Forward School

## Program Code: J620-002-4:2020

## Program Name: FRONT-END SOFTWARE DEVELOPMENT

## Title : Exe23 - Dimension Reduction Exercise

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**Date : 25/07/2023**

**Introduction :**

**Conclusion :**

# Dimension Reduction Exercise

## Principal Component Analysis

Let's begin by importing the various library

In [5]:
```
import pandas as pd
import numpy as np
```

In [130]:
```
from sklearn.datasets import load_breast_cancer
breast = load_breast_cancer()
# Combine the data and target arrays
data = breast.data

# Create a dictionary with column names as keys and data arrays as values
data_dict = {name: data[:, i] for i, name in enumerate(breast.feature_names)}

# Create the DataFrame
df = pd.DataFrame(data_dict)
df['target'] = breast.target
df
```

Out[130]:

| | mean radius | mean texture | mean perimeter | mean area | mean smoothness | mean compactness | mean concavity | mean concave points | mea symmetr |
|---|---|---|---|---|---|---|---|---|---|
| **0** | 17.99 | 10.38 | 122.80 | 1001.0 | 0.11840 | 0.27760 | 0.30010 | 0.14710 | 0.241 |
| **1** | 20.57 | 17.77 | 132.90 | 1326.0 | 0.08474 | 0.07864 | 0.08690 | 0.07017 | 0.181 |
| **2** | 19.69 | 21.25 | 130.00 | 1203.0 | 0.10960 | 0.15990 | 0.19740 | 0.12790 | 0.206 |
| **3** | 11.42 | 20.38 | 77.58 | 386.1 | 0.14250 | 0.28390 | 0.24140 | 0.10520 | 0.259 |
| **4** | 20.29 | 14.34 | 135.10 | 1297.0 | 0.10030 | 0.13280 | 0.19800 | 0.10430 | 0.180 |
| **...** | ... | ... | ... | ... | ... | ... | ... | ... | . |
| **564** | 21.56 | 22.39 | 142.00 | 1479.0 | 0.11100 | 0.11590 | 0.24390 | 0.13890 | 0.172 |
| **565** | 20.13 | 28.25 | 131.20 | 1261.0 | 0.09780 | 0.10340 | 0.14400 | 0.09791 | 0.175 |
| **566** | 16.60 | 28.08 | 108.30 | 858.1 | 0.08455 | 0.10230 | 0.09251 | 0.05302 | 0.159 |
| **567** | 20.60 | 29.33 | 140.10 | 1265.0 | 0.11780 | 0.27700 | 0.35140 | 0.15200 | 0.239 |
| **568** | 7.76 | 24.54 | 47.92 | 181.0 | 0.05263 | 0.04362 | 0.00000 | 0.00000 | 0.158 |

569 rows × 31 columns

In [131]:
```
breast.keys()
```

Out[131]:
```
dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_name
s', 'filename', 'data_module'])
```

In [132]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
 30  target                   569 non-null    int32  
dtypes: float64(30), int32(1)
memory usage: 135.7 KB
```

In [133]:
```

```

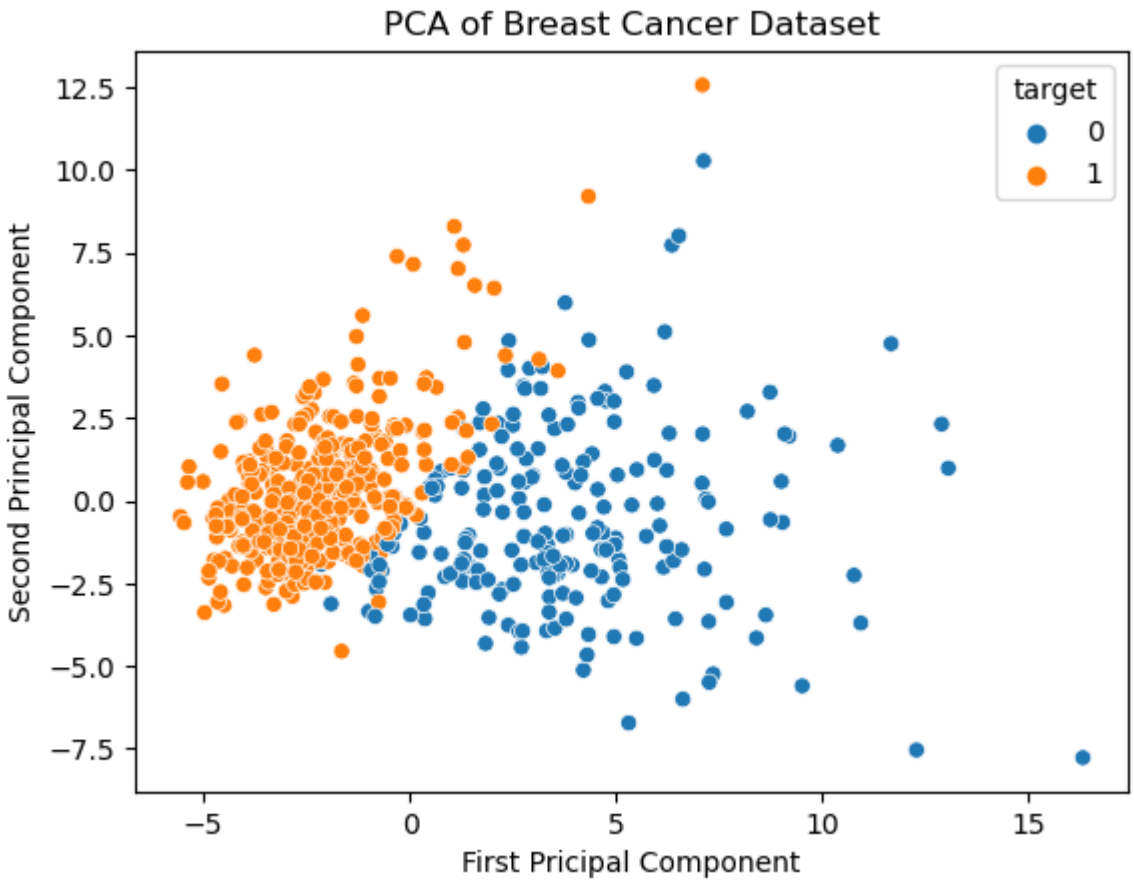
In [135]:
```
data.shape
```

Out[135]:
```
(569, 30)
```

In [158]:
```
from sklearn.preprocessing import StandardScaler
X = df.iloc[:, 0:30].values
scaler = StandardScaler()
scaled_data = scaler.fit_transform(X)

