

Program Code: J620-002-4:2020

Program Name: FRONT-END SOFTWARE DEVELOPMENT

Title: Exe23 - Dimension Reduction Exercise

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Introduction: Learning on Dimension Reduction using python.

Conclusion: Managed to complete tasks relating to the topic.

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	sym
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	С
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	C
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	C
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	C
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	С
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	С
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	С
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	С
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	С
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	С

569 rows × 31 columns

→

In [131]:

```
breast.keys()
```

Out[131]:

```
dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR', 'feature_na
mes', '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)

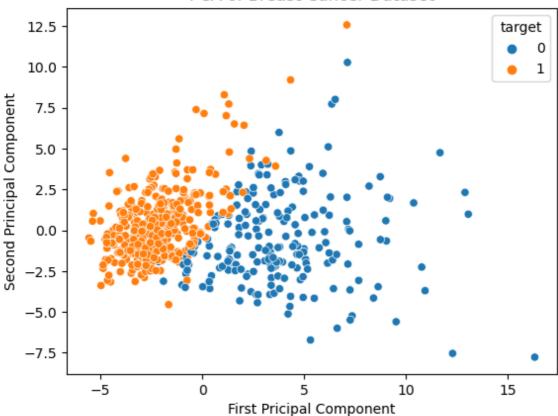
pca = PCA(copy=True, iterated_power='auto', n_components=2, random_state=None,svd_solver
pca.fit(scaled_data)
x_pca = pca.fit_transform(scaled_data)
x_pca.shape
```

Out[158]:

(569, 2)

In [159]:

PCA of Breast Cancer Dataset



In [161]:

```
pca.components_
```

Out[161]:

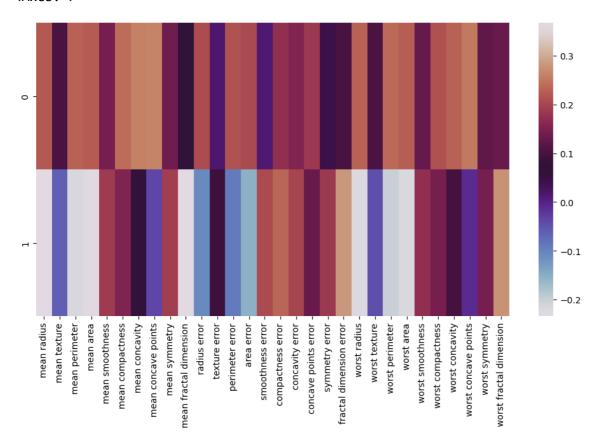
```
array([[ 0.21890244,
                      0.10372458,
                                   0.22753729,
                                                0.22099499, 0.14258969,
         0.23928535,
                      0.25840048,
                                   0.26085376,
                                                0.13816696,
                                                              0.06436335,
         0.20597878,
                      0.01742803,
                                   0.21132592,
                                                              0.01453145,
                                                0.20286964,
         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,
        \hbox{-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 two componed
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]:

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
	67 (44) 1 (44)	(-)	

dtypes: float64(11), int64(3)

memory usage: 19.6 KB

In [6]:

data.describe()

Out[6]:

	Alcohol	Malic_Acid	Ash	Ash_Alcanity	Magnesium	Total_PhenoIs	Flavan
count	178.000000	178.000000	178.000000	178.000000	178.000000	178.000000	178.000
mean	13.000618	2.336348	2.366517	19.494944	99.741573	2.295112	2.029
std	0.811827	1.117146	0.274344	3.339564	14.282484	0.625851	0.998
min	11.030000	0.740000	1.360000	10.600000	70.000000	0.980000	0.340
25%	12.362500	1.602500	2.210000	17.200000	88.000000	1.742500	1.205
50%	13.050000	1.865000	2.360000	19.500000	98.000000	2.355000	2.135
75%	13.677500	3.082500	2.557500	21.500000	107.000000	2.800000	2.875
max	14.830000	5.800000	3.230000	30.000000	162.000000	3.880000	5.080
4							•

In [7]:

```
#2. Split the dataset into the Training and the Test set. Set the test set to 0.3
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, random_state=42
```

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 first two prin 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]]
```

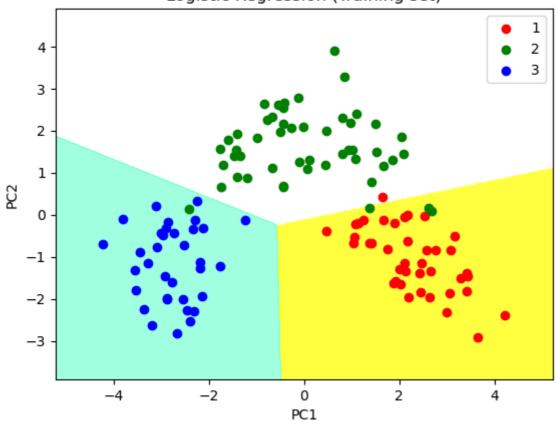
In [119]:

```
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: Use rWarning: *c* argument looks like a single numeric RGB or RGBA sequence, w hich should be avoided as value-mapping will have precedence in case its l ength matches 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 for all points.

