deliverable2-task3

October 16, 2023

TASK 1

[56]:
```python
import sklearn.datasets
from sklearn.datasets import load_breast_cancer

cancer = load_breast_cancer()
print(cancer.keys())
print(cancer.DESCR)
```

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

|details-start|
References
|details-split|

- 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.

|details-end|

[57]:
```
cancer = load_breast_cancer(return_X_y = True, as_frame = True)

a = cancer[0]
a['typeofcancer'] = cancer[1]
a.iloc[0:2, :]
```

[57]:
```
   mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
0        17.99         10.38           122.8     1001.0          0.11840
1        20.57         17.77           132.9     1326.0          0.08474

   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

   mean fractal dimension  …  worst texture  worst perimeter  worst area  \
0                 0.07871  …          17.33            184.6      2019.0
1                 0.05667  …          23.41            158.8      1956.0

   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

   worst symmetry  worst fractal dimension  typeofcancer
0          0.4601                  0.11890             0
1          0.2750                  0.08902             0

[2 rows x 31 columns]
```

[58]:
```
a.shape
```

[58]:
```
(569, 31)
```

[59]:
```
df = a.iloc[:, [0, 6, 7, 8, 30]]
df.iloc[0:2, :] #Show the first two rows
```

[59]:
```
   mean radius  mean concavity  mean concave points  mean symmetry  \
0        17.99          0.3001              0.14710         0.2419
1        20.57          0.0869              0.07017         0.1812

   typeofcancer
0             0
1             0
```

[60]:
```
df.iloc[[17, 18, 19, 20, 21], :] #Show row indices; 17, 18, 19, 20, 21
```

[60]:
```
    mean radius  mean concavity  mean concave points  mean symmetry  \
17       16.130         0.17220              0.10280         0.2164
```

```
18      19.810      0.14790         0.09498      0.1582
19      13.540      0.06664         0.04781      0.1885
20      13.080      0.04568         0.03110      0.1967
21       9.504      0.02956         0.02076      0.1815

    typeofcancer
17             0
18             0
19             1
20             1
21             1
```

