Sp25 CS 477/577: Python for Machine Learning

Homework 1: Python for basic data processing

This homework aims to practice basic Python programing skills using the breast cancer wisconsin dataset.

Tasks:

Task 1: Explore the dataset. 40 points

Task 2: Data search. 15 points

Task 3: Study the 'area' feature. 15 points

Task 4: Count data samples. 10 poits

Task 5:Define a function. 20 points

Dataset

```
- Number of data samples/rows: 569
```

- Each data sample has 30 numeric features/attributes. All features of a data sample form
- a `feature vector' (each row).
- The first 10 features were directly calculated using mean featuues of all nuclei in an H&E image(Fig. 1).
- Only the first 10 features of each data sample will be used in this assignment.
- Each data sample is associated with one class label: 0 or 1
 - : 212 Malignant (0)
 - : 357 Benign (1)
- Get more details at:

https://scikit-

learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html#sklearn.datasets.loa

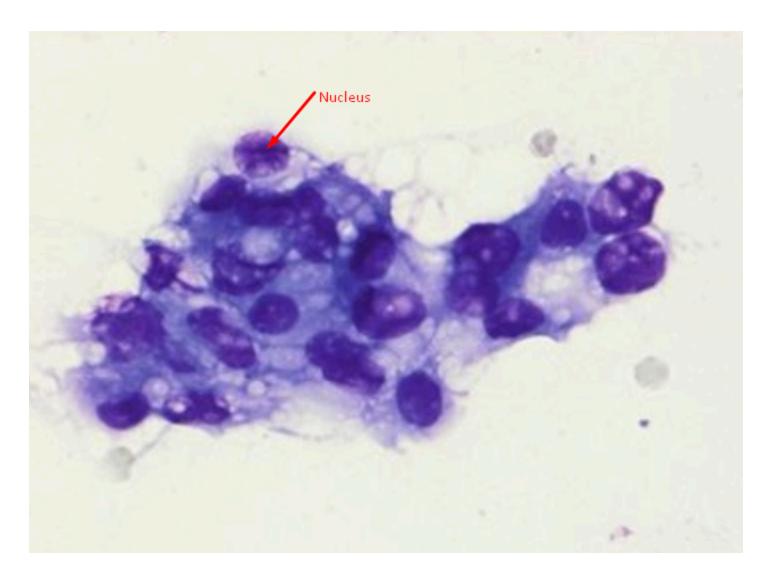


Fig. 1. Cell nuclei in a breast histopathology image

Fine Needle Aspiration (FNA) biopsy: https://www.cancer.org/cancer/breast-cancer/screening-tests-and-early-detection/breast-biopsy/fine-needle-aspiration-biopsy-of-the-breast.html

H&E stain: https://en.wikipedia.org/wiki/H%26E_stain

```
In [18]: import sklearn.datasets as ds
import numpy as np

In [19]: #load dataset
breast_ds = ds.load_breast_cancer()
print('Data fields in breast_ds: \n', dir(breast_ds))
print('\n Dataset description:\n', breast_ds['DESCR'])
```

```
Data fields in breast ds:
 ['DESCR', 'data', 'data module', 'feature names', 'filename', 'frame', 'target', 'target names']
Dataset description:
 .. _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
                                    43.79 188.5
perimeter (mean):
area (mean):
                                   143.5 2501.0
                                    0.053 0.163
smoothness (mean):
compactness (mean):
                                    0.019 0.345
concavity (mean):
                                          0.427
                                    0.0
                                          0.201
concave points (mean):
                                    0.0
symmetry (mean):
                                    0.106 0.304
fractal dimension (mean):
                                    0.05 0.097
radius (standard error):
                                    0.112 2.873
                                    0.36 4.885
texture (standard error):
                                    0.757 21.98
perimeter (standard error):
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):
                                          0.053
                                    0.0
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
                                          0.291
concave points (worst):
                                    0.0
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.

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.

```
tgts = breast ds.target # class labels
print('Size of feature vectors: ', ftrs.shape)
print('Size of targets: ', tgts.shape)
print('Target labels:\n', tgts)
Size of feature vectors: (569, 10)
Size of targets: (569,)
Target labels:
1 1 1 1 1 1 1 0 0 0 0 0 0 1
```

Task 1: Explore the dataset. 40 points

```
In [21]: #Task 1.1 check the data type of 'ftrs' and 'tgts', and print it out. 5 points
    print(type(ftrs))
    print(type(tgts))

<class 'numpy.ndarray'>
    <class 'numpy.ndarray'>

In [22]: #Task 1.2 print out the the features and class label of the 10th data samples. 5 points
    #each row is one data sample
    # Features
    print(ftrs[9])
```

```
# Labels
         print(tgts[9])
        [1.246e+01 2.404e+01 8.397e+01 4.759e+02 1.186e-01 2.396e-01 2.273e-01
         8.543e-02 2.030e-01 8.243e-021
        0
In [23]: #Task 1.3 count and print out the number of malignant samples (class label: 0). 5 points
         # traditional
         malignant count = 0
         for i in tqts:
             if i == 0:
                 malignant count+=1
         print(malignant count)
         # using numpy library for numpy.ndarray
         count = np.sum(tgts == 0)
         print(count)
        212
        212
In [24]: #Task 1.4 count and print out the number of benign samples (class label: 1). 5 points
         benign count = np.sum(tgts == 1)
         print(benign count)
         # Alternatively, malignant is known from above: 212. Number of Instances: 569
         print(569-212)
        357
        357
In [25]: #Task 1.5 calculate the average (mean) of feature vectors of benign samples: 5 values
         benign type = ftrs[tgts == 1]
         b mean = np.mean(benign type, axis=0)
         print('Mean:', b_mean)
        Mean: [1.21465238e+01 1.79147619e+01 7.80754062e+01 4.62790196e+02
         9.24776471e-02 8.00846218e-02 4.60576210e-02 2.57174062e-02
         1.74185994e-01 6.28673950e-021
```

Task 2: Data search. 15 points.

Let the user input an index (0 to 568) of a data sample, and print out the feature vector and the corresponding class label of that sample.

```
Require multiple searches in one run**Extra 5 points for dealing with abnormal input, e.g., out-of-range index
```

Task 3. Study the 'area' (index = 3) feature. 15 points

```
In [29]: #Task 3.1: Calculate and print out the mean, min and max values
# of the feature 'area (index 3)' for all benign samples.
```

```
benign_area = benign_type[:, 3]
mean_area = np.mean(benign_area)
min_area = np.min(benign_area)
max_area = np.max(benign_area)

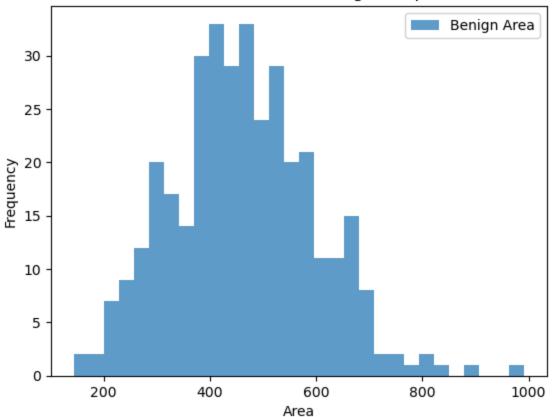
print('Mean area:', mean_area)
print('Min area:', min_area)
print('Max area:', max_area)

# plot the area features of all benign samples
plt.hist(benign_area, bins=30, alpha=0.7, label='Benign Area')
plt.xlabel('Area')
plt.ylabel('Frequency')
plt.title('Area Features of all benign samples')
plt.legend()
plt.show()
```

Mean area: 462.7901960784313

Min area: 143.5 Max area: 992.1

Area Features of all benign samples



In [30]: #Task 3.2: Calculate and print out the mean, min and max values
of the feature 'area (index 3)' for all malignant samples.

malignant_area = malignant_type[:, 3]
mean_area = np.mean(malignant_area)
min_area = np.min(malignant_area)
max_area = np.max(malignant_area)

print('Mean area:', mean_area)
print('Min area:', min_area)
print('Max area:', max_area)

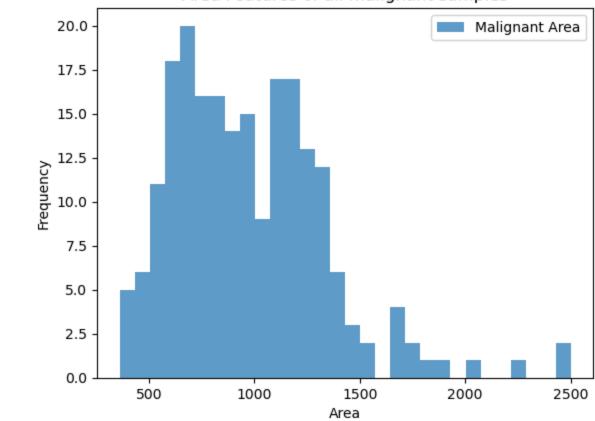
plot the area features of all malignant samples
plt.hist(malignant_area, bins=30, alpha=0.7, label='Malignant Area')

```
plt.xlabel('Area')
plt.ylabel('Frequency')
plt.title('Area Features of all malignant samples')
plt.legend()
plt.show()
```

Mean area: 978.3764150943397

Min area: 361.6 Max area: 2501.0

Area Features of all malignant samples



Task 3.3: What observations can you get from the results of Tasks 3.1 and 3.2?

Response:

Task 4: Count data samples. 10 points

```
In [31]: # Task 4.1 Count the number of malignant samples that have 'area (index 3)' value less than 600. 10 points
    malignant600 = np.sum(malignant_area < 600)
    print(malignant600)

31
In [32]: # Task 4.2 Count the number of benign samples that have 'area (index 3)' values less than 600. 10 points
    benign600 = np.sum(benign_area < 600)
    print(benign600)
304</pre>
```

Task 5: Define a function. 20 points

Define a function that calculates and returns the Euclidean distance between any two given data samples

```
In [33]: # Task 5.1
         def Eclidean(a, b):
                 inputs:a, b: feature vectors of two patients
                 return: d: the distance
             1.1.1
             d = np.linalg.norm(a - b)
             return d
         # test
         print('two malignant samples:', Eclidean(ftrs[1], ftrs[2])) # two malignant samples
         print('two benign samples:', Eclidean(ftrs[19], ftrs[20])) # two benign samples
         print('between two mean vectors:', Eclidean(b mean, m mean)) # between means
        two malignant samples: 123.08662898837753
        two benign samples: 46.35812850705252
        between two mean vectors: 516.9734937120693
In [34]: # Task 5.2 calculate and print out the Eclidean distance between
         # every feature vector (ftrs[i]) and the mean feature vector of maliganant samples (m_mean)
```

```
for i in range(len(ftrs)):
    distance = Eclidean(ftrs[i], m_mean)
    print(f"Distance between feature vector {i} and mean malignant vector: {distance}")
```

```
Distance between feature vector 0 and mean malignant vector: 26.33286841188874
Distance between feature vector 1 and mean malignant vector: 348.100547954307
Distance between feature vector 2 and mean malignant vector: 225.11112082189712
Distance between feature vector 3 and mean malignant vector: 593.5125407983936
Distance between feature vector 4 and mean malignant vector: 319.32932515401563
Distance between feature vector 5 and mean malignant vector: 502.40778179535
Distance between feature vector 6 and mean malignant vector: 61.795325836513186
Distance between feature vector 7 and mean malignant vector: 401.2846200083299
Distance between feature vector 8 and mean malignant vector: 459.4439860471249
Distance between feature vector 9 and mean malignant vector: 503.48703014490815
Distance between feature vector 10 and mean malignant vector: 181.0332464755555
Distance between feature vector 11 and mean malignant vector: 197.76883065979666
Distance between feature vector 12 and mean malignant vector: 145.6684522159039
Distance between feature vector 13 and mean malignant vector: 196.04450674669724
Distance between feature vector 14 and mean malignant vector: 400.6866907488999
Distance between feature vector 15 and mean malignant vector: 320.1876522604738
Distance between feature vector 16 and mean malignant vector: 294.6161712899466
Distance between feature vector 17 and mean malignant vector: 179.73066216538615
Distance between feature vector 18 and mean malignant vector: 282.0138745004371
Distance between feature vector 19 and mean malignant vector: 413.10237695597965
Distance between feature vector 20 and mean malignant vector: 459.3986357986808
Distance between feature vector 21 and mean malignant vector: 706.726381566751
Distance between feature vector 22 and mean malignant vector: 274.3848730362856
Distance between feature vector 23 and mean malignant vector: 426.2017365311438
Distance between feature vector 24 and mean malignant vector: 73.97606494559071
Distance between feature vector 25 and mean malignant vector: 65.88638397603917
Distance between feature vector 26 and mean malignant vector: 334.0717584016947
Distance between feature vector 27 and mean malignant vector: 115.83316744985136
Distance between feature vector 28 and mean malignant vector: 246.3546411922511
Distance between feature vector 29 and mean malignant vector: 24.184880491289793
Distance between feature vector 30 and mean malignant vector: 110.09086873547199
Distance between feature vector 31 and mean malignant vector: 539.1149593138027
Distance between feature vector 32 and mean malignant vector: 79.15495353921617
Distance between feature vector 33 and mean malignant vector: 184.1240715500901
Distance between feature vector 34 and mean malignant vector: 171.42636000463608
Distance between feature vector 35 and mean malignant vector: 109.0060656347418
Distance between feature vector 36 and mean malignant vector: 346.07460671194207
Distance between feature vector 37 and mean malignant vector: 455.78773691015635
Distance between feature vector 38 and mean malignant vector: 280.3124855035749
Distance between feature vector 39 and mean malignant vector: 420.0624745033168
Distance between feature vector 40 and mean malignant vector: 416.4199389573172
Distance between feature vector 41 and mean malignant vector: 608.8648211528222
```

```
Distance between feature vector 42 and mean malignant vector: 126.33865143090208
Distance between feature vector 43 and mean malignant vector: 434.10552387464344
Distance between feature vector 44 and mean malignant vector: 447.8992474060053
Distance between feature vector 45 and mean malignant vector: 98.06773690071056
Distance between feature vector 46 and mean malignant vector: 779.1509766177085
Distance between feature vector 47 and mean malignant vector: 444.7787209421317
Distance between feature vector 48 and mean malignant vector: 530.4648914839066
Distance between feature vector 49 and mean malignant vector: 418.36475441634684
Distance between feature vector 50 and mean malignant vector: 552.0044298453313
Distance between feature vector 51 and mean malignant vector: 407.60210529462614
Distance between feature vector 52 and mean malignant vector: 542.2670373148247
Distance between feature vector 53 and mean malignant vector: 54.928128713072034
Distance between feature vector 54 and mean malignant vector: 266.20370699082633
Distance between feature vector 55 and mean malignant vector: 570.9633365114181
Distance between feature vector 56 and mean malignant vector: 173.95437401617775
Distance between feature vector 57 and mean malignant vector: 322.0982991050606
Distance between feature vector 58 and mean malignant vector: 452.3912651548184
Distance between feature vector 59 and mean malignant vector: 756.4577613174755
Distance between feature vector 60 and mean malignant vector: 668.4844525142494
Distance between feature vector 61 and mean malignant vector: 759.0599564000124
Distance between feature vector 62 and mean malignant vector: 333.2313758885394
Distance between feature vector 63 and mean malignant vector: 719.7608498461
Distance between feature vector 64 and mean malignant vector: 480.51774356550777
Distance between feature vector 65 and mean malignant vector: 310.6167890241415
Distance between feature vector 66 and mean malignant vector: 711.1716127545313
Distance between feature vector 67 and mean malignant vector: 585.9362924903929
Distance between feature vector 68 and mean malignant vector: 730.1330557435878
Distance between feature vector 69 and mean malignant vector: 477.1395687551554
Distance between feature vector 70 and mean malignant vector: 151.85452113429386
Distance between feature vector 71 and mean malignant vector: 736.635282836788
Distance between feature vector 72 and mean malignant vector: 49.07765062573198
Distance between feature vector 73 and mean malignant vector: 395.1239087680631
Distance between feature vector 74 and mean malignant vector: 508.81568826007975
Distance between feature vector 75 and mean malignant vector: 161.08876206176845
Distance between feature vector 76 and mean malignant vector: 420.228373193496
Distance between feature vector 77 and mean malignant vector: 28.575209293036508
Distance between feature vector 78 and mean malignant vector: 268.1493343244469
Distance between feature vector 79 and mean malignant vector: 473.20777675943646
Distance between feature vector 80 and mean malignant vector: 578.4028226585929
Distance between feature vector 81 and mean malignant vector: 459.33944898130517
Distance between feature vector 82 and mean malignant vector: 901.4126923063918
Distance between feature vector 83 and mean malignant vector: 154.31617914211452
```

```
Distance between feature vector 84 and mean malignant vector: 536.51452853716
Distance between feature vector 85 and mean malignant vector: 96.84790559142846
Distance between feature vector 86 and mean malignant vector: 330.86439526561276
Distance between feature vector 87 and mean malignant vector: 97.90668591429404
Distance between feature vector 88 and mean malignant vector: 513.5363054036027
Distance between feature vector 89 and mean malignant vector: 327.13806479916445
Distance between feature vector 90 and mean malignant vector: 316.3826570165137
Distance between feature vector 91 and mean malignant vector: 250.64705534828622
Distance between feature vector 92 and mean malignant vector: 427.8494391274009
Distance between feature vector 93 and mean malignant vector: 424.28459659229327
Distance between feature vector 94 and mean malignant vector: 273.2084595194698
Distance between feature vector 95 and mean malignant vector: 286.14832960223805
Distance between feature vector 96 and mean malignant vector: 528.6534187855679
Distance between feature vector 97 and mean malignant vector: 685.9918502553204
Distance between feature vector 98 and mean malignant vector: 567.3598971789111
Distance between feature vector 99 and mean malignant vector: 336.54390095705315
Distance between feature vector 100 and mean malignant vector: 396.65123596167456
Distance between feature vector 101 and mean malignant vector: 838.0443901325493
Distance between feature vector 102 and mean malignant vector: 521.1024535809685
Distance between feature vector 103 and mean malignant vector: 682.062979869247
Distance between feature vector 104 and mean malignant vector: 644.1061387791233
Distance between feature vector 105 and mean malignant vector: 449.12171745705854
Distance between feature vector 106 and mean malignant vector: 567.3415452848034
Distance between feature vector 107 and mean malignant vector: 513.0009063012709
Distance between feature vector 108 and mean malignant vector: 531.9677567453571
Distance between feature vector 109 and mean malignant vector: 583.486890417219
Distance between feature vector 110 and mean malignant vector: 690.2622106632627
Distance between feature vector 111 and mean malignant vector: 499.10704879576195
Distance between feature vector 112 and mean malignant vector: 348.93754185539615
Distance between feature vector 113 and mean malignant vector: 645.9077886973453
Distance between feature vector 114 and mean malignant vector: 749.9159736355675
Distance between feature vector 115 and mean malignant vector: 541.1999709642598
Distance between feature vector 116 and mean malignant vector: 735.4323446438849
Distance between feature vector 117 and mean malignant vector: 296.4011951700786
Distance between feature vector 118 and mean malignant vector: 196.02643615496012
Distance between feature vector 119 and mean malignant vector: 4.157554880384549
Distance between feature vector 120 and mean malignant vector: 576.742570820695
Distance between feature vector 121 and mean malignant vector: 98.91702205290912
Distance between feature vector 122 and mean malignant vector: 784.3035028668614
Distance between feature vector 123 and mean malignant vector: 338.5166901579703
Distance between feature vector 124 and mean malignant vector: 425.9347316962329
Distance between feature vector 125 and mean malignant vector: 390.6470117301695
```

```
Distance between feature vector 126 and mean malignant vector: 406.7443149552021
Distance between feature vector 127 and mean malignant vector: 159.85580959416959
Distance between feature vector 128 and mean malignant vector: 304.3400001205328
Distance between feature vector 129 and mean malignant vector: 214.19350587547373
Distance between feature vector 130 and mean malignant vector: 523.9271916530114
Distance between feature vector 131 and mean malignant vector: 229.9014898020938
Distance between feature vector 132 and mean malignant vector: 168.83044300576884
Distance between feature vector 133 and mean malignant vector: 217.23096087353966
Distance between feature vector 134 and mean malignant vector: 96.75000646302132
Distance between feature vector 135 and mean malignant vector: 473.2979503381949
Distance between feature vector 136 and mean malignant vector: 556.3150149145716
Distance between feature vector 137 and mean malignant vector: 580.1857105539394
Distance between feature vector 138 and mean malignant vector: 300.8842633048096
Distance between feature vector 139 and mean malignant vector: 595.17519601239
Distance between feature vector 140 and mean malignant vector: 692.1066200702954
Distance between feature vector 141 and mean malignant vector: 165.7383794652634
Distance between feature vector 142 and mean malignant vector: 581.920089776351
Distance between feature vector 143 and mean malignant vector: 467.304794349295
Distance between feature vector 144 and mean malignant vector: 624.9258015842759
Distance between feature vector 145 and mean malignant vector: 546.9194849163026
Distance between feature vector 146 and mean malignant vector: 547.6382738397688
Distance between feature vector 147 and mean malignant vector: 289.4323450452123
Distance between feature vector 148 and mean malignant vector: 339.0267264040428
Distance between feature vector 149 and mean malignant vector: 394.35372273557647
Distance between feature vector 150 and mean malignant vector: 460.1029680272141
Distance between feature vector 151 and mean malignant vector: 777.0172632869445
Distance between feature vector 152 and mean malignant vector: 680.2083496783409
Distance between feature vector 153 and mean malignant vector: 598.2278094291946
Distance between feature vector 154 and mean malignant vector: 440.5686165973266
Distance between feature vector 155 and mean malignant vector: 519.4418827070984
Distance between feature vector 156 and mean malignant vector: 14.843636181632586
Distance between feature vector 157 and mean malignant vector: 98.44864336017697
Distance between feature vector 158 and mean malignant vector: 531.2768263844604
Distance between feature vector 159 and mean malignant vector: 613.4510198962145
Distance between feature vector 160 and mean malignant vector: 559.9857679256761
Distance between feature vector 161 and mean malignant vector: 179.05593696940412
Distance between feature vector 162 and mean malignant vector: 236.15693094687967
Distance between feature vector 163 and mean malignant vector: 515.1280929556177
Distance between feature vector 164 and mean malignant vector: 708.6003706813999
Distance between feature vector 165 and mean malignant vector: 288.8770197744973
Distance between feature vector 166 and mean malignant vector: 622.6719866642201
Distance between feature vector 167 and mean malignant vector: 92.32116899603885
```

```
Distance between feature vector 168 and mean malignant vector: 6.980974413136859
Distance between feature vector 169 and mean malignant vector: 293.14997282387696
Distance between feature vector 170 and mean malignant vector: 515.6791541385904
Distance between feature vector 171 and mean malignant vector: 414.0548909051305
Distance between feature vector 172 and mean malignant vector: 242.02225244263525
Distance between feature vector 173 and mean malignant vector: 607.4300287809883
Distance between feature vector 174 and mean malignant vector: 630.6661719988838
Distance between feature vector 175 and mean malignant vector: 753.7299776663776
Distance between feature vector 176 and mean malignant vector: 677.9313714251776
Distance between feature vector 177 and mean malignant vector: 145.6139320890012
Distance between feature vector 178 and mean malignant vector: 453.22788993418595
Distance between feature vector 179 and mean malignant vector: 470.9117196290401
Distance between feature vector 180 and mean malignant vector: 1273.410912657245
Distance between feature vector 181 and mean malignant vector: 333.80154635800335
Distance between feature vector 182 and mean malignant vector: 212.26094057703503
Distance between feature vector 183 and mean malignant vector: 577.9630778352914
Distance between feature vector 184 and mean malignant vector: 268.29105188292027
Distance between feature vector 185 and mean malignant vector: 662.9611481189444
Distance between feature vector 186 and mean malignant vector: 62.78579487039438
Distance between feature vector 187 and mean malignant vector: 559.6045017332978
Distance between feature vector 188 and mean malignant vector: 550.9825065576069
Distance between feature vector 189 and mean malignant vector: 516.0289462865203
Distance between feature vector 190 and mean malignant vector: 369.09145095628645
Distance between feature vector 191 and mean malignant vector: 472.1787646662126
Distance between feature vector 192 and mean malignant vector: 692.4868323617773
Distance between feature vector 193 and mean malignant vector: 502.19709736993997
Distance between feature vector 194 and mean malignant vector: 307.356204188982
Distance between feature vector 195 and mean malignant vector: 463.19429086141713
Distance between feature vector 196 and mean malignant vector: 390.279162819955
Distance between feature vector 197 and mean malignant vector: 45.673794040330776
Distance between feature vector 198 and mean malignant vector: 170.0680604081999
Distance between feature vector 199 and mean malignant vector: 336.3412484286526
Distance between feature vector 200 and mean malignant vector: 518.7157680483197
Distance between feature vector 201 and mean malignant vector: 26.87526167341295
Distance between feature vector 202 and mean malignant vector: 708.0055170808301
Distance between feature vector 203 and mean malignant vector: 381.3437443925046
Distance between feature vector 204 and mean malignant vector: 497.69227501244467
Distance between feature vector 205 and mean malignant vector: 262.35800550469077
Distance between feature vector 206 and mean malignant vector: 685.042833058915
Distance between feature vector 207 and mean malignant vector: 74.3063976537016
Distance between feature vector 208 and mean malignant vector: 449.8923318426801
Distance between feature vector 209 and mean malignant vector: 253.618998459326
```

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In []: