

LogisticRegression

August 19, 2022

```
[1]: import pandas as pd
     from sklearn.datasets import load_breast_cancer
```

```
[2]: cancer_data = load_breast_cancer()
```

```
[3]: print(cancer_data.DESCR)
```

```
.. _breast_cancer_dataset:
```

```
Breast cancer wisconsin (diagnostic) dataset
```

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```

```
**Data Set Characteristics:**
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```
:Number of Instances: 569
```

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

```
:Attribute Information:
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- 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 (perimeter² / 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

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:Donor: Nick Street

:Date: November, 1995

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

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

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

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

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

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

.. topic:: References

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

```
[4]: features = pd.DataFrame(cancer_data.data, columns=cancer_data.feature_names)
     target = pd.DataFrame(cancer_data.target, columns=['Target'])
```

```
[5]: features.head()
```

```

[5]: 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]

```
[6]: target.head()
```

```

[6]: Target
0      0
1      0
2      0
3      0
4      0

```

```
[7]: from sklearn.model_selection import train_test_split
      from sklearn.linear_model import LogisticRegression
      from sklearn.metrics import accuracy_score
```

```
[8]: X_train, X_test, y_train, y_test = train_test_split(features, target,
      ↪random_state=10)
      print(X_train.shape)
      print(X_test.shape)
      print(y_train.shape)
      print(y_test.shape)
```

```
(426, 30)
(143, 30)
(426, 1)
(143, 1)
```

```
[9]: my_logreg_model = LogisticRegression().fit(X_train, y_train)
```

```
/usr/local/lib/python3.7/site-packages/sklearn/utils/validation.py:993:
DataConversionWarning: A column-vector y was passed when a 1d array was
expected. Please change the shape of y to (n_samples, ), for example using
ravel().
```

```
    y = column_or_1d(y, warn=True)
```

```
/usr/local/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:818:
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

```
    extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
```