PCA_LDA_T-SNE_COMPARISON

February 19, 2025

[63]:
```
data_url = 'https://raw.githubusercontent.com/pkmklong/
↪Breast-Cancer-Wisconsin-Diagnostic-DataSet/master/data.csv'
```

[64]:
```
import numpy as np
import pandas as pd
import seaborn as sns
sns.set()
import matplotlib.pyplot as plt
```

[65]:
```
df = pd.read_csv(data_url)
df.head()
```

[65]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	…	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	…	17.33	184.60	2019.0	0.1622	
1	…	23.41	158.80	1956.0	0.1238	
2	…	25.53	152.50	1709.0	0.1444	
3	…	26.50	98.87	567.7	0.2098	
4	…	16.67	152.20	1575.0	0.1374	

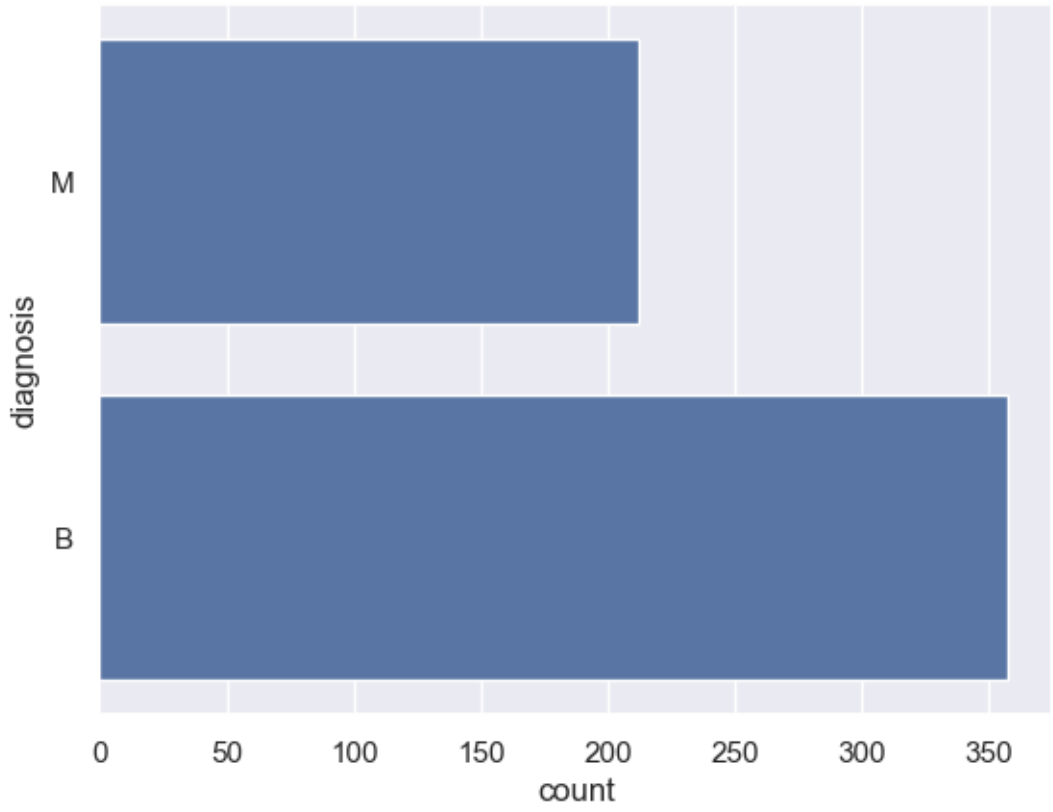
	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.6656	0.7119	0.2654	0.4601	
1	0.1866	0.2416	0.1860	0.2750	
2	0.4245	0.4504	0.2430	0.3613	
3	0.8663	0.6869	0.2575	0.6638	

```
4             0.2050           0.4000                0.1625          0.2364

   fractal_dimension_worst  Unnamed: 32
0                  0.11890          NaN
1                  0.08902          NaN
2                  0.08758          NaN
3                  0.17300          NaN
4                  0.07678          NaN

[5 rows x 33 columns]
```

