

# Breast cancer Wisconsin 特徵資訊解析

## 1. ID number

患者編號

## 2. Diagnosis (M = malignant, B = benign)

診斷結果(M:惡性，B:良性)

Ten real-valued features are computed for each cell nucleus:

以下的 10 種特徵皆是以細胞核為基準計算

## 1. radius (mean of distances from center to points on the perimeter)

半徑(癌細胞核的中心至其圓周的長度的平均值)

## 2. texture (standard deviation of gray-scale values)

紋理(灰階值的標準差)

## 3. perimeter

癌細胞之周長

## 4. area

癌細胞所占面積

5. smoothness (local variation in radius lengths)

平滑度(癌細胞在其半徑長度內的局部變化)

6. compactness ( $\text{perimeter}^2 / \text{area} - 1.0$ )

癌細胞緊緻性(半徑<sup>2</sup> / 癌細胞面積 - 1)

7. concavity (severity of concave portions of the contour)

凹陷度(輪廓凹陷的嚴重程度)

8. concave points (number of concave portions of the contour)

凹陷點(輪廓凹陷處的數量)

9. symmetry

對稱

10. fractal dimension (“coastline approximation” — 1)

分形維度(水平近似值 - 1)

# Python code

## Breast cancer Wisconsin

```
In [1]: 1 import numpy as np
2 import matplotlib.pyplot as plt
3 import pandas as pd
4 from sklearn.neighbors import KNeighborsClassifier
5 from sklearn import metrics
6 from sklearn.model_selection import train_test_split
7 from sklearn.metrics import roc_curve, auc
8 from sklearn.model_selection import KFold
```

```
In [2]: 1 # Import cancer data
2
3 dataset = pd.read_csv('C:/Users/accel/cancer.csv')
4 X = dataset.iloc[:, 2:32].values # 從 radius_mean 開始作為資料集
5 Y = dataset.iloc[:, 0].values # 將 diagnosis 作為 label
6
7 dataset.head()
```

Out[2]:

	diagnosis	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	radius_worst
0	M	842302	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...	25.06
1	M	842517	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...	33.97
2	M	84300903	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...	26.54
3	M	84348301	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...	18.08
4	M	84358402	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...	24.30

5 rows x 32 columns

```
In [3]: 1 print('cancer dataset dimensions:{}'.format(dataset.shape))

cancer dataset dimensions:(569, 32)
```

```
In [4]: 1 # Define the score
2
3 def TP():
4     x = 0
5     for i in range(len(Pred_test)):
6         if Pred_test[i] == Y_test[i]:
7             if Pred_test[i] == 'B':
8                 x += 1
9     return x
10
11 def TN():
12     x = 0
13     for i in range(len(Pred_test)):
14         if Pred_test[i] == Y_test[i]:
15             if Pred_test[i] == 'M':
16                 x += 1
17     return x
18
19 def FP():
20     x = 0
21     for i in range(len(Pred_test)):
22         if Pred_test[i] != Y_test[i]:
23             if Pred_test[i] == 'B':
24                 x += 1
25     return x
26
27 def FN():
28     x = 0
29     for i in range(len(Pred_test)):
30         if Pred_test[i] != Y_test[i]:
31             if Pred_test[i] == 'M':
32                 x += 1
33     return x
```



```

In [9]: 1 # roc curve & auc
2
3 roc_auc = auc(fpr, tpr) ### 计算auc的值
4
5 plt.figure()
6 lw = 2
7 plt.figure(figsize=(10,10))
8 plt.plot(fpr, tpr, color='darkorange',
9          lw=lw, label='ROC curve (area = %0.3f)' % roc_auc) ###FPR:row , TPR:column
10 plt.plot([0, 1], [0, 1], color='navy', lw=lw, linestyle='--')
11 plt.xlim([0.0, 1.0])
12 plt.ylim([0.0, 1.05])
13 plt.xlabel('False Positive Rate')
14 plt.ylabel('True Positive Rate')
15 plt.title('Receiver operating characteristic example')
16 plt.legend(loc="lower right")
17
18 plt.show()

```

<Figure size 432x288 with 0 Axes>