pca = PCA(copy=True, iterated_power='auto', n_components=2, random_state=None,
pca.fit(scaled_data)
x_pca = pca.fit_transform(scaled_data)
x_pca.shape
```

Out[158]:
```
(569, 2)
```

In [159]:
```
import seaborn as sns
import matplotlib.pyplot as plt

pca_df = pd.DataFrame(x_pca,
                      columns=['First Pricipal Component',
                               'Second Principal Component'])

pca_df['target'] = breast.target

sns.scatterplot(x='First Pricipal Component',
                y='Second Principal Component',
                hue='target',
                data=pca_df)

plt.title('PCA of Breast Cancer Dataset')
plt.show()
```

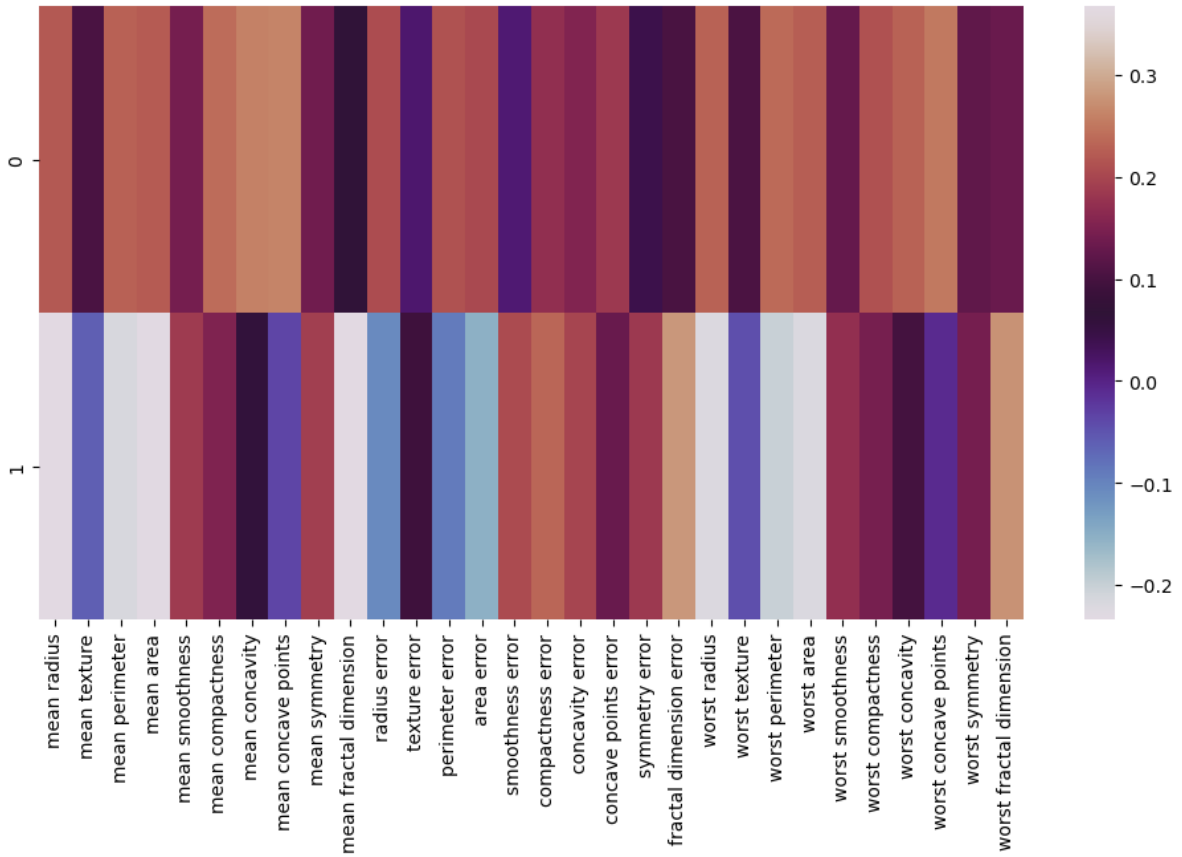


In [161]:
```
pca.components_
```

Out[161]:
```
array([[ 0.21890244,  0.10372458,  0.22753729,  0.22099499,  0.14258969,
         0.23928535,  0.25840048,  0.26085376,  0.13816696,  0.06436335,
         0.20597878,  0.01742803,  0.21132592,  0.20286964,  0.01453145,
         0.17039345,  0.15358979,  0.1834174 ,  0.04249842,  0.10256832,
         0.22799663,  0.10446933,  0.23663968,  0.22487053,  0.12795256,
         0.21009588,  0.22876753,  0.25088597,  0.12290456,  0.13178394],
       [-0.23385713, -0.05970609, -0.21518136, -0.23107671,  0.18611302,
         0.15189161,  0.06016536, -0.0347675 ,  0.19034877,  0.36657547,
        -0.10555215,  0.08997968, -0.08945723, -0.15229263,  0.20443045,
         0.2327159 ,  0.19720728,  0.13032156,  0.183848  ,  0.28009203,
        -0.21986638, -0.0454673 , -0.19987843, -0.21935186,  0.17230435,
         0.14359317,  0.09796411, -0.00825724,  0.14188335,  0.27533947]])
```

In [165]:
```
map_df = pd.DataFrame(pca.components_, columns=breast['feature_names'])
plt.figure(figsize=(12,6))
sns.heatmap(map_df,cmap='twilight')
```

Out[165]:
```
<Axes: >
```



# PCA Exercise

In [3]:
```
#1. Import the wine dataset and assign it to a variable. Split the data into t
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
data = pd.read_csv("./Wine.csv")
data.head()
X = data.iloc[:, 0:13].values
y = data.iloc[:, 13].values
```

In [4]:
```
data['Customer_Segment'].values
```

Out[4]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 3, 3,
       3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,
       3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,
       3, 3], dtype=int64)
```

In [5]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 14 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   Alcohol               178 non-null    float64
 1   Malic_Acid            178 non-null    float64
 2   Ash                   178 non-null    float64
 3   Ash_Alcanity          178 non-null    float64
 4   Magnesium             178 non-null    int64  
 5   Total_Phenols         178 non-null    float64
 6   Flavanoids            178 non-null    float64
 7   Nonflavanoid_Phenols  178 non-null    float64
 8   Proanthocyanins       178 non-null    float64
 9   Color_Intensity       178 non-null    float64
 10  Hue                   178 non-null    float64
 11  OD280                 178 non-null    float64
 12  Proline               178 non-null    int64  
 13  Customer_Segment      178 non-null    int64  
dtypes: float64(11), int64(3)
memory usage: 19.6 KB
```

In [6]:
```
data.describe()
```

Out[6]:

| | Alcohol | Malic_Acid | Ash | Ash_Alcanity | Magnesium | Total_Phenols | Flavanoids |
|---|---|---|---|---|---|---|---|
| **count** | 178.000000 | 178.000000 | 178.000000 | 178.000000 | 178.000000 | 178.000000 | 178.000000 |
| **mean** | 13.000618 | 2.336348 | 2.366517 | 19.494944 | 99.741573 | 2.295112 | 2.029270 |
| **std** | 0.811827 | 1.117146 | 0.274344 | 3.339564 | 14.282484 | 0.625851 | 0.998859 |
| **min** | 11.030000 | 0.740000 | 1.360000 | 10.600000 | 70.000000 | 0.980000 | 0.340000 |
| **25%** | 12.362500 | 1.602500 | 2.210000 | 17.200000 | 88.000000 | 1.742500 | 1.205000 |
| **50%** | 13.050000 | 1.865000 | 2.360000 | 19.500000 | 98.000000 | 2.355000 | 2.135000 |
| **75%** | 13.677500 | 3.082500 | 2.557500 | 21.500000 | 107.000000 | 2.800000 | 2.875000 |
| **max** | 14.830000 | 5.800000 | 3.230000 | 30.000000 | 162.000000 | 3.880000 | 5.080000 |

In [7]:
```
#2. Split the dataset into the Training and the Test set. Set the test set to (
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, rando
```

In [106]:
```
#3. Scale the train and test set using the StandardScaler
from sklearn.preprocessing import StandardScaler
model = StandardScaler()
X_train_scaled = model.fit_transform(X_train)
X_test_scaled = model.transform(X_test)
```

In [107]:
```
from sklearn.decomposition import PCA
pca = PCA(n_components=2)
X_train_pca = pca.fit_transform(X_train_scaled)
X_test_pca = pca.transform(X_test_scaled)
```

In [108]:
```
#4. Apply the PCA function to both the test and train set, to extract the firs
pca.explained_variance_ratio_
```

Out[108]:
```
array([0.36196226, 0.18763862])
```

In [114]:
```
from sklearn.linear_model import LogisticRegression
logr = LogisticRegression()
logr.fit(X_train_pca, y_train)
```

Out[114]:
```
LogisticRegression()
```

**In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.**
**On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.**

In [115]:
```
#5. Create a Logistic Regression based on the training set
```

In [116]:
```
#6. Apply the created LR model onto the test data
# Predicting the test set result using
# predict function under LogisticRegression
from sklearn.linear_model import LogisticRegression
y_pred = logr.predict(X_test_pca)
y_pred
```

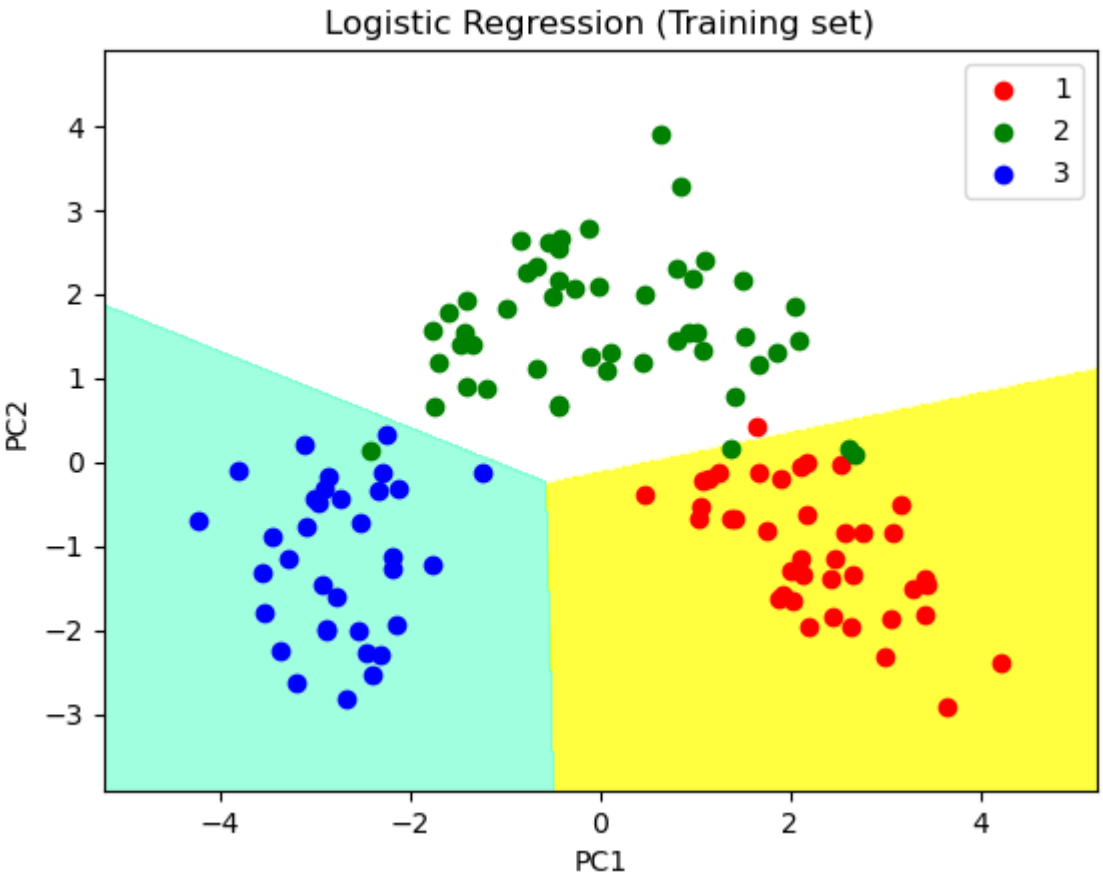
Out[116]:
```
array([1, 1, 3, 1, 2, 1, 2, 3, 2, 3, 2, 3, 1, 2, 1, 2, 2, 2, 1, 2, 1, 2,
       2, 3, 3, 3, 2, 2, 2, 1, 1, 2, 3, 1, 1, 1, 3, 3, 2, 3, 2, 2, 2, 2,
       3, 1, 2, 2, 3, 1, 2, 1, 1, 3], dtype=int64)
```

In [117]:
```
#7. Create a confusion matrix to score the prediction performed
from sklearn.metrics import confusion_matrix
confusion_matrix = confusion_matrix(y_test, y_pred)
print(confusion_matrix)
```

```
[[17  2  0]
 [ 0 21  0]
 [ 0  0 14]]
```

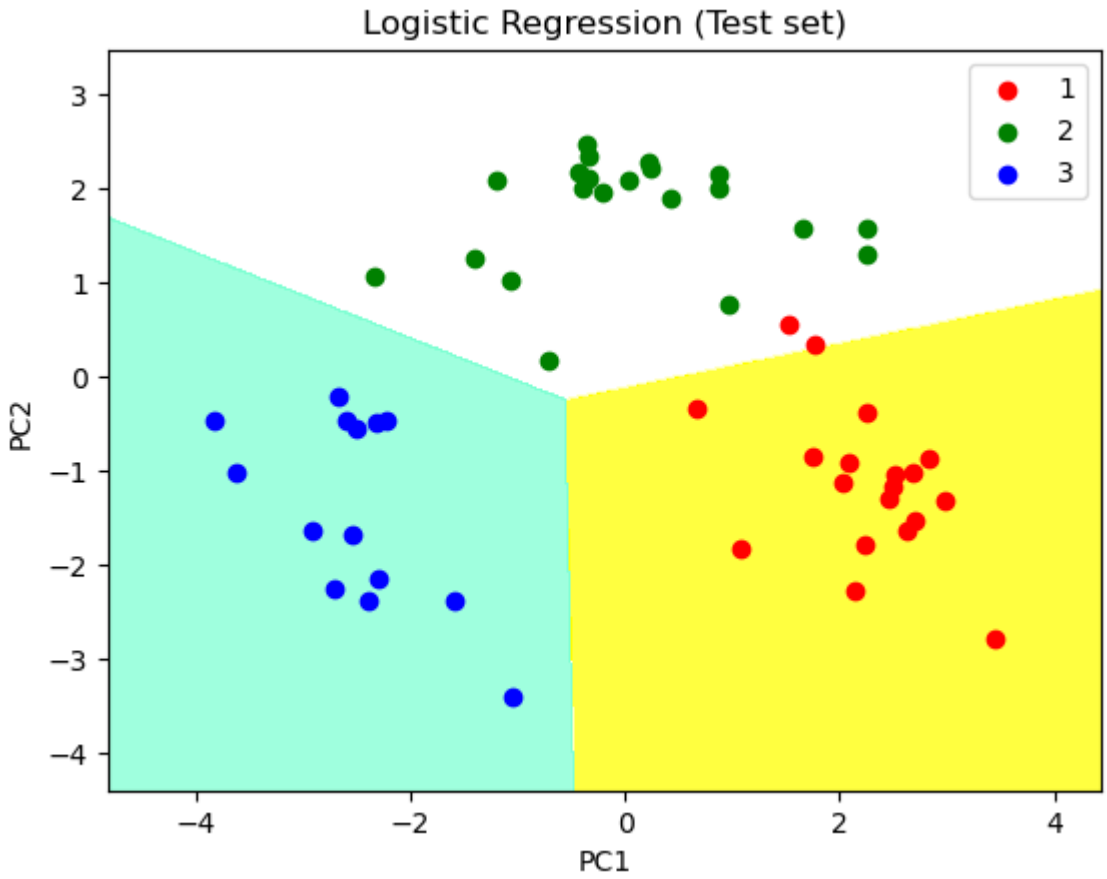
In [119]:
```
from matplotlib.colors import ListedColormap

X_set, y_set = X_train_pca, y_train
X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1,
                     stop = X_set[:, 0].max() + 1, step = 0.01),
                     np.arange(start = X_set[:, 1].min() - 1,
                     stop = X_set[:, 1].max() + 1, step = 0.01))

plt.contourf(X1, X2, logr.predict(np.array([X1.ravel(),
             X2.ravel()]).T).reshape(X1.shape), alpha = 0.75,
             cmap = ListedColormap(('yellow', 'white', 'aquamarine')))

plt.xlim(X1.min(), X1.max())
plt.ylim(X2.min(), X2.max())

for i, j in enumerate(np.unique(y_set)):
    plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
                c = ListedColormap(('red', 'green', 'blue'))(i), label = j)

plt.title('Logistic Regression (Training set)')
plt.xlabel('PC1') # for Xlabel
plt.ylabel('PC2') # for Ylabel
plt.legend() # to show legend

# show scatter plot
plt.show()
```

```
C:\Users\Xiang Ze\AppData\Local\Temp\ipykernel_11056\2160364856.py:17: UserWa
rning: *c* argument looks like a single numeric RGB or RGBA sequence, which s
hould be avoided as value-mapping will have precedence in case its length mat
ches with *x* & *y*.  Please use the *color* keyword-argument or provide a 2D
array with a single row if you intend to specify the same RGB or RGBA value f
or all points.
  plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
```


Logistic Regression (Training set)
1
2
3
PC2
PC1
4
3
2
1
0
−1
−2
−3
−4
−2
0
2
4

In [121]:
```
# Visualising the Test set results through scatter plot

from matplotlib.colors import ListedColormap

X_set, y_set = X_test_pca, y_test

X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1,
                     stop = X_set[:, 0].max() + 1, step = 0.01),
                     np.arange(start = X_set[:, 1].min() - 1,
                     stop = X_set[:, 1].max() + 1, step = 0.01))

plt.contourf(X1, X2, logr.predict(np.array([X1.ravel(),
             X2.ravel()]).T).reshape(X1.shape), alpha = 0.75,
             cmap = ListedColormap(('yellow', 'white', 'aquamarine')))

plt.xlim(X1.min(), X1.max())
plt.ylim(X2.min(), X2.max())

for i, j in enumerate(np.unique(y_set)):
    plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
                c = ListedColormap(('red', 'green', 'blue'))(i), label = j)

# title for scatter plot
plt.title('Logistic Regression (Test set)')
plt.xlabel('PC1') # for Xlabel
plt.ylabel('PC2') # for Ylabel
plt.legend()

# show scatter plot
plt.show()
# show scatter plot
```

```
C:\Users\Xiang Ze\AppData\Local\Temp\ipykernel_11056\1590122172.py:20: UserWa
rning: *c* argument looks like a single numeric RGB or RGBA sequence, which s
hould be avoided as value-mapping will have precedence in case its length mat
ches with *x* & *y*.  Please use the *color* keyword-argument or provide a 2D
array with a single row if you intend to specify the same RGB or RGBA value f
or all points.
  plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
```




# Exercise 1. Take home test / challenge test

Repeat this exercise but this time do it without dimension reduction. What do you get?

In [10]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score
model = DecisionTreeClassifier()
model.fit(X_train, y_train)
y_pred = model.predict(X_test)
accuracy_rf = accuracy_score(y_test, y_pred)
print("Random Forest Accuracy:", accuracy_rf)
```

```
Random Forest Accuracy: 0.9444444444444444
```

# Random Forest Feature Selection

Let's do a guided walkthrough for a RF feature selection )
(https://chrisalbon.com/machine_learning/trees_and_forests/feature_selection_using_random_for
(https://chrisalbon.com/machine_learning/trees_and_forests/feature_selection_using_random_for

In [19]:
```
import numpy as np
from sklearn.ensemble import RandomForestClassifier
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.feature_selection import SelectFromModel
from sklearn.metrics import accuracy_score
```

In [20]:
```
# Load the iris dataset
iris = datasets.load_iris()

# Create a list of feature names
feat_labels = ['Sepal Length','Sepal Width','Petal Length','Petal Width']

# Create X from the features
X = iris.data

# Create y from output
y = iris.target
```

In [21]:
```
# View the features
X[:5]
```

Out[21]:
```
array([[5.1, 3.5, 1.4, 0.2],
       [4.9, 3. , 1.4, 0.2],
       [4.7, 3.2, 1.3, 0.2],
       [4.6, 3.1, 1.5, 0.2],
       [5. , 3.6, 1.4, 0.2]])
```

In [22]:
```
# View the target data
iris.target
```

Out[22]:
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2])
```

In [ ]:
```
```

In [23]:
```
# Split the data into 40% test and 60% training
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4, rando
```

In [24]:
```
from sklearn.ensemble import RandomForestClassifier
# Create a random forest classifier
model = RandomForestClassifier(criterion="gini", max_depth = 2)

# Train the classifier
model.fit(X_train, y_train)

gini_importance = model.feature_importances_
print('Sepal Length', gini_importance[0])
print('Sepal Width', gini_importance[1])
print('Petal Length', gini_importance[2])
print('Petal Width', gini_importance[3])
```

```
Sepal Length 0.12883574204615036
Sepal Width 0.0027025199853343575
Petal Length 0.43459171536344887
Petal Width 0.4338700226050663
```

In [ ]:
```

```

In [25]:
```
# Create a selector object that will use the random forest classifier to ident
# features that have an importance of more than 0.15
feature_selector = SelectFromModel(estimator=model, threshold=0.15)

# Train the selector
feature_selector.fit(X_train, y_train)
```

Out[25]:
```
SelectFromModel(estimator=RandomForestClassifier(max_depth=2), threshold=0.1
5)
```
**In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.**
**On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.**

In [26]:
```
# Print the names of the most important features
feature_selector.fit(X_train, y_train)
selected_feature_names = [iris.feature_names[i] for i in feature_selector.get_
print(selected_feature_names)
```

```
['petal length (cm)', 'petal width (cm)']
```

In [27]:
```
# Transform the data to create a new dataset containing only the most importan
# Note: We have to apply the transform to both the training X and test X data.
X_train_selected = feature_selector.transform(X_train)
X_test_selected = feature_selector.transform(X_test)
```

In [28]:
```
# Create a new random forest classifier for the most important features
new_model = RandomForestClassifier(n_estimators=10000, random_state=0, n_jobs=

# Train the new classifier on the new dataset containing the most important fe
new_model.fit(X_train_selected, y_train)
```

Out[28]:
```
RandomForestClassifier(n_estimators=10000, n_jobs=-1, random_state=0)
```
**In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.**
**On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.**

In [29]:
```
# Apply the limited classifier to the test data
y_pred = model.predict(X_test)

# View The Accuracy Of Our Full Feature (4 Features) Model
accuracy_score(y_test, y_pred)
```

Out[29]:
```
0.8833333333333333
```

In [30]:
```
y_pred_two = new_model.predict(X_test_selected)
accuracy_selected = accuracy_score(y_test, y_pred_two)
print("Accuracy with selected features:", accuracy_selected)
```

```
Accuracy with selected features: 0.9
```

In [31]:
```
# Apply The Full Featured Classifier To The Test Data


# View The Accuracy Of Our Full Feature (4 Features) Model
```

In [32]:
```
# Apply The Full Featured Classifier To The Test Data

# View The Accuracy Of Our Limited Feature (2 Features) Model
```

# Exercise 2. Now repeat RF feature selection but now use the wine dataset

In [36]:
```
from sklearn.ensemble import RandomForestClassifier
data = pd.read_csv("./Wine.csv")
X = data.drop('Customer_Segment', axis = 1)
y = data['Customer_Segment']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4, rando
model = RandomForestClassifier(criterion="gini", max_depth = 2)

# Train the classifier
model.fit(X_train, y_train)
feature_selector = SelectFromModel(estimator=model, threshold=0.15)

# Train the selector
feature_selector.fit(X_train, y_train)
X_train_selected = feature_selector.transform(X_train)
X_test_selected = feature_selector.transform(X_test)
new_model = RandomForestClassifier(n_estimators=10000, random_state=0, n_jobs=

# Train the new classifier on the new dataset containing the most important fe
new_model.fit(X_train_selected, y_train)

y_pred_two = new_model.predict(X_test_selected)
accuracy_selected = accuracy_score(y_test, y_pred_two)
print("Accuracy with selected features:", accuracy_selected)
```

```
Accuracy with selected features: 0.8888888888888888
```

# RFE Walkthrough

In [12]:
```
# Automatically select the features
# automatically select the number of features for RFE
from numpy import mean
from numpy import std
from sklearn.datasets import make_classification
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.feature_selection import RFECV
from sklearn.tree import DecisionTreeClassifier
from sklearn.pipeline import Pipeline
# define dataset
X, y = make_classification(n_samples=1000, n_features=10, n_informative=5, n_r

# create pipeline
model = DecisionTreeClassifier()
rfe = RFECV(estimator=model, step=1)
pipeline = Pipeline(steps=[('feature_selection', rfe), ('classifier', model)])

# evaluate model
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
scores = cross_val_score(pipeline, X, y, scoring='accuracy', cv=cv)

# report performance
print("Accuracy:", mean(scores), (std(scores)))
```

```
Accuracy: 0.882 0.026255158223353628
```

In [30]:
```
# report which features were selected by RFE
from sklearn.datasets import make_classification
from sklearn.feature_selection import RFE
# define dataset
X, y = make_classification(n_samples=1000, n_features=10, n_informative=5, n_r
# define RFE
rfe = RFE(estimator=DecisionTreeClassifier(), n_features_to_select=5)
# fit RFE
rfe.fit(X, y)
# summarize all features
for i in range(X.shape[1]):
    print('Column: %d, Selected %s, Rank: %.3f' % (i, rfe.support_[i], rfe.ra
```

```
Column: 0, Selected False, Rank: 5.000
Column: 1, Selected False, Rank: 4.000
Column: 2, Selected True, Rank: 1.000
Column: 3, Selected True, Rank: 1.000
Column: 4, Selected True, Rank: 1.000
Column: 5, Selected False, Rank: 6.000
Column: 6, Selected True, Rank: 1.000
Column: 7, Selected False, Rank: 2.000
Column: 8, Selected True, Rank: 1.000
Column: 9, Selected False, Rank: 3.000
```

# Exercise 3. Now repeat RF feature selection but now use the iris dataset

In [38]:
```
#Starter code for Exercise 3
# Load libraries

from sklearn import datasets
import matplotlib.pyplot as plt

# Load digits dataset
iris = datasets.load_iris()

# Create feature matrix
X = iris.data

# Create target vector
y = iris.target

# View the first observation's feature values
iris.data[0]
```

Out[38]:
```
array([5.1, 3.5, 1.4, 0.2])
```

In [39]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4, rando
model = RandomForestClassifier(criterion="gini", max_depth = 2)

# Train the classifier
model.fit(X_train, y_train)
feature_selector = SelectFromModel(estimator=model, threshold=0.15)

# Train the selector
feature_selector.fit(X_train, y_train)
X_train_selected = feature_selector.transform(X_train)
X_test_selected = feature_selector.transform(X_test)
new_model = RandomForestClassifier(n_estimators=10000, random_state=0, n_jobs=

# Train the new classifier on the new dataset containing the most important fe
new_model.fit(X_train_selected, y_train)

y_pred_two = new_model.predict(X_test_selected)
accuracy_selected = accuracy_score(y_test, y_pred_two)
print("Accuracy with selected features:", accuracy_selected)
```

```
Accuracy with selected features: 0.9
```

## t-SNE Walkthrough ([https://cmdlinetips.com/2019/07/dimensionality-reduction-with-tsne/ (https://cmdlinetips.com/2019/07/dimensionality-reduction-with-tsne/)](https://cmdlinetips.com/2019/07/dimensionality-reduction-with-tsne/))

In [40]:
```
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import pandas as pd
```

In [41]:
```
from sklearn.datasets import load_digits
digits = load_digits()
digits
```

Out[41]:
```
{'data': array([[ 0.,  0.,  5., ...,  0.,  0.,  0.],
        [ 0.,  0.,  0., ..., 10.,  0.,  0.],
        [ 0.,  0.,  0., ..., 16.,  9.,  0.],
        ...,
        [ 0.,  0.,  1., ...,  6.,  0.,  0.],
        [ 0.,  0.,  2., ..., 12.,  0.,  0.],
        [ 0.,  0., 10., ..., 12.,  1.,  0.]]),
 'target': array([0, 1, 2, ..., 8, 9, 8]),
 'frame': None,
 'feature_names': ['pixel_0_0',
  'pixel_0_1',
  'pixel_0_2',
  'pixel_0_3',
  'pixel_0_4',
  'pixel_0_5',
  'pixel_0_6',
  'pixel_0_7',
  'pixel_1_0',
  'pixel_1_1',
```

In [42]:
```
digits.data.shape
```

Out[42]:
```
(1797, 64)
```

In [43]:
```
digits.target
```

Out[43]:
```
array([0, 1, 2, ..., 8, 9, 8])
```

In [45]:
```
data_X = digits.data[:600]
y = digits.target[:600]
```

In [17]:
```
from sklearn.manifold import TSNE
tsne = TSNE(n_components=2, random_state=0)
tsne_obj= tsne.fit_transform(data_X)
tsne_obj
```

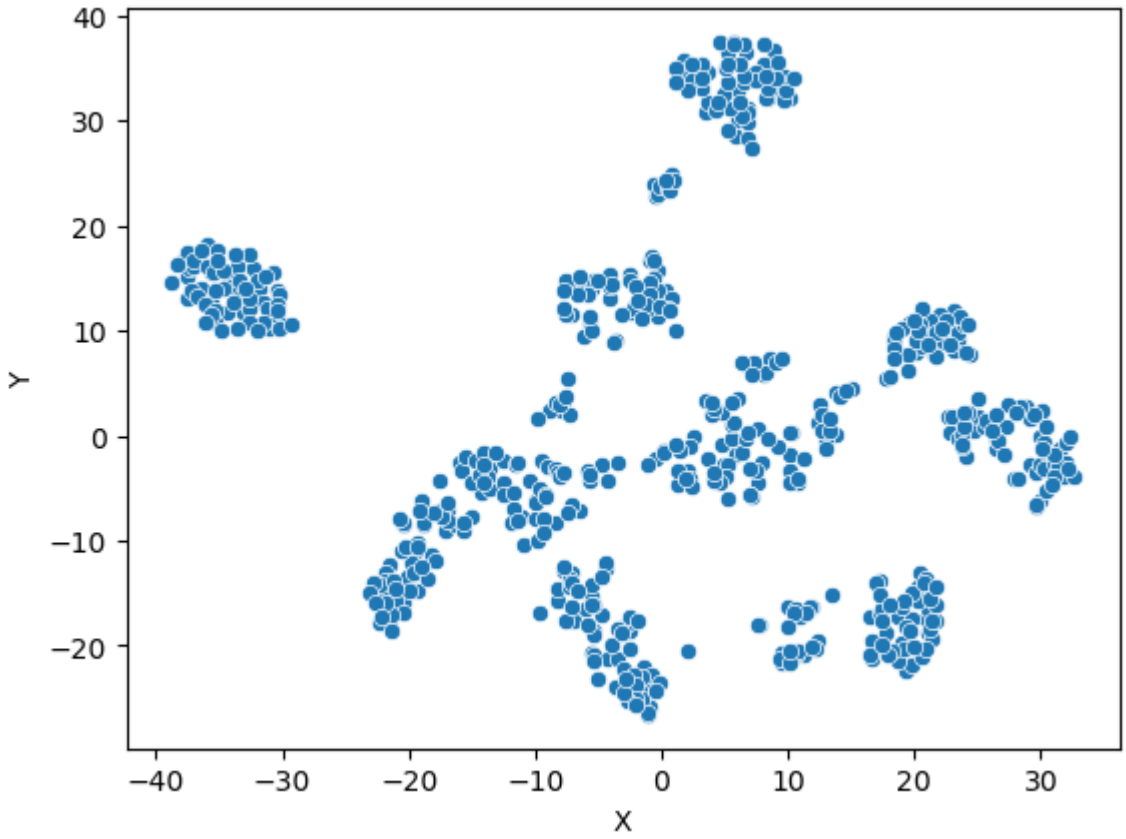
Out[17]:
```
array([[-33.064045 ,  11.775319 ],
       [ 17.76624  ,   5.4796257],
       [  8.055402 ,   5.8756485],
       ...,
       [ 18.094622 , -16.057703 ],
       [  5.6653833,  37.35514  ],
       [ -7.595555 ,   3.655271 ]], dtype=float32)
```

In [25]:
```
tsne_df = pd.DataFrame({'X':tsne_obj[:,0],'Y':tsne_obj[:,1],'digit':y})
tsne_df.head()
```

Out[25]:

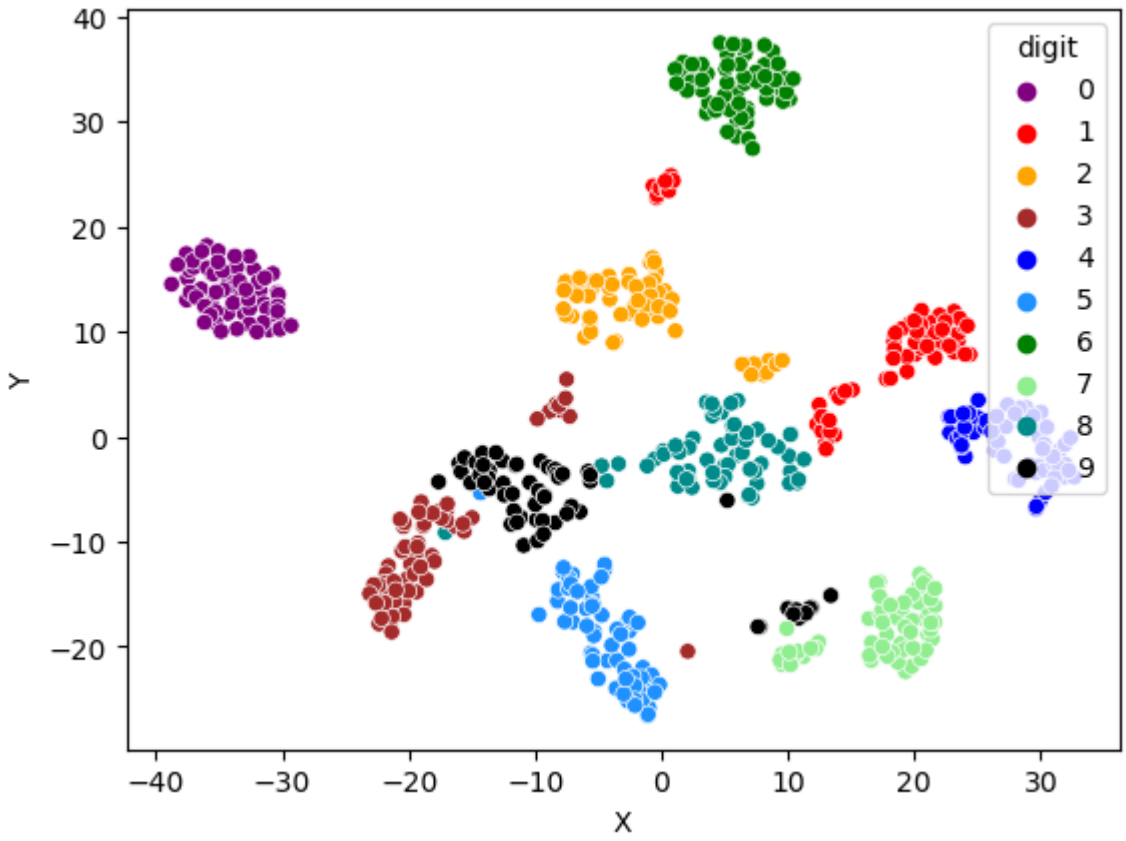
| | X | Y | digit |
|---|---|---|---|
| **0** | -33.064045 | 11.775319 | 0 |
| **1** | 17.766239 | 5.479626 | 1 |
| **2** | 8.055402 | 5.875648 | 2 |
| **3** | -18.861454 | -8.514892 | 3 |
| **4** | 30.009453 | 2.323586 | 4 |

In [20]:
```
import seaborn as sns
sns.scatterplot(x="X", y="Y", data=tsne_df);
```



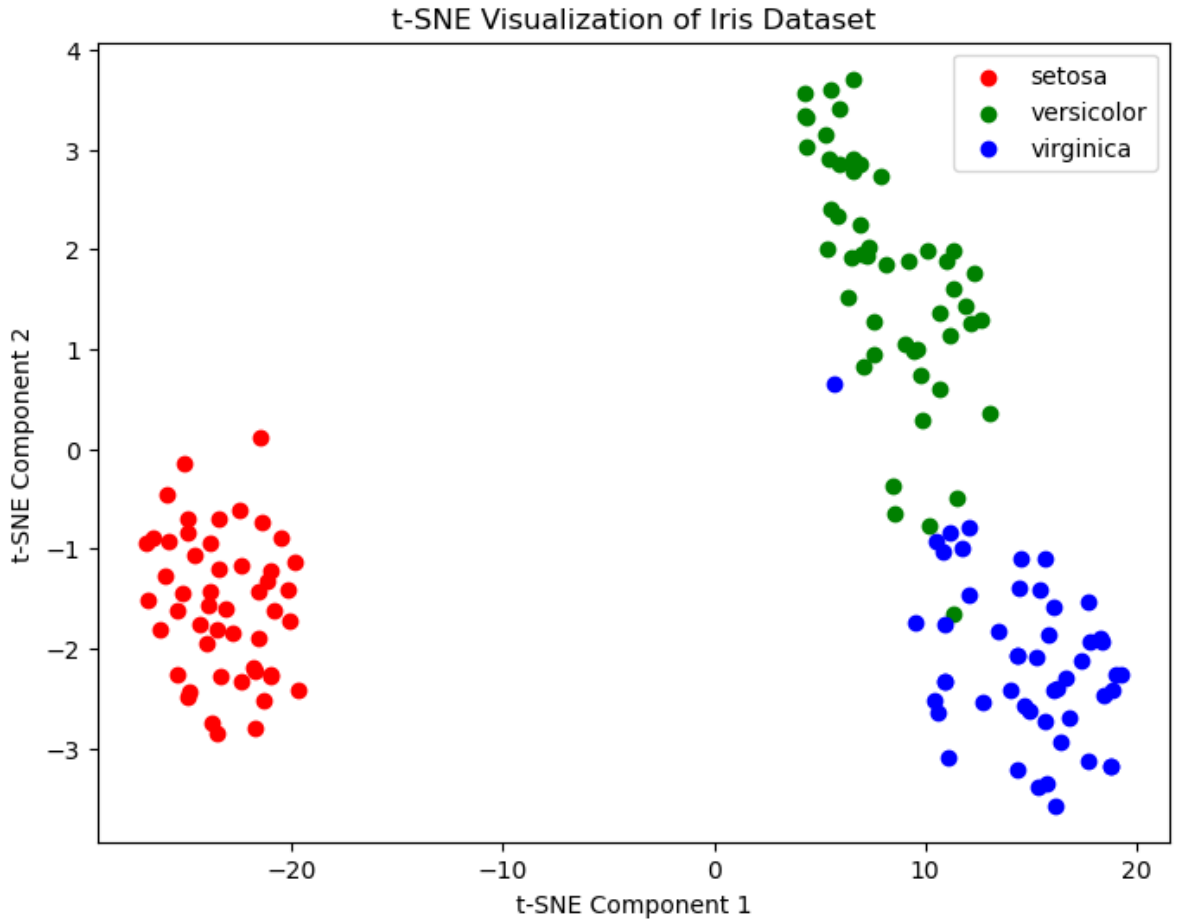
In [28]:
```
sns.scatterplot(x="X", y="Y",hue="digit",
                palette=['purple','red','orange','brown','blue','dodgerblue','
                legend='full',data=tsne_df)
```

Out[28]: <Axes: xlabel='X', ylabel='Y'>




## Exercise 4. Now repeat t-SNE feature selection but now use the iris dataset

In [47]:
```
from sklearn.datasets import load_iris

# Load the Iris dataset
iris = load_iris()
X = iris.data
y = iris.target

from sklearn.manifold import TSNE

tsne = TSNE(n_components=2, random_state=42)
X_tsne = tsne.fit_transform(X)

import matplotlib.pyplot as plt
plt.figure(figsize=(8, 6))
colors = ['red', 'green', 'blue']
for i in range(len(colors)):
    plt.scatter(X_tsne[y == i, 0], X_tsne[y == i, 1], c=colors[i], label=iris.

plt.xlabel('t-SNE Component 1')
plt.ylabel('t-SNE Component 2')
plt.title('t-SNE Visualization of Iris Dataset')
plt.legend()
plt.show()
```



In [ ]: