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 `load_breast_cancer` function is part of the scikit-learn library, and its data comes from the Breast Cancer Wisconsin dataset.

```
from sklearn.datasets import load_breast_cancer
bc = load_breast_cancer()
print('{}\n'.format(repr(bc.data)))
print('Data shape: {}\n'.format(bc.data.shape))

# Class labels
print('{}\n'.format(repr(bc.target)))
print('Labels shape: {}\n'.format(bc.target.shape))

# Label names
print('{}\n'.format(list(bc.target_names)))

malignant = bc.data[bc.target == 0]
print('Malignant shape: {}\n'.format(malignant.shape))

benign = bc.data[bc.target == 1]
print('Benign shape: {}\n'.format(benign.shape))
```

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, `get_label_info`, 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,
                   class_label, label_names):
  # CODE HERE
  pass
```

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.

Create a `for` loop that iterates variable `class_label` through `range(len(label_names))`.

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,
                  label_names):
  # CODE HERE
  pass
```

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).

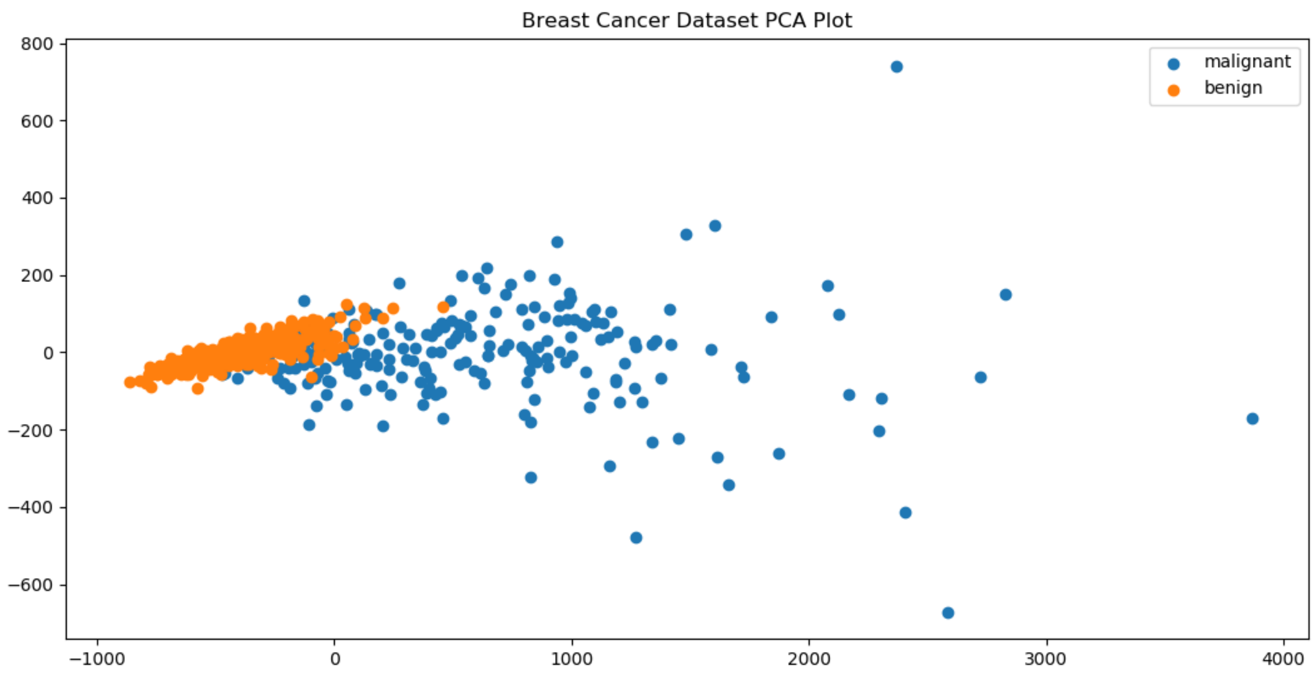
```
from sklearn.datasets import load_breast_cancer
from sklearn.decomposition import PCA
bc = load_breast_cancer()
pca_obj = PCA(n_components=2)
component_data = pca_obj.fit_transform(bc.data)
labels = bc.target
label_names = bc.target_names
# Using the completed separate_data function
separated_data = separate_data(component_data,
                               labels, label_names)

# Plotting the data
```

```
import matplotlib.pyplot as plt
for label_name, label_data in separated_data:
  col1 = label_data[:, 0]  # 1st column (1st pr. comp.)

  col2 = label_data[:, 1]  # 2nd column (2nd pr. comp.)
  plt.scatter(col1, col2, label=label_name) # scatterplot
plt.legend()  # adds legend to plot
plt.title('Breast Cancer Dataset PCA Plot')
plt.show()
```

The result of the above code is this plot:


Breast Cancer Dataset PCA Plot
malignant
benign