	0.438742		0.2
437	0.334091	0.212039	0.317808	0.198557	0.288435	0.121373	0.082802	0.146322	0.330303	0.196986		0.3
113	0.167022	0.354413	0.171723	0.080959	0.537781	0.340225	0.151734	0.152485	0.435354	0.608430		0.1
204	0.259785	0.300643	0.257757	0.143664	0.424483	0.265076	0.187559	0.189911	0.436869	0.300721		0.2
519	0.273037	0.236388	0.267570	0.148716	0.540489	0.283173	0.090909	0.148857	0.535354	0.355318		0.2
411	0.192106	0.240785	0.187478	0.097516	0.497156	0.179928	0.071368	0.123260	0.330303	0.293514		0.1
8	0.284869	0.409537	0.302052	0.159754	0.674099	0.533157	0.435567	0.464861	0.651515	0.522603		0.3
73	0.322732	0.205614	0.322300	0.187052	0.433962	0.333170	0.182498	0.251938	0.304040	0.342870		0.3
400	0.517251	0.382482	0.557045	0.361070	0.635280	0.730691	0.747188	0.595427	0.531818	0.462765		0.5
118	0.416442	0.446398	0.427821	0.271322	0.567572	0.477946	0.499766	0.471123	0.523232	0.509937		0.4
206	0.137015	0.255665	0.132195	0.064487	0.507990	0.162383	0.041143	0.097018	0.441414	0.281503		0.0

455 rows × 30 columns

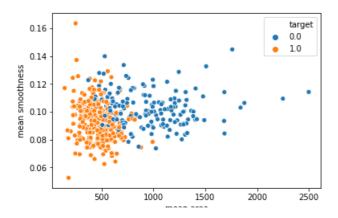
In [37]:

4

sns.scatterplot(x = X_train['mean area'], y = X_train['mean smoothness'], hue = y_train)

Out[37]:

<matplotlib.axes._subplots.AxesSubplot at 0x1c93fb7dac8>

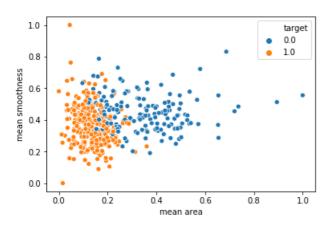


In [38]:

```
sns.scatterplot(x = X_train_scaled['mean area'], y = X_train_scaled['mean smoothness'], hue = y_train)
```

Out[38]:

<matplotlib.axes. subplots.AxesSubplot at 0x1c93fc637f0>



In [39]:

```
min_test = X_test.min()
range_test = (X_test - min_test).max()
X_test_scaled = (X_test - min_test)/range_test
```

In [40]:

```
from sklearn.svm import SVC
from sklearn.metrics import classification_report, confusion_matrix
svc_model = SVC()
svc_model.fit(X_train_scaled, y_train)
```

Out[40]:

```
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
  decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
  max_iter=-1, probability=False, random_state=None, shrinking=True,
  tol=0.001, verbose=False)
```

In [41]:

```
y_predict = svc_model.predict(X_test_scaled)
cm = confusion_matrix(y_test, y_predict)
sns.heatmap(cm,annot=True,fmt="d")
```

Out[41]:

<matplotlib.axes._subplots.AxesSubplot at 0x1c94022fc50>



0 1

In [42]:

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

support	f1-score	recall	precision	
48	0.95	0.90	1.00	0.0
66	0.96	1.00	0.93	1.0
114	0.96	0.96	0.96	avg / total

IMPROVING THE MODEL - PART 2

```
In [43]:
```

```
param_grid = {'C': [0.1, 1, 10, 100], 'gamma': [1, 0.1, 0.01, 0.001], 'kernel': ['rbf']}
```

In [44]:

