
Dimensionality Reduction

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Part 1: Dimensionality Reduction

Introduction:

Dimensionality reduction is the process of decreasing the dimensions (the number of attributes) in a given data. There could be several compelling reasons to do so, including the convenience of visualizing, reduction in noise, representing the data in a more comprehensive way by removing redundant attributes etc. One technique of dimensionality reduction is known as Principal Component Analysis (PCA).

Principal Component Analysis (PCA): In PCA, we discover a new set of dimensions against which to represent, describe or evaluate the data where each new dimension is known as a Principal Component and each principal component is mutually orthogonal to all other Principal components.

Implementation:

From a bird's eye view, the process of finding the principal components is as follows:

- Let X^* the mean vector found by taking the mean of all rows.
- The original data is adjusted by subtracting each value of each row by X
 - $x' = x - X^*$;
- Next, the covariance matrix, S , is calculated from the above adjusted data(X).

$$S = (1/n-1)XTX$$

- Now, the eigenvectors and eigenvalues of S are found such that $Sa = \lambda a$
- The eigenvalues λ_j corresponds to variance on each component j , so the λ values are sorted.
- Finally, we take the first 'd' eigenvectors a_i and these represent the directions with largest variance.

The new dimensions (principal components) are produced as:

$$y_1 = a_{11}x_1 + a_{12}x_2 + \dots + a_{1k}x_k$$

$$y_2 = a_{21}x_1 + a_{22}x_2 + \dots + a_{2k}x_k$$

$$\dots$$

$$y_k = a_{k1}x_1 + a_{k2}x_2 + \dots + a_{kk}x_k$$

Code Snippets:

The following piece of code is used to calculate the mean of all rows

```
for col in range(matrix.shape[1]):
    sum = 0
    for row in range(matrix.shape[0]):
        sum+=matrix[row,col]
    meanList.append(sum/n)
```

After the mean (X^*) is found, the following method is used to adjust the original data:

```
def adjustment(matrix, meanList):
    tmp = 0
    for col in range(matrix.shape[1]):
        for row in range(matrix.shape[0]):
            matrix[row,col] = matrix[row,col] - meanList[tmp]
        tmp+=1
    return matrix
```

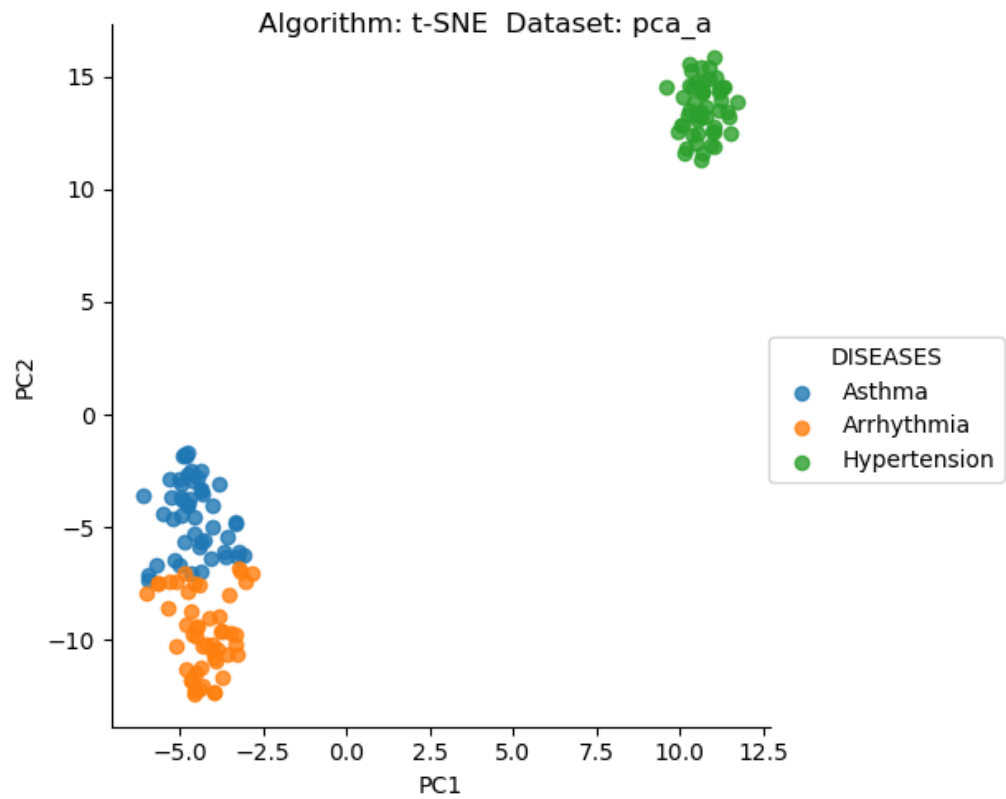
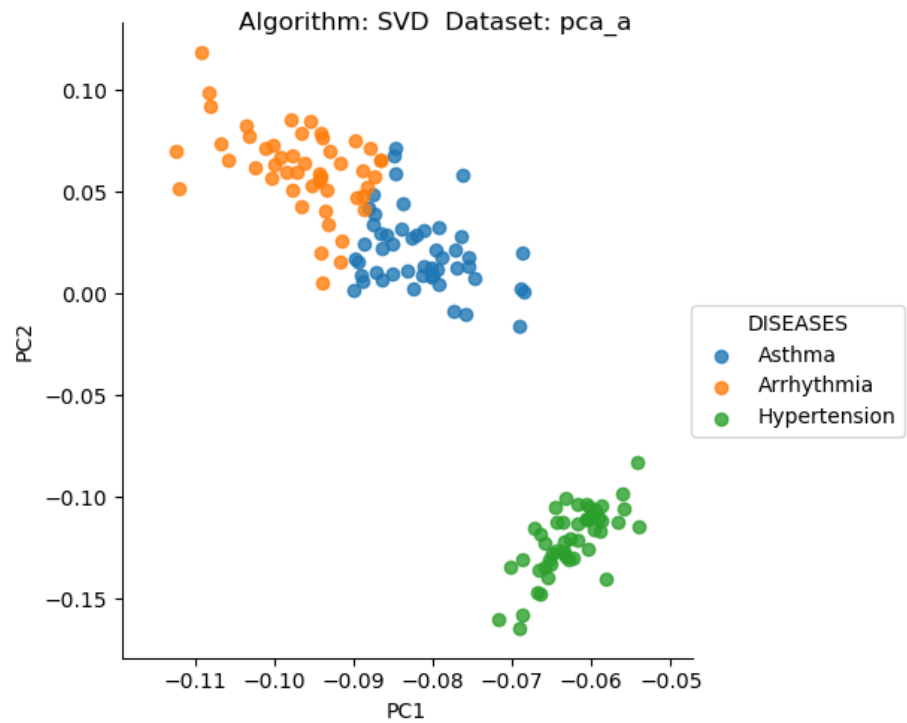
To calculate the eigen vectors, the following code is used (using the numpy library methods for matrix multiplication and finding the eigen vectors)

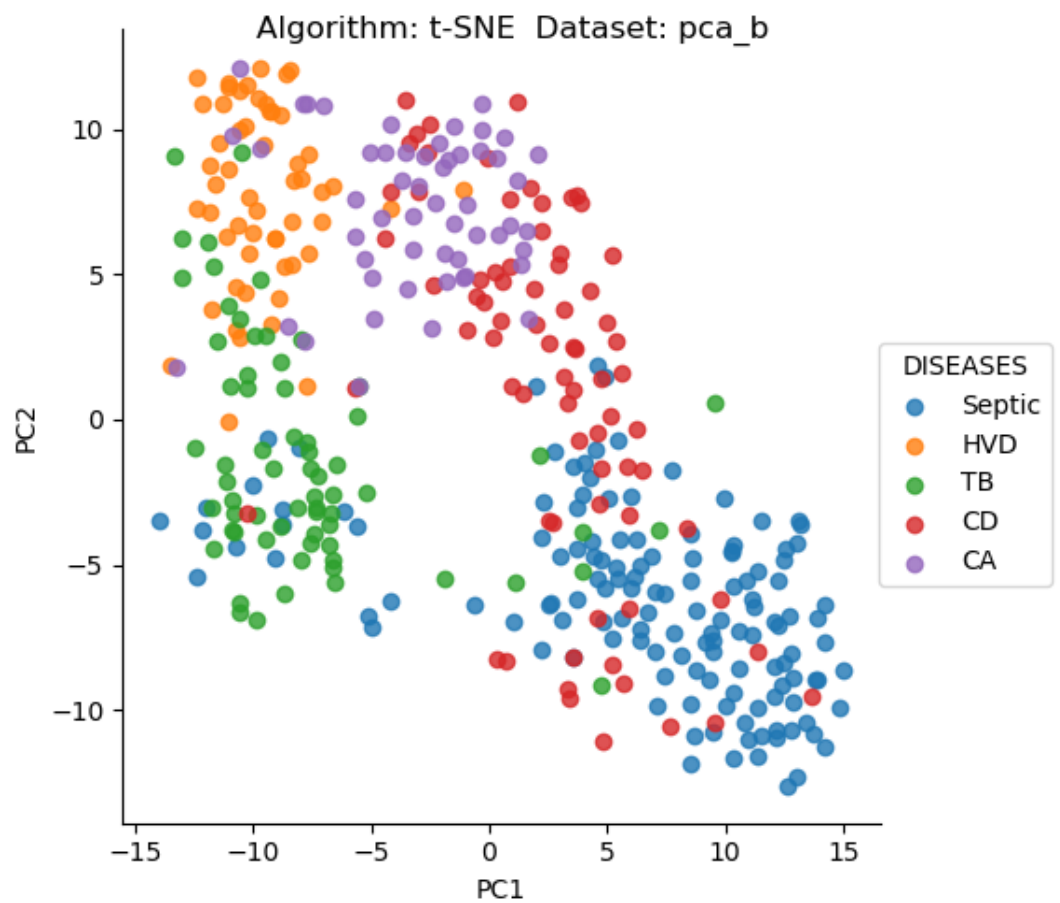
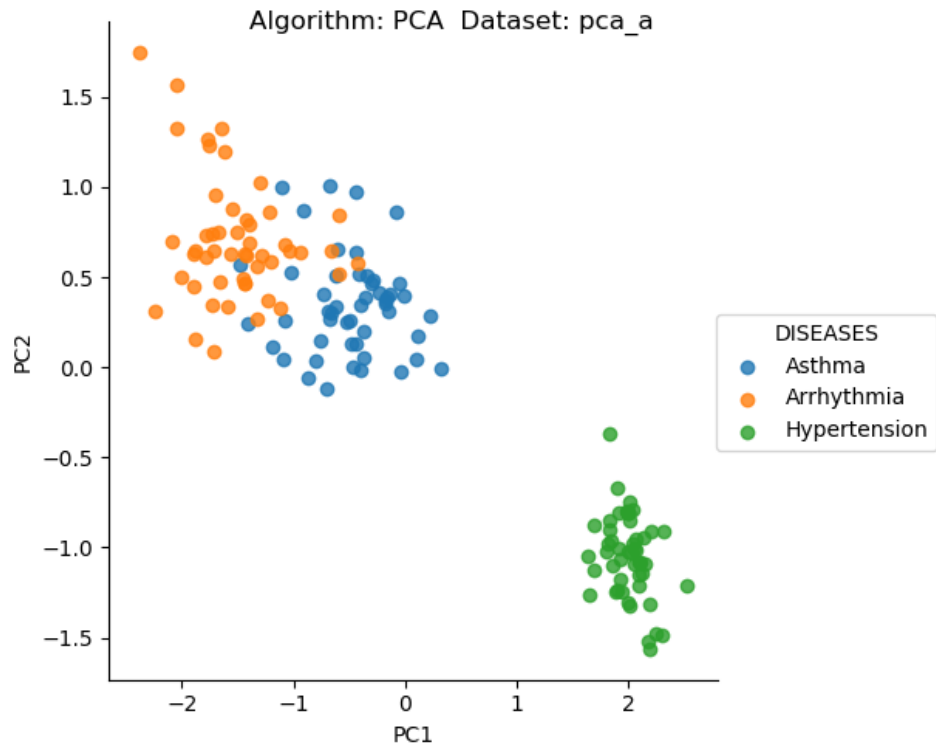
```
S = (1/(n-1))*np.matmul(matrix.T,matrix)
eigenValues, eigenVectors = np.linalg.eig(S)
```

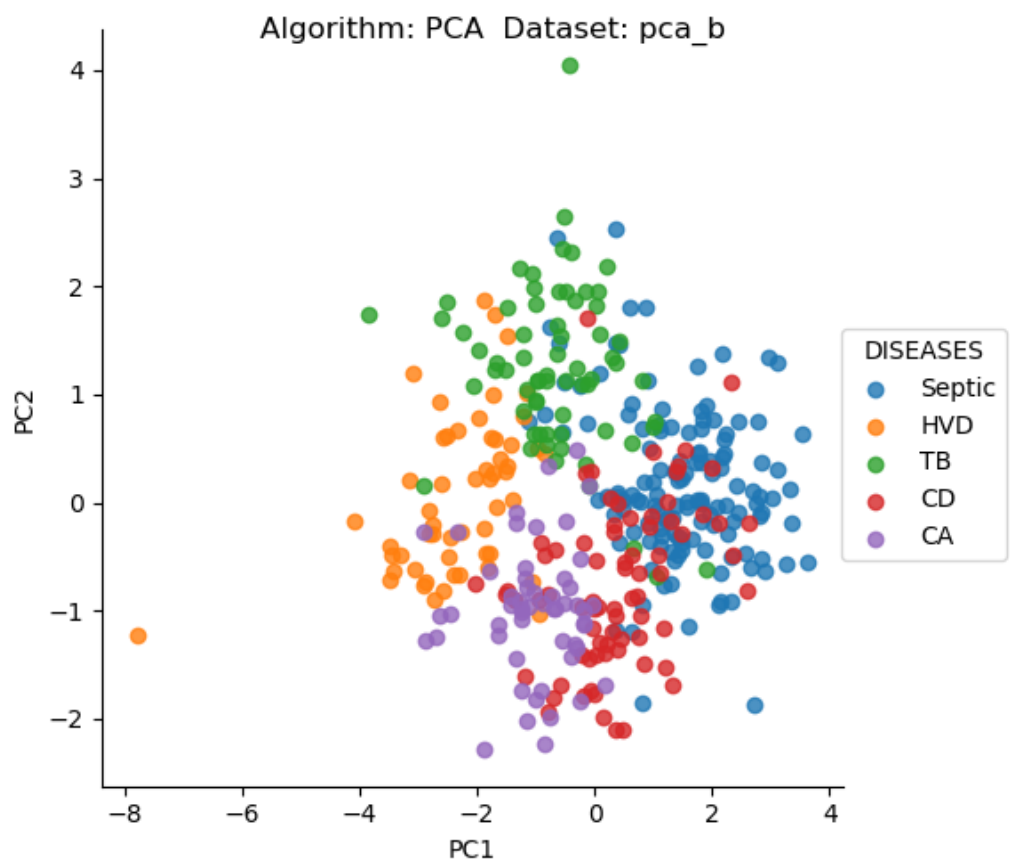
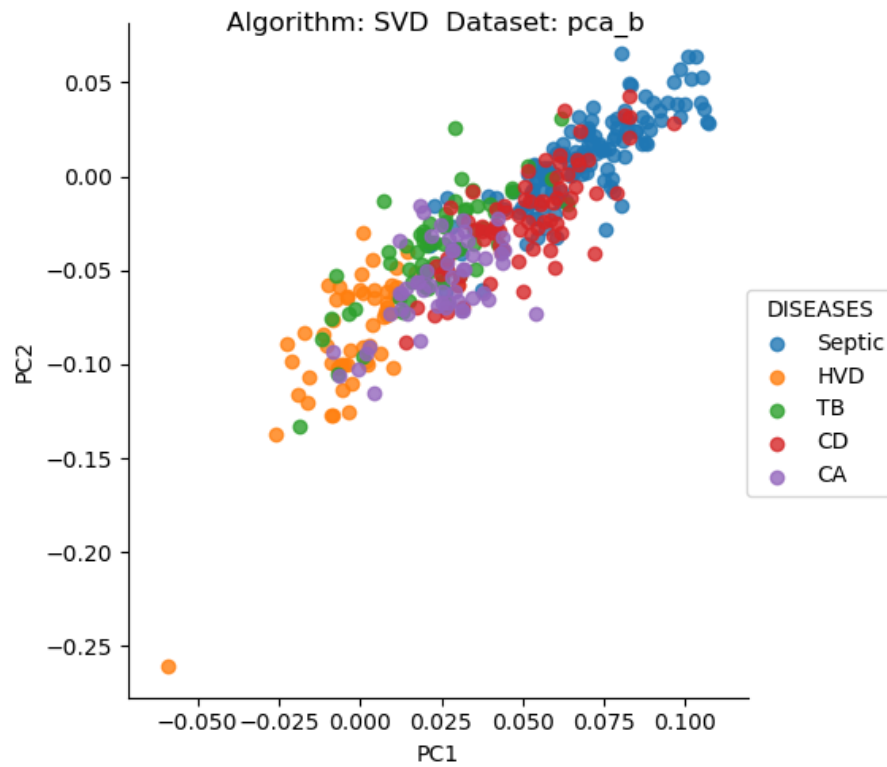
Finally, the top n principal components are found using the following method:

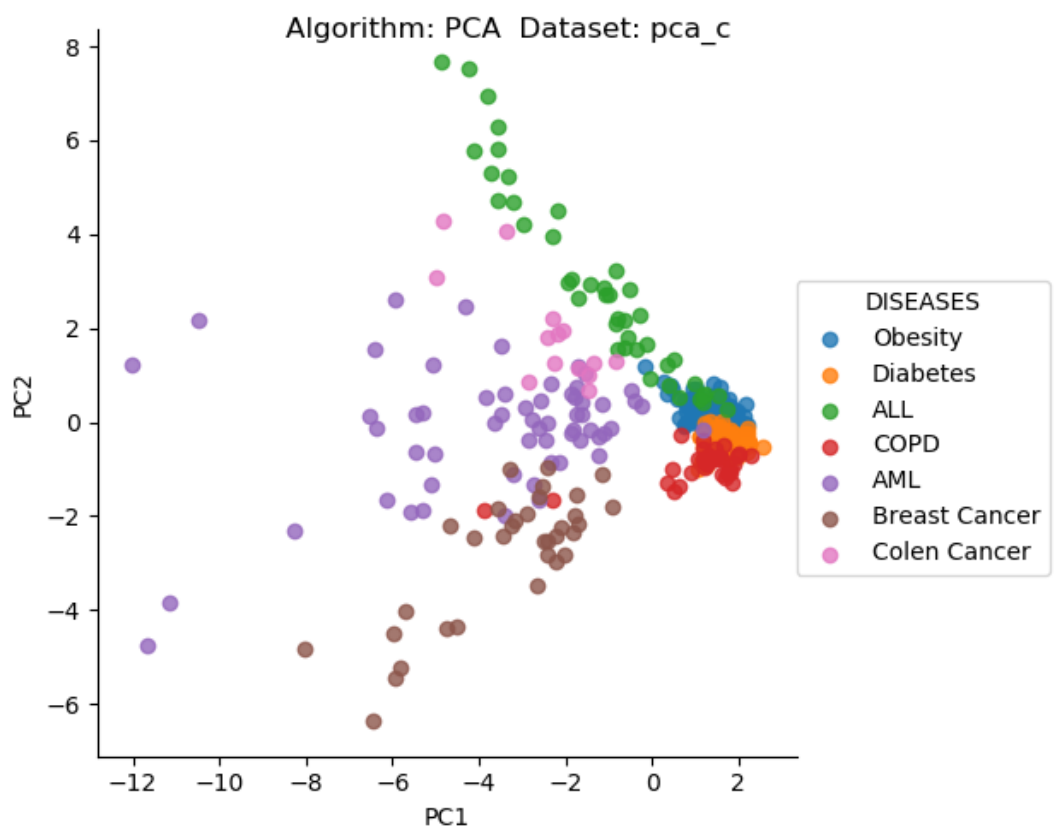
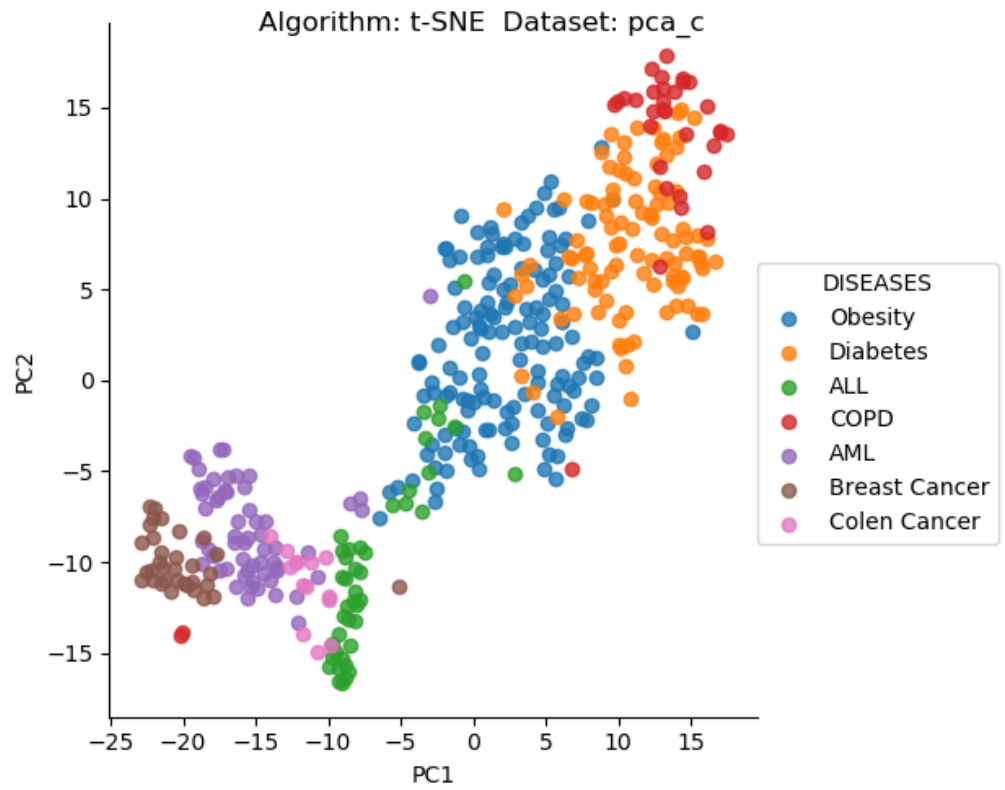
```
def topN(eigenValues, eigenVectors,n = 2):
    indices = eigenValues.argsort()[::-1][:n]
    return eigenVectors[indices[0]],eigenVectors[indices[1]]
```

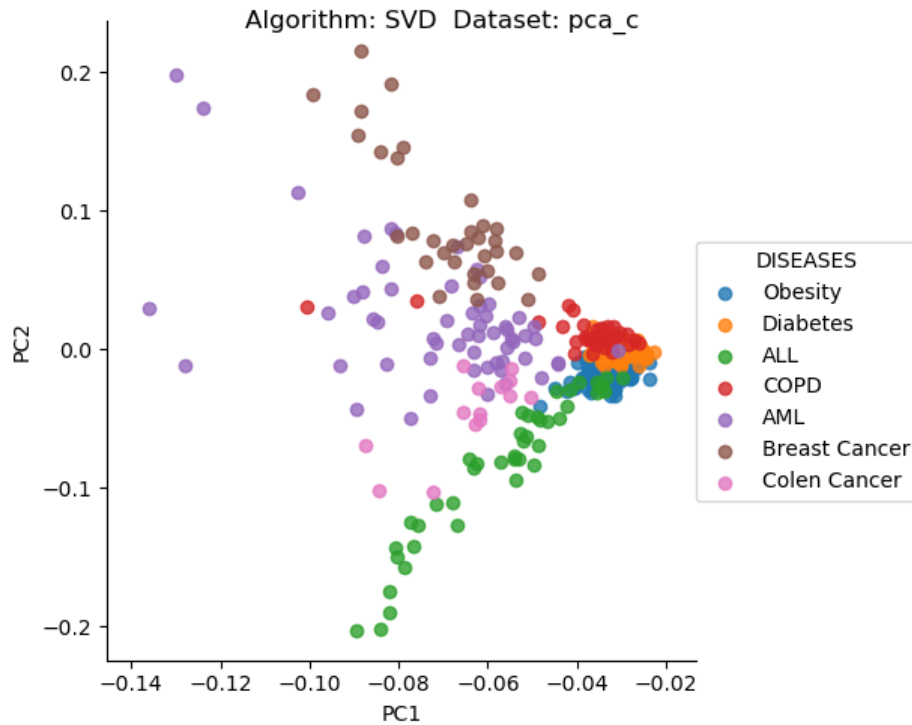
Results:











Inferences:

As it can be evidently seen, the scatter plots for PCA and SVD are much similar as both the algorithms follow a somewhat similar process for determining the principal components. PCA is just a special case of SVD where it needs the data to be normalized and hence, this justifies why the graphs for PCA and SVD are similar.

t-SNE (short for t-Distributed Stochastic Neighbor Embedding) maps the multi-dimensional data to a lower dimensional space by minimizing the divergence between two distributions: a distribution that measures pairwise similarities of the input objects and a distribution that measures pairwise similarities of the corresponding low-dimensional points in the embedding and attempts to find patterns in the data by identifying observed clusters based on similarity of data points with multiple features. When t-SNE is compared to PCA, PCA is just a linear technique for reducing the dimensions while keeping the information intact. Whereas in t-SNE, after the process, the input features are no longer identifiable, and no inference can be made based only on the output of t-SNE.