Breast Cancer Detection Using Machine Learning

Importing libraries

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

!pip install scikit-learn
```

```
Requirement already satisfied: scikit-learn in c:\users\nishita\
appdata\local\packages\
pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\localcache\local-
packages\python311\site-packages (1.6.1)
Requirement already satisfied: numpy>=1.19.5 in c:\users\nishita\
appdata\local\packages\
pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\localcache\local-
packages\python311\site-packages (from scikit-learn) (1.26.2)
Requirement already satisfied: scipy>=1.6.0 in c:\users\nishita\
appdata\local\packages\
pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\localcache\local-
packages\python311\site-packages (from scikit-learn) (1.15.3)
Requirement already satisfied: joblib>=1.2.0 in c:\users\nishita\
appdata\local\packages\
pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\localcache\local-
packages\python311\site-packages (from scikit-learn) (1.5.1)
Requirement already satisfied: threadpoolctl>=3.1.0 in c:\users\
nishita\appdata\local\packages\
pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\localcache\local-
packages\python311\site-packages (from scikit-learn) (3.6.0)


[notice] A new release of pip is available: 24.0 -> 25.1.1
[notice] To update, run: C:\Users\Nishita\AppData\Local\Microsoft\
WindowsApps\PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\
python.exe -m pip install --upgrade pip
```

```
from sklearn.datasets import load_breast_cancer
cancer_dataset = load_breast_cancer()

cancer_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]]),
 'target': array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
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        0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
0,
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0,
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0,
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0,
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0,
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1,
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1,
        1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0,
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        0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
0,
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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,
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       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1,
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0,
       1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1,
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       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]),
 'frame': None,
 'target_names': array(['malignant', 'benign'], dtype='<U9'),
 'DESCR': '.. _breast_cancer_dataset:\n\nBreast cancer wisconsin
(diagnostic) dataset\n--------------------------------------------\n\
n**Data Set Characteristics:**\n\n:Number of Instances: 569\n\n:Number
of Attributes: 30 numeric, predictive attributes and the class\n\
n:Attribute Information:\n    - radius (mean of distances from center
to points on the perimeter)\n    - texture (standard deviation of
gray-scale values)\n    - perimeter\n    - area\n    - smoothness
(local variation in radius lengths)\n    - compactness (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    worst/largest values) of these
features were computed for each image,\n    resulting in 30 features.
For instance, field 0 is Mean Radius, field\n    10 is Radius SE,
field 20 is Worst Radius.\n\n    - class:\n            - WDBC-
Malignant\n            - WDBC-Benign\n\n:Summary Statistics:\n\
n===================================== ====== ======\n
Min    Max\n===================================== ====== ======\
nradius (mean):                        6.981  28.11\ntexture (mean):
9.71   39.28\nperimeter (mean):                      43.79  188.5\narea
(mean):                        143.5  2501.0\nsmoothness (mean):
0.053  0.163\ncompactness (mean):                  0.019  0.345\
nconcavity (mean):                     0.0    0.427\nconcave points
(mean):                0.0    0.201\nsymmetry (mean):
0.106  0.304\nfractal dimension (mean):            0.05   0.097\
nradius (standard error):              0.112  2.873\ntexture (standard
error):             0.36   4.885\nperimeter (standard error):
0.757  21.98\narea (standard error):               6.802  542.2\
nsmoothness (standard error):          0.002  0.031\ncompactness
(standard error):         0.002  0.135\nconcavity (standard error):
0.0    0.396\nconcave points (standard error):      0.0    0.053\
nsymmetry (standard error):            0.008  0.079\nfractal dimension
(standard error):   0.001  0.03\nradius (worst):
```

```
7.93   36.04\ntexture (worst):                        12.02  49.54\
nperimeter (worst):                   50.41  251.2\narea (worst):
185.2  4254.0\nsmoothness (worst):                   0.071  0.223\
ncompactness (worst):                  0.027  1.058\nconcavity
(worst):                    0.0    1.252\nconcave points (worst):
0.0    0.291\nsymmetry (worst):                       0.156  0.664\
nfractal dimension (worst):            0.055  0.208\
n================================== ====== ======\n\n:Missing
Attribute Values: None\n\n: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.\
nhttps://goo.gl/U2Uwz2\n\nFeatures are computed from a digitized image
of a fine needle\naspirate (FNA) of a breast mass.  They describe\
ncharacteristics of the cell nuclei present in the image.\n\
nSeparating plane described above 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\nfeatures and 1-3 separating planes.\n\nThe
actual linear program 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].\n\nThis database is also available through the UW CS ftp
server:\n\nftp ftp.cs.wisc.edu\ncd math-prog/cpo-dataset/machine-
learn/WDBC/\n\n.. dropdown:: References\n\n  - W.N. Street, W.H.
Wolberg and O.L. Mangasarian. Nuclear feature extraction\n    for
breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on\n
Electronic Imaging: Science and Technology, volume 1905, pages 861-
870,\n    San Jose, CA, 1993.\n  - O.L. Mangasarian, W.N. Street and
W.H. Wolberg. Breast cancer diagnosis and\n    prognosis 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',
        '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',
 'data_module': 'sklearn.datasets.data'}
```

```
type(cancer_dataset)
```

```
sklearn.utils._bunch.Bunch
```

```
cancer_dataset.keys()
```

```
dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR',
'feature_names', 'filename', 'data_module'])
```

```
cancer_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]])
```

```
type(cancer_dataset['data'])
```

```
numpy.ndarray
```

```
cancer_dataset['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, 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,
```

```
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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,
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0,
       0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0,
0,
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0,
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1,
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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, 1, 0, 0, 0, 0, 0, 0, 1])
```

```
cancer_dataset['target_names']
```

```
array(['malignant', 'benign'], dtype='<U9')
```

```
print(cancer_dataset['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

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/

.. dropdown:: 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_dataset['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']

print(cancer_dataset['filename'])

breast_cancer.csv

cancer_df =
pd.DataFrame(np.c_[cancer_dataset['data'],cancer_dataset['target']],
             columns = np.append(cancer_dataset['feature_names'],
['target']))

cancer_df.head(6)

   mean radius  mean texture  mean perimeter  mean area  mean
smoothness  \
```

```
0        17.99         10.38          122.80     1001.0
0.11840
1        20.57         17.77          132.90     1326.0
0.08474
2        19.69         21.25          130.00     1203.0
0.10960
3        11.42         20.38           77.58      386.1
0.14250
4        20.29         14.34          135.10     1297.0
0.10030
5        12.45         15.70           82.57      477.1
0.12780

   mean compactness  mean concavity  mean concave points  mean
symmetry  \
0           0.27760          0.3001              0.14710
0.2419
1           0.07864          0.0869              0.07017
0.1812
2           0.15990          0.1974              0.12790
0.2069
3           0.28390          0.2414              0.10520
0.2597
4           0.13280          0.1980              0.10430
0.1809
5           0.17000          0.1578              0.08089
0.2087

   mean fractal dimension  ...  worst texture  worst perimeter  worst
area  \
0                 0.07871  ...          17.33           184.60
2019.0
1                 0.05667  ...          23.41           158.80
1956.0
2                 0.05999  ...          25.53           152.50
1709.0
3                 0.09744  ...          26.50            98.87
567.7
4                 0.05883  ...          16.67           152.20
1575.0
5                 0.07613  ...          23.75           103.40
741.6

   worst smoothness  worst compactness  worst concavity  worst concave
points  \
0            0.1622             0.6656           0.7119
0.2654
1            0.1238             0.1866           0.2416
0.1860
2            0.1444             0.4245           0.4504
```

```
0.2430
3           0.2098             0.8663           0.6869
0.2575
4           0.1374             0.2050           0.4000
0.1625
5           0.1791             0.5249           0.5355
0.1741

   worst symmetry  worst fractal dimension  target
0          0.4601                  0.11890     0.0
1          0.2750                  0.08902     0.0
2          0.3613                  0.08758     0.0
3          0.6638                  0.17300     0.0
4          0.2364                  0.07678     0.0
5          0.3985                  0.12440     0.0

[6 rows x 31 columns]
```

```
cancer_df.tail(6)
```

```
     mean radius  mean texture  mean perimeter  mean area  mean
smoothness  \
563        20.92         25.09          143.00     1347.0
0.10990
564        21.56         22.39          142.00     1479.0
0.11100
565        20.13         28.25          131.20     1261.0
0.09780
566        16.60         28.08          108.30      858.1
0.08455
567        20.60         29.33          140.10     1265.0
0.11780
568         7.76         24.54           47.92      181.0
0.05263

     mean compactness  mean concavity  mean concave points  mean
symmetry  \
563           0.22360         0.31740              0.14740
0.2149
564           0.11590         0.24390              0.13890
0.1726
565           0.10340         0.14400              0.09791
0.1752
566           0.10230         0.09251              0.05302
0.1590
567           0.27700         0.35140              0.15200
0.2397
568           0.04362         0.00000              0.00000
0.1587
```

```
     mean fractal dimension  ...  worst texture  worst perimeter
worst area  \
563                 0.06879  ...          29.41           179.10
1819.0
564                 0.05623  ...          26.40           166.10
2027.0
565                 0.05533  ...          38.25           155.00
1731.0
566                 0.05648  ...          34.12           126.70
1124.0
567                 0.07016  ...          39.42           184.60
1821.0
568                 0.05884  ...          30.37            59.16
268.6

     worst smoothness  worst compactness  worst concavity  \
563           0.14070            0.41860           0.6599
564           0.14100            0.21130           0.4107
565           0.11660            0.19220           0.3215
566           0.11390            0.30940           0.3403
567           0.16500            0.86810           0.9387
568           0.08996            0.06444           0.0000

     worst concave points  worst symmetry  worst fractal dimension
target
563                0.2542          0.2929                  0.09873
0.0
564                0.2216          0.2060                  0.07115
0.0
565                0.1628          0.2572                  0.06637
0.0
566                0.1418          0.2218                  0.07820
0.0
567                0.2650          0.4087                  0.12400
0.0
568                0.0000          0.2871                  0.07039
1.0

[6 rows x 31 columns]

cancer_df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
```

```
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
 30  target                   569 non-null    float64
dtypes: float64(31)
memory usage: 137.9 KB

cancer_df.describe()

       mean radius  mean texture  mean perimeter    mean area  \
count   569.000000    569.000000      569.000000   569.000000
mean     14.127292     19.289649       91.969033   654.889104
std       3.524049      4.301036       24.298981   351.914129
min       6.981000      9.710000       43.790000   143.500000
25%      11.700000     16.170000       75.170000   420.300000
50%      13.370000     18.840000       86.240000   551.100000
75%      15.780000     21.800000      104.100000   782.700000
max      28.110000     39.280000      188.500000  2501.000000

       mean smoothness  mean compactness  mean concavity  mean concave
points  \
count       569.000000        569.000000      569.000000
569.000000
mean          0.096360          0.104341        0.088799
0.048919
std           0.014064          0.052813        0.079720
```

```
0.038803
min           0.052630          0.019380        0.000000
0.000000
25%           0.086370          0.064920        0.029560
0.020310
50%           0.095870          0.092630        0.061540
0.033500
75%           0.105300          0.130400        0.130700
0.074000
max           0.163400          0.345400        0.426800
0.201200

       mean symmetry  mean fractal dimension  ...  worst texture  \
count     569.000000              569.000000  ...     569.000000
mean        0.181162                0.062798  ...      25.677223
std         0.027414                0.007060  ...       6.146258
min         0.106000                0.049960  ...      12.020000
25%         0.161900                0.057700  ...      21.080000
50%         0.179200                0.061540  ...      25.410000
75%         0.195700                0.066120  ...      29.720000
max         0.304000                0.097440  ...      49.540000

       worst perimeter   worst area  worst smoothness  worst
compactness  \
count       569.000000   569.000000        569.000000
569.000000
mean        107.261213   880.583128          0.132369
0.254265
std          33.602542   569.356993          0.022832
0.157336
min          50.410000   185.200000          0.071170
0.027290
25%          84.110000   515.300000          0.116600
0.147200
50%          97.660000   686.500000          0.131300
0.211900
75%         125.400000  1084.000000          0.146000
0.339100
max         251.200000  4254.000000          0.222600
1.058000

       worst concavity  worst concave points  worst symmetry  \
count       569.000000            569.000000      569.000000
mean          0.272188              0.114606        0.290076
std           0.208624              0.065732        0.061867
min           0.000000              0.000000        0.156500
25%           0.114500              0.064930        0.250400
50%           0.226700              0.099930        0.282200
75%           0.382900              0.161400        0.317900
max           1.252000              0.291000        0.663800
```

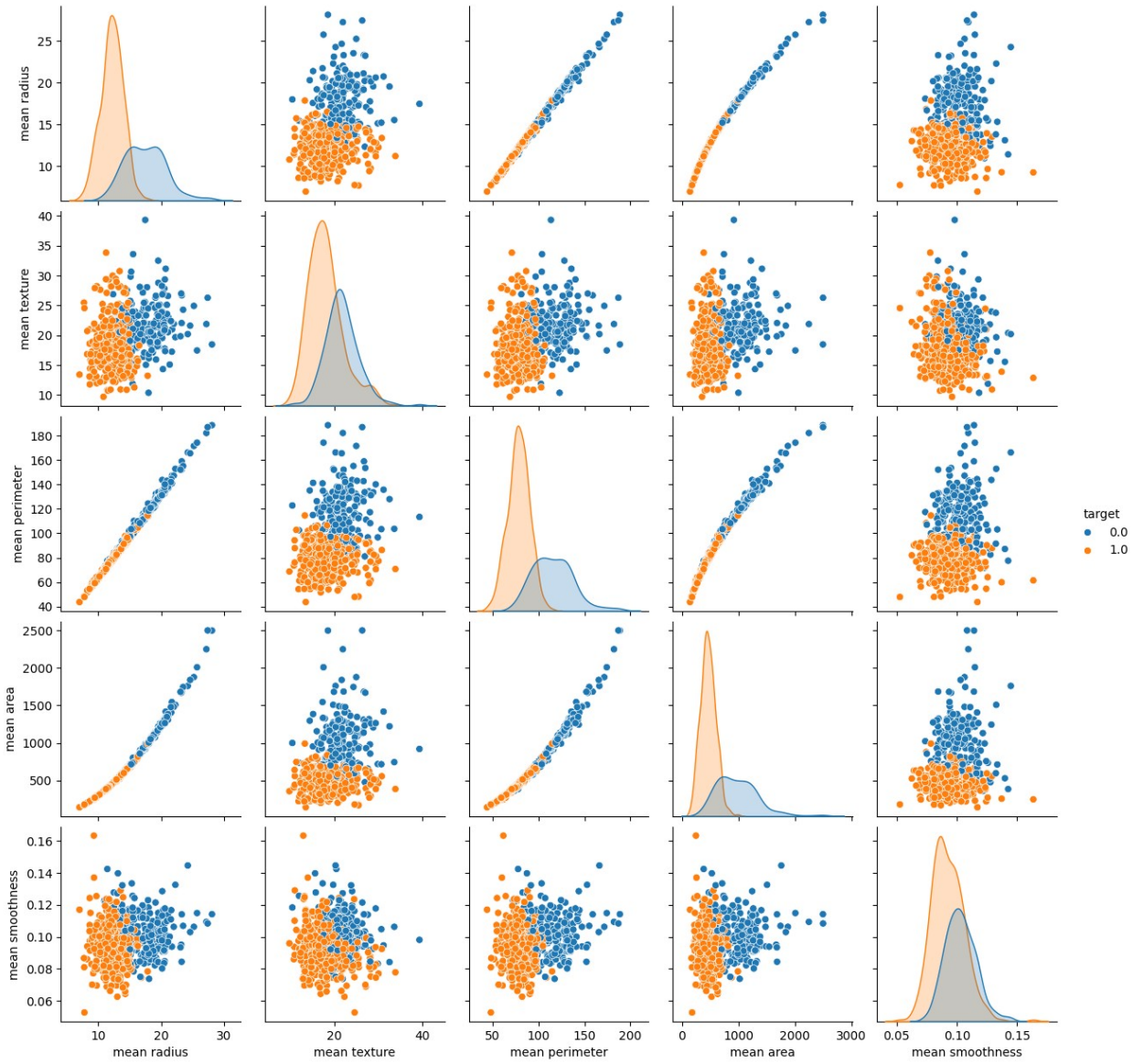
```
       worst fractal dimension      target
count               569.000000  569.000000
mean                  0.083946    0.627417
std                   0.018061    0.483918
min                   0.055040    0.000000
25%                   0.071460    0.000000
50%                   0.080040    1.000000
75%                   0.092080    1.000000
max                   0.207500    1.000000

[8 rows x 31 columns]
```

```
sns.pairplot(cancer_df, hue = 'target')
```

```
<seaborn.axisgrid.PairGrid at 0x2282f5bf010>
```

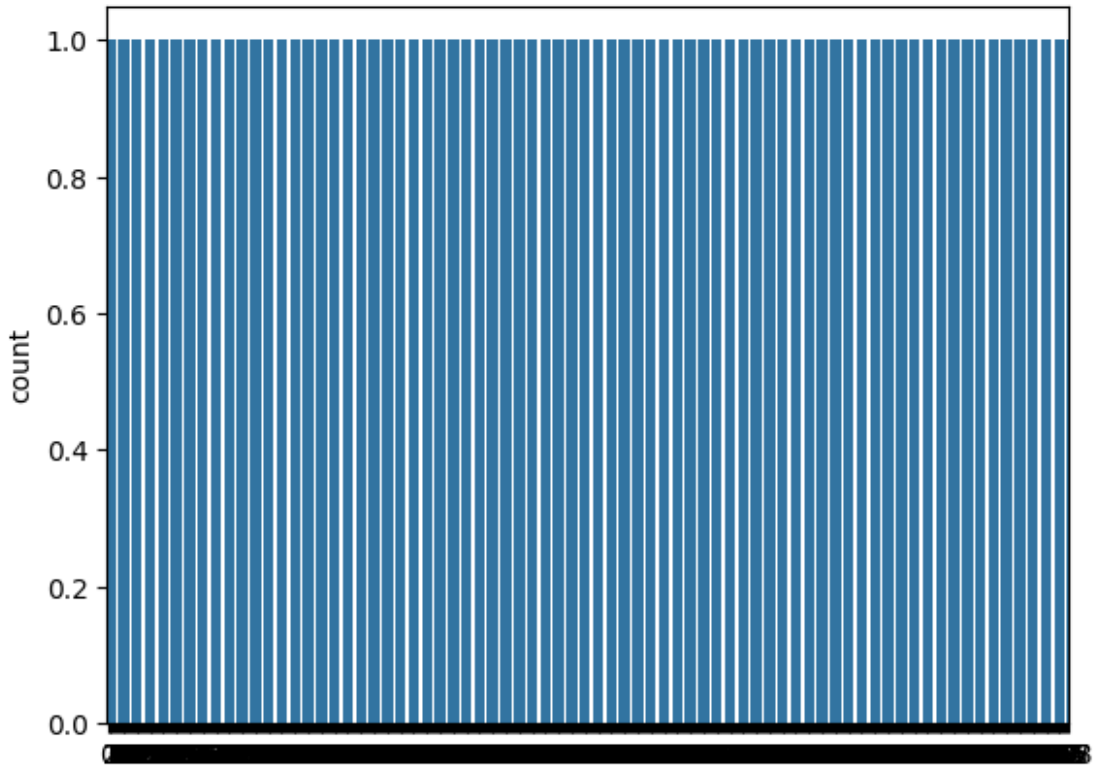
```
sns.pairplot(cancer_df, hue = 'target',
             vars = ['mean radius', 'mean texture', 'mean perimeter',
'mean area', 'mean smoothness'] )
```

```
<seaborn.axisgrid.PairGrid at 0x2286377a9d0>
```



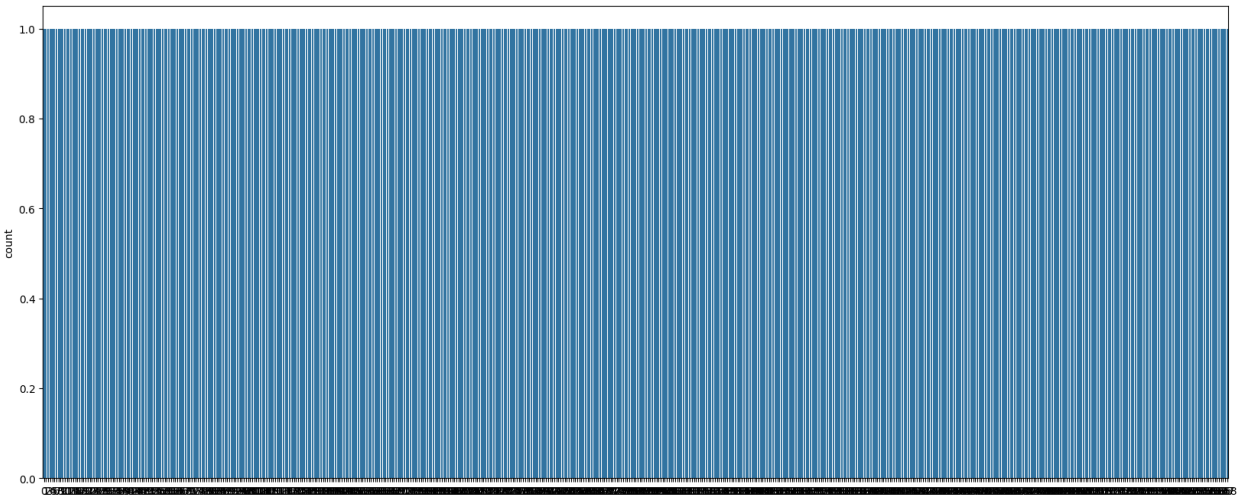

```
sns.countplot(cancer_df['target'])
```

```
<Axes: ylabel='count'>
```



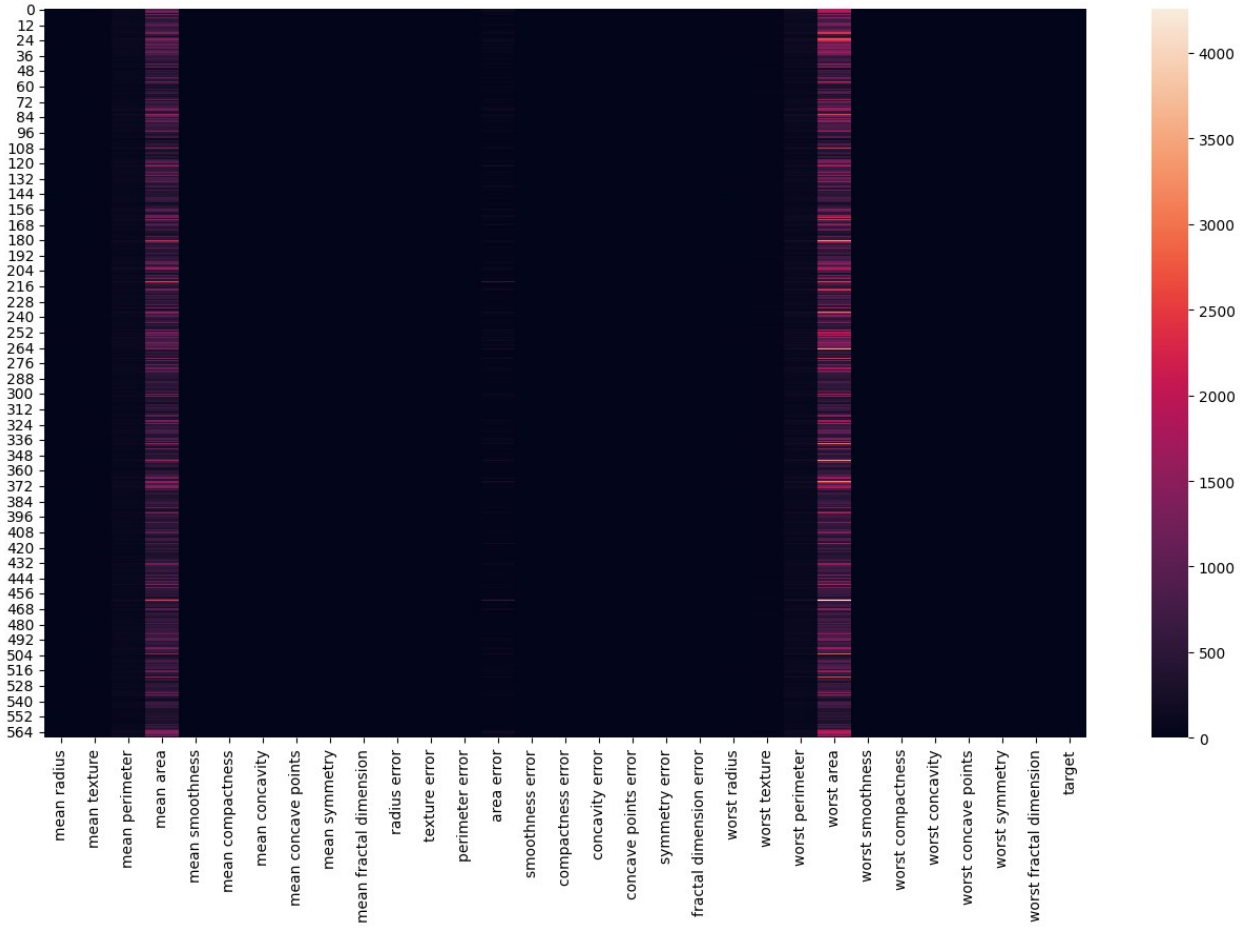

```
plt.figure(figsize = (20,8))
sns.countplot(cancer_df['mean radius'])
```

```
<Axes: ylabel='count'>
```



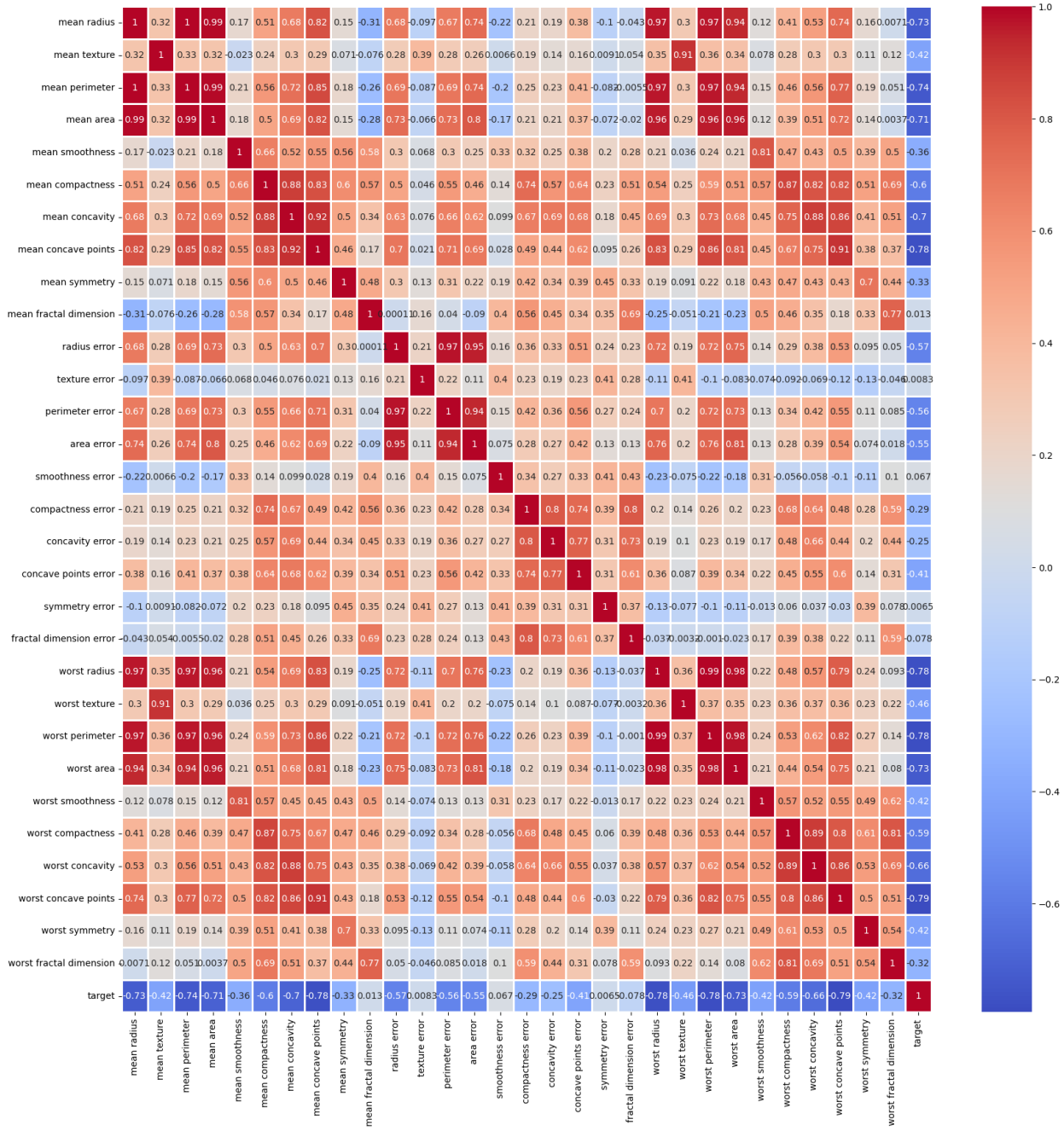

```
plt.figure(figsize=(16,9))
sns.heatmap(cancer_df)
```

```
<Axes: >
```




```
plt.figure(figsize=(20,20))
sns.heatmap(cancer_df.corr(), annot = True, cmap ='coolwarm',
linewidths=2)
```

```
<Axes: >
```

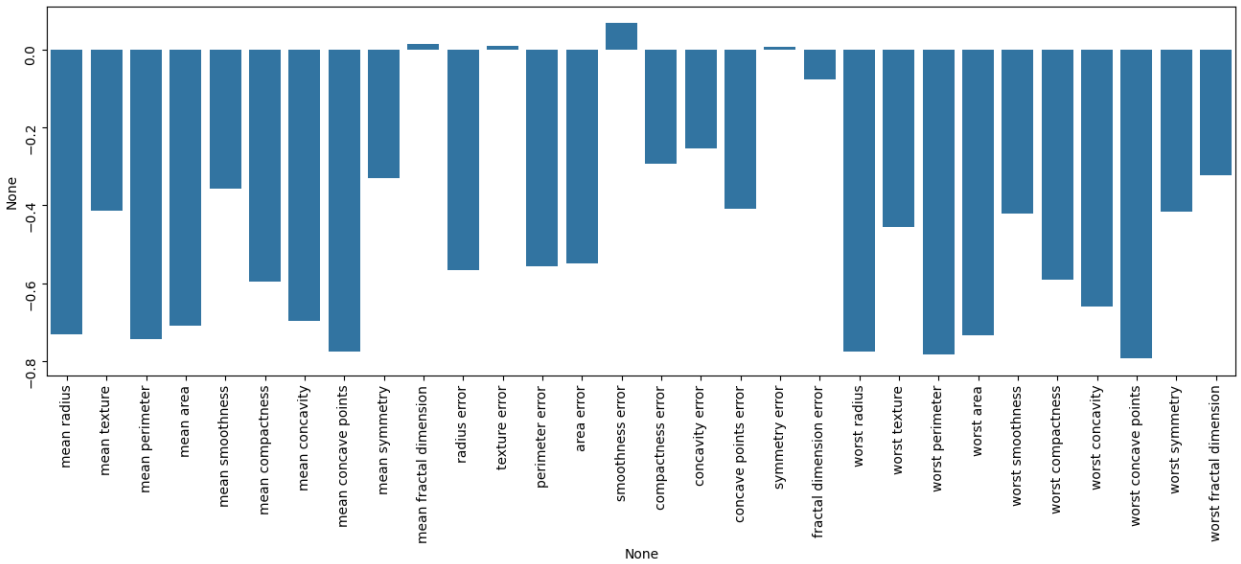



```
# create second DataFrame by droping target
cancer_df2 = cancer_df.drop(['target'], axis = 1)
print("The shape of 'cancer_df2' is : ", cancer_df2.shape)
```

```
The shape of 'cancer_df2' is :  (569, 30)
```

```
# visualize correlation barplot
plt.figure(figsize=(16, 5))
ax = sns.barplot(
    x=cancer_df2.corrwith(cancer_df.target).index,
```

```
    y=cancer_df2.corrwith(cancer_df.target)
)
ax.tick_params(labelrotation=90)
plt.show()
```




```
# input variable
X = cancer_df.drop(['target'], axis = 1)
X.head(6)
```

```
   mean radius  mean texture  mean perimeter  mean area  mean
smoothness  \
0        17.99         10.38          122.80     1001.0
0.11840
1        20.57         17.77          132.90     1326.0
0.08474
2        19.69         21.25          130.00     1203.0
0.10960
3        11.42         20.38           77.58      386.1
0.14250
4        20.29         14.34          135.10     1297.0
0.10030
5        12.45         15.70           82.57      477.1
0.12780

   mean compactness  mean concavity  mean concave points  mean
symmetry  \
0           0.27760          0.3001              0.14710
0.2419
1           0.07864          0.0869              0.07017
0.1812
2           0.15990          0.1974              0.12790
0.2069
```

```
3           0.28390          0.2414               0.10520
0.2597
4           0.13280          0.1980               0.10430
0.1809
5           0.17000          0.1578               0.08089
0.2087

   mean fractal dimension  ...  worst radius  worst texture  worst
perimeter  \
0                 0.07871  ...         25.38          17.33
184.60
1                 0.05667  ...         24.99          23.41
158.80
2                 0.05999  ...         23.57          25.53
152.50
3                 0.09744  ...         14.91          26.50
98.87
4                 0.05883  ...         22.54          16.67
152.20
5                 0.07613  ...         15.47          23.75
103.40

   worst area  worst smoothness  worst compactness  worst concavity  \
0      2019.0            0.1622             0.6656           0.7119
1      1956.0            0.1238             0.1866           0.2416
2      1709.0            0.1444             0.4245           0.4504
3       567.7            0.2098             0.8663           0.6869
4      1575.0            0.1374             0.2050           0.4000
5       741.6            0.1791             0.5249           0.5355

   worst concave points  worst symmetry  worst fractal dimension
0                0.2654          0.4601                  0.11890
1                0.1860          0.2750                  0.08902
2                0.2430          0.3613                  0.08758
3                0.2575          0.6638                  0.17300
4                0.1625          0.2364                  0.07678
5                0.1741          0.3985                  0.12440

[6 rows x 30 columns]
```

```
# output variable
y = cancer_df['target']
y.head(6)

0    0.0
1    0.0
2    0.0
3    0.0
4    0.0
```

```
5    0.0
Name: target, dtype: float64
```

```
# split dataset into train and test
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)

# Feature scaling
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train_sc = sc.fit_transform(X_train)
X_test_sc = sc.transform(X_test)

from sklearn.metrics import confusion_matrix, classification_report,
accuracy_score

# Support vector classifier
from sklearn.svm import SVC
svc_classifier = SVC()
svc_classifier.fit(X_train, y_train)
y_pred_scv = svc_classifier.predict(X_test)
accuracy_score(y_test, y_pred_scv)
```

```
0.9385964912280702
```

```
# Train with Standard scaled Data
svc_classifier2 = SVC()
svc_classifier2.fit(X_train_sc, y_train)
y_pred_svc_sc = svc_classifier2.predict(X_test_sc)
accuracy_score(y_test, y_pred_svc_sc)
```

```
0.9649122807017544
```

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score

lr_classifier = LogisticRegression(random_state=51, penalty='l1',
solver='liblinear')
lr_classifier.fit(X_train, y_train)
y_pred_lr = lr_classifier.predict(X_test)
accuracy_score(y_test, y_pred_lr)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\svm\_base.py:1249:
ConvergenceWarning: Liblinear failed to converge, increase the number
of iterations.
  warnings.warn(
```

```
0.9649122807017544
```

```
# Train with Standard scaled Data
#lr_classifier2 = LogisticRegression(random_state = 51, penalty =
'l1')
lr_classifier2 = LogisticRegression(random_state=51, penalty='l1',
solver='liblinear')

lr_classifier2.fit(X_train_sc, y_train)
y_pred_lr_sc = lr_classifier.predict(X_test_sc)
accuracy_score(y_test, y_pred_lr_sc)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\utils\validation.py:2739:
UserWarning: X does not have valid feature names, but
LogisticRegression was fitted with feature names
  warnings.warn(
```

```
0.6052631578947368
```

```
# K – Nearest Neighbor Classifier
from sklearn.neighbors import KNeighborsClassifier
knn_classifier = KNeighborsClassifier(n_neighbors = 5, metric =
'minkowski', p = 2)
knn_classifier.fit(X_train, y_train)
y_pred_knn = knn_classifier.predict(X_test)
accuracy_score(y_test, y_pred_knn)
```

```
0.9385964912280702
```

```
# Train with Standard scaled Data
knn_classifier2 = KNeighborsClassifier(n_neighbors = 5, metric =
'minkowski', p = 2)
knn_classifier2.fit(X_train_sc, y_train)
y_pred_knn_sc = knn_classifier.predict(X_test_sc)
accuracy_score(y_test, y_pred_knn_sc)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\utils\validation.py:2739:
UserWarning: X does not have valid feature names, but
KNeighborsClassifier was fitted with feature names
  warnings.warn(
```

```
0.5789473684210527
```

```
# Naive Bayes Classifier
from sklearn.naive_bayes import GaussianNB
nb_classifier = GaussianNB()
nb_classifier.fit(X_train, y_train)
y_pred_nb = nb_classifier.predict(X_test)
accuracy_score(y_test, y_pred_nb)
```

```
0.9473684210526315
```

```
# Train with Standard scaled Data
nb_classifier2 = GaussianNB()
nb_classifier2.fit(X_train_sc, y_train)
y_pred_nb_sc = nb_classifier2.predict(X_test_sc)
accuracy_score(y_test, y_pred_nb_sc)
```

```
0.9385964912280702
```

```
# Decision Tree Classifier
from sklearn.tree import DecisionTreeClassifier
dt_classifier = DecisionTreeClassifier(criterion = 'entropy',
random_state = 51)
dt_classifier.fit(X_train, y_train)
y_pred_dt = dt_classifier.predict(X_test)
accuracy_score(y_test, y_pred_dt)
```

```
0.9473684210526315
```

```
# Train with Standard scaled Data
dt_classifier2 = DecisionTreeClassifier(criterion = 'entropy',
random_state = 51)
dt_classifier2.fit(X_train_sc, y_train)
y_pred_dt_sc = dt_classifier.predict(X_test_sc)
accuracy_score(y_test, y_pred_dt_sc)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\utils\validation.py:2739:
UserWarning: X does not have valid feature names, but
DecisionTreeClassifier was fitted with feature names
  warnings.warn(
```

```
0.7543859649122807
```

```
# Random Forest Classifier
from sklearn.ensemble import RandomForestClassifier
rf_classifier = RandomForestClassifier(n_estimators = 20, criterion =
'entropy', random_state = 51)
rf_classifier.fit(X_train, y_train)
y_pred_rf = rf_classifier.predict(X_test)
accuracy_score(y_test, y_pred_rf)
```

```
0.9736842105263158
```

```
# Train with Standard scaled Data
rf_classifier2 = RandomForestClassifier(n_estimators = 20, criterion =
'entropy', random_state = 51)
rf_classifier2.fit(X_train_sc, y_train)
```

```
y_pred_rf_sc = rf_classifier.predict(X_test_sc)
accuracy_score(y_test, y_pred_rf_sc)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\utils\validation.py:2739:
UserWarning: X does not have valid feature names, but
RandomForestClassifier was fitted with feature names
  warnings.warn(
```

```
0.7543859649122807
```

```
import sklearn
print(sklearn.__version__)
```

```
1.6.1
```

```
from sklearn.ensemble import AdaBoostClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score

adb_classifier = AdaBoostClassifier(
    estimator=DecisionTreeClassifier(criterion='entropy',
random_state=200),
    n_estimators=2000,
    learning_rate=0.1,
    algorithm='SAMME',
    random_state=1
)

adb_classifier.fit(X_train, y_train)
y_pred_adb = adb_classifier.predict(X_test)
print("Accuracy:", accuracy_score(y_test, y_pred_adb))
```

```
Accuracy: 0.9473684210526315
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\ensemble\
_weight_boosting.py:519: FutureWarning: The parameter 'algorithm' is
deprecated in 1.6 and has no effect. It will be removed in version
1.8.
  warnings.warn(
```

```
# Train with Standard scaled Data
adb_classifier2 =
AdaBoostClassifier(estimator=DecisionTreeClassifier(criterion =
'entropy', random_state = 200),
                                    n_estimators=2000,
                                    learning_rate=0.1,
                                    algorithm='SAMME',
```

```
                                    random_state=1,)
adb_classifier2.fit(X_train_sc, y_train)
y_pred_adb_sc = adb_classifier2.predict(X_test_sc)
accuracy_score(y_test, y_pred_adb_sc)
```

```
C:\Users\Nishita\AppData\Local\Packages\
PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\LocalCache\local-
packages\Python311\site-packages\sklearn\ensemble\
_weight_boosting.py:519: FutureWarning: The parameter 'algorithm' is
deprecated in 1.6 and has no effect. It will be removed in version
1.8.
  warnings.warn(
```

```
0.9473684210526315
```

```
!pip install xgboost
```

```
Collecting xgboost
  Downloading xgboost-3.0.2-py3-none-win_amd64.whl.metadata (2.1 kB)
Requirement already satisfied: numpy in c:\users\nishita\appdata\
local\packages\pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\
localcache\local-packages\python311\site-packages (from xgboost)
(1.26.2)
Requirement already satisfied: scipy in c:\users\nishita\appdata\
local\packages\pythonsoftwarefoundation.python.3.11_qbz5n2kfra8p0\
localcache\local-packages\python311\site-packages (from xgboost)
(1.15.3)
Downloading xgboost-3.0.2-py3-none-win_amd64.whl (150.0 MB)
   ---------------------------------------- 0.0/150.0 MB ? eta -:--:--
   ---------------------------------------- 0.5/150.0 MB 11.1 MB/s eta
0:00:14
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Installing collected packages: xgboost
Successfully installed xgboost-3.0.2


[notice] A new release of pip is available: 24.0 -> 25.1.1
[notice] To update, run: C:\Users\Nishita\AppData\Local\Microsoft\
WindowsApps\PythonSoftwareFoundation.Python.3.11_qbz5n2kfra8p0\
python.exe -m pip install --upgrade pip
```

```python
# XGBoost Classifier
from xgboost import XGBClassifier
xgb_classifier = XGBClassifier()
xgb_classifier.fit(X_train, y_train)
```

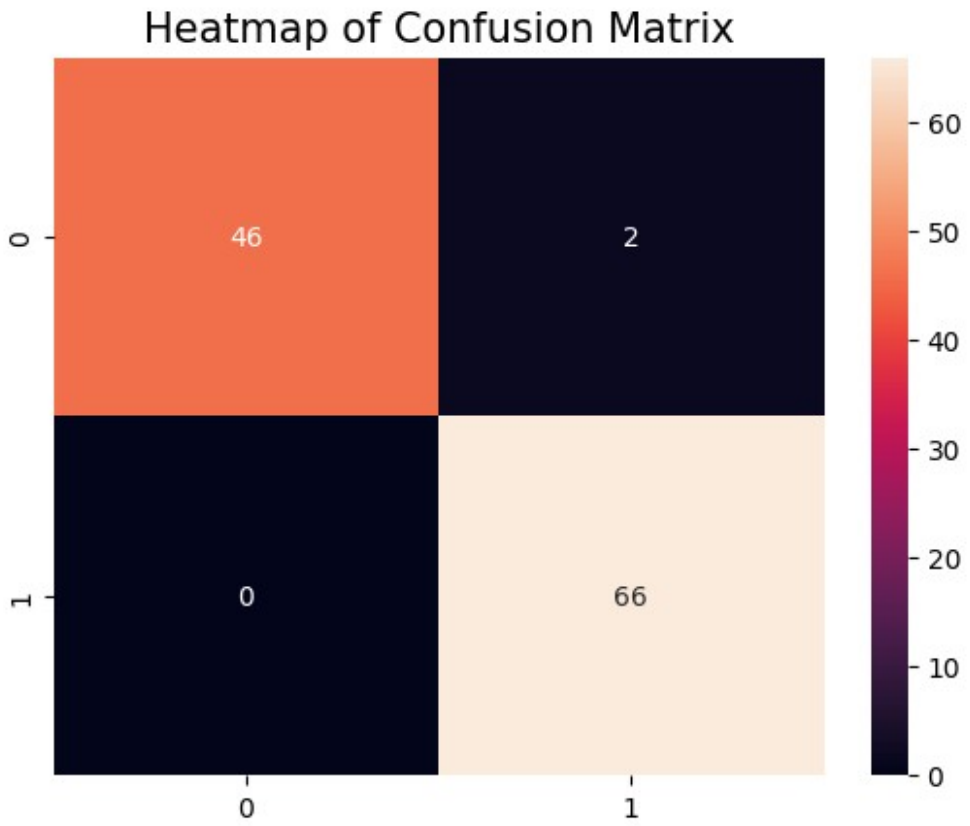
```
y_pred_xgb = xgb_classifier.predict(X_test)
accuracy_score(y_test, y_pred_xgb)
```

```
0.9824561403508771
```

```
# Train with Standard scaled Data
xgb_classifier2 = XGBClassifier()
xgb_classifier2.fit(X_train_sc, y_train)
y_pred_xgb_sc = xgb_classifier2.predict(X_test_sc)
accuracy_score(y_test, y_pred_xgb_sc)
```

```
0.9824561403508771
```

```
cm = confusion_matrix(y_test, y_pred_xgb)
plt.title('Heatmap of Confusion Matrix', fontsize = 15)
sns.heatmap(cm, annot = True)
plt.show()
```




```
print(classification_report(y_test, y_pred_xgb))
```

```
              precision    recall  f1-score   support

         0.0       1.00      0.96      0.98        48
         1.0       0.97      1.00      0.99        66
```

```
    accuracy                           0.98       114
   macro avg       0.99      0.98      0.98       114
weighted avg       0.98      0.98      0.98       114
```

```
from xgboost import XGBClassifier

# Define and train the XGBoost model
xgb_classifier_pt = XGBClassifier()
xgb_classifier_pt.fit(X_train_sc, y_train)
```

```
XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, device=None,
early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None,
feature_types=None,
              feature_weights=None, gamma=None, grow_policy=None,
              importance_type=None, interaction_constraints=None,
              learning_rate=None, max_bin=None,
max_cat_threshold=None,
              max_cat_to_onehot=None, max_delta_step=None,
max_depth=None,
              max_leaves=None, min_child_weight=None, missing=nan,
              monotone_constraints=None, multi_strategy=None,
n_estimators=None,
              n_jobs=None, num_parallel_tree=None, ...)
```

```
# Cross validation
from sklearn.model_selection import cross_val_score

cross_validation = cross_val_score(estimator = xgb_classifier_pt, X =
X_train_sc, y = y_train, cv = 10)
print("Cross validation accuracy of XGBoost model = ",
cross_validation)
print("\nCross validation mean accuracy of XGBoost model = ",
cross_validation.mean())
```

```
Cross validation accuracy of XGBoost model =  [1.         0.97826087
0.97826087 1.         0.93478261 0.97777778
 1.         1.         0.97777778 0.91111111]

Cross validation mean accuracy of XGBoost model =  0.9757971014492753
```