[66]:
```
df.columns
```

[66]:
```
Index(['id', 'diagnosis', 'radius_mean', 'texture_mean', 'perimeter_mean',
       'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
       'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
       'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'smoothness_worst',
       'compactness_worst', 'concavity_worst', 'concave points_worst',
       'symmetry_worst', 'fractal_dimension_worst', 'Unnamed: 32'],
      dtype='object')
```

[67]:
```
sns.countplot(df['diagnosis'])
plt.show()
```



[68]:
```
df.drop(['Unnamed: 32'], axis = 1, inplace = True)
```

[69]:
```
df.head()
```

[69]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	…	radius_worst	texture_worst	perimeter_worst	area_worst	\
0	…	25.38	17.33	184.60	2019.0	
1	…	24.99	23.41	158.80	1956.0	

```
2  …         23.57          25.53           152.50      1709.0
3  …         14.91          26.50            98.87       567.7
4  …         22.54          16.67           152.20      1575.0

   smoothness_worst  compactness_worst  concavity_worst  concave points_worst  \
0            0.1622             0.6656           0.7119                0.2654
1            0.1238             0.1866           0.2416                0.1860
2            0.1444             0.4245           0.4504                0.2430
3            0.2098             0.8663           0.6869                0.2575
4            0.1374             0.2050           0.4000                0.1625

   symmetry_worst  fractal_dimension_worst
0          0.4601                  0.11890
1          0.2750                  0.08902
2          0.3613                  0.08758
3          0.6638                  0.17300
4          0.2364                  0.07678

[5 rows x 32 columns]
```

[70]:
```
df.drop(['id'], axis = 1, inplace = True)
```

[71]:
```
df.head()
```

[71]:
```
  diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0         M        17.99         10.38          122.80     1001.0
1         M        20.57         17.77          132.90     1326.0
2         M        19.69         21.25          130.00     1203.0
3         M        11.42         20.38           77.58      386.1
4         M        20.29         14.34          135.10     1297.0

   smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
0          0.11840           0.27760          0.3001              0.14710
1          0.08474           0.07864          0.0869              0.07017
2          0.10960           0.15990          0.1974              0.12790
3          0.14250           0.28390          0.2414              0.10520
4          0.10030           0.13280          0.1980              0.10430

   symmetry_mean  …  radius_worst  texture_worst  perimeter_worst  \
0         0.2419  …         25.38          17.33           184.60
1         0.1812  …         24.99          23.41           158.80
2         0.2069  …         23.57          25.53           152.50
3         0.2597  …         14.91          26.50            98.87
4         0.1809  …         22.54          16.67           152.20

   area_worst  smoothness_worst  compactness_worst  concavity_worst  \
0      2019.0            0.1622             0.6656           0.7119
```

```
1      1956.0           0.1238            0.1866           0.2416
2      1709.0           0.1444            0.4245           0.4504
3       567.7           0.2098            0.8663           0.6869
4      1575.0           0.1374            0.2050           0.4000

   concave points_worst  symmetry_worst  fractal_dimension_worst
0                0.2654          0.4601                  0.11890
1                0.1860          0.2750                  0.08902
2                0.2430          0.3613                  0.08758
3                0.2575          0.6638                  0.17300
4                0.1625          0.2364                  0.07678

[5 rows x 31 columns]
```

[72]:
```
df.columns
```

[72]:
```
Index(['diagnosis', 'radius_mean', 'texture_mean', 'perimeter_mean',
       'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
       'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
       'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'smoothness_worst',
       'compactness_worst', 'concavity_worst', 'concave points_worst',
       'symmetry_worst', 'fractal_dimension_worst'],
      dtype='object')
```

[73]:
```
X = df.iloc[:, 1:].values
y = df['diagnosis'].values
```

[74]:
```
X.shape
```

[74]:
```
(569, 30)
```

[75]:
```
y.shape
```

[75]:
```
(569,)
```

[76]:
```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X,y, test_size = 0.2,␣
 ↪random_state= 0)
```

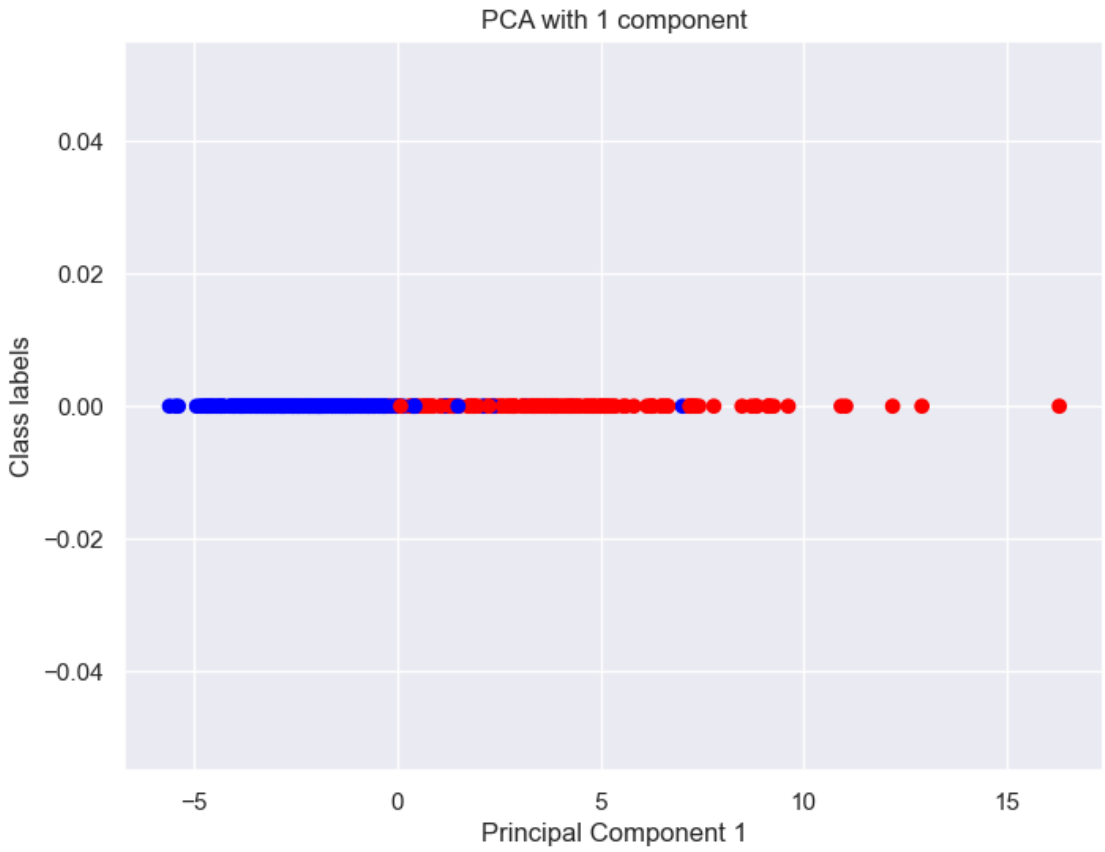
0.0.1 Feature Scaling

[77]:
```
from sklearn.preprocessing import StandardScaler

sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

0.1 PCA (Principal Component Analysis)

[84]:
```
from sklearn.decomposition import PCA

pca = PCA(n_components = 1)

X_train = pca.fit_transform(X_train)
X_test = pca.transform(X_test)
```

[86]:
```
import matplotlib.pyplot as plt
import numpy as np

# Map class labels to colors
colors = {'B': 'blue', 'M': 'red'}

# Create a list of colors based on the class labels
c = [colors[label] for label in y_train]

plt.figure(figsize=(8, 6))
plt.scatter(X_train, np.zeros(len(X_train)), c=c)
plt.title('PCA with 1 component')
plt.xlabel('Principal Component 1')
plt.ylabel('Class labels')
plt.show()
```



0.1.1 Conclusion

PCA has no concern with the class labels. It summarizes the feature set without considering the output. PCA tries to find the directions of the maximum variance in the dataset. In a high cardinality feature set, there are possibilities of duplicate features which would add redundancy to the dataset, increase the computation cost and add unneccessary model complexity. **The role of PCA is to find such highly correlated or duplicate features and to come up with a new feature set where there is minimum correlation between the features or in other words feature set with maximum variance between the features.**

0.2 t-SNE (t-Distributed Stochastic Neighbor)

[ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size = 0.2,␣
↪random_state= 0)
```

[ ]:
```
from sklearn.preprocessing import StandardScaler

sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

[ ]:
```
from sklearn.manifold import TSNE
```

[ ]:
```
tsne = TSNE(n_components = 2, random_state = 0)
```

[ ]:
```
tsne_obj = tsne.fit_transform(X_train)
```

```
c:\Users\Neil\anaconda3\Lib\site-
packages\joblib\externals\loky\backend\context.py:136: UserWarning: Could not
find the number of physical cores for the following reason:
[WinError 2] The system cannot find the file specified
Returning the number of logical cores instead. You can silence this warning by
setting LOKY_MAX_CPU_COUNT to the number of cores you want to use.
  warnings.warn(
  File "c:\Users\Neil\anaconda3\Lib\site-
packages\joblib\externals\loky\backend\context.py", line 257, in
_count_physical_cores
    cpu_info = subprocess.run(
               ^^^^^^^^^^^^^^^

  File "c:\Users\Neil\anaconda3\Lib\subprocess.py", line 548, in run
    with Popen(*popenargs, **kwargs) as process:
         ^^^^^^^^^^^^^^^^^^^^^^^^^^^

  File "c:\Users\Neil\anaconda3\Lib\subprocess.py", line 1026, in __init__
    self._execute_child(args, executable, preexec_fn, close_fds,
  File "c:\Users\Neil\anaconda3\Lib\subprocess.py", line 1538, in _execute_child
    hp, ht, pid, tid = _winapi.CreateProcess(executable, args,
                       ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
```

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

[ ]:
```
tsne_df.head()
```

[ ]:

	X	Y	classification
0	-7.053003	-2.806510	B
1	-8.142869	-9.293004	B
2	-13.934480	8.887429	B
3	-2.931662	-9.876837	B
4	-9.162365	-12.554125	B

[ ]:
```
tsne_df['classification'].value_counts()
```

[ ]:
```
classification
B    290
M    165
Name: count, dtype: int64
```