from sklearn.model_selection import GridSearchCV

In [45]:

```
grid = GridSearchCV(SVC(),param_grid,refit=True,verbose=4)
```

In [46]:

```
grid.fit(X_train_scaled,y_train)
```

```
Fitting 3 folds for each of 16 candidates, totalling 48 fits
[CV] C=0.1, gamma=1, kernel=rbf .....
[CV] C=0.1, gamma=1, kernel=rbf, score=0.9671052631578947, total= 0.0s
[CV] C=0.1, gamma=1, kernel=rbf ......
   C=0.1, gamma=1, kernel=rbf, score=0.9210526315789473, total=
[CV] C=0.1, gamma=1, kernel=rbf .....
[CV] C=0.1, gamma=1, kernel=rbf, score=0.9470198675496688, total= 0.0s
[CV] C=0.1, gamma=0.1, kernel=rbf .....
[CV] C=0.1, gamma=0.1, kernel=rbf, score=0.9144736842105263, total= 0.0s
[CV] C=0.1, gamma=0.1, kernel=rbf ......
[CV] C=0.1, gamma=0.1, kernel=rbf, score=0.8881578947368421, total= 0.0s
[CV] C=0.1, gamma=0.1, kernel=rbf ......
[CV] C=0.1, gamma=0.1, kernel=rbf, score=0.8675496688741722, total=
[CV] C=0.1, gamma=0.01, kernel=rbf ......
    C=0.1, gamma=0.01, kernel=rbf, score=0.6381578947368421, total=
[CV]
[CV] C=0.1, gamma=0.01, kernel=rbf .....
[CV] C=0.1, gamma=0.01, kernel=rbf, score=0.6381578947368421, total=
[CV] C=0.1, gamma=0.01, kernel=rbf .....
[CV] C=0.1, gamma=0.01, kernel=rbf, score=0.6423841059602649, total=
                                                     0.0s
C=0.1, gamma=0.001, kernel=rbf, score=0.6381578947368421, total=
[CV] C=0.1, gamma=0.001, kernel=rbf, score=0.6381578947368421, total=
[CV] C=0.1, gamma=0.001, kernel=rbf ......
[CV] C=0.1, gamma=0.001, kernel=rbf, score=0.6423841059602649, total=
[CV] C=1, gamma=1, kernel=rbf .....
   C=1, gamma=1, kernel=rbf, score=0.993421052631579, total= 0.0s
[CV]
[CV] C=1, gamma=1, kernel=rbf .....
[CV] C=1, gamma=1, kernel=rbf, score=0.9473684210526315, total= 0.0s
[CV] C=1, gamma=1, kernel=rbf ......
[CV] C=1, gamma=1, kernel=rbf, score=0.9801324503311258, total= 0.0s
[CV] C=1, gamma=0.1, kernel=rbf .....
[CV] C=1, gamma=0.1, kernel=rbf, score=0.9736842105263158, total= 0.0s
[CV] C=1, gamma=0.1, kernel=rbf .....
[CV] C=1, gamma=0.1, kernel=rbf, score=0.9276315789473685, total=
```

```
[CV] C=1, gamma=0.1, kernel=rbf .....
[CV] C=1, gamma=0.1, kernel=rbf, score=0.9403973509933775, total= 0.0s
[CV] C=1, gamma=0.01, kernel=rbf ......
[CV] C=1, gamma=0.01, kernel=rbf, score=0.9144736842105263, total= 0.0s
[CV] C=1, gamma=0.01, kernel=rbf .....
                      1 out of
                               1 | elapsed:
                                           0.0s remaining:
                                                          0.0s
[Parallel(n jobs=1)]: Done
[Parallel(n jobs=1)]: Done
                      2 out of
                               2 | elapsed:
                                           0.0s remaining:
                                                          0.0s
[Parallel(n jobs=1)]: Done
                      3 out of
                               3 | elapsed:
                                           0.0s remaining:
                                                          0.0s
[CV] C=1, gamma=0.01, kernel=rbf, score=0.8947368421052632, total= 0.0s
[CV] C=1, gamma=0.01, kernel=rbf ......
   C=1, gamma=0.01, kernel=rbf, score=0.8675496688741722, total= 0.0s
[CV]
[CV] C=1, gamma=0.001, kernel=rbf .....
[CV] C=1, gamma=0.001, kernel=rbf, score=0.6381578947368421, total= 0.0s
[CV] C=1, qamma=0.001, kernel=rbf .....
[CV] C=1, gamma=0.001, kernel=rbf, score=0.6381578947368421, total= 0.0s
[CV] C=1, gamma=0.001, kernel=rbf ......
   C=1, gamma=0.001, kernel=rbf, score=0.6423841059602649, total=
[CV] C=10, gamma=1, kernel=rbf .....
[CV] C=10, gamma=1, kernel=rbf, score=0.993421052631579, total= 0.0s
[CV] C=10, gamma=1, kernel=rbf .....
[CV] C=10, gamma=1, kernel=rbf, score=0.9605263157894737, total= 0.0s
[CV] C=10, gamma=1, kernel=rbf .....
   C=10, gamma=1, kernel=rbf, score=0.9735099337748344, total= 0.0s
[CV]
[CV] C=10, gamma=0.1, kernel=rbf .....
[CV] C=10, gamma=0.1, kernel=rbf, score=0.993421052631579, total= 0.0s
[CV] C=10, gamma=0.1, kernel=rbf .....
[CV] C=10, gamma=0.1, kernel=rbf, score=0.9671052631578947, total= 0.0s
[CV] C=10, gamma=0.1, kernel=rbf ......
   C=10, gamma=0.1, kernel=rbf, score=0.9735099337748344, total=
[CV]
[CV] C=10, qamma=0.01, kernel=rbf ......
[CV] C=10, gamma=0.01, kernel=rbf, score=0.9736842105263158, total=
[CV] C=10, gamma=0.01, kernel=rbf ......
[CV] C=10, gamma=0.01, kernel=rbf, score=0.9210526315789473, total=
[CV] C=10, gamma=0.01, kernel=rbf .....
[CV] C=10, gamma=0.01, kernel=rbf, score=0.9403973509933775, total=
                                                       0.0s
[CV] C=10, gamma=0.001, kernel=rbf .....
[CV] C=10, gamma=0.001, kernel=rbf, score=0.9144736842105263, total=
                                                        0.0s
[CV] C=10, gamma=0.001, kernel=rbf .....
   C=10, gamma=0.001, kernel=rbf, score=0.8947368421052632, total=
[CV]
[CV] C=10, gamma=0.001, kernel=rbf .....
[CV] C=10, gamma=0.001, kernel=rbf, score=0.8675496688741722, total=
[CV] C=100, gamma=1, kernel=rbf .....
[CV] C=100, gamma=1, kernel=rbf, score=0.9605263157894737, total= 0.0s
[CV] C=100, gamma=1, kernel=rbf .....
   C=100, gamma=1, kernel=rbf, score=0.9539473684210527, total=
[CV] C=100, gamma=1, kernel=rbf ......
[CV] C=100, gamma=1, kernel=rbf, score=0.9801324503311258, total= 0.0s
[CV] C=100, gamma=0.1, kernel=rbf, score=0.9868421052631579, total= 0.0s
[CV] C=100, gamma=0.1, kernel=rbf .......
[CV]
   C=100, gamma=0.1, kernel=rbf, score=0.9539473684210527, total=
[CV] C=100, gamma=0.1, kernel=rbf ......
[CV] C=100, gamma=0.1, kernel=rbf, score=0.9801324503311258, total=
[CV] C=100, gamma=0.01, kernel=rbf .....
[CV] C=100, gamma=0.01, kernel=rbf, score=0.993421052631579, total=
[CV] C=100, gamma=0.01, kernel=rbf ......
[CV] C=100, gamma=0.01, kernel=rbf, score=0.9671052631578947, total=
[CV] C=100, qamma=0.01, kernel=rbf .....
[CV] C=100, gamma=0.01, kernel=rbf, score=0.9735099337748344, total=
                                                        0.0s
[CV] C=100, gamma=0.001, kernel=rbf ......
   C=100, gamma=0.001, kernel=rbf, score=0.9736842105263158, total=
[CV] C=100, gamma=0.001, kernel=rbf .....
[CV] C=100, gamma=0.001, kernel=rbf, score=0.9210526315789473, total=
                                                         0.0s
[CV] C=100, gamma=0.001, kernel=rbf .....
[CV] C=100, gamma=0.001, kernel=rbf, score=0.9403973509933775, total=
                                                         0.0s
[Parallel(n jobs=1)]: Done 48 out of 48 | elapsed: 0.3s finished
```

```
max_teer i, productitey=raise, raindom_state=None, Shiringfilde,
tol=0.001, verbose=False),
   fit_params=None, iid=True, n_jobs=1,
   param_grid={'C': [0.1, 1, 10, 100], 'gamma': [1, 0.1, 0.01, 0.001], 'kernel': ['rbf']},
   pre_dispatch='2*n_jobs', refit=True, return_train_score='warn',
   scoring=None, verbose=4)
```

In [47]:

```
grid.best_params_
```

Out[47]:

```
{'C': 10, 'gamma': 0.1, 'kernel': 'rbf'}
```

In [48]:

```
grid.best_estimator_
```

Out[48]:

```
SVC(C=10, cache_size=200, class_weight=None, coef0=0.0,
  decision_function_shape='ovr', degree=3, gamma=0.1, kernel='rbf',
  max_iter=-1, probability=False, random_state=None, shrinking=True,
  tol=0.001, verbose=False)
```

In [49]:

```
grid_predictions = grid.predict(X_test_scaled)
```

In [50]:

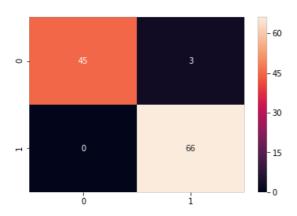
```
cm = confusion_matrix(y_test, grid_predictions)
```

In [51]:

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

Out[51]:

<matplotlib.axes. subplots.AxesSubplot at 0x1c94162d400>



In [52]:

 $\verb|print(classification_report(y_test, grid_predictions))|\\$

support	f1-score	recall	precision	
48	0.97	0.94	1.00	0.0
66	0.98	1.00	0.96	1.0
114	0.97	0.97	0.97	avg / total

Classification of each Datapoint whether the cancer is benign or malignant acheived Precision, Recall and F1 score of 97%...... Hence, our Model can be Deployed into Production.