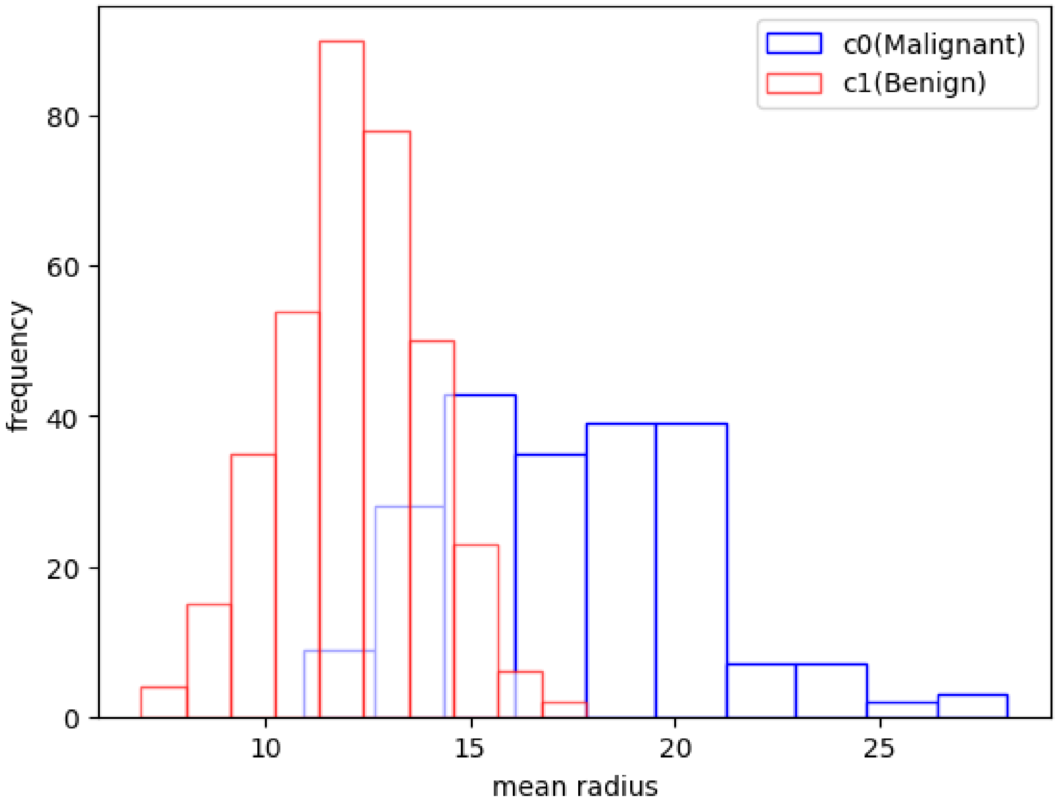
TASK 2

[ ]:

```

```

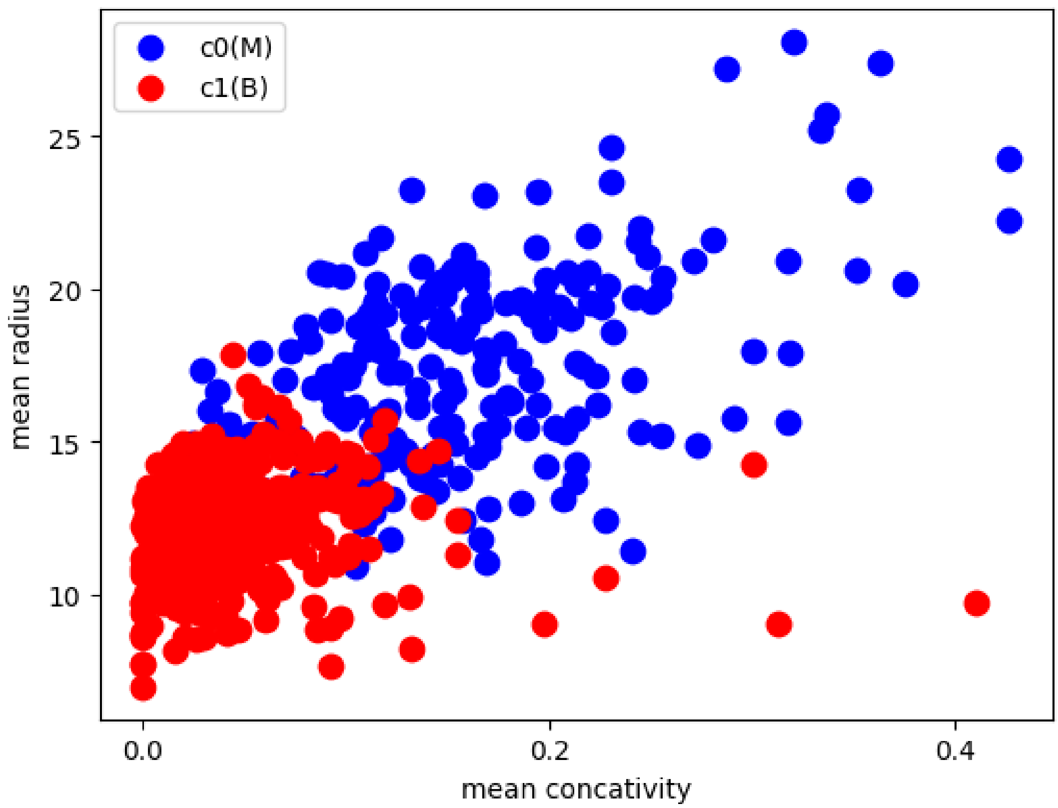
[61]:

```
import matplotlib.pyplot as plt
fig, ax = plt.subplots()

import numpy as np
mean_radius = np.array(df.iloc[:, 4])

pos = 0
mean_radius_malignant = np.array([])
mean_radius_benign = np.array([])

for row in mean_radius:
    if row == 0:
        mean_radius_malignant = np.append(mean_radius_malignant, df.iloc[pos,␣
 ↪0])
    else:
        mean_radius_benign = np.append(mean_radius_benign, df.iloc[pos, 0])
    pos += 1

plt.hist(mean_radius_malignant, bins=10, color='w', edgecolor='b', alpha=1.0,␣
 ↪label='c0(Malignant)')
plt.hist(mean_radius_benign, bins=10, color = 'w', edgecolor='r', alpha=0.65,␣
 ↪label='c1(Benign)')


plt.xlabel("mean radius")
plt.ylabel("frequency")
plt.legend()
plt.show()
```