```
[ ]: plt.figure(figsize = (10,10))
     sns.scatterplot(x = "X", y = 'Y', hue = 'classification', legend = 'full', data␣
       ↪= tsne_df)
     plt.show()
```

0.2.1 Conclusion

t-SNE is an unsupervised dimensionality reduction technique that does not take class labels into account. It focuses on preserving the local structure of the data rather than maximizing variance. t-SNE maps high-dimensional data into a lower-dimensional space, typically for visualization purposes, by minimizing the divergence between pairwise similarities in the original and reduced space. In datasets with high cardinality, complex structures can make it difficult to interpret relationships between data points. The role of t-SNE is to capture and reveal hidden structures in high-dimensional data by clustering similar points together while maintaining meaningful separa-

tions, making it particularly useful for visualizing patterns and groupings in complex datasets.

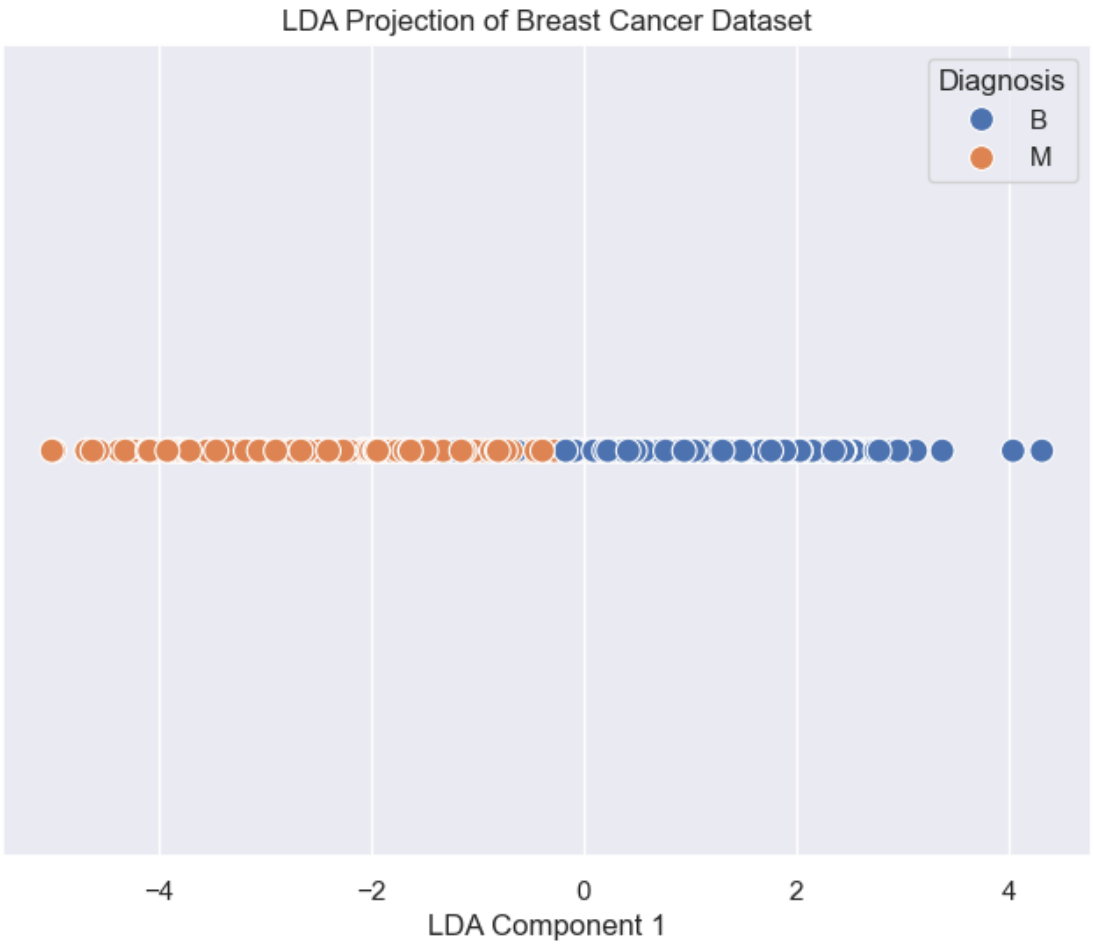
0.3 LDA (Linear Discriminant Analysis)

0.3.1 Performing LDA (Linear Discriminant Analysis)

[ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size = 0.2,␣
↪random_state= 0)

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

[ ]:
```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA

lda = LDA(n_components = 1)
X_train = lda.fit_transform(X_train, y_train)
X_test = lda.transform(X_test)
```

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

# Create a DataFrame for plotting
import pandas as pd
df_lda = pd.DataFrame({'LDA1': X_train[:, 0], 'Diagnosis': y_train})

# Plot using Seaborn
plt.figure(figsize=(8,6))
sns.scatterplot(x=df_lda['LDA1'], y=[0] * len(df_lda), hue=df_lda['Diagnosis'],␣
↪palette="deep", s=100)
plt.xlabel('LDA Component 1')
plt.title('LDA Projection of Breast Cancer Dataset')
plt.yticks([])  # Remove y-axis labels since it's 1D
plt.legend(title='Diagnosis')
plt.show()
```



1 What's the difference from PCA?

LDA tries to reduce the dimensionality by taking into consideration the information that discriminates the output classes. LDA tries to find the decision boundary around each cluster of class. It projects the data points to new dimension in a way that the clusters are as seperate from each other as possible and individual elements within a class are as close to the centroid as possible. **In other words, the inter-class seperability is increased in LDA. Intra-class seperability is reduced.** The new dimensions are the linear discriminants of the feature set.