

# Labeled Data

Separate the PCA components of a dataset by class.

### **Chapter Goals:**

- Learn about labeled datasets
- Separate principle component data by class label

#### A. Class labels

A big part of data science is classifying observations in a dataset into separate categories, or *classes*. A popular use case of data classification is in separating a dataset into "good" and "bad" categories. For example, we can classify a dataset of breast tumors as either malignant or benign.

The code below separates a breast cancer dataset into malignant and benign categories. The <code>load\_breast\_cancer</code> (https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load\_breast\_cancer. html#sklearn.datasets.load\_breast\_cancer) function is part of the scikit-learn library, and its data comes from the Breast Cancer Wisconsin (https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+ (Diagnostic)) dataset.

```
1 from sklearn.datasets import load_breast_cancer
 2 bc = load_breast_cancer()
 3 print('{}\n'.format(repr(bc.data)))
 4 print('Data shape: {}\n'.format(bc.data.shape))
 6 # Class labels
    print('{}\n'.format(repr(bc.target)))
    print('Labels shape: {}\n'.format(bc.target.shape))
 9
   # Label names
   print('{}\n'.format(list(bc.target_names)))
11
12
13 malignant = bc.data[bc.target == 0]
    print('Malignant shape: {}\n'.format(malignant.shape))
14
15
16
    benign = bc.data[bc.target == 1]
    print('Benign shape: {}\n'.format(benign.shape))
17
```

```
Output

Output

1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1])

Labels shape: (569,)

['malignant', 'benign']

Malignant shape: (212, 30)

Benign shape: (357, 30)
```

In the example above, the bc.data array contains all the dataset values, while the bc.target array contains the class ID labels for each row in bc.data. A class ID of 0 corresponds to a malignant tumor, while a class ID of 1 corresponds to a benign tumor.

Using the bc.target class IDs, we separated the dataset into malignant and benign data arrays. In other words, the malignant array contains the rows of bc.data corresponding to the indexes in bc.target containing 0, while the benign array contains the rows of bc.data corresponding to the indexes in bc.target containing 1. There are 212 malignant data observations and 357 benign observations.

## Time to Code!

The coding exercise in this chapter involves completing the separate\_components function, which will separate principal component data by class.

To do this, we first need to complete a helper function, <code>get\_label\_info</code>, which returns the label name and data for an input class label.

The component\_data input represents the principal component data

The labels input is a 1-D array containing the class label IDs corresponding to each row of component\_data. We can use it to separate the principle components by class.

The class\_label input represents a particular class label ID.

The label\_names input represents all the string names for the class labels.

Set label\_name equal to the string at index class\_label of label\_names.

Set label\_data equal to the rows of component\_data corresponding to the indexes where labels equals class\_label. Then return the tuple (label\_name, label\_data).

```
def get_label_info(component_data, labels,
2
                       class_label, label_names):
3
     # CODE HERE
     pass
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                                                               \leftarrow
      ·Ω·
                                                                              Ø
                                   Solution
                                                                             G
      def get_label_info(component_data, labels,
  2
                          class_label, label_names):
  3
        label_name = label_names[class_label]
  4
        label_data = component_data[labels == class_label]
  5
        return (label name, label data)
  6
  7
```

Now, inside the main separate\_data function, we'll iterate through each label in the label\_names list.

Set separated\_data equal to an empty list.



Inside the for loop, we can use our helper function to obtain the separated data for each class.

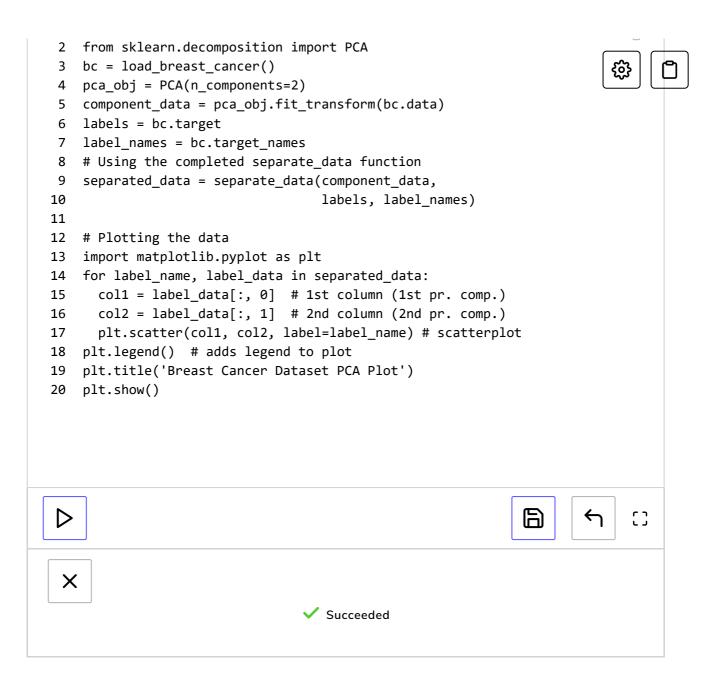
Inside the for loop, call get\_label\_info with inputs component\_data, labels, class\_label, and label\_names. Append the function's output to separated\_data.

After finalizing the list of principle components separated by class, we return it.

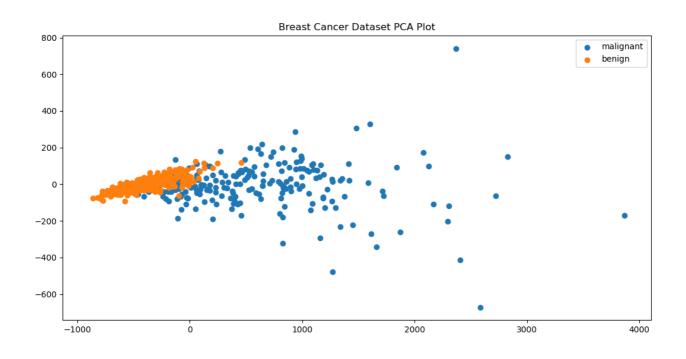
### Outside the for loop, return separated\_data.

```
def separate_data(component_data, labels,
1
2
                       label_names):
3
     # CODE HERE
4
     pass
5
               \odot
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                                                                          Ø
                                                                                G
                                     Solution
      def separate_data(component_data, labels,
   2
                          label_names):
   3
        separated_data = []
   4
        for class_label in range(len(label_names)):
   5
           separated_data.append(get_label_info(
             component_data, labels, class_label, label_names))
   6
   7
        return separated data
   8
   9
```

The separate\_data function is incredibly useful for visualizing the components. We can use matplotlib to create nice plots of the separated data (shown in the code below).

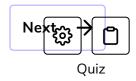


## The result of the above code is this plot:





PCA



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