Dimensionality Reduction Techniques

In [1]:

```
import os
import sys
import logging

logging.basicConfig(filename="SA1_SVD.log",
                    filemode='w',
                    level=logging.INFO,
                    format="%(asctime)s : %(levelname)s : %(message)s")

try :
    logging.info("#### Packages import ####")
    import numpy as np
    import pandas as pd
    import matplotlib.pyplot as plt
    import seaborn as sns
    import sklearn
    from sklearn import datasets
    import scipy
except ImportError as ie:
    # Output expected ImportErrors
```

```
        logging.error(msg=ie.__class__.__name__  + " :: Missing Package --> " + ie.name)
    except Exception as exception:
        # Output unexpected Exceptions
        logging.info("#### Exceptions other than ModuleImportError ####")
        logging.log(msg=(exception, False))
        logging.log(msg=exception.__class__.__name__ + " :: " + exception.name)

    %matplotlib inline
```

SVD-(Singular_Value_Decomposition)

Lets first understand how SVD works using a dummy dataset, then we will apply the same concept on Breast Cancer Dataset. There are multiple ways by which we can apply SVD on our dataset. First, I'll demonstrate the same using Numpy then via Sklearn.

Using--Numpy

In [2]:
```
X = pd.DataFrame({'col1':[9,4,7,4],
                  'col2':[3,2,1,2]})
```

In [3]:
```
X
```

Out[3]:

	col1	col2
0	9	3
1	4	2
2	7	1
3	4	2

In [4]:
```
X.shape, X.ndim
```

Out[4]:
```
((4, 2), 2)
```

In [5]:
```
from numpy.linalg import svd
```

In [6]:
```
U,S,VT = svd(X,full_matrices=True,compute_uv=True,hermitian=False)
```

In [7]:
```
pd.DataFrame(U)
```

Out[7]:

	0	1	2	3
0	-0.711633	-0.113179	-0.642945	-0.259597
1	-0.331229	-0.466058	0.650505	-0.499920
2	-0.523597	0.743485	0.385767	0.155758
3	-0.331229	-0.466058	0.121029	0.811436

In [13]:
```
Sigma = np.zeros((X.shape[0],X.shape[1]))
Sigma
```

Out[13]:
```
array([[0., 0.],
       [0., 0.],
```

```
       [0., 0.],
       [0., 0.]])
```

In [14]:
```
Sigma[:X.shape[1],:X.shape[1]] = np.diag(S)
Sigma
```

Out[14]:
```
array([[13.32885697,  0.        ],
       [ 0.        ,  1.53021959],
       [ 0.        ,  0.        ],
       [ 0.        ,  0.        ]])
```

In [15]:
```
pd.DataFrame(VT)
```

Out[15]:

	0	1
0	-0.954298	-0.298856
1	0.298856	-0.954298

Re-construct

How to re-construct the main dataset from U, Sigma and VT?

Way-1 : Using Dot Product

In [13]:
```
np.dot(U,np.dot(Sigma,VT))
```

Out[13]:
```
array([[9., 3.],
       [4., 2.],
       [7., 1.],
       [4., 2.]])
```

Way-2 : Using Matrix Multiplication

In [14]:
```
U @ Sigma @ VT
```

Out[14]:
```
array([[9., 3.],
       [4., 2.],
       [7., 1.],
       [4., 2.]])
```

Truncated_SVD

Contrary to PCA, this estimator does not center the data before computing the singular value decomposition. This means it can work with sparse matrices efficiently.

In particular, truncated SVD works on term count/tf-idf matrices as returned by the vectorizers in :mod: `sklearn.feature_extraction.text` . In that context, it is known as `latent semantic analysis (LSA)` .

This estimator supports two algorithms: a fast randomized SVD solver, and a "naive" algorithm that uses ARPACK as an eigensolver on `X * X.T` or `X.T * X` , whichever is more efficient.

Using--Sklearn

In [15]:
```
from sklearn.decomposition import TruncatedSVD
```

In [16]:
```
tsvd = TruncatedSVD(n_components=2)
```

In [17]:
```
X2 = pd.DataFrame({'col1':[9,4,7,4],
                   'col2':[3,2,1,2],
                   'col3':[5,6,7,1]})
```

In [18]:
```
X2.shape, X2.ndim
```

Out[18]:
```
((4, 3), 2)
```

In [19]:
```
X_transf = tsvd.fit_transform(X2)
```

Variance of every component

In [20]:
```
vect_magnitude = tsvd.explained_variance_                ## The magnitude or amount
vect_magnitude
```

Out[20]:
```
array([6.42468871, 3.2616684 ])
```

Here, explained_variance_ represents the variance of both the components.

In [21]:
```
np.var(X_transf[:,0]), np.var(X_transf[:,1])
```

Out[21]:
```
(6.4246887130369394, 3.2616683951751866)
```

Percentage of variations explained by components

In [22]:
```
expln_var_ratio = tsvd.explained_variance_ratio_          ## Percentage of variatio
expln_var_ratio
```

Out[22]:
```
array([0.63064429, 0.32016377])
```

Here, explained_variance_ratio is the ratio of the variances in the components and the sum of the variance in the original dataset.

In [23]:
```
np.var(X_transf,axis=0)/np.sum(np.var(X2,axis=0))
```

Out[23]:
```
array([0.63064429, 0.32016377])
```

Total percentage of variations explained by components

In [24]:
```
tot_var_expln = np.sum((expln_var_ratio))*100            ## Total variation explai
print('Total variation explained by the components is {0:.3f}%'.format(tot_var_expln
```

```
Total variation explained by the components is 95.081%
```

It is just the addition of components individual percentage of variances.

In [25]:
```
np.sum(np.var(X_transf,axis=0)/np.sum(np.var(X2,axis=0)))
```

Out[25]:
```
0.9508080597018038
```

Number of components

In [26]:
```
tsvd.n_components          ## Number of generated components
```

Out[26]: 2

VT

In [27]:
```
VT_x2 = tsvd.components_     ## These are the values of VT's i.e. the EIGEN VECTORS
VT_x2
```

Out[27]:
```
array([[ 0.75687368,  0.23209938,  0.61095999],
       [ 0.53103415,  0.32653333, -0.7819071 ]])
```

So, one thing to understand here is that the above VT_x2 is representing the two eigen vectors whose amount of variation or magnitude(means the eigen value) is represented by singular*values*.

In [28]:
```
tsvd.singular_values_        ## These are the values of the sigma's i.e. the EIGEN V
```

Out[28]:
```
array([16.60761964,  3.62068869])
```

In [29]:
```
U_Sigma_x2 = X_transf        ## The fit_transform function returns us the product of
U_Sigma_x2
```

Out[29]:
```
array([[10.56296122,  1.84937181],
       [ 7.15745341, -1.91423937],
       [ 9.80693507, -1.42957735],
       [ 4.10265348,  1.99529615]])
```

Here, one point to understand is that SVD is nothing but breaking the higher rank dataset into one set(U,Singma and VT) of Rank-1 matrices or closest approximation of main dataset is achieved by the addition of more than one set(U,Sigma and VT) of Rank-1 matrices which can yield a higher rank dataset.

Fit*transform returns the product of U and Sigma, so if we want to reconstruct our main dataset then we just need to peform its matrix multiplication with the VT's or components*.

`Re-construct(TSVD)`

`How to re-construct the main dataset from U, Sigma and VT?`

Way-1 : Using Matrix Multiplication

In [30]:
```
retrv_x2 = pd.DataFrame(U_Sigma_x2 @ VT_x2).apply(lambda val : np.round(val,4))
retrv_x2
```

Out[30]:

	0	1	2
0	8.9769	3.0555	5.0075
1	4.4008	1.0362	5.8697
2	6.6635	1.8094	7.1094

	0	1	2
3	4.1648	1.6038	0.9464

Way-2 : Using Dot Product

In [31]:
```
pd.DataFrame(np.dot(U_Sigma_x2, VT_x2)).apply(lambda val : np.round(val,4))
```

Out[31]:

	0	1	2
0	8.9769	3.0555	5.0075
1	4.4008	1.0362	5.8697
2	6.6635	1.8094	7.1094
3	4.1648	1.6038	0.9464

We have reterieved X2 that was our dataset of shape (4,3) with 12 elements and it is the closest approximate with two components having 8 elements.

Here, it might feels like we have saved a very little space but imagine if we have 1000 x 1000 dataset then in such as case we will only consume space of 2000 elements instead of 10,00,000.

In [30]:
```
X2
```

Out[30]:

	col1	col2	col3
0	9	3	5
1	4	2	6
2	7	1	7
3	4	2	1

SVDS

It is SVD for sparse matirces. It computes the largest or smallest k singular values/vectors for a sparse matrix. The order of the singular values is not guaranteed. It can use the following Eigen Value solvers:

- `##### ARPACK(Stands for ARNoldi Package)`
- `##### LOBPCG(Stand for Locally Optimal Block Preconditioned Conjugate Gradient)`

Using--Scipy

In [41]:
```
X3 = pd.DataFrame({'col1':[9,0,0,4,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0],
                   'col2':[0,2,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0],
```

```
                   'col3':[0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,6,0,1],
                   'col4':[0,0,3,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9]})
```

In [46]:
```
X3.shape
```

Out[46]: (23, 4)

In [42]:
```
from scipy.sparse.linalg import svds
```

In [60]:
```
U_svds_x3, Sigma_svds_x3, VT_svds_x3 = svds(A=X3,k=2,solver='lobpcg')
```

In [61]:
```
U_svds_x3
```

Out[61]:
```
array([[0.        , 0.91381155],
       [0.        , 0.        ],
       [0.30945484, 0.        ],
       [0.        , 0.40613847],
       [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.        ],
       [0.10223039, 0.        ],
       [0.        , 0.        ],
       [0.9454029 , 0.        ]])
```

In [63]:
```
pd.DataFrame(U_svds_x3).shape
```

Out[63]: (23, 2)

In [64]:
```
Sigma_svds_x3
```

Out[64]: array([9.56486299, 9.8488578])

In [65]:
```
pd.DataFrame(VT_svds_x3)
```

Out[65]:

	0	1	2	3
0	0.0	0.0	0.16297	0.986631
1	1.0	0.0	0.00000	0.000000

In [66]:
```
VT_svds_x3.shape
```

Out[66]: (2, 4)

Re-construct(SVDS)

How to re-construct the main dataset from U, Sigma and VT?

Matrix Multiplication

In [90]:
```
sigma_val_svds_X3 = np.zeros((X3.shape[1]-2,X3.shape[1]-2))
sigma_val_svds_X3
```

Out[90]:
```
array([[0., 0.],
       [0., 0.]])
```

In [91]:
```
sigma_val_svds_X3[:,:] = np.diag(Sigma_svds_x3)
sigma_val_svds_X3
```

Out[91]:
```
array([[9.56486299, 0.        ],
       [0.        , 9.8488578 ]])
```

In [92]:
```
pd.DataFrame(U_svds_x3 @ sigma_val_svds_X3 @ VT_svds_x3)
```

Out[92]:

	0	1	2	3
0	9.0	0.0	0.000000	0.000000
1	0.0	0.0	0.000000	0.000000
2	0.0	0.0	0.482374	2.920322
3	4.0	0.0	0.000000	0.000000
4	0.0	0.0	0.000000	0.000000
5	0.0	0.0	0.000000	0.000000
6	0.0	0.0	0.000000	0.000000
7	0.0	0.0	0.000000	0.000000
8	0.0	0.0	0.000000	0.000000
9	0.0	0.0	0.000000	0.000000
10	0.0	0.0	0.000000	0.000000
11	0.0	0.0	0.000000	0.000000
12	0.0	0.0	0.000000	0.000000
13	0.0	0.0	0.000000	0.000000
14	0.0	0.0	0.000000	0.000000
15	0.0	0.0	0.000000	0.000000
16	0.0	0.0	0.000000	0.000000
17	0.0	0.0	0.000000	0.000000
18	0.0	0.0	0.000000	0.000000
19	0.0	0.0	0.000000	0.000000
20	0.0	0.0	0.159355	0.964747
21	0.0	0.0	0.000000	0.000000
22	0.0	0.0	1.473680	8.921758

In [84]:
```
X3
```

Out[84]:

	col1	col2	col3	col4
0	9	0	0	0
1	0	2	0	0
2	0	0	0	3
3	4	0	0	0
4	0	0	0	0
5	0	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	0
15	0	0	0	0
16	0	0	0	0
17	0	0	0	0
18	0	0	0	0
19	0	0	0	0
20	0	0	6	0
21	0	1	0	0
22	0	0	1	9

Numpy(SVD)_on_Sparse_Matrix

In [102...
```
svd_x3 = np.linalg.svd(X3)
```

In [103...
```
U_svd_x3, Sigma_svd_x3, VT_svd_x3 = svd_x3
```

In [104...
```
pd.DataFrame(U_svd_x3)
```

Out[104...

	0	1	2	3	4	5	6	7	8	9	...	13	14	15	16	17
0	-0.913812	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
1	0.000000	0.000000	0.000000	-0.894427	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
2	0.000000	-0.309455	-0.082041	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
3	-0.406138	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0

	0	1	2	3	4	5	6	7	8	9	...	13	14	15	16	17
4	0.000000	0.000000	0.000000	0.000000	1.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
5	0.000000	0.000000	0.000000	0.000000	0.0	1.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
6	0.000000	0.000000	0.000000	0.000000	0.0	0.0	1.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
7	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	1.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
8	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	1.0	0.0	...	0.0	0.0	0.0	0.0	0.0
9	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	1.0	...	0.0	0.0	0.0	0.0	0.0
10	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
11	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
12	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
13	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	1.0	0.0	0.0	0.0	0.0
14	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	1.0	0.0	0.0	0.0
15	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	1.0	0.0	0.0
16	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	1.0	0.0
17	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	1.0
18	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
19	0.000000	0.000000	0.000000	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
20	0.000000	-0.102230	0.993367	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
21	0.000000	0.000000	0.000000	-0.447214	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0
22	0.000000	-0.945403	-0.080563	0.000000	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	0.0	0.0

23 rows × 23 columns

In [97]:
```
Sigma_svd_x3
```

Out[97]:
```
array([9.8488578 , 9.56486299, 5.95931171, 2.23606798])
```

In [98]:
```
VT_svd_x3
```

Out[98]:
```
array([[-1.        , -0.        , -0.        , -0.        ],
       [-0.        , -0.        , -0.16296995, -0.98663103],
       [-0.        , -0.        ,  0.98663103, -0.16296995],
       [-0.        , -1.        , -0.        , -0.        ]])
```

In [105…
```
sigma_val_svd_x3 = np.zeros((X3.shape[0],X3.shape[1]))
sigma_val_svd_x3[:4,:] = np.diag(Sigma_svd_x3)
sigma_val_svd_x3
```

Out[105…
```
array([[9.8488578 , 0.        , 0.        , 0.        ],
       [0.        , 9.56486299, 0.        , 0.        ],
       [0.        , 0.        , 5.95931171, 0.        ],
       [0.        , 0.        , 0.        , 2.23606798],
       [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.        , 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.        ]])
```

In [106…

```
pd.DataFrame(U_svd_x3 @ (sigma_val_svd_x3 @ VT_svd_x3)).apply(lambda val : np.round(
```

Out[106…

	0	1	2	3
0	9.0	0.0	0.0	0.0
1	0.0	2.0	0.0	0.0
2	0.0	0.0	-0.0	3.0
3	4.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0
5	0.0	0.0	0.0	0.0
6	0.0	0.0	0.0	0.0
7	0.0	0.0	0.0	0.0
8	0.0	0.0	0.0	0.0
9	0.0	0.0	0.0	0.0
10	0.0	0.0	0.0	0.0
11	0.0	0.0	0.0	0.0
12	0.0	0.0	0.0	0.0
13	0.0	0.0	0.0	0.0
14	0.0	0.0	0.0	0.0
15	0.0	0.0	0.0	0.0
16	0.0	0.0	0.0	0.0
17	0.0	0.0	0.0	0.0
18	0.0	0.0	0.0	0.0
19	0.0	0.0	0.0	0.0
20	0.0	0.0	6.0	0.0
21	0.0	1.0	0.0	0.0
22	0.0	0.0	1.0	9.0

In [107…

```
X3
```

Out[107…

	col1	col2	col3	col4
0	9	0	0	0

	col1	col2	col3	col4
1	0	2	0	0
2	0	0	0	3
3	4	0	0	0
4	0	0	0	0
5	0	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	0
15	0	0	0	0
16	0	0	0	0
17	0	0	0	0
18	0	0	0	0
19	0	0	0	0
20	0	0	6	0
21	0	1	0	0
22	0	0	1	9

Matrix-Free--Solver

Scipy SVDS

In [151…
```
from scipy.sparse import random as sparse_random
from sklearn.random_projection import sparse_random_matrix
```

In [109…
```
X_sp_mat = sparse_random(2000, 2000, density=0.01, format='csr',random_state=42)
```

In [110…
```
X_sp_mat.shape
```

Out[110… (2000, 2000)

In [111…
```
X_sp_mat.ndim
```

Out[111… 2

In [149…
```
## Memory space required for storing the data of Sparse Matrix
```

```
## *****(We are here talking about the data of Sparse matrix not the spase object it
print(X_sp_mat.data.nbytes, X_sp_mat.indptr.nbytes, X_sp_mat.indices.nbytes)

print("\nTotal number of bytes required to store the data of above sparse matrix is
```

```
320000 8004 160000

Total number of bytes required to store the data of above sparse matrix is 488004
```

In [131…

```
## Size of whole object(size of stored data + overhead)
print("Size of Sparse Matrix object(size of stored data + overhead) is {} bytes".for
```

```
Size of Sparse Matrix object(size of stored data + overhead) is 56 bytes
```

Constructing Pandas DataFrame from Sparse Matrix

In [119…

```
X_sp_mat_df = pd.DataFrame.sparse.from_spmatrix(X_sp_mat)
X_sp_mat_df.head()
```

Out[119…

	0	1	2	3	4	5	6	7	8	9	...	1990	1991	1992	1993	1994	1995	1996	1
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	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	
2	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	
3	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	
4	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	

5 rows × 2000 columns

In [120…

```
X_sp_mat_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2000 entries, 0 to 1999
Columns: 2000 entries, 0 to 1999
dtypes: Sparse[float64, 0](2000)
memory usage: 468.9 KB
```

In [146…

```
## Size of whole object(size of stored data + overhead)
print("Size of Pandas Df formed from the Sparse Matrix(size of stored data + overhea
```

```
Size of Pandas Df formed from the Sparse Matrix(size of stored data + overhead) is 4
80152 bytes
```

In [48]:

```
X_sp_matrix.ndim
```

Out[48]: 2

In [49]:

```
X_sp_matrix.shape
```

Out[49]: (2000, 2000)

Re-Constructing Sparse Matrix from Pandas DataFrame

In [125…

```
X_sp_mat_recons = scipy.sparse.csr_matrix(X_sp_mat_df)
```

In [126…

```
X_sp_mat_recons.data.nbytes + X_sp_mat_recons.indptr.nbytes + X_sp_mat_recons.indice
```

Out[126… 488004

In [147…
```
## Size of whole object(size of stored data + overhead)
print("Size of re-constructed Sparse Matrix (size of stored data + overhead) is {} b
```

```
Size of re-constructed Sparse Matrix (size of stored data + overhead) is 56 bytes
```

Here, we found that Sparse objects requires less storage space or memory, however, if we store the same data in the pandas dataframe object then its storage becomes inefficient in terms of space consumption.

Execution_time_diff

Difference in execution time of SVDS on Sparse Matrix and Pandas DataFrame

In [152…
```
%timeit scipy.sparse.linalg.svds(X_sp_mat,k=200)
```

```
4.35 s ± 550 ms per loop (mean ± std. dev. of 7 runs, 1 loop each)
```

In [154…
```
%timeit scipy.sparse.linalg.svds(X_sp_mat_df,k=200)
```

```
9.32 s ± 377 ms per loop (mean ± std. dev. of 7 runs, 1 loop each)
```

For 200 largest singular values, time consumption with the dataframe object is more than double as compared to the Sparse object.

SVD_on_Breast_Cancer_Datset

In [155…
```
breast_cancer = datasets.load_breast_cancer()
```

In [156…
```
print(breast_cancer.DESCR)
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

    :Number of Instances: 569

    :Number of Attributes: 30 numeric, predictive attributes and the class

    :Attribute Information:
        - radius (mean of distances from center to points on the perimeter)
        - texture (standard deviation of gray-scale values)
        - perimeter
        - area
        - smoothness (local variation in radius lengths)
        - compactness (perimeter^2 / area - 1.0)
        - concavity (severity of concave portions of the contour)
        - concave points (number of concave portions of the contour)
        - symmetry
        - fractal dimension ("coastline approximation" - 1)

        The mean, standard error, and "worst" or largest (mean of the three
        worst/largest values) of these features were computed for each image,
        resulting in 30 features.  For instance, field 0 is Mean Radius, field
        10 is Radius SE, field 20 is Worst Radius.
```

```
        - class:
                - WDBC-Malignant
                - WDBC-Benign

    :Summary Statistics:

    ===================================== ====== ======
                                           Min    Max
    ===================================== ====== ======
    radius (mean):                        6.981  28.11
    texture (mean):                       9.71   39.28
    perimeter (mean):                     43.79  188.5
    area (mean):                          143.5  2501.0
    smoothness (mean):                    0.053  0.163
    compactness (mean):                   0.019  0.345
    concavity (mean):                     0.0    0.427
    concave points (mean):                0.0    0.201
    symmetry (mean):                      0.106  0.304
    fractal dimension (mean):             0.05   0.097
    radius (standard error):              0.112  2.873
    texture (standard error):             0.36   4.885
    perimeter (standard error):           0.757  21.98
    area (standard error):                6.802  542.2
    smoothness (standard error):          0.002  0.031
    compactness (standard error):         0.002  0.135
    concavity (standard error):           0.0    0.396
    concave points (standard error):      0.0    0.053
    symmetry (standard error):            0.008  0.079
    fractal dimension (standard error):   0.001  0.03
    radius (worst):                       7.93   36.04
    texture (worst):                      12.02  49.54
    perimeter (worst):                    50.41  251.2
    area (worst):                         185.2  4254.0
    smoothness (worst):                   0.071  0.223
    compactness (worst):                  0.027  1.058
    concavity (worst):                    0.0    1.252
    concave points (worst):               0.0    0.291
    symmetry (worst):                     0.156  0.664
    fractal dimension (worst):            0.055  0.208
    ===================================== ====== ======

    :Missing Attribute Values: None

    :Class Distribution: 212 - Malignant, 357 - Benign

    :Creator:  Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

    :Donor: Nick Street

    :Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2

Features are computed from a digitized image of a fine needle
aspirate (FNA) of a breast mass.  They describe
characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using
Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree.  Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
```

```
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. topic:: References

   - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
     for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
     Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
     San Jose, CA, 1993.
   - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
     prognosis via linear programming. Operations Research, 43(4), pages 570-577,
     July-August 1995.
   - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
     to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994)
     163-171.
```

In [157…

```
cancer_df = pd.concat([pd.DataFrame(breast_cancer.data,columns=breast_cancer.feature
                       pd.DataFrame(breast_cancer.target,columns=['Label'])],axis=1)

cancer_df.head()
```

Out[157…

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	di
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	

5 rows × 31 columns

In [158…

```
cancer_df.shape
```

Out[158… (569, 31)

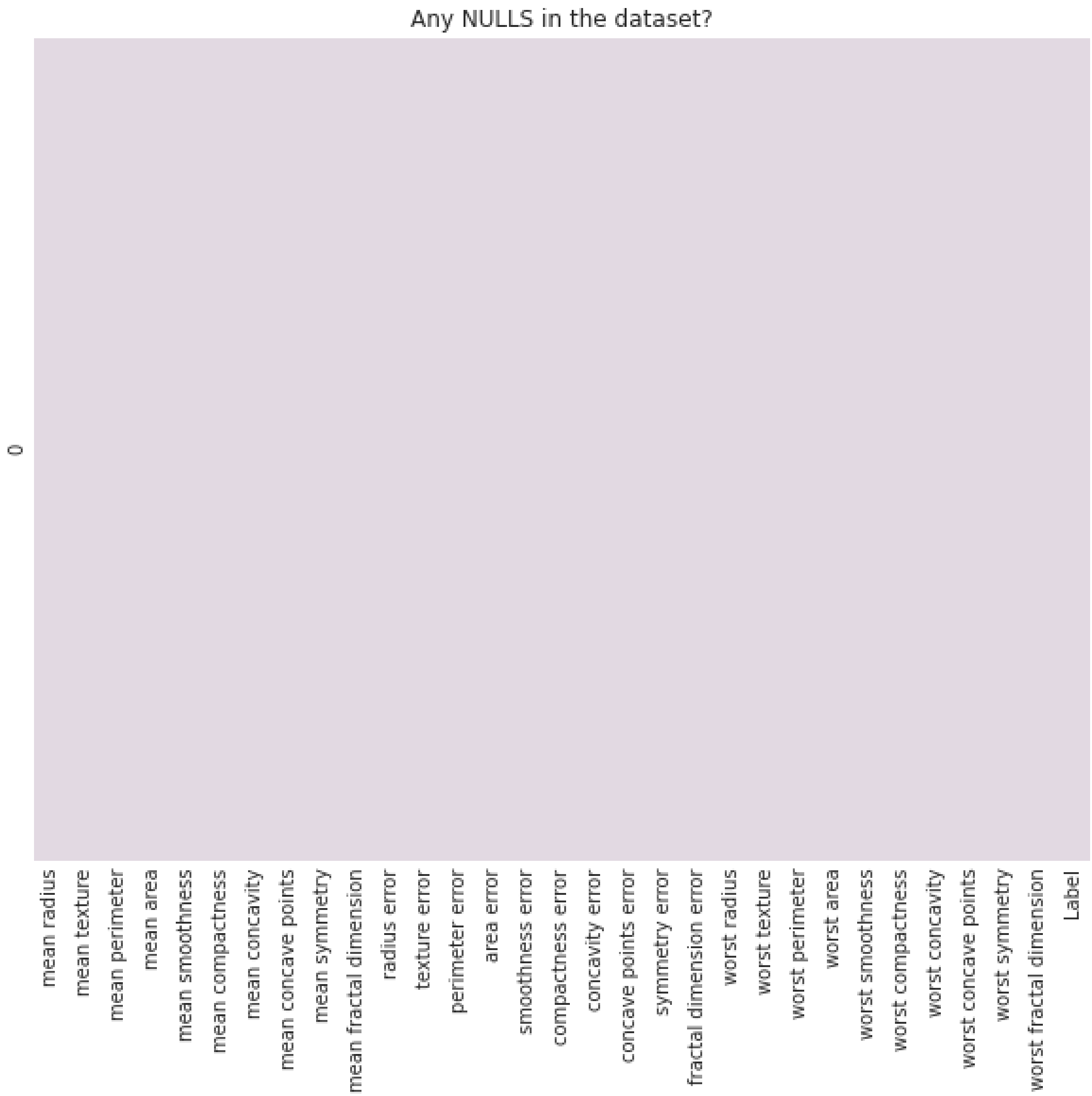
In [159…

```
cancer_df.ndim
```

Out[159… 2

In [204…

```
with plt.style.context('seaborn-dark'):
    plt.figure(figsize=(10,8))
    sns.heatmap(data=pd.DataFrame(cancer_df.isna().sum()).T,annot=False,cmap='twilig
    plt.title("Any NULLS in the dataset?")
```



In [176…

```
X_cancer_df = cancer_df.iloc[:,0:-1]
```

In [177…

```
X_cancer_df.head()
```

Out[177…

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	di
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	

5 rows × 30 columns

In [174…

```
from sklearn.decomposition import TruncatedSVD
```

In [175…

```
tsvd_cancer_data = TruncatedSVD(n_components=4)
```

In [178…
```
cancer_transf = tsvd_cancer_data.fit_transform(X_cancer_df)
```

In [189…
```
pd.DataFrame(tsvd_cancer_data.components_)  ### Eigen Vectors
```

Out[189…

	0	1	2	3	4	5	6	7	8
0	0.010742	0.013405	0.070451	0.572522	0.000065	0.000080	0.000081	0.000045	0.000122
1	-0.031086	-0.048312	-0.197365	-0.770224	-0.000262	-0.000175	-0.000041	-0.000017	-0.000498
2	-0.076244	-0.177050	-0.473078	0.248295	-0.000901	-0.000651	0.000087	0.000065	-0.001707
3	0.046589	0.139147	0.300983	-0.120163	0.000809	0.000767	0.000420	0.000056	0.001547

4 rows × 30 columns

In [190…
```
tsvd_cancer_data.singular_values_  ### Eigen Values
```

Out[190…
```
array([30786.44462784,  2480.44578339,   880.46294478,   555.12328791])
```

In [184…
```
tsvd_cancer_data.explained_variance_
```

Out[184…
```
array([439557.66669002,   9783.78914599,   1186.68181281,    524.75476533])
```

In [185…
```
tsvd_cancer_data.explained_variance_ratio_
```

Out[185…
```
array([0.97440781, 0.02168862, 0.00263063, 0.00116327])
```

In [192…
```
cancer_transf = pd.DataFrame(cancer_transf,columns=['PC1','PC2','PC3','PC4'])
cancer_transf = pd.concat([cancer_transf,cancer_df['Label']],axis=1)
cancer_transf.head()
```

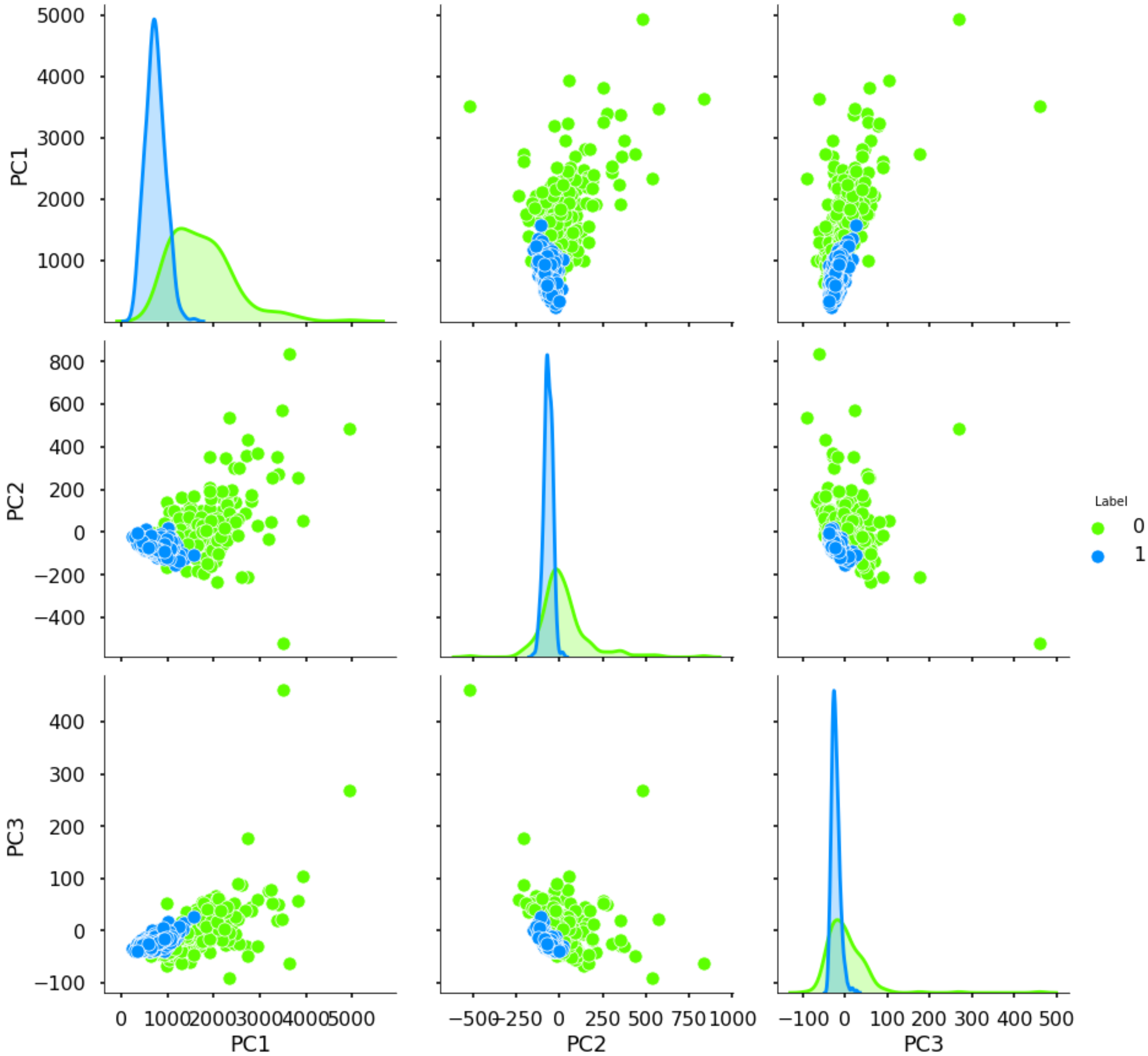
Out[192…

	PC1	PC2	PC3	PC4	Label
0	2241.974276	347.715560	-27.537419	59.801498	0
1	2372.408403	56.901670	23.863162	-48.564064	0
2	2101.840280	11.947627	30.411386	-12.071248	0
3	697.432105	-2.127700	-46.793073	27.242121	0
4	2047.087229	-137.765113	67.523948	-20.172432	0

In [193…
```
cancer_transf.shape
```

Out[193…
```
(569, 5)
```

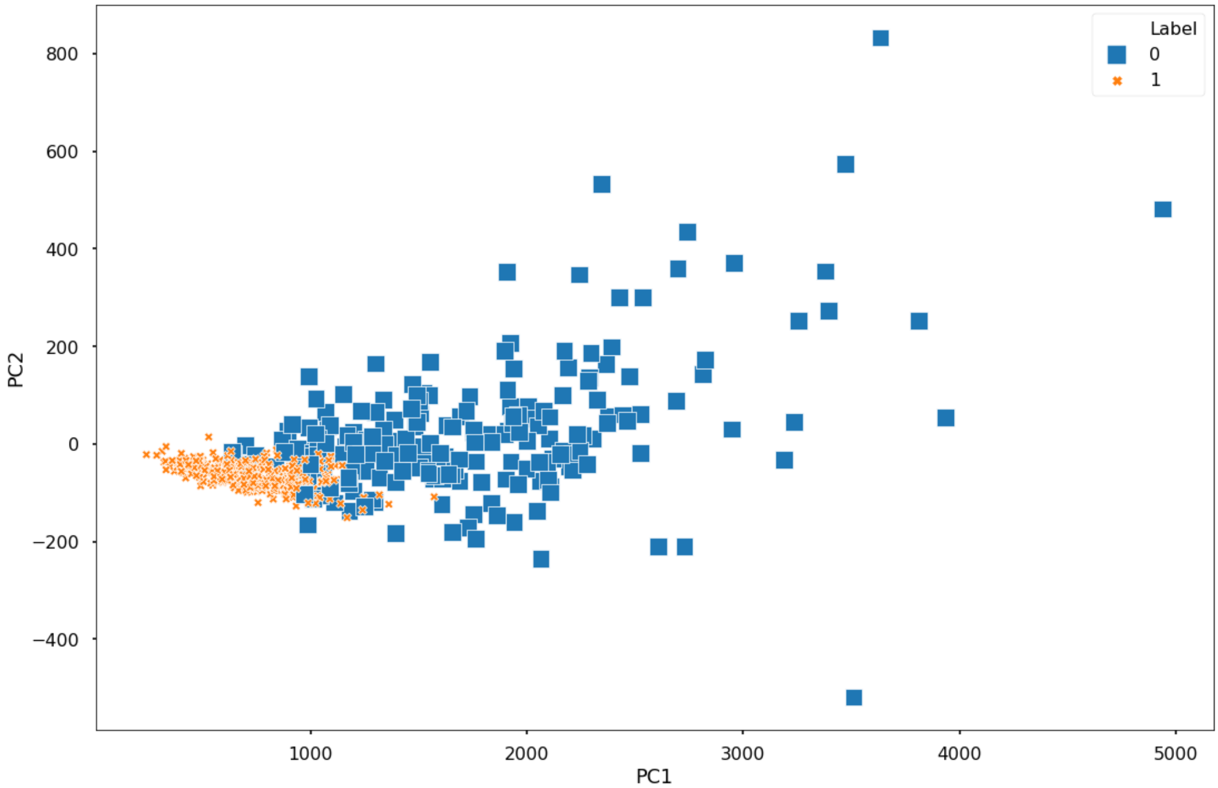
In [203…
```
with plt.style.context('seaborn-poster'):
    sns.pairplot(data=cancer_transf[['PC1','PC2','PC3','Label']],hue='Label',height=
```



First impression gave me the look of overlapping of data values and for further analysis I'll go ahead with the first two components.

In [258…

```
markers = {0: "s", 1: "X"}
with plt.style.context('seaborn-poster'):
    plt.figure(figsize=(18,12))
    sns.scatterplot(data=cancer_transf,x='PC1',y='PC2',hue='Label',size=cancer_trans
                    style='Label',
                    markers=markers)
```

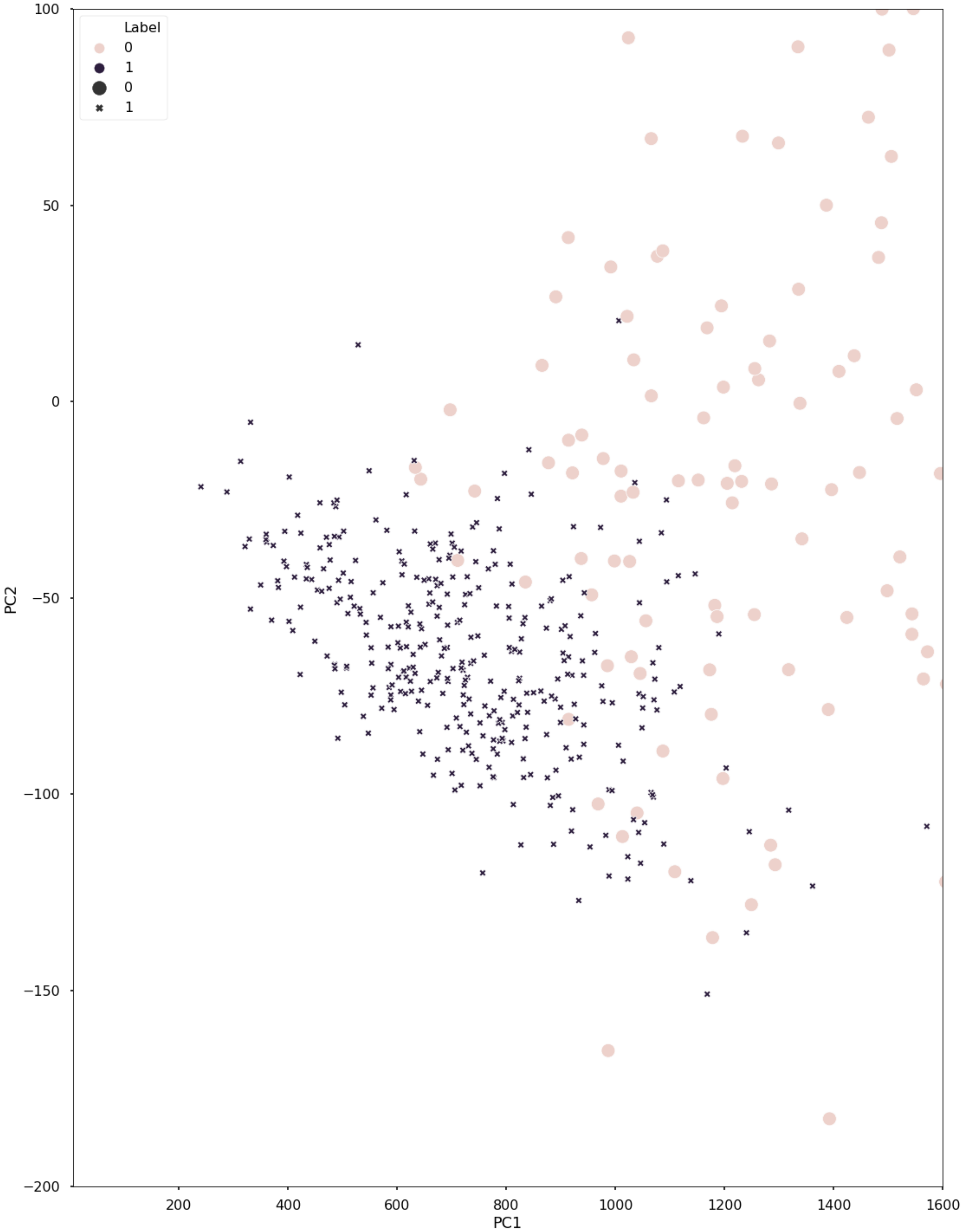


Positive patients are very tightly packed and yes there is some overlapping of both types of patients. One thing thats striking in my mind here is the close approximity of postive cases.

One more close look...

In [275…

```
with plt.style.context('seaborn-poster'):
    plt.figure(figsize=(18,25))
    sns.scatterplot(data=cancer_transf,x='PC1',y='PC2',hue='Label',size=cancer_trans
    plt.xlim(right=1600)
    plt.ylim(bottom=-200,top=100)
```



Models_Performance

Lets run some models

In [337…

```
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.linear_model import Perceptron, LogisticRegression
from sklearn.neighbors import KNeighborsClassifier as knn
from sklearn.metrics import accuracy_score, precision_score, recall_score
```

In [319…

```
X_train,X_test,y_train,y_test = train_test_split(cancer_transf[['PC1','PC2']],cancer
```

In [320…
```
X_train.shape, y_train.shape, X_test.shape, y_test.shape
```
Out[320…
```
((398, 2), (398,), (171, 2), (171,))
```

Perceptron

In [321…
```
pc = Perceptron()
```
In [322…
```
pc_model = pc.fit(X_train,y_train)
```
In [323…
```
pc_y_pred = pc_model.predict(X_test)
```
In [324…
```
accuracy_score(y_test,pc_y_pred)
```
Out[324…
```
0.8713450292397661
```
In [325…
```
precision_score(y_test,pc_y_pred)
```
Out[325…
```
0.8859649122807017
```
In [326…
```
recall_score(y_test,pc_y_pred)
```
Out[326…
```
0.9181818181818182
```
In [327…
```
cross_val_score(pc_model,X_test,y_test,cv=10)
```
Out[327…
```
array([0.66666667, 0.70588235, 0.88235294, 0.58823529, 0.82352941,
       0.82352941, 0.82352941, 0.82352941, 0.35294118, 0.94117647])
```
In [328…
```
np.mean(cross_val_score(pc_model,X_test,y_test,cv=10))
```
Out[328…
```
0.7431372549019607
```

Logistic_Regression

In [329…
```
lr = LogisticRegression()
```
In [330…
```
lr_model = lr.fit(X_train,y_train)
```
In [331…
```
lr_y_pred = lr_model.predict(X_test)
```
In [332…
```
accuracy_score(y_test,lr_y_pred)
```
Out[332…
```
0.9298245614035088
```
In [333…
```
precision_score(y_test,lr_y_pred)
```
Out[333…
```
0.9375
```
In [334…
```
recall_score(y_test,lr_y_pred)
```
Out[334…
```
0.9545454545454546
```
In [335…
```
cross_val_score(lr_model,X_test,y_test,cv=10)
```
Out[335…
```
array([0.88888889, 0.94117647, 1.        , 0.82352941, 0.94117647,
```

```
        0.94117647, 0.94117647, 0.88235294, 0.94117647, 0.82352941])
```

In [336…
```
np.mean(cross_val_score(lr_model,X_test,y_test,cv=10))
```

Out[336…
```
0.9124183006535949
```

KNN

In [339…
```
KNN = knn(n_neighbors=7)
```

In [344…
```
knn_model = KNN.fit(X=X_train,y=y_train)
```

In [345…
```
knn_y_pred = knn_model.predict(X_test)
```

In [346…
```
accuracy_score(y_test,knn_y_pred)
```

Out[346…
```
0.9473684210526315
```

In [347…
```
precision_score(y_test,knn_y_pred)
```

Out[347…
```
0.954954954954955
```

In [348…
```
recall_score(y_test,knn_y_pred)
```

Out[348…
```
0.9636363636363636
```

In [349…
```
cross_val_score(knn_model,X_test,y_test,cv=10)
```

Out[349…
```
array([0.88888889, 0.88235294, 1.        , 0.94117647, 0.94117647,
       0.94117647, 0.94117647, 0.94117647, 0.88235294, 0.88235294])
```

In [350…
```
np.mean(cross_val_score(knn_model,X_test,y_test,cv=10))
```

Out[350…
```
0.9241830065359478
```

Reference Links

https://machinelearningmastery.com/singular-value-decomposition-for-machine-learning/

https://www.analyticsvidhya.com/blog/2019/08/5-applications-singular-value-decomposition-svd-data-science/

https://www.youtube.com/watch?v=46Hpy4FiGls&list=PLMrJAkhIeNNSVjnsviglFoY2nXildDCcv&index=10