```
plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
```

Logistic Regression (Training set)



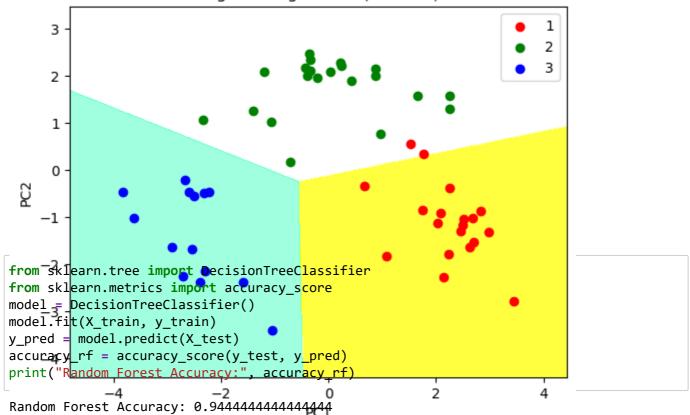
In [121]:

```
# 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: Use rWarning: *c* argument looks like a single numeric RGB or RGBA sequence, w hich should be avoided as value-mapping will have precedence in case its l ength matches 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 for all points.

```
plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
```

Logistic Regression (Test set)



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_forest/)) (https://chrisalbon.com/machine_learning/trees_and_forests/feature_selection_using_random_forest/))

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]:
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 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, random_state=0)
```

```
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 identify
# 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=
0.15)

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_support(in print(selected_feature_names)
```

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

```
In [27]:
```

```
# Transform the data to create a new dataset containing only the most important features
# 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=-1)
# Train the new classifier on the new dataset containing the most important features
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, random_state=0)
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=-1)
# Train the new classifier on the new dataset containing the most important features
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)
```

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_redundant=5
# 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_redundant=5
# 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.ranking_[i])
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
```

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

Column: 9, Selected False, Rank: 3.000

```
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, random_state=0)
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=-1)
# Train the new classifier on the new dataset containing the most important features
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)
```

Accuracy with selected features: 0.9

print("Accuracy with selected features:", accuracy_selected)

t-SNE Walkthrough

(<u>https://cmdlinetips.com/2019/07/dimensionality-reduction-with-tsne/ (https://cmdlinetips.com/2019/07/dimensionality-reduction-with-tsne/)</u>

```
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., \ldots, 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',
  'mixel 1 0'.
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]:

In [25]:

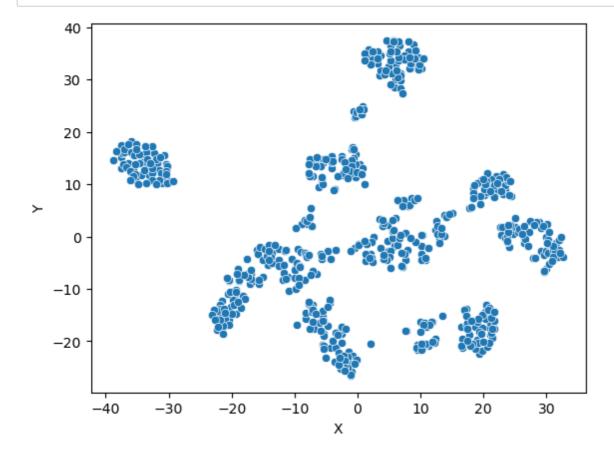
```
tsne_df = pd.DataFrame({'X':tsne_obj[:,0],'Y':tsne_obj[:,1],'digit':y})
tsne_df.head()
```

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]:

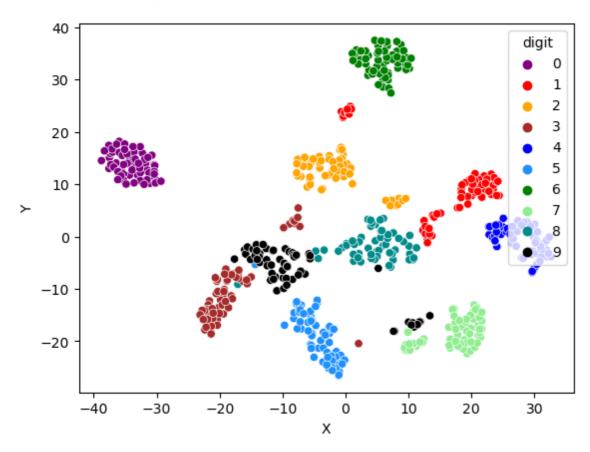
```
import seaborn as sns
sns.scatterplot(x="X", y="Y", data=tsne_df);
```



In [28]:

Out[28]:

<Axes: xlabel='X', ylabel='Y'>

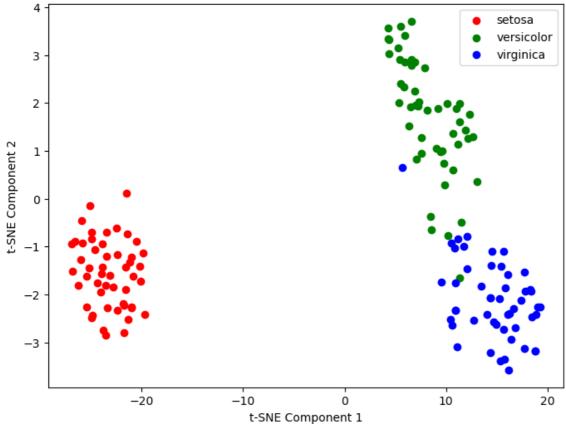


Exercise 4. Now repeat t-SNE feature selection but now use the iris dataset

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.target_nam
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 []: