

breast-cancer-classification

August 19, 2024

SOUMAJIT DEY

PROJECT NAME :- Breast Cancer Classification using Machine Learning

Breast cancer is the most-commonly diagnosed malignant tumor in women in the world, as well as the first cause of death from malignant tumors. The incidence of breast cancer is constantly increasing in all regions of the world. For this reason, despite the progress in its detection and treatment, which translates into improved mortality rates, it seems necessary to look for new therapeutic methods, predictive and prognostic factors. The article presents a review of the literature on breast carcinoma - a disease affecting women in the world.

Abstract

Breast cancer is the most-commonly diagnosed malignant tumor in women in the world, as well as the first cause of death from malignant tumors. The incidence of breast cancer is constantly increasing in all regions of the world. For this reason, despite the progress in its detection and treatment, which translates into improved mortality rates, it seems necessary to look for new therapeutic methods, and predictive and prognostic factors. Treatment strategies vary depending on the molecular subtype. Breast cancer treatment is multidisciplinary; it includes approaches to locoregional therapy (surgery and radiation therapy) and systemic therapy. Systemic therapies include hormone therapy for hormone-positive disease, chemotherapy, anti-HER2 therapy for HER2-positive disease, and quite recently, immunotherapy. Triple negative breast cancer is responsible for more than 15–20% of all breast cancers. It is of particular research interest as it presents a therapeutic challenge, mainly due to its low response to treatment and its highly invasive nature. Future therapeutic concepts for breast cancer aim to individualize therapy and de-escalate and escalate treatment based on cancer biology and early response to therapy. The article presents a review of the literature on breast carcinoma—a disease affecting women in the world.

What Is a Tumor

A tumor is an abnormal mass or growth of tissue that serves no specific purpose. It can develop when cells grow and divide too quickly. Tumors can be located anywhere in the body. They grow and behave differently depending on whether they are benign (noncancerous) or malignant (cancerous).

Benign (Noncancerous) Tumors

A benign tumor is made up of cells that don't threaten to invade other tissues. The tumor cells are contained within the tumor and aren't abnormal or very different from surrounding cells.

Usually, benign types of tumors are harmless unless they are:

Pressing on nearby tissues, nerves, or blood vessels

Taking up space in the brain

Causing damage

Causing excess hormone production

Malignant (Cancerous) Tumors

Malignant tumors are made of cancer cells that can grow uncontrollably and invade nearby tissues. The cancer cells in a malignant tumor tend to be abnormal and very different from the normal surrounding tissue.

Cancerous tumors can occur anywhere in the body. The most frequently diagnosed malignant tumors worldwide include:

Breast cancer

Lung cancer

Colorectal cancer

Prostate cancer

Stomach cancer

Some cancer cells can travel through the bloodstream or lymph system to other parts of the body. This spreading process is called metastasis.

For example, breast cancer begins in the breast tissue and may spread to lymph nodes in the armpit if not caught and treated early enough. Once this occurs, the cancer cells can travel (metastasize) to the liver, bones, or other parts of the body.

#importing the Dependencies

```
[ ]: import numpy as np
import pandas as pd
import sklearn.datasets
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

1 Data Collection & Processing

```
[ ]: # loading the data from sklearn
breast_cancer_dataset = sklearn.datasets.load_breast_cancer()
```

```
[ ]: print(breast_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, 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, 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, 1, 0, 1, 1, 0, 1, 0, 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, 1, 0, 1, 0, 0, 1, 0, 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, 0, 0, 1, 0, 1, 0, 1, 1,
1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1]), '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\n      - radius (mean of distances from center to points on the
perimeter)\n\n      - texture (standard deviation of gray-scale values)\n
- perimeter\n\n      - area\n\n      - smoothness (local variation in radius
lengths)\n\n      - compactness (perimeter^2 / area - 1.0)\n\n      - concavity
(severity of concave portions of the contour)\n\n      - concave points (number
of concave portions of the contour)\n\n      - symmetry\n\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.

```


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.', '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'}

```
[ ]: # loading the data to a data frame
data_frame = pd.DataFrame(breast_cancer_dataset.data, columns =_
↳breast_cancer_dataset.feature_names)
```

```
[ ]: # print the first 5 rows of the dataframe
data_frame.head()
```

```
[ ]:      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

      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

      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

      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

	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 rows x 30 columns]

```
[ ]: # adding the 'target' column to the data frame
data_frame['label'] = breast_cancer_dataset.target
```

```
[ ]: # print last 5 rows of the dataframe
data_frame.tail()
```

```
[ ]:      mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
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
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
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
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	label
564	0.2216	0.2060	0.07115	0
565	0.1628	0.2572	0.06637	0
566	0.1418	0.2218	0.07820	0
567	0.2650	0.4087	0.12400	0
568	0.0000	0.2871	0.07039	1

[5 rows x 31 columns]

```
[ ]: # number of rows and columns in the dataset
data_frame.shape
```

```
[ ]: (569, 31)
```

```
[ ]: # getting some information about the data
data_frame.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  label               569 non-null    int64
dtypes: float64(30), int64(1)
memory usage: 137.9 KB

```

```

[ ]: # checking for missing values
data_frame.isnull().sum()

```

```

[ ]: mean radius          0
mean texture             0
mean perimeter           0
mean area               0
mean smoothness          0
mean compactness         0
mean concavity           0
mean concave points      0
mean symmetry            0
mean fractal dimension    0
radius error             0
texture error            0
perimeter error          0
area error               0
smoothness error         0
compactness error        0
concavity error          0
concave points error     0
symmetry error           0
fractal dimension error  0
worst radius             0
worst texture            0
worst perimeter          0
worst area              0
worst smoothness         0
worst compactness        0
worst concavity          0
worst concave points     0
worst symmetry           0
worst fractal dimension  0
label                   0
dtype: int64

```



```
[ ]: # statistical measures about the data
data_frame.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	label
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]

```
[ ]: # checking the distribution of Target Varibale
data_frame['label'].value_counts()
```

```
[ ]: label
1      357
0      212
Name: count, dtype: int64
```

Class Distribution:

- 0(Malignant) - 212
- 1(Benign) - 357

2 1 — Benign

3 0 — Malignant

```
[ ]: data_frame.groupby('label').mean()
```

```
[ ]:      mean radius  mean texture  mean perimeter  mean area  mean smoothness \
label
0      17.462830    21.604906    115.365377    978.376415    0.102898
1      12.146524    17.914762     78.075406    462.790196    0.092478

      mean compactness  mean concavity  mean concave points  mean symmetry \
label
0      0.145188      0.160775      0.087990      0.192909
1      0.080085      0.046058      0.025717      0.174186
```

	mean fractal dimension	...	worst radius	worst texture	\
label		...			
0	0.062680	...	21.134811	29.318208	
1	0.062867	...	13.379801	23.515070	

	worst perimeter	worst area	worst smoothness	worst compactness	\
label					
0	141.370330	1422.286321	0.144845	0.374824	
1	87.005938	558.899440	0.124959	0.182673	

	worst concavity	worst concave points	worst symmetry	\
label				
0	0.450606	0.182237	0.323468	
1	0.166238	0.074444	0.270246	

	worst fractal dimension
label	
0	0.091530
1	0.079442

[2 rows x 30 columns]

All the values of Malignant Cases are greater in compare with Benign Cases

4 Separating the features and target

```
[ ]: X = data_frame.drop(columns='label', axis=1)
      Y = data_frame['label']
```

```
[ ]: print(X)
```

	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	
..	
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	\
0	0.27760	0.30010	0.14710	0.2419	
1	0.07864	0.08690	0.07017	0.1812	

2	0.15990	0.19740	0.12790	0.2069
3	0.28390	0.24140	0.10520	0.2597
4	0.13280	0.19800	0.10430	0.1809
..
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 radius	worst texture	\
0	0.07871	...	25.380	17.33	
1	0.05667	...	24.990	23.41	
2	0.05999	...	23.570	25.53	
3	0.09744	...	14.910	26.50	
4	0.05883	...	22.540	16.67	
..	
564	0.05623	...	25.450	26.40	
565	0.05533	...	23.690	38.25	
566	0.05648	...	18.980	34.12	
567	0.07016	...	25.740	39.42	
568	0.05884	...	9.456	30.37	

	worst perimeter	worst area	worst smoothness	worst compactness	\
0	184.60	2019.0	0.16220	0.66560	
1	158.80	1956.0	0.12380	0.18660	
2	152.50	1709.0	0.14440	0.42450	
3	98.87	567.7	0.20980	0.86630	
4	152.20	1575.0	0.13740	0.20500	
..	
564	166.10	2027.0	0.14100	0.21130	
565	155.00	1731.0	0.11660	0.19220	
566	126.70	1124.0	0.11390	0.30940	
567	184.60	1821.0	0.16500	0.86810	
568	59.16	268.6	0.08996	0.06444	

	worst concavity	worst concave points	worst symmetry	\
0	0.7119	0.2654	0.4601	
1	0.2416	0.1860	0.2750	
2	0.4504	0.2430	0.3613	
3	0.6869	0.2575	0.6638	
4	0.4000	0.1625	0.2364	
..	
564	0.4107	0.2216	0.2060	
565	0.3215	0.1628	0.2572	
566	0.3403	0.1418	0.2218	
567	0.9387	0.2650	0.4087	
568	0.0000	0.0000	0.2871	

	worst fractal dimension
0	0.11890
1	0.08902
2	0.08758
3	0.17300
4	0.07678
..	...
564	0.07115
565	0.06637
566	0.07820
567	0.12400
568	0.07039

[569 rows x 30 columns]

```
[ ]: print(Y)
```

```
0      0
1      0
2      0
3      0
4      0
..
564    0
565    0
566    0
567    0
568    1
```

Name: label, Length: 569, dtype: int64

5 splitting the data into training data & Testing data

```
[ ]: X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2,
↳random_state=2)
```

```
[ ]: print(X.shape, X_train.shape, X_test.shape)
```

(569, 30) (455, 30) (114, 30)

6 Modeling Training

7 Logistic Regression

```
[ ]: model = LogisticRegression()
```

```
[ ]: # training the Logistic Regression model using Training data
```

```
model.fit(X_train, Y_train)
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458:  
ConvergenceWarning: lbfgs failed to converge (status=1):  
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

```
n_iter_i = _check_optimize_result(
```

```
[ ]: LogisticRegression()
```

8 Model Evalution

9 Accuracy Score

```
[ ]: # accuracy on training data
```

```
X_train_prediction = model.predict(X_train)
```

```
training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
```

```
[ ]: print('Accuracy on training data = ', training_data_accuracy)
```

```
Accuracy on training data = 0.9472527472527472
```

```
[ ]: # accuracy on test data
```

```
X_test_prediction = model.predict(X_test)
```

```
test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
```

```
[ ]: print('Accuracy on test data = ', test_data_accuracy)
```

```
Accuracy on test data = 0.9298245614035088
```

10 Building a Predictive System

```
[ ]: input_data = (13.54,14.36,87.46,566.3,0.09779,0.08129,0.06664,0.04781,0.1885,0.  
    ↳05766,0.2699,0.7886,2.058,23.56,0.008462,0.0146,0.02387,0.01315,0.0198,0.  
    ↳0023,15.11,19.26,99.7,711.2,0.144,0.1773,0.239,0.1288,0.2977,0.07259)
```

```
# change the input data to a numpy array
```

```
input_data_as_numpy_array = np.asarray(input_data)
```

```
# reshape the numpy array as we are predicting for one datapoint
input_data_resaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_resaped)
print(prediction)

if (prediction[0] == 0):
    print('The Breast cancer is Malignant')
else:
    print('The Breast Cancer is Benign')
```

[1]

The Breast Cancer is Benign

/usr/local/lib/python3.10/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fitted with feature names

```
warnings.warn(
```