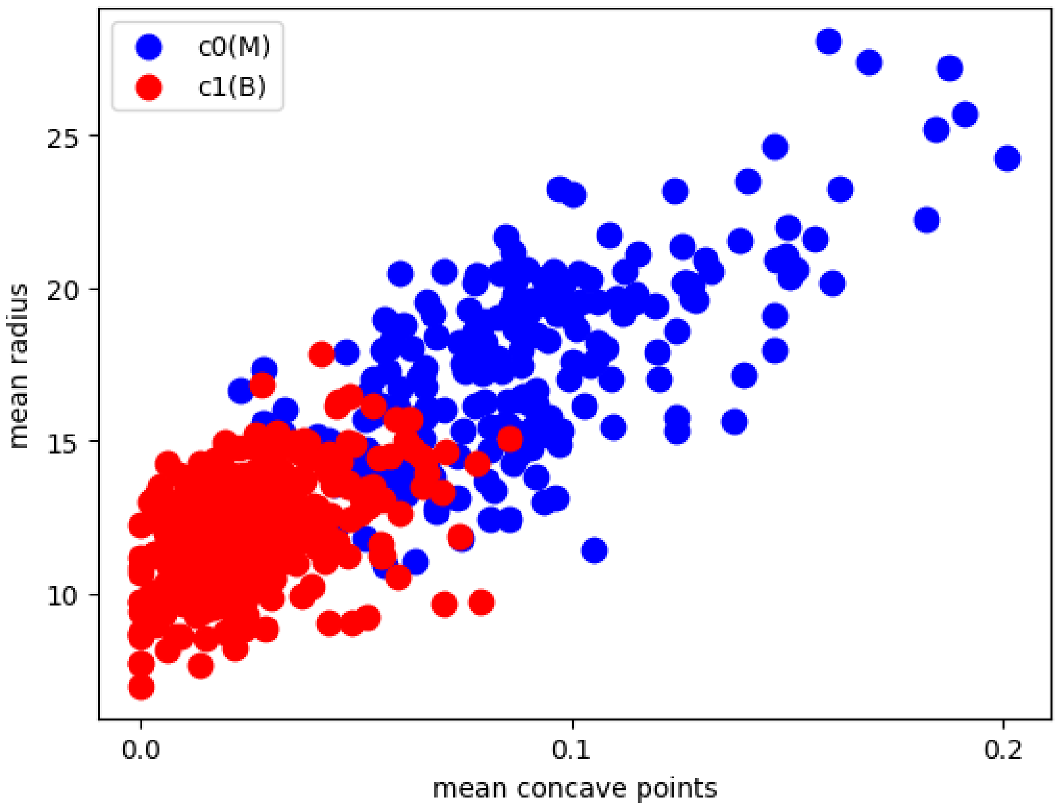
[70]:
```
import matplotlib.pyplot as plt
fig, ax = plt.subplots()

import numpy as np
mean_radius = np.array(df.iloc[:, 4])
pos = 0
mean_radius_malignant = np.array([])
mean_radius_benign = np.array([])
mean_concativity_malignant = np.array([])
mean_concativity_benign = np.array([])

for row in mean_radius:
    if row == 0:
        mean_radius_malignant = np.append(mean_radius_malignant, df.iloc[pos,␣
 ↪0])
        mean_concativity_malignant = np.append(mean_concativity_malignant, df.
 ↪iloc[pos, 1])
    else:
        mean_radius_benign = np.append(mean_radius_benign, df.iloc[pos, 0])
        mean_concativity_benign = np.append(mean_concativity_benign, df.
 ↪iloc[pos, 1])
```

```
    pos += 1

ax.scatter(mean_concativity_malignant, mean_radius_malignant, c='b',␣
↪marker='o', s=80, label="c0(M)")
ax.scatter(mean_concativity_benign, mean_radius_benign, c='r', marker='o',␣
↪s=80, label="c1(B)")


plt.xticks([0.0, 0.2, 0.4],['0.0', '0.2', '0.4'])
plt.xlabel("mean concativity")
plt.ylabel("mean radius")
plt.legend()
plt.show()
```



[76]:
```
import matplotlib.pyplot as plt
fig, ax = plt.subplots()

import numpy as np
mean_radius = np.array(df.iloc[:, 4])
pos = 0
mean_radius_malignant = np.array([])
```

```
mean_radius_benign = np.array([])
mean_concave_malignant = np.array([])
mean_concave_benign = np.array([])

for row in mean_radius:
    if row == 0:
        mean_radius_malignant = np.append(mean_radius_malignant, df.iloc[pos, 0])
        mean_concave_malignant = np.append(mean_concave_malignant, df.iloc[pos, 2])
    else:
        mean_radius_benign = np.append(mean_radius_benign, df.iloc[pos, 0])
        mean_concave_benign = np.append(mean_concave_benign, df.iloc[pos, 2])
    pos += 1

ax.scatter(mean_concave_malignant, mean_radius_malignant, c='b', marker='o', s=80, label="c0(M)")
ax.scatter(mean_concave_benign, mean_radius_benign, c='r', marker='o', s=80, label="c1(B)")


plt.xticks([0.0, 0.1, 0.2],['0.0', '0.1', '0.2'])
plt.xlabel("mean concave points")
plt.ylabel("mean radius")
plt.legend()
plt.show()
```



[77]:
```
import matplotlib.pyplot as plt
fig, ax = plt.subplots()

import numpy as np
mean_radius = np.array(df.iloc[:, 4])
pos = 0
mean_radius_malignant = np.array([])
mean_radius_benign = np.array([])
mean_symmetry_malignant = np.array([])
mean_symmetry_benign = np.array([])

for row in mean_radius:
    if row == 0:
        mean_radius_malignant = np.append(mean_radius_malignant, df.iloc[pos,␣
 ↪0])
        mean_symmetry_malignant = np.append(mean_symmetry_malignant, df.
 ↪iloc[pos, 3])
    else:
        mean_radius_benign = np.append(mean_radius_benign, df.iloc[pos, 0])
        mean_symmetry_benign = np.append(mean_symmetry_benign, df.iloc[pos, 3])
    pos += 1
```

```
ax.scatter(mean_symmetry_malignant, mean_radius_malignant, c='b', marker='o',␣
↪s=80, label="c0(M)")
ax.scatter(mean_symmetry_benign, mean_radius_benign, c='r', marker='o', s=80,␣
↪label="c1(B)")


plt.xticks([0.1, 0.2, 0.3],['0.1', '0.2', '0.3'])
plt.xlabel("mean symmetry")
plt.ylabel("mean radius")
plt.legend()
plt.show()
```