Lab 9 - CCPS 844 Data Mining

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Answer the following questions and submit a PDF file on the D2L.

Select a dataset of your choice.

- Find number of optimal features from your dataset using the Recursive feature elimination with cross-validation.
- Prepare a dataset with optimal features and call info and describe methods on it
- Apply PCA on the dataset (with optimal features) to get a dataset with reduced dimenion
- There should be a reason to pick n_components to reduce the dimension of the dataset by using PCA
- What is the dimension of the dataset before and after applying PCA?

In [ ]:

```
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.svm import SVC
from sklearn.model_selection import StratifiedKFold
from sklearn.feature_selection import RFECV
from sklearn.datasets import make_classification
%matplotlib inline
```

In [ ]:

```
df= pd.read_csv("pima-indians-diabetes.csv",index_col=0)
df

features = ['pregnant','glucose','bp','skin','insulin','bmi','pedigree','age']
X=df[features]
y=df.label
X
```

Out[ ]:

	pregnant	glucose	bp	skin	insulin	bmi	pedigree	age
1	6	148	72	35	0	33.6	0.627	50
2	1	85	66	29	0	26.6	0.351	31
3	8	183	64	0	0	23.3	0.672	32
4	1	89	66	23	94	28.1	0.167	21
5	0	137	40	35	168	43.1	2.288	33
...	...	...	...	...	...	...	...	...
764	10	101	76	48	180	32.9	0.171	63
765	2	122	70	27	0	36.8	0.340	27
766	5	121	72	23	112	26.2	0.245	30

	pregnant	glucose	bp	skin	insulin	bmi	pedigree	age
767	1	126	60	0	0	30.1	0.349	47
768	1	93	70	31	0	30.4	0.315	23

768 rows × 8 columns

In [ ]:
```
from sklearn.linear_model import LogisticRegression
logit=LogisticRegression(multi_class='ovr',solver='lbfgs',max_iter=1000)
```

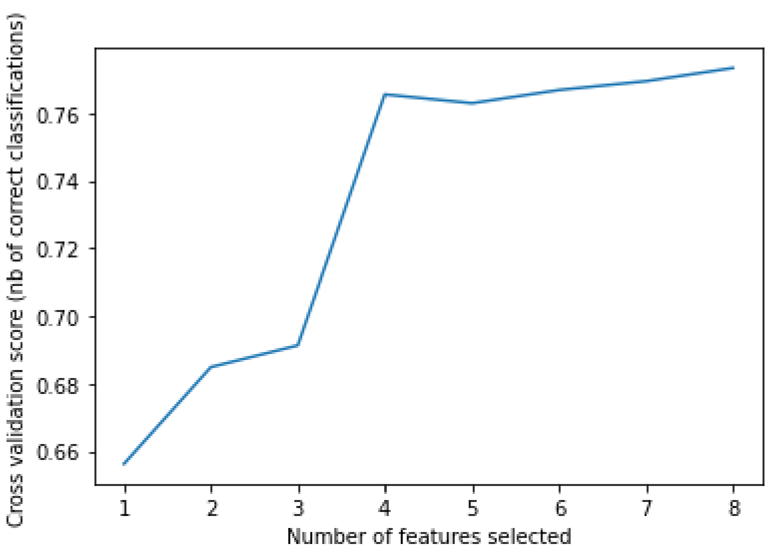
In [ ]:
```
rfecv = RFECV(estimator=logit, step=1, cv=StratifiedKFold(10), scoring='accuracy')
rfecv.fit(X, y)
```

Out[ ]:
```
RFECV(cv=StratifiedKFold(n_splits=10, random_state=None, shuffle=False),
      estimator=LogisticRegression(max_iter=1000, multi_class='ovr'),
      scoring='accuracy')
```

In [ ]:
```
print(f"Optimal number of features : {rfecv.n_features_}")
```

```
Optimal number of features : 8
```

In [ ]:
```
plt.figure()
plt.xlabel("Number of features selected")
plt.ylabel("Cross validation score (nb of correct classifications)")
plt.plot(range(1, len(rfecv.grid_scores_) + 1), rfecv.grid_scores_)
plt.show()
```



In [ ]:
```
print(df.info())
print(df.describe())
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 768 entries, 1 to 768
Data columns (total 9 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   pregnant  768 non-null    int64
```

```
 1   glucose   768 non-null    int64
 2   bp        768 non-null    int64
 3   skin      768 non-null    int64
 4   insulin   768 non-null    int64
 5   bmi       768 non-null    float64
 6   pedigree  768 non-null    float64
 7   age       768 non-null    int64
 8   label     768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 60.0 KB
None
         pregnant     glucose          bp        skin     insulin         bmi  \
count  768.000000  768.000000  768.000000  768.000000  768.000000  768.000000
mean     3.845052  120.894531   69.105469   20.536458   79.799479   31.992578
std      3.369578   31.972618   19.355807   15.952218  115.244002    7.884160
min      0.000000    0.000000    0.000000    0.000000    0.000000    0.000000
25%      1.000000   99.000000   62.000000    0.000000    0.000000   27.300000
50%      3.000000  117.000000   72.000000   23.000000   30.500000   32.000000
75%      6.000000  140.250000   80.000000   32.000000  127.250000   36.600000
max     17.000000  199.000000  122.000000   99.000000  846.000000   67.100000

         pedigree         age       label
count  768.000000  768.000000  768.000000
mean     0.471876   33.240885    0.348958
std      0.331329   11.760232    0.476951
min      0.078000   21.000000    0.000000
25%      0.243750   24.000000    0.000000
50%      0.372500   29.000000    0.000000
75%      0.626250   41.000000    1.000000
max      2.420000   81.000000    1.000000
```

PCA

In [ ]:

```python
from sklearn import decomposition
pca_X = X
pca = decomposition.PCA(n_components=2)
pca.fit(pca_X)
pca_X = pca.transform(X)
pca_X.shape
print(f"Dimenstions before PCA: {X.shape}\nDimenstions after PCA: {pca_X.shape}")
```

```
Dimenstions before PCA: (768, 8)
Dimenstions after PCA: (768, 2)
```

In [ ]:

In [ ]: