Capstone Project 1: Healthcare

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```
DESCRIPTION

Problem Statement:

ICMR wants to analyze different types of cancers, such as breast cancer, renal
cancer, colon cancer, lung cancer, and prostate cancer becoming a cause of
worry in recent years. They would like to identify the probable cause of these
cancers in terms of genes responsible for each cancer type. This would lead us
to early identification of each type of cancer reducing the fatality rate.



Dataset Details:

The input dataset contains 802 samples for the corresponding 802 people who
have been detected with different types of cancer. Each sample contains
expression values of more than 20K genes. Samples have one of the types of
tumors: BRCA, KIRC, COAD, LUAD, and PRAD.
```

```
Project Task: Week 1

Exploratory Data Analysis:

Merge both the datasets.

Plot the merged dataset as a hierarchically-clustered heatmap.

Perform Null-hypothesis testing.

Dimensionality Reduction:

Each sample has expression values for around 20K genes. However, it may not be
necessary to include all 20K genes expression values to analyze each cancer
type. Therefore, we will identify a smaller set of attributes which will then
be used to fit multiclass classification models. So, the first task targets the
dimensionality reduction using various techniques such as,
PCA, LDA, and t-SNE.

Input: Complete dataset including all genes (20531)

Output: Selected Genes from each dimensionality reduction method


Project Task: Week 2

Clustering Genes and Samples:
```

Our next goal is to identify groups of genes that behave similarly across samples and identify the distribution of samples corresponding to each cancer type. Therefore, this task focuses on applying various clustering techniques, e.g., k-means, hierarchical and mean shift clustering, on genes and samples.

First, apply the given clustering technique on all genes to identify:

Genes whose expression values are similar across all samples

Genes whose expression values are similar across samples of each cancer type

Next, apply the given clustering technique on all samples to identify:

Samples of the same class (cancer type) which also correspond to the same cluster

Samples identified to be belonging to another cluster but also to the same class (cancer type)

Building Classification Model(s) with Feature Selection:

Our final task is to build a robust classification model(s) for identifying each type of cancer. It also aims at the to do feature selection in order to identify the genes that help in classifying each cancer type.

Sub-tasks:

Build a classification model(s) using multiclass SVM, Random Forest, and Deep Neural Network to classify the input data into five cancer types

Apply the feature selection algorithms, forward selection and backward elimination to refine selected attributes (selected in Task-2) using the classification model from the previous step

Validate the genes selected from the last step using statistical significance testing (t-test for one vs. all and F-test)

In [2]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import scipy.stats

from sklearn.decomposition import PCA
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
colors = ['royalblue','red','deeppink', 'maroon', 'mediumorchid', 'tan', 'forestg
vectorizer = np.vectorize(lambda x: colors[x % len(colors)])

import warnings
warnings.filterwarnings(action='ignore',category=DeprecationWarning)
warnings.filterwarnings(action='ignore',category=FutureWarning)
```

Project Task: Week 1: Exploratory Data Analysis:

In [3]:
```
#  Load the data and labels in dataframe

data = pd.read_csv('data.csv',delimiter=',')
label = pd.read_csv('labels.csv',delimiter=',',)
```

In [4]:
```
print(type(data))
print(type(label))
```

```
<class 'pandas.core.frame.DataFrame'>
<class 'pandas.core.frame.DataFrame'>
```

In [5]:
```
print("=========================================================================")
print("The dimension of data:")
print("The data has ", data.shape[0], " rows and ", data.shape[1], "columns")

print(" ")

print("The dimension of label:")
print("The label has ", label.shape[0], " rows and ", label.shape[1], "columns")
print("=========================================================================")
```

```
=========================================================================
The dimension of data:
The data has  801  rows and  20532 columns

The dimension of label:
The label has  801  rows and  2 columns
=========================================================================
```

In [6]:
```
data.head(3) # display 3 rows of data
```

Out[6]:

	Unnamed: 0	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_
0	sample_0	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0
1	sample_1	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0
2	sample_2	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0

3 rows × 20532 columns

In [7]:
```
label.head(3) # display 3 rows of label
```

Out[7]:

	Unnamed: 0	Class
0	sample_0	PRAD
1	sample_1	LUAD
2	sample_2	PRAD

In [8]:
```
data.describe()
```

Out[8]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_
count	801.000000	801.000000	801.000000	801.000000	801.000000	801.0	801.000000	801.00000
mean	0.026642	3.010909	3.095350	6.722305	9.813612	0.0	7.405509	0.49988
std	0.136850	1.200828	1.065601	0.638819	0.506537	0.0	1.108237	0.50879
min	0.000000	0.000000	0.000000	5.009284	8.435999	0.0	3.930747	0.00000
25%	0.000000	2.299039	2.390365	6.303346	9.464466	0.0	6.676042	0.00000
50%	0.000000	3.143687	3.127006	6.655893	9.791599	0.0	7.450114	0.44307
75%	0.000000	3.883484	3.802534	7.038447	10.142324	0.0	8.121984	0.78935
max	1.482332	6.237034	6.063484	10.129528	11.355621	0.0	10.718190	2.77900

8 rows × 20531 columns

In [9]:
```
# Project Task: Week 1: Exploratory Data Analysis: Merge both the datasets based
merged_data = pd.merge(label,data)
merged_data.head(10)
```

Out[9]:

	Unnamed: 0	Class	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7
0	sample_0	PRAD	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871
1	sample_1	LUAD	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000
2	sample_2	PRAD	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595
3	sample_3	PRAD	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882
4	sample_4	BRCA	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982
5	sample_5	PRAD	0.0	3.467853	3.581918	6.620243	9.706829	0.0	7.758510	0.000000
6	sample_6	KIRC	0.0	1.224966	1.691177	6.572007	9.640511	0.0	6.754888	0.531868
7	sample_7	PRAD	0.0	2.854853	1.750478	7.226720	9.758691	0.0	5.952103	0.000000
8	sample_8	BRCA	0.0	3.992125	2.772730	6.546692	10.488252	0.0	7.690222	0.352307
9	sample_9	PRAD	0.0	3.642494	4.423558	6.849511	9.464466	0.0	7.947216	0.724214

10 rows × 20533 columns

In [10]:
```
#Unique values in the label for the target column Class
merged_data.Class.unique() # There are five unique categories or levels for the t
# breast cancer -'BRCA', renal cancer - 'KIRC', colon cancer - 'COAD', lung cance
```

Out[10]:
```
array(['PRAD', 'LUAD', 'BRCA', 'KIRC', 'COAD'], dtype=object)
```

In [11]:
```
merged_data.isnull().sum()
```

Out[11]:
```
Unnamed: 0    0
Class         0
gene_0        0
gene_1        0
gene_2        0
             ..
gene_20526    0
gene_20527    0
gene_20528    0
gene_20529    0
gene_20530    0
Length: 20533, dtype: int64
```

In [12]:
```
print(merged_data.isnull().sum()[merged_data.isnull().sum() > 0])
```

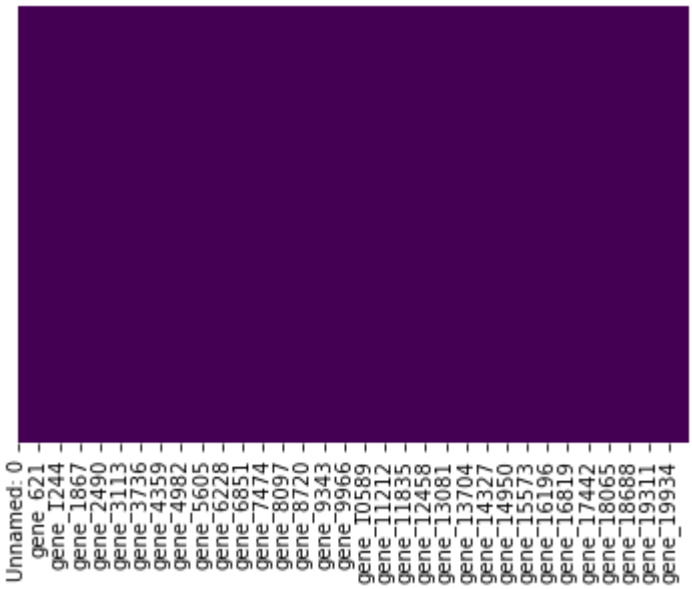
```
Series([], dtype: int64)
```

In [13]:
```
#display the list of column names with nans: There are no columns with nans
[features for features in merged_data.columns if merged_data[features].isnull().s
```

Out[13]:
```
[]
```

In [14]:
```
sns.heatmap(merged_data.isnull(),yticklabels=False,cbar=False,cmap='viridis') # H
```

Out[14]:
```
<AxesSubplot:>
```



In [15]:
```
# Describe the quantitative variables in the data frame
merged_data.describe()
```

Out[15]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_
count	801.000000	801.000000	801.000000	801.000000	801.000000	801.0	801.000000	801.00000
mean	0.026642	3.010909	3.095350	6.722305	9.813612	0.0	7.405509	0.49988
std	0.136850	1.200828	1.065601	0.638819	0.506537	0.0	1.108237	0.50879
min	0.000000	0.000000	0.000000	5.009284	8.435999	0.0	3.930747	0.00000
25%	0.000000	2.299039	2.390365	6.303346	9.464466	0.0	6.676042	0.00000
50%	0.000000	3.143687	3.127006	6.655893	9.791599	0.0	7.450114	0.44307
75%	0.000000	3.883484	3.802534	7.038447	10.142324	0.0	8.121984	0.78935
max	1.482332	6.237034	6.063484	10.129528	11.355621	0.0	10.718190	2.77900

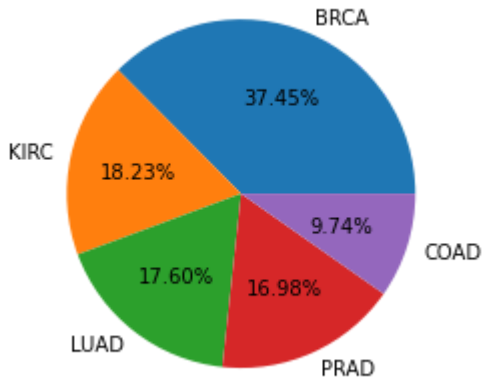
8 rows × 20531 columns

In [16]:
```
#Count of the items for the categrical variable Class
merged_data.Class.value_counts() # index is Class and values are the counts
```

Out[16]:
```
BRCA    300
KIRC    146
LUAD    141
PRAD    136
COAD     78
Name: Class, dtype: int64
```

In [17]:
```
class_values = merged_data.Class.value_counts().values
class_index = merged_data.Class.value_counts().index
plt.pie(class_values[:5],labels=class_index[:5],autopct='%1.2f%%')
# There are five unique categories or levels for the target feature "Class"
# breast cancer -'BRCA', renal cancer - 'KIRC', colon cancer - 'COAD', lung cance
# Majority of the data are from BRCA patients, andeee1wt4fr3d  the least represer
# The other three categoriesrepresented nearly 17%-18% of the data
```

Out[17]:
```
([<matplotlib.patches.Wedge at 0x1cba5e741c0>,
  <matplotlib.patches.Wedge at 0x1cba5e74820>,
  <matplotlib.patches.Wedge at 0x1cba5e74e20>,
  <matplotlib.patches.Wedge at 0x1cba5e8a460>,
  <matplotlib.patches.Wedge at 0x1cba5e8aa60>],
 [Text(0.42244602842489287, 1.0156472581895915, 'BRCA'),
  Text(-1.0745060009455198, 0.23545032157987564, 'KIRC'),
  Text(-0.6751858801228837, -0.8684031479000334, 'LUAD'),
  Text(0.45410058834857936, -1.001894533202709, 'PRAD'),
  Text(1.0489263693942839, -0.3312906150033935, 'COAD')],
 [Text(0.2304251064135779, 0.5539894135579589, '37.45%'),
  Text(-0.5860941823339199, 0.12842744813447762, '18.23%'),
  Text(-0.3682832073397547, -0.47367444430910904, '17.60%'),
  Text(0.247691230008316, -0.5464879272014775, '16.98%'),
  Text(0.5721416560332456, -0.1807039718200328, '9.74%')])
```



In [18]:
```
#Project Task: Week 1: Exploratory Data Analysis: Plot the merged dataset as a hi

heatmap_data = pd.pivot_table(merged_data, index=['Class'])

heatmap_data.head()
```

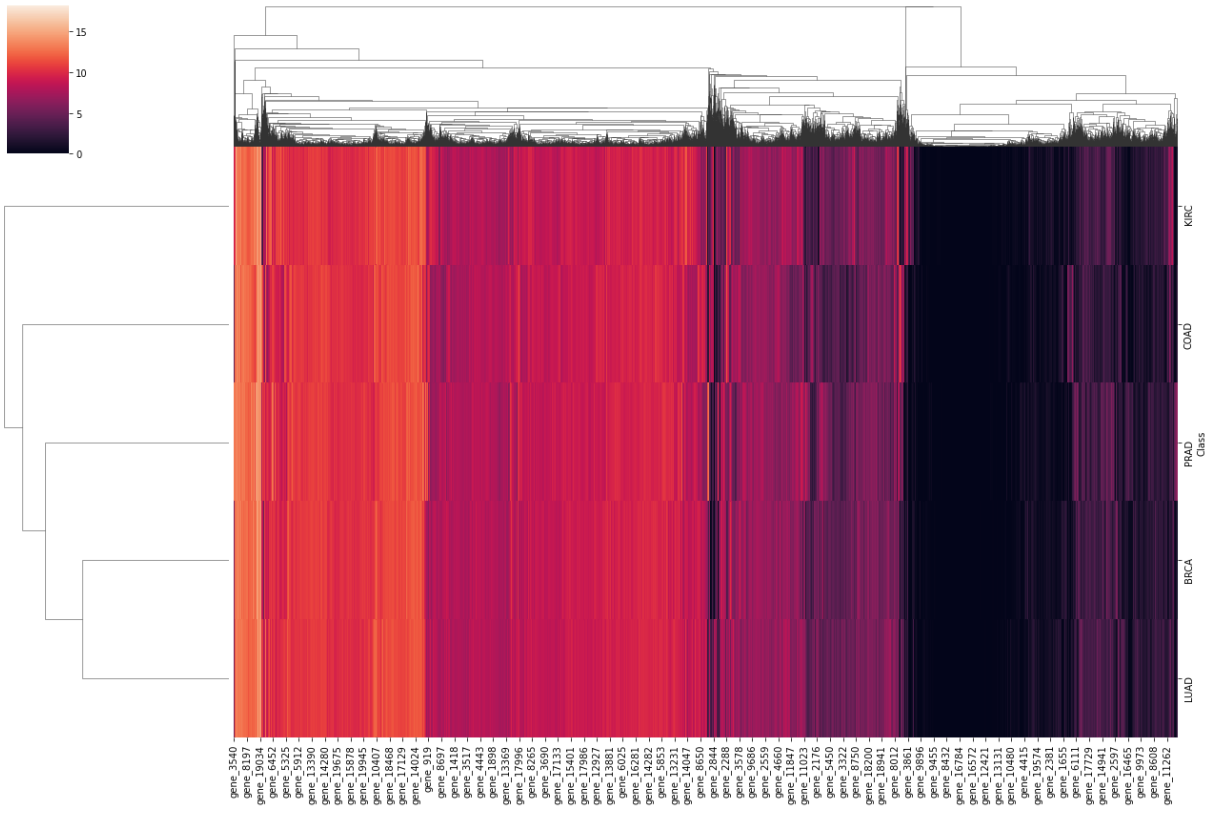
Out[18]:

Class	gene_0	gene_1	gene_10	gene_100	gene_1000	gene_10000	gene_10001	gene_10002
BRCA	0.011362	2.839739	0.544066	10.681488	10.303568	3.258028	7.339461	7.900497
COAD	0.022212	3.438381	0.357278	11.015745	9.951124	3.462039	5.526673	7.487396
KIRC	0.046544	2.398129	1.166824	10.238999	11.148094	1.651798	6.895752	7.686932
LUAD	0.041088	3.358260	0.607541	10.517670	10.503698	3.754181	7.281878	7.041924
PRAD	0.026544	3.441041	0.765608	10.282936	9.967433	1.949878	7.946141	8.529695

5 rows × 20531 columns

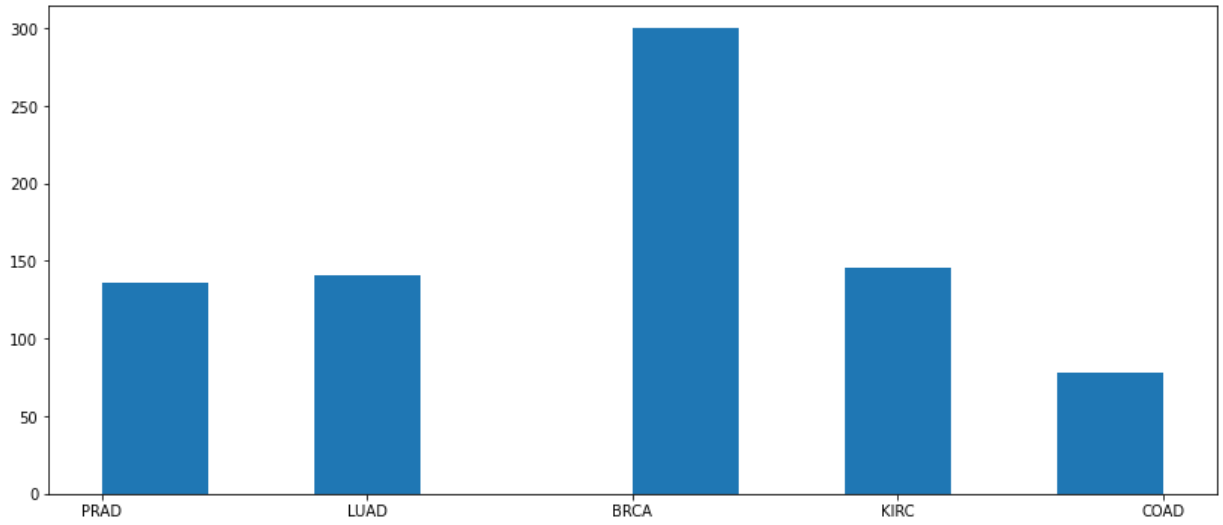
In [19]:
```
sns.clustermap(heatmap_data, figsize=(18,12))
plt.savefig('Hierarchically-clustered_heatmap_with_Seaborn.jpg',dpi=150)
```

```
C:\Users\Byju\Anaconda3\lib\site-packages\seaborn\matrix.py:649: UserWarning: C
lustering large matrix with scipy. Installing `fastcluster` may give better per
formance.
  warnings.warn(msg)
```



In [20]:
```
#Project Task: Week 1: Exploratory Data Analysis: Perform Null-hypothesis testing
# We will do the F-test for ANOVA.

df_f_test=merged_data
```

In [21]:
```
# Use histogram plot to check if the data is normally distributed
plt.figure(figsize=(14,6))
plt.hist(merged_data['Class'])
plt.show()
```



In [22]:
```
# The df loaded from csv have an unwanted index column named unnamed:0. Handle th
non_cat_data = merged_data.drop(['Unnamed: 0'], axis=1)
non_cat_data
```

Out[22]:

	Class	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_8
0	PRAD	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0.0
1	LUAD	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0.0
2	PRAD	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0.0
3	PRAD	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882	0.0
4	BRCA	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982	0.0
...	...	...	...	...	...	...	...	...	...	...
796	BRCA	0.0	1.865642	2.718197	7.350099	10.006003	0.0	6.764792	0.496922	0.0
797	LUAD	0.0	3.942955	4.453807	6.346597	10.056868	0.0	7.320331	0.000000	0.0
798	COAD	0.0	3.249582	3.707492	8.185901	9.504082	0.0	7.536589	1.811101	0.0
799	PRAD	0.0	2.590339	2.787976	7.318624	9.987136	0.0	9.213464	0.000000	0.0
800	PRAD	0.0	2.325242	3.805932	6.530246	9.560367	0.0	7.957027	0.000000	0.0

801 rows × 20532 columns

```
# Null Hypothesis: The mean['PRAD'] =  mean['LUAD'] = mean['BRCA'] =
mean['KIRC'] = mean['COAD']
# Alternate Hypothesis: The means for different categories or level of the
variable "Class" are not the same.
```

In [23]:
```
def f_test(df_f_test,gene):
    df_anova = df_f_test[[gene,'Class']]
    grps = pd.unique(df_anova.Class.values)
    grps
    d_data = {grp:df_anova[gene][df_anova.Class == grp] for grp in grps}
    F, p = scipy.stats.f_oneway(d_data['LUAD'], d_data['PRAD'], d_data['BRCA'], d
    print("F_statistics:-",F)
    print("p_values:-",p)
    if p<0.05:
        print("reject null hypothesis")
    else:
        print("accept null hypothesis")

    return
```

In [24]:
```
f_test(df_f_test,"gene_0")
```

```
F_statistics:- 2.1322967854919392
p_values:- 0.07505540778266195
accept null hypothesis
```

In [25]:
```
f_test(df_f_test,"gene_1000")
```

```
F_statistics:- 180.0931919092308
p_values:- 7.612856287347603e-110
reject null hypothesis
```

In [26]:
```
f_test(df_f_test,"gene_1000")
```

```
F_statistics:- 180.0931919092308
p_values:- 7.612856287347603e-110
reject null hypothesis
```

In [27]:
```
f_test(df_f_test,"gene_20000")
```

```
F_statistics:- 17.31965303056122
p_values:- 1.23614927542531e-13
reject null hypothesis
```

In [28]:
```
f_test(df_f_test,"gene_20530")
```

```
F_statistics:- 4.581248855684393
p_values:- 0.0011587473461475769
reject null hypothesis
```

In [29]:
```
f_test(df_f_test,"gene_5")
```

```
F_statistics:- nan
p_values:- nan
accept null hypothesis

C:\Users\Byju\Anaconda3\lib\site-packages\scipy\stats\stats.py:3709: F_onewayCo
nstantInputWarning: Each of the input arrays is constant;the F statistic is not
defined or infinite
  warnings.warn(F_onewayConstantInputWarning())
```

In [30]:
```
f_test(df_f_test,"gene_8")
```

```
F_statistics:- 0.7062282419800234
p_values:- 0.5877913885898287
accept null hypothesis
```

In [31]:
```
df_catmapped = merged_data
df_catmapped['Class'] = df_catmapped['Class'].map({'PRAD': 1, 'LUAD': 2, 'BRCA':
df_catmapped = df_catmapped.drop(['Unnamed: 0'],axis=1)
```

```
Shapiro test
The null hypothesis for the Shapiro-Wilk test is that a variable is normally
distributed (i.e., simple random sample from a normal distribution) in some
population.
As a rule of thumb, we reject the null hypothesis if p < 0.05
```

In [32]:
```
#Shapiro test
from scipy.stats import shapiro
stat, p = shapiro(df_catmapped)
print('stat=%.2f, p=%.30f' %(stat, p))

if p > 0.05:
    print('Normal Distribution')
else:
    print('Not Normal')
```

```
stat=0.92, p=0.000000000000000000000000000000
Not Normal

C:\Users\Byju\Anaconda3\lib\site-packages\scipy\stats\morestats.py:1681: UserWa
rning: p-value may not be accurate for N > 5000.
  warnings.warn("p-value may not be accurate for N > 5000.")
```

```
k2test - In statistics, D'Agostino's K2 test, named for Ralph D'Agostino, is a
goodness-of-fit measure of departure from normality, that is the test aims to
establish whether or not the given sample comes from a normally distributed
population
```

In [33]:
```
# K2 normality test
from scipy.stats import normaltest
k2_test = df_catmapped['Class']

stat, p = normaltest(k2_test)
print('stat=%.2f, p=%.30f' %(stat, p))

if p > 0.05:
    print('Normal Distribution')
else:
    print('Not Normal')
```

```
stat=48.54, p=0.000000000028833417148493984116
Not Normal
```

```
Project Task: Week 2: Dimensionality Reduction:

Each sample has expression values for around 20K genes. However, it may not be
necessary to include all 20K genes expression values to analyze each cancer
type. Therefore, we will identify a smaller set of attributes which will then
be used to fit multiclass classification models. So, the first task targets the
dimensionality reduction using various techniques such as, PCA, LDA, and t-SNE.

Input: Complete dataset including all genes (20531)
Output: Selected Genes from each dimensionality reduction method
```

```
Principal Component Analysis (PCA): It seeks a projection that preserves as
much information as possible in the data.
Linear Discriminant Analysis (LDA):- It seeks a projection that best
discriminates the data.
```

Week 2: Dimensionality Reduction using PCA

In [34]:
```
# Define data

# The df loaded from csv have an unwanted index column named unnamed:0. Handle th
df_pca = merged_data.drop(['Unnamed: 0'], axis=1)

# Also drop the categorical target variable Class
df_pca = df_pca.drop(['Class'], axis=1)
df_pca.head()
```

Out[34]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_8	gene_9
0	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0.0	0.0
1	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0.0	0.0
2	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0.0	0.0
3	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882	0.0	0.0
4	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982	0.0	0.0

5 rows × 20531 columns

In [35]:
```
df_pca.values.shape
```

Out[35]:
```
(801, 20531)
```

In [36]:
```
x_pca = df_pca.values
```

Week2: Scaling the data using standard scaler method

In [37]:
```
from sklearn.preprocessing import StandardScaler
stdscaler = StandardScaler()
X_Scaled = stdscaler.fit_transform(x_pca)
X_Scaled
```

Out[37]:
```
array([[-0.19479935, -0.82802988,  0.15980044, ..., -1.18793812,
        -0.11648251, -0.26190144],
       [-0.19479935, -2.01501735, -1.415042  , ..., -0.34227662,
        -1.65688871, -0.26190144],
       [-0.19479935,  0.41734754,  1.15673547, ...,  0.88686027,
        -1.85526414, -0.26190144],
       ...,
       [-0.19479935,  0.19888076,  0.57481583, ..., -0.22008186,
        -0.41046699,  1.3485582 ],
       [-0.19479935, -0.35045311, -0.28863152, ...,  1.43719268,
         0.09195083, -0.26190144],
       [-0.19479935, -0.57135218,  0.66725377, ...,  0.45087581,
        -0.47161901, -0.26190144]])
```

Week2: Perform PCA with n_components=2

In [38]:
```
# Import PCA from sklearn and define the n_components as 2
from sklearn.decomposition import PCA
pca_cancer = PCA(n_components=2)
```

In [39]:
```
#Perform fit transform on the scaled data
X_pca_twoPC = pca_cancer.fit_transform(X_Scaled)
X_pca_twoPC.shape
```

Out[39]:
```
(801, 2)
```

In [40]:
```
X_pca_twoPC
```

Out[40]:
```
array([[-57.44698695,  95.41098075],
       [-16.91943004,   0.73247011],
       [-70.3452179 , -19.30332634],
       ...,
       [ -4.1330897 ,  15.6900136 ],
       [-30.81475746,  33.52642261],
       [-22.34455669,   4.05235641]])
```

In [41]:
```
print('Explained variation per principal component: {}'.format(pca_cancer.explair
```

```
Explained variation per principal component: [0.10539781 0.08754232]
```

The above output suggest that the principal component 1 holds 10.5% of the information while the principal component 2 holds 8.75% of the information.

In [42]:
```
# Put the data back on the 2 columns defined
df_pca = pd.DataFrame(X_pca_twoPC)
df_pca.columns = ['pca1','pca2']

# Add the convereted categorical data for
df_pca['cancer_class']=df_catmapped['Class']
df_pca
```

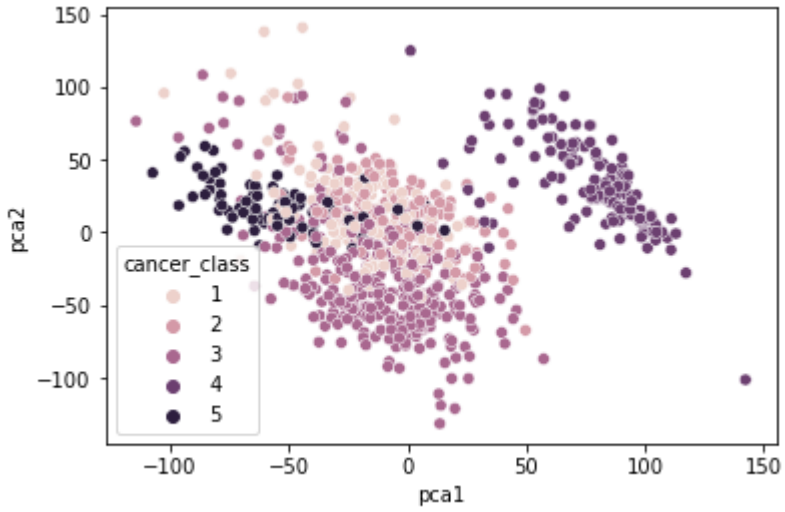
Out[42]:

	pca1	pca2	cancer_class
0	-57.446987	95.410981	1
1	-16.919430	0.732470	2
2	-70.345218	-19.303326	1
3	-49.161591	-9.227586	1
4	-18.132534	-51.327797	3
...	...	...	...
796	-12.417385	-42.321574	3
797	-29.415554	28.526281	2
798	-4.133090	15.690014	5
799	-30.814757	33.526423	1
800	-22.344557	4.052356	1

801 rows × 3 columns

In [43]:
```
# Use seaborn maps to plot the data on the 5 clusters
sns.scatterplot(x='pca1',y='pca2', hue = 'cancer_class',data=df_pca)
```

Out[43]: <AxesSubplot:xlabel='pca1', ylabel='pca2'>



Week2: PCA with n_components=.995

In [44]:
```
pca_99point5 = PCA(.995)
X_pca_99point5 = pca_99point5.fit_transform(x_pca)
X_pca_99point5.shape
```

Out[44]:
```
(801, 747)
```

In [45]:
```
X_pca_99point5
```

Out[45]:
```
array([[-6.27554152e+01, -9.40719735e+01,  8.95198311e+01, ...,
         3.09258084e+00,  7.13597730e-01, -8.21221710e-02],
       [-2.43289636e+00,  9.05858418e+01, -1.06730787e+00, ...,
         1.39674724e-02, -3.95175744e-01, -9.49947250e-01],
       [-7.12668528e+01, -8.06460774e+00,  6.61124549e+01, ...,
         1.28898532e-01, -2.64530262e-01,  3.84594189e-01],
       ...,
       [ 1.04862615e+01,  2.15705946e+01,  4.13458784e+01, ...,
        -6.47882986e-01, -2.07256774e-01,  1.38942922e-01],
       [-5.50636049e+01, -9.23947780e+01,  8.00500394e+01, ...,
         1.74673062e+00,  2.02232239e+00, -1.92708948e+00],
       [-4.91030338e+01, -5.09976391e+01,  4.05037544e+01, ...,
         1.80367340e+00,  2.22994027e+00, -8.07255452e-01]])
```

In [46]:
```
print('Explained variation per principal component: {}'.format(pca_99point5.expla
```

```
Explained variation per principal component: [1.58385502e-01 1.05039600e-01
9.47222083e-02 6.50080336e-02
 3.61561783e-02 2.97266705e-02 2.65714239e-02 1.56273075e-02
 1.40707327e-02 1.22687325e-02 9.60110033e-03 8.90219244e-03
 7.58205527e-03 7.23021295e-03 6.64002139e-03 6.37713380e-03
 5.69484775e-03 5.17577102e-03 4.62121409e-03 4.45511704e-03
 4.43458295e-03 4.06433767e-03 3.95469831e-03 3.73193404e-03
 3.68555898e-03 3.55682493e-03 3.48486339e-03 3.16722678e-03
 3.10381215e-03 2.95236028e-03 2.89217028e-03 2.76294055e-03
 2.73106816e-03 2.62048411e-03 2.51405018e-03 2.51115763e-03
 2.40637037e-03 2.35678917e-03 2.32169987e-03 2.25441828e-03
 2.22014731e-03 2.17486887e-03 2.12139803e-03 2.10345082e-03
 2.08597543e-03 2.04290041e-03 1.96472299e-03 1.95728543e-03
 1.93418289e-03 1.89133509e-03 1.81771843e-03 1.78520804e-03
 1.75768926e-03 1.72698808e-03 1.70410487e-03 1.67957902e-03
 1.64251866e-03 1.62876591e-03 1.61259105e-03 1.57999194e-03
 1.57141842e-03 1.55484061e-03 1.54252341e-03 1.51270505e-03
 1.48299684e-03 1.47660342e-03 1.45686263e-03 1.43049748e-03
 1.39928385e-03 1.38588278e-03 1.37362530e-03 1.36753069e-03
```

In [47]:
```
# 747 principal components were needed to explain 99.5% variance in the data
len(pca_99point5.explained_variance_ratio_)
```

Out[47]:
```
747
```

In [48]:
```
# Put the data back on the x columns
df_pca_995 = pd.DataFrame(X_pca_99point5)


# Add the convereted categorical data to the above dataframe
df_pca_995['cancer_class']=df_catmapped['Class']
df_pca_995
```

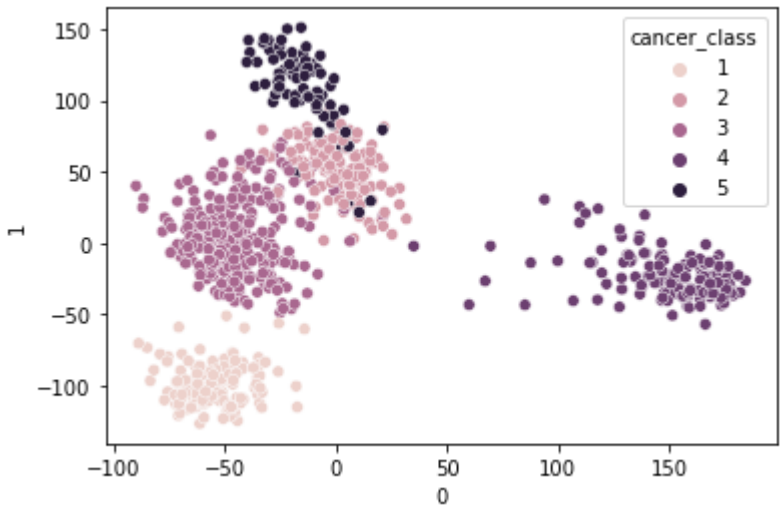
Out[48]:

	0	1	2	3	4	5	6	7
0	-62.755415	-94.071973	89.519831	-15.942567	81.423539	-13.998292	7.716073	-22.936551
1	-2.432896	90.585842	-1.067308	-53.083120	-15.676684	60.842472	10.257369	-48.822959
2	-71.266853	-8.064608	66.112455	81.381475	-7.525685	109.824273	5.519407	-13.364480
3	-84.770785	-73.244566	74.181000	27.022697	-18.044895	50.116433	-3.495197	-11.318520
4	-69.560171	-9.612940	-67.497549	34.868543	-1.795849	-6.676780	-2.840781	16.780157
...	...	...	...	...	...	...	...	...
796	-60.861882	-22.278633	-80.927167	42.670292	7.843763	-4.545218	-27.602910	-8.840676
797	-14.465433	53.392194	38.153904	-63.217345	22.799082	39.543441	-47.899401	39.925172
798	10.486261	21.570595	41.345878	-59.639929	-2.163066	-96.453878	38.375897	46.997294
799	-55.063605	-92.394778	80.050039	-7.782015	15.180574	2.563620	8.487660	10.571657
800	-49.103034	-50.997639	40.503754	-31.495505	-10.361908	-1.272555	9.185948	-31.629661

801 rows × 748 columns

In [49]:
```
# Use seaborn maps to plot the data on the 5 clusters
sns.scatterplot(x = 0,y = 1, hue = 'cancer_class',data = df_pca_995)
```

Out[49]: <AxesSubplot:xlabel='0', ylabel='1'>



Week2: Dimensionality reduction using t-SNE

PCA is great, but it does have some drawbacks. One of the major drawbacks of PCA is that it does not retain non-linear variance. This means PCA will not be able to get results for figures like Trefoil Knot.In simple terms, PCA works on retaining only global variance, and thus retaining local variance was the motivation behind t-SNE.

The t-SNE (t-distributed Stochastic Neighbor Embedding) is a nonlinear dimensionality reduction technique to visualize high-dimensional data (t-SNE is well suited for embedding high dimension data into lower dimensional data (2D or 3D) for data visualization). T-SNE converts similarities between data points to joint probabilities and tries to minimize the Kullback-Leibler divergence between the joint probabilities of the low-dimensional embedding and the high-dimensional data. t-SNE has a cost function that is not convex, i.e. with different initializations we can get different results. Lower perplexity values might result in fewer clusters. It is hence recommended to try various perplexity values ranging from 2 to the number of data points to obtain better results.

How does t-SNE work?
Step 1: t-SNE constructs a probability distribution on pairs in higher dimensions such that similar objects are assigned a higher probability and dissimilar objects are assigned lower probability.

Step 2: Then, t-SNE replicates the same probability distribution on lower dimensions iteratively till the Kullback-Leibler divergence is minimized.

Kullback-Leibler divergence is a measure of the difference between the probability distributions from Step1 and Step2. KL divergence is mathematically given as the expected value of the logarithm of the difference of these probability distributions.

In [50]:
```
merged_df_tsne = merged_data
non_numeric = ['Unnamed: 0','Class']
merged_df_tsne = merged_df_tsne.drop(non_numeric, axis=1)
merged_df_tsne
```

Out[50]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_8	gene_
0	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0.0	0.
1	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0.0	0.
2	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0.0	0.
3	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882	0.0	0.
4	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982	0.0	0.
...	...	...	...	...	...	...	...	...	...	.
796	0.0	1.865642	2.718197	7.350099	10.006003	0.0	6.764792	0.496922	0.0	0.
797	0.0	3.942955	4.453807	6.346597	10.056868	0.0	7.320331	0.000000	0.0	0.
798	0.0	3.249582	3.707492	8.185901	9.504082	0.0	7.536589	1.811101	0.0	0.
799	0.0	2.590339	2.787976	7.318624	9.987136	0.0	9.213464	0.000000	0.0	0.
800	0.0	2.325242	3.805932	6.530246	9.560367	0.0	7.957027	0.000000	0.0	0.

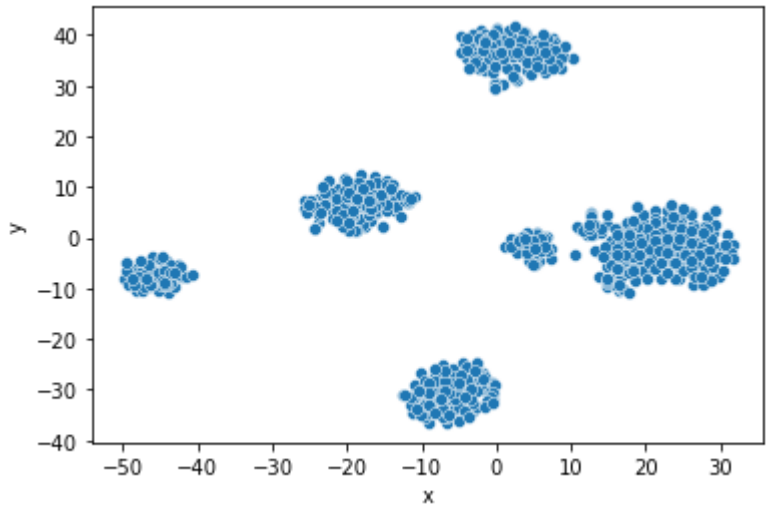
801 rows × 20531 columns

In [51]:
```
#import T-SNE library from sklearn
from sklearn.manifold import TSNE
tsne_model = TSNE(learning_rate=50)
```

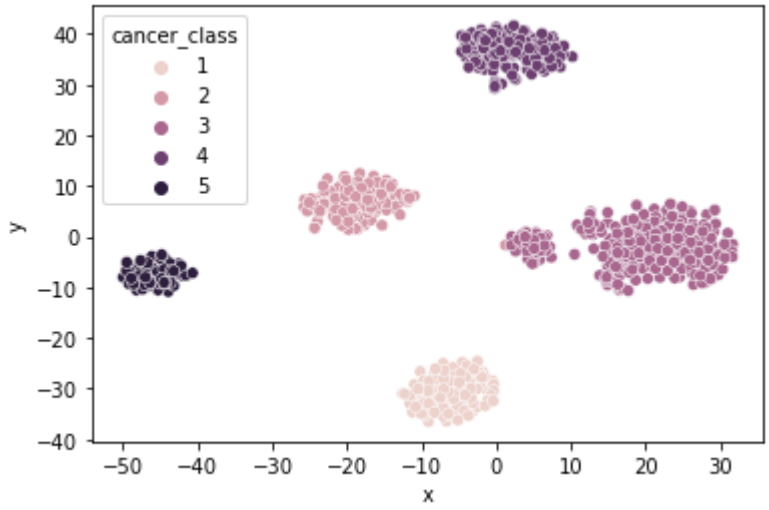
In [52]:
```
tnse_features = tsne_model.fit_transform(merged_df_tsne)
tnse_features[1:4,:]
```

Out[52]:
```
array([[-13.69347 ,   5.532149],
       [ -6.690077, -36.395447],
       [ -6.537254, -35.288013]], dtype=float32)
```

In [53]:
```
merged_df_tsne['x'] = tnse_features[:,0]
merged_df_tsne['y'] = tnse_features[:,1]

import seaborn as sns
g = sns.scatterplot(x='x',y='y', data=merged_df_tsne)
plt.show()
```



In [54]:
```
merged_df_tsne['cancer_class']=df_catmapped['Class']
sns.scatterplot(x='x',y='y',hue = 'cancer_class', data=merged_df_tsne)
plt.show()
```



Week2: Dimensionality reduction using LDA

```
Linear Discriminant Analysis (LDA), is a ML algorithm for multi-class
classification.
Used as a dimensionality reduction technique, LDA provides a projection of a
training
dataset that best separates the data points by their assigned class.
```

In [55]:
```
merged_df_lda = merged_data.drop(['Unnamed: 0'], axis=1)
merged_df_lda = merged_df_lda.drop(['Class'], axis=1)
x_lda = merged_df_lda
x_lda
```

Out[55]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_8	gene_
0	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0.0	0.
1	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0.0	0.
2	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0.0	0.
3	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882	0.0	0.
4	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982	0.0	0.
...	...	...	...	...	...	...	...	...	...	.
796	0.0	1.865642	2.718197	7.350099	10.006003	0.0	6.764792	0.496922	0.0	0.
797	0.0	3.942955	4.453807	6.346597	10.056868	0.0	7.320331	0.000000	0.0	0.
798	0.0	3.249582	3.707492	8.185901	9.504082	0.0	7.536589	1.811101	0.0	0.
799	0.0	2.590339	2.787976	7.318624	9.987136	0.0	9.213464	0.000000	0.0	0.
800	0.0	2.325242	3.805932	6.530246	9.560367	0.0	7.957027	0.000000	0.0	0.

801 rows × 20531 columns

In [56]:
```
x_lda.shape
```

Out[56]:
```
(801, 20531)
```

In [57]:
```
y_lda = merged_data['Class']
y_lda.values
```

Out[57]:
```
array([1, 2, 1, 1, 3, 1, 4, 1, 3, 1, 3, 4, 1, 3, 3, 3, 2, 4, 4, 1, 3, 4,
       2, 3, 4, 2, 5, 3, 3, 3, 3, 3, 4, 3, 1, 3, 4, 2, 3, 3, 4, 1, 1, 4,
       4, 3, 1, 5, 3, 2, 3, 2, 3, 1, 5, 3, 3, 5, 4, 3, 2, 4, 3, 2, 1, 5,
       3, 1, 4, 3, 4, 3, 3, 2, 3, 2, 3, 4, 1, 5, 3, 1, 3, 3, 1, 1, 3, 3,
       4, 3, 1, 1, 3, 3, 3, 1, 5, 3, 1, 3, 3, 4, 3, 4, 2, 4, 2, 5, 2, 2,
       1, 3, 2, 1, 3, 4, 4, 4, 3, 3, 2, 4, 2, 3, 1, 1, 1, 3, 4, 2, 5, 3,
       5, 3, 3, 4, 2, 3, 4, 5, 3, 1, 3, 4, 2, 5, 1, 3, 2, 2, 2, 2, 3, 3,
       2, 3, 3, 1, 1, 2, 1, 2, 4, 3, 1, 2, 5, 4, 2, 3, 4, 2, 3, 2, 3, 3,
       3, 1, 3, 4, 5, 4, 3, 1, 1, 1, 2, 2, 3, 2, 2, 4, 2, 1, 2, 3, 3, 3,
       2, 2, 3, 4, 4, 4, 4, 1, 3, 1, 3, 2, 2, 3, 1, 3, 1, 3, 3, 3, 2, 3,
       4, 2, 4, 4, 2, 3, 4, 1, 3, 2, 2, 1, 5, 3, 4, 1, 4, 5, 3, 4, 4, 2,
       1, 1, 2, 2, 4, 3, 3, 5, 3, 1, 5, 3, 1, 4, 1, 1, 1, 3, 5, 5, 2, 5,
       5, 1, 2, 3, 3, 4, 4, 3, 5, 1, 4, 1, 3, 3, 4, 3, 3, 3, 3, 2, 2, 3,
       3, 3, 4, 4, 4, 4, 3, 3, 3, 4, 3, 3, 2, 1, 3, 3, 5, 2, 1, 3, 3, 3,
       5, 3, 1, 3, 5, 2, 2, 1, 4, 3, 4, 4, 2, 5, 4, 3, 3, 3, 3, 4, 3, 3,
       1, 3, 4, 3, 2, 1, 4, 3, 1, 5, 3, 3, 3, 2, 2, 2, 3, 3, 1, 2, 3, 4,
       3, 5, 5, 2, 3, 4, 3, 3, 3, 5, 2, 5, 4, 1, 4, 3, 3, 4, 3, 5, 1, 2,
       1, 3, 4, 1, 3, 5, 4, 4, 5, 5, 1, 3, 3, 5, 4, 3, 1, 3, 3, 3, 2, 2,
       4, 2, 3, 4, 5, 1, 3, 2, 1, 3, 3, 3, 2, 3, 3, 1, 3, 1, 5, 3, 2, 3,
       3, 2, 3, 3, 3, 4, 2, 1, 3, 1, 4, 3, 4, 5, 3, 1, 2, 4, 3, 3, 4, 3,
       2, 3, 3, 1, 5, 3, 4, 2, 1, 3, 1, 3, 3, 3, 3, 4, 2, 3, 4, 3, 3, 2,
       2, 4, 5, 1, 5, 3, 4, 4, 3, 1, 4, 5, 2, 2, 3, 1, 1, 3, 1, 2, 4, 1,
       3, 2, 1, 2, 3, 3, 5, 2, 4, 5, 2, 3, 1, 3, 3, 1, 3, 5, 3, 5, 4, 3,
       3, 2, 2, 2, 5, 4, 2, 2, 3, 3, 4, 1, 2, 1, 3, 4, 3, 4, 4, 1, 1, 2,
       3, 4, 5, 5, 3, 4, 4, 3, 3, 1, 4, 5, 3, 3, 5, 2, 3, 3, 3, 4, 1, 2,
       2, 3, 4, 5, 4, 4, 3, 1, 2, 4, 3, 5, 2, 2, 2, 1, 2, 4, 3, 3, 5, 1,
       3, 3, 3, 4, 2, 2, 3, 1, 2, 2, 3, 4, 1, 5, 2, 1, 5, 2, 5, 4, 4, 3,
       3, 4, 4, 5, 3, 2, 1, 1, 4, 3, 2, 3, 3, 5, 3, 1, 1, 3, 3, 5, 3, 4,
       3, 3, 5, 3, 1, 3, 3, 4, 1, 2, 3, 3, 4, 3, 3, 3, 3, 3, 5, 2, 2, 3,
       3, 3, 1, 3, 3, 4, 2, 2, 4, 4, 2, 4, 5, 3, 5, 4, 3, 3, 1, 1, 1, 2,
       1, 1, 5, 3, 3, 5, 2, 4, 3, 4, 5, 3, 3, 3, 1, 2, 4, 3, 1, 4, 1, 3,
       2, 4, 1, 2, 1, 1, 3, 4, 1, 2, 5, 5, 3, 3, 3, 2, 4, 4, 4, 3, 2, 4,
       1, 3, 2, 1, 3, 1, 3, 4, 3, 5, 1, 1, 4, 1, 4, 3, 2, 2, 3, 3, 4, 3,
       3, 3, 3, 4, 4, 1, 5, 4, 3, 3, 4, 3, 2, 3, 3, 1, 3, 1, 3, 5, 3, 3,
       4, 2, 3, 3, 1, 3, 1, 5, 3, 3, 3, 2, 3, 2, 3, 2, 4, 4, 5, 5, 3, 3,
       3, 2, 3, 2, 4, 3, 2, 4, 2, 2, 2, 4, 3, 1, 3, 3, 4, 3, 1, 4, 3, 3,
       3, 3, 1, 2, 3, 2, 5, 1, 1], dtype=int64)
```

In [58]:
```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
lda = LDA(n_components=2)
x_lda_m2 = lda.fit(x_lda,y_lda).transform(x_lda)
```

In [59]:
```
lda.explained_variance_ratio_
```

Out[59]:
```
array([0.36219022, 0.30156109])
```

In [60]:
```
x_lda_m3 = pd.DataFrame(data=x_lda_m2)
x_lda_m3['cancer_class']=y_lda
x_lda_m3
```

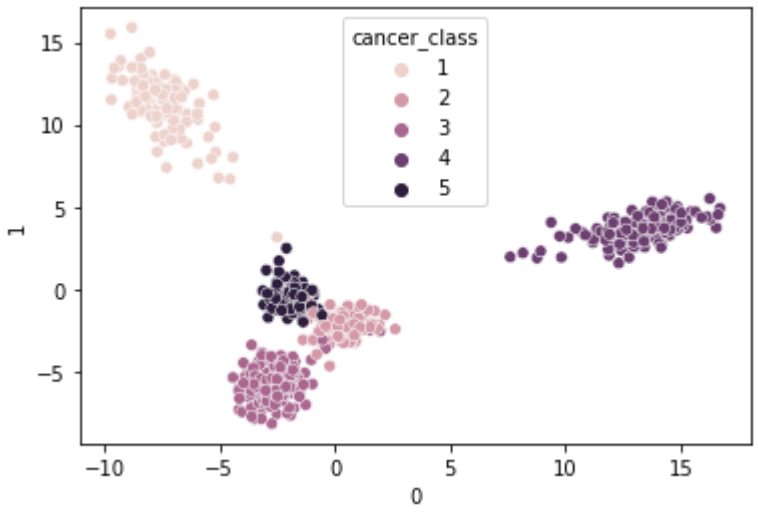
Out[60]:

	0	1	cancer_class
0	-7.958125	10.922818	1
1	-0.301563	-2.780898	2
2	-6.424952	8.870978	1
3	-6.934259	10.417199	1
4	-2.872004	-4.912284	3
...	...	...	...
796	-2.491183	-6.516482	3
797	0.217789	-1.859410	2
798	-1.426674	-0.474514	5
799	-7.800641	12.104337	1
800	-7.306312	7.388476	1

801 rows × 3 columns

In [61]:
```
sns.scatterplot(x=0, y=1, hue = 'cancer_class', data=x_lda_m3)
```

Out[61]:
```
<AxesSubplot:xlabel='0', ylabel='1'>
```



Project Task: Week 3: Clustering Genes and Samples:

Week 3: Clustering Genes and Samples:

```
Our next goal is to identify groups of genes that behave similarly across
samples and identify the distribution of samples corresponding to each cancer
type. Therefore, this task focuses on applying various clustering techniques,
e.g., k-means, hierarchical, and mean-shift clustering, on genes and samples.

First, apply the given clustering technique on all genes to identify:

Genes whose expression values are similar across all samples: i.e., find
clusters which has maximum number of observations

Genes whose expression values are similar across samples of each cancer type

Next, apply the given clustering technique on all samples to identify:

Samples of the same class (cancer type) which also correspond to the same
cluster

Samples identified to be belonging to another cluster but also to the same
class (cancer type)
```

KMEANS Clustering with PCA = 2

In [62]:
```
from sklearn.cluster import KMeans
clusters = KMeans(5, n_init = 5)
clusters.fit(X_pca_twoPC) # X_pca_twoPCA corresponds to PCA output with component

clusters.labels_
```

Out[62]:
```
array([4, 3, 0, 0, 2, 0, 1, 3, 2, 0, 3, 1, 3, 4, 2, 2, 3, 1, 1, 0, 2, 3,
       3, 0, 1, 3, 0, 2, 3, 2, 2, 2, 1, 4, 0, 2, 1, 3, 0, 4, 1, 0, 3, 1,
       1, 2, 4, 0, 2, 3, 2, 0, 2, 0, 0, 0, 2, 0, 1, 3, 3, 3, 2, 3, 0, 0,
       3, 0, 1, 0, 1, 3, 0, 3, 2, 0, 2, 4, 3, 0, 2, 0, 2, 2, 4, 3, 2, 0,
       1, 0, 0, 0, 2, 4, 2, 0, 0, 2, 2, 3, 2, 1, 2, 1, 3, 1, 0, 0, 0, 3,
       4, 2, 3, 0, 2, 1, 1, 1, 2, 2, 3, 1, 0, 0, 3, 3, 0, 2, 1, 0, 0, 0,
       4, 3, 2, 1, 1, 2, 1, 0, 2, 0, 2, 1, 3, 0, 4, 2, 3, 0, 3, 3, 2, 2,
       3, 3, 2, 3, 0, 3, 4, 3, 1, 3, 3, 3, 0, 1, 3, 2, 1, 3, 2, 0, 2, 0,
       3, 3, 3, 1, 0, 1, 2, 3, 0, 3, 3, 3, 2, 3, 3, 1, 4, 2, 3, 2, 4, 2,
       0, 3, 2, 1, 1, 1, 1, 2, 4, 0, 3, 3, 3, 2, 3, 0, 3, 2, 2, 2, 3, 3,
       1, 3, 1, 1, 3, 2, 1, 0, 2, 3, 4, 2, 0, 4, 1, 3, 1, 0, 3, 1, 1, 2,
       0, 3, 3, 0, 1, 3, 2, 0, 2, 0, 3, 2, 3, 1, 4, 3, 3, 2, 3, 0, 2, 0,
       0, 0, 3, 0, 2, 1, 1, 2, 0, 4, 1, 0, 2, 2, 1, 2, 2, 2, 4, 0, 3, 2,
       2, 2, 1, 1, 1, 1, 4, 2, 2, 1, 2, 2, 3, 3, 3, 2, 4, 3, 0, 2, 2, 2,
       4, 3, 2, 2, 0, 0, 3, 0, 1, 0, 1, 1, 2, 0, 3, 2, 2, 2, 2, 1, 2, 2,
       0, 0, 1, 2, 3, 3, 1, 2, 0, 0, 3, 2, 2, 3, 4, 3, 2, 2, 0, 3, 2, 1,
       2, 0, 3, 3, 2, 1, 2, 2, 0, 0, 3, 0, 1, 0, 1, 3, 2, 1, 2, 0, 0, 3,
       0, 4, 1, 0, 2, 0, 1, 1, 0, 0, 0, 2, 4, 0, 1, 4, 0, 0, 2, 2, 3, 3,
       1, 3, 2, 1, 0, 2, 2, 3, 3, 0, 4, 2, 0, 2, 0, 3, 3, 0, 0, 2, 2, 2,
       2, 3, 2, 3, 2, 1, 3, 2, 2, 3, 1, 0, 1, 4, 2, 0, 3, 1, 2, 2, 1, 2,
       3, 0, 2, 3, 4, 0, 1, 3, 4, 0, 0, 2, 2, 2, 2, 1, 2, 3, 1, 2, 2, 0,
       3, 1, 0, 3, 0, 3, 1, 1, 0, 3, 1, 0, 3, 0, 2, 3, 3, 3, 3, 2, 1, 3,
       3, 4, 3, 4, 2, 2, 0, 0, 1, 0, 0, 0, 0, 4, 3, 3, 2, 0, 2, 4, 1, 2,
       2, 0, 2, 2, 0, 1, 3, 0, 2, 2, 3, 3, 0, 3, 2, 1, 0, 1, 1, 4, 3, 3,
       3, 1, 0, 0, 2, 1, 1, 2, 3, 3, 1, 0, 3, 2, 0, 3, 2, 3, 2, 1, 3, 0,
       3, 0, 1, 0, 1, 1, 0, 3, 0, 1, 2, 0, 0, 3, 3, 3, 3, 1, 2, 2, 0, 0,
       2, 3, 2, 1, 3, 0, 0, 0, 0, 2, 2, 1, 0, 4, 0, 3, 0, 3, 4, 1, 1, 2,
       2, 1, 1, 0, 2, 3, 0, 0, 1, 2, 3, 2, 3, 0, 3, 4, 3, 3, 2, 4, 2, 1,
       2, 3, 3, 2, 3, 0, 2, 1, 0, 3, 2, 2, 1, 3, 2, 2, 2, 4, 0, 3, 3, 0,
       2, 2, 3, 2, 2, 1, 0, 2, 1, 1, 3, 1, 0, 3, 4, 1, 2, 2, 3, 3, 0, 3,
       0, 2, 0, 2, 2, 0, 0, 1, 2, 1, 0, 2, 2, 3, 2, 3, 1, 2, 2, 1, 0, 2,
       3, 1, 0, 3, 3, 3, 4, 1, 0, 3, 0, 0, 2, 3, 2, 3, 1, 1, 1, 3, 3, 1,
       3, 2, 3, 4, 2, 0, 2, 1, 3, 3, 3, 3, 1, 3, 1, 2, 3, 3, 2, 4, 1, 2,
       0, 2, 0, 1, 1, 3, 0, 1, 0, 4, 1, 2, 3, 3, 0, 2, 4, 0, 3, 0, 3, 2,
       1, 3, 2, 2, 3, 2, 0, 3, 2, 3, 2, 3, 2, 0, 3, 3, 1, 1, 0, 0, 2, 2,
       2, 0, 2, 3, 3, 3, 3, 1, 0, 3, 0, 1, 2, 4, 0, 0, 1, 2, 2, 3, 2, 2,
       2, 2, 3, 3, 2, 0, 3, 0, 3])
```

In [63]:
```
pca_with_twoPC_df = pd.DataFrame(data=X_pca_twoPC,columns=['pca1','pca2'])
pca_with_twoPC_df.head()
```

Out[63]:

	pca1	pca2
0	-57.446987	95.410981
1	-16.919430	0.732470
2	-70.345218	-19.303326
3	-49.161591	-9.227586
4	-18.132534	-51.327797

In [64]:
```
pca_with_twoPC_df['Class_label'] = clusters.labels_
pca_with_twoPC_df['given_cancer_class'] = label.Class.values
pca_with_twoPC_df
```

Out[64]:

	pca1	pca2	Class_label	given_cancer_class
0	-57.446987	95.410981	4	PRAD
1	-16.919430	0.732470	3	LUAD
2	-70.345218	-19.303326	0	PRAD
3	-49.161591	-9.227586	0	PRAD
4	-18.132534	-51.327797	2	BRCA
...	...	...	...	...
796	-12.417385	-42.321574	2	BRCA
797	-29.415554	28.526281	0	LUAD
798	-4.133090	15.690014	3	COAD
799	-30.814757	33.526423	0	PRAD
800	-22.344557	4.052356	3	PRAD

801 rows × 4 columns

In [65]:
```
brca = pca_with_twoPC_df.groupby('given_cancer_class').get_group('BRCA')
brca.Class_label.value_counts()
```

Out[65]:
```
2    198
3     47
0     36
4     19
Name: Class_label, dtype: int64
```

In [66]:
```
coad = pca_with_twoPC_df.groupby('given_cancer_class').get_group('COAD')
coad.Class_label.value_counts()
```

Out[66]:
```
0    61
4    10
3     7
Name: Class_label, dtype: int64
```

In [67]:
```
luad = pca_with_twoPC_df.groupby('given_cancer_class').get_group('LUAD')
luad.Class_label.value_counts()
```

Out[67]:
```
3    92
0    33
2    10
4     5
1     1
Name: Class_label, dtype: int64
```

In [68]:
```
kirc = pca_with_twoPC_df.groupby('given_cancer_class').get_group('KIRC')
kirc.Class_label.value_counts()
```

Out[68]:
```
1    139
3      6
4      1
Name: Class_label, dtype: int64
```

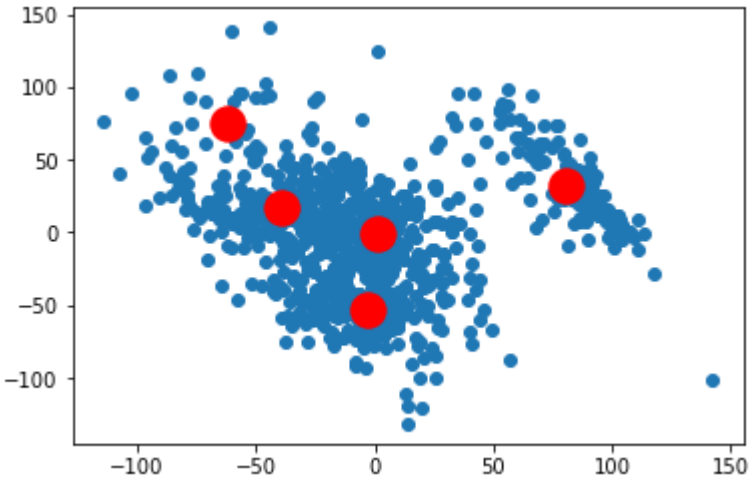
In [69]:
```
prad = pca_with_twoPC_df.groupby('given_cancer_class').get_group('PRAD')
prad.Class_label.value_counts()
```

Out[69]:
```
3    56
0    55
4    13
2    12
Name: Class_label, dtype: int64
```

In [70]:
```
clusters.cluster_centers_
```

Out[70]:
```
array([[-41.92422247,  16.28080653],
       [ 80.53911417,  32.98851346],
       [ -2.19479126, -52.95519389],
       [ -0.56774771,   2.28012936],
       [-60.8031089 ,  73.86530534]])
```

In [71]:
```
kmeans = KMeans(n_clusters=5, init='k-means++', max_iter=300, n_init=10, random_s
pred_y = kmeans.fit_predict(X_pca_twoPC)
plt.scatter(X_pca_twoPC[:,0], X_pca_twoPC[:,1])
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], s=300,
plt.show()
```



KMEANS Clustering with PCA = .995

In [72]:
```
#from sklearn.cluster import KMeans
clusters_995 = KMeans(5, n_init = 5)
clusters_995.fit(X_pca_99point5)
clusters_995.labels_
```

Out[72]:
```
array([2, 3, 2, 2, 1, 2, 0, 2, 1, 2, 1, 0, 2, 1, 1, 1, 3, 0, 0, 2, 1, 0,
       3, 1, 0, 3, 4, 1, 1, 1, 1, 1, 0, 1, 2, 1, 0, 3, 1, 1, 0, 2, 2, 0,
       0, 1, 2, 4, 1, 3, 1, 3, 1, 2, 4, 1, 1, 4, 0, 1, 3, 1, 1, 3, 2, 4,
       1, 2, 0, 1, 0, 1, 1, 3, 1, 3, 1, 0, 2, 4, 1, 2, 1, 1, 2, 2, 1, 1,
       0, 1, 2, 2, 1, 1, 1, 2, 4, 1, 2, 1, 1, 0, 1, 0, 3, 0, 3, 4, 3, 3,
       2, 1, 3, 2, 1, 0, 0, 0, 1, 1, 3, 0, 3, 1, 2, 2, 2, 1, 0, 1, 4, 1,
       4, 1, 1, 0, 3, 1, 0, 4, 1, 2, 1, 0, 3, 4, 2, 1, 3, 3, 3, 3, 1, 1,
       3, 1, 1, 2, 2, 3, 2, 3, 0, 1, 2, 3, 4, 0, 3, 1, 0, 3, 1, 3, 1, 1,
       1, 2, 1, 0, 4, 0, 1, 2, 2, 2, 3, 3, 1, 3, 3, 0, 3, 2, 3, 1, 1, 1,
       3, 3, 1, 0, 0, 0, 0, 2, 1, 2, 1, 3, 3, 1, 2, 1, 2, 1, 1, 1, 3, 1,
       0, 3, 0, 0, 3, 1, 0, 2, 1, 3, 3, 2, 4, 1, 0, 2, 0, 4, 1, 0, 0, 3,
       2, 2, 3, 3, 0, 1, 1, 4, 1, 2, 4, 1, 2, 0, 2, 2, 2, 1, 4, 4, 3, 4,
       4, 2, 3, 1, 1, 0, 0, 1, 4, 2, 0, 2, 1, 1, 0, 1, 1, 1, 1, 3, 3, 1,
       1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 1, 1, 3, 2, 1, 1, 4, 3, 2, 1, 1, 1,
       4, 1, 2, 1, 4, 3, 3, 2, 0, 1, 0, 0, 3, 4, 0, 1, 1, 1, 1, 0, 1, 1,
       2, 1, 0, 1, 3, 2, 0, 1, 2, 4, 1, 1, 1, 3, 3, 3, 1, 1, 2, 3, 1, 0,
       1, 4, 4, 3, 1, 0, 1, 1, 1, 4, 3, 4, 0, 2, 0, 1, 1, 0, 1, 4, 2, 3,
       2, 1, 0, 2, 1, 4, 0, 0, 4, 4, 2, 1, 1, 4, 0, 1, 2, 1, 1, 1, 3, 3,
       0, 3, 1, 0, 4, 2, 1, 3, 2, 1, 1, 1, 3, 1, 1, 2, 1, 2, 4, 1, 3, 1,
       1, 3, 1, 1, 1, 0, 3, 2, 1, 2, 0, 1, 0, 4, 1, 2, 3, 0, 1, 1, 0, 1,
       3, 1, 1, 2, 4, 1, 0, 3, 2, 1, 2, 1, 1, 1, 1, 0, 3, 1, 0, 1, 1, 3,
       3, 0, 4, 2, 4, 1, 0, 0, 1, 2, 0, 4, 3, 3, 1, 2, 2, 1, 2, 3, 0, 2,
       1, 3, 2, 3, 1, 1, 4, 3, 0, 4, 3, 1, 2, 1, 1, 2, 1, 4, 1, 4, 0, 1,
       1, 3, 3, 3, 4, 0, 3, 3, 1, 1, 0, 2, 3, 2, 1, 0, 1, 0, 0, 2, 2, 3,
       1, 0, 4, 4, 1, 0, 0, 1, 1, 2, 0, 4, 1, 1, 4, 3, 1, 1, 1, 0, 2, 3,
       3, 1, 0, 4, 0, 0, 1, 2, 3, 0, 1, 4, 3, 3, 3, 2, 3, 0, 1, 1, 4, 2,
       1, 1, 1, 0, 3, 3, 1, 2, 3, 3, 1, 0, 2, 4, 3, 2, 4, 3, 4, 0, 0, 1,
       1, 0, 0, 4, 1, 1, 2, 2, 0, 1, 3, 1, 1, 4, 1, 2, 2, 1, 1, 4, 1, 0,
       1, 1, 4, 1, 2, 1, 1, 0, 2, 3, 1, 1, 0, 1, 1, 1, 1, 1, 4, 3, 3, 1,
       1, 1, 2, 1, 1, 0, 3, 3, 0, 0, 3, 0, 4, 1, 4, 0, 1, 1, 2, 2, 2, 3,
       2, 2, 4, 1, 1, 4, 3, 0, 1, 0, 4, 1, 1, 1, 2, 3, 0, 1, 2, 0, 2, 1,
       3, 0, 2, 3, 2, 2, 1, 0, 2, 3, 4, 4, 1, 1, 1, 3, 0, 0, 0, 1, 3, 0,
       2, 1, 3, 2, 1, 2, 1, 0, 1, 4, 2, 2, 0, 2, 0, 1, 3, 3, 1, 1, 0, 1,
       1, 1, 1, 0, 0, 2, 4, 0, 1, 1, 0, 1, 3, 1, 1, 2, 1, 2, 1, 4, 1, 1,
       0, 3, 1, 1, 2, 1, 2, 4, 1, 1, 1, 3, 1, 3, 1, 3, 0, 0, 4, 4, 1, 1,
       1, 3, 1, 3, 0, 1, 3, 0, 3, 3, 3, 0, 1, 2, 1, 1, 0, 1, 2, 0, 1, 1,
       1, 1, 2, 3, 1, 3, 3, 2, 2])
```

In [73]:
```
pca_99point5_df = pd.DataFrame(data=X_pca_twoPC,columns=['pca1','pca2'])
pca_99point5_df.head()
```

Out[73]:

	pca1	pca2
0	-57.446987	95.410981
1	-16.919430	0.732470
2	-70.345218	-19.303326
3	-49.161591	-9.227586
4	-18.132534	-51.327797

In [74]:
```
pca_99point5_df['Class_label'] = clusters.labels_
pca_99point5_df['given_cancer_class'] = label.Class.values
```

In [75]:
```
pca_99point5_df.shape
```

Out[75]:
```
(801, 4)
```

In [76]:
```
brca_995 = pca_99point5_df.groupby('given_cancer_class').get_group('BRCA')
brca_995.Class_label.value_counts()
```

Out[76]:
```
2    198
3     47
0     36
4     19
Name: Class_label, dtype: int64
```

In [77]:
```
coad_995 = pca_99point5_df.groupby('given_cancer_class').get_group('COAD')
coad_995.Class_label.value_counts()
```

Out[77]:
```
0    61
4    10
3     7
Name: Class_label, dtype: int64
```

In [78]:
```
luad_995 = pca_99point5_df.groupby('given_cancer_class').get_group('LUAD')
luad_995.Class_label.value_counts()
```

Out[78]:
```
3    92
0    33
2    10
4     5
1     1
Name: Class_label, dtype: int64
```

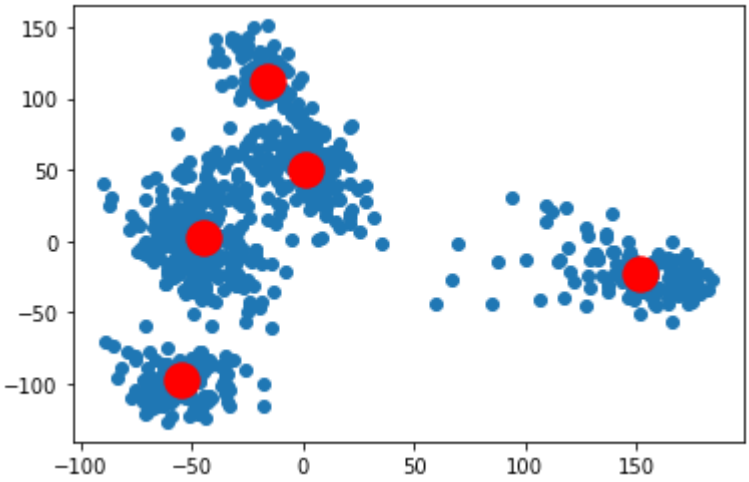
In [79]:
```
kirc_995 = pca_99point5_df.groupby('given_cancer_class').get_group('KIRC')
kirc_995.Class_label.value_counts()
```

Out[79]:
```
1    139
3      6
4      1
Name: Class_label, dtype: int64
```

In [80]:
```
prad_995 = pca_99point5_df.groupby('given_cancer_class').get_group('PRAD')
prad_995.Class_label.value_counts()
```

Out[80]:
```
3    56
0    55
4    13
2    12
Name: Class_label, dtype: int64
```

In [81]:
```
kmeans = KMeans(n_clusters=5, init='k-means++', max_iter=300, n_init=10, random_s
pred_y = kmeans.fit_predict(X_pca_99point5)
plt.scatter(X_pca_99point5[:,0], X_pca_99point5[:,1])
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], s=300,
plt.show()
```



Project Task: Week 4: Build Classification Models

Week 4: Building Classification Model(s) with Feature Selection:

```
Our final task is to build a robust classification model(s) for identifying
each type of cancer.

Sub-tasks:

Build a classification model(s) using multiclass SVM, Random Forest, and Deep
Neural Network to classify the input data into five cancer types

Apply the feature selection algorithms, forward selection, and backward
elimination to refine selected attributes (selected in Task-2) using the
classification model from the previous step

Validate the genes selected from the last step using statistical significance
testing (t-test for one vs. all and F-test)
```

Decision Tree Classifier

```
Decision Tree is a Supervised Machine Learning Algorithm that uses a set of
rules to predict the class of the new previously unseen input.
```

In [82]:
```
x_ml = x_lda
y_ml = y_lda
print(x_ml.shape)
print(y_ml.shape)
```

```
(801, 20531)
(801,)
```

In [83]:
```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x_ml,y_ml,test_size=0.30,rand
```

In [84]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score

dt_model = DecisionTreeClassifier(max_depth=5)
dt_model.fit(x_train,y_train)

dt_model.score(x_test,y_test)

y_pred=dt_model.predict(x_test)
print(dt_model.score(x_test,y_test))
```

```
0.9585062240663901
```

Support Vector Machine Classifier

```
The goal of support vector machine algorithm is to find a hyperplane in an N-
dimensional space( where N is the number of features) to distinctly classify
the data points.
```

In [85]:
```
from sklearn.metrics import accuracy_score
from sklearn.svm import SVC

sv_model = SVC(probability=True, kernel='linear')
sv_model.fit(x_train,y_train)
sv_model.score(x_test,y_test)


y_pred = sv_model.predict(x_test)
print(accuracy_score(y_test,y_pred))
```

```
1.0
```

Random Forest Classifier

```
Random forest is an ensemble of a large number of individual decision trees.
Each individual tree in the random forest returns a class prediction and the
class with the most votes becomes our model’s prediction. The basic idea behind
Randm forest is that a large number of relatively uncorrelated models (
decision trees) operating as a ensemble will outperform any of the individual
constituent models.
```

In [86]:
```
from sklearn import ensemble
rf_model = ensemble.RandomForestClassifier(n_estimators=100)
rf_model.fit(x_train,y_train)
rf_model.score(x_test,y_test)
```

Out[86]: 0.9875518672199171

Naive Bayes Classifier

```
A probabilistic machine learning model used for classification task.
```

In [87]:
```
from sklearn.naive_bayes import GaussianNB

gnb_model = GaussianNB()
gnb_model.fit(x_train,y_train)
gnb_model.score(x_test,y_test)
```

Out[87]: 0.7385892116182573

Gradient Boosting Classifier

In [88]:
```
gb_model = ensemble.GradientBoostingClassifier(n_estimators=40)
gb_model.fit(x_train,y_train)
gb_model.score(x_test,y_test)
```

Out[88]: 0.9626556016597511

K-nearest neighbors (KNN) Classifier

In [89]:
```
from sklearn.neighbors import KNeighborsClassifier
knn_model= KNeighborsClassifier(n_neighbors=5)
knn_model.fit(x_train,y_train)
knn_model.score(x_test,y_test)
```

Out[89]: 0.995850622406639

Recursive Feature Elimination

```
We will evaluate an RFE feature selection algorithm on the dataset. We will use
a DecisionTreeClassifier to choose features and set the number of features to
five. We will then fit a new DecisionTreeClassifier model on the selected
features.

We will evaluate the model using repeated stratified k-fold cross-validation,
with three repeats and 10 folds. We will report the mean and standard deviation
of the accuracy of the model across all repeats and folds.
```

In [90]:
```
# automatically select the number of features via 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 = X_pca_99point5
y = merged_data['Class']
#X, y = make_classification(n_samples=1000, n_features=10, n_informative=5, n_rec
# create pipeline
rfe = RFECV(estimator=DecisionTreeClassifier())
model = DecisionTreeClassifier()
pipeline = Pipeline(steps=[('s',rfe),('m',model)])
# evaluate model'mmnm
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
#cv = RepeatedStratifiedKFold(n_splits=2, n_repeats=1, random_state=1)
n_scores = cross_val_score(pipeline, X, y, scoring='accuracy', cv=cv, n_jobs=-1,
# report performance
print('Accuracy: %.3f (%.3f)' % (mean(n_scores), std(n_scores)))
```

```
Accuracy: 0.975 (0.016)
```

One way F Test

In [103]:
```
df_tsne = pd.DataFrame(data=tnse_features,columns=['tsne1','tsne2'])
df_tsne['cancer_type']=label['Class']
df_tsne
```

Out[103]:

	tsne1	tsne2	cancer_type
0	-0.597084	-30.755308	PRAD
1	-13.693470	5.532149	LUAD
2	-6.690077	-36.395447	PRAD
3	-6.537254	-35.288013	PRAD
4	23.679300	-1.491317	BRCA
...	...	...	...
796	24.331879	-0.355141	BRCA
797	-25.114609	6.746962	LUAD
798	-40.703033	-7.175969	COAD
799	-4.194886	-31.243105	PRAD
800	-8.176849	-26.034245	PRAD

801 rows × 3 columns

In [105]:
```
import scipy.stats as stats

df_anova_tsne = df_tsne[['tsne1','cancer_type']]
grps_tsne = pd.unique(df_anova_tsne.cancer_type.values)

d_data = {grp:df_anova_tsne['tsne1'][df_anova_tsne.cancer_type == grp] for grp in

F, p = stats.f_oneway(d_data['LUAD'], d_data['PRAD'], d_data['BRCA'], d_data['KI

if p<0.05:
    print("reject null hypothesis")
else:
    print("accept null hypothesis")
```

```
reject null hypothesis
```

In [106]:
```
df_anova_tsne = df_tsne[['tsne2','cancer_type']]
grps_tsne = pd.unique(df_anova_tsne.cancer_type.values)

d_data = {grp:df_anova_tsne['tsne2'][df_anova_tsne.cancer_type == grp] for grp in

F, p = stats.f_oneway(d_data['LUAD'], d_data['PRAD'], d_data['BRCA'], d_data['KI

if p<0.05:
    print("reject null hypothesis")
else:
    print("accept null hypothesis")
```

```
reject null hypothesis
```

Forward Feature Selection

In [107]:
```
# install the mlxtend library for forward selection or backward elimination
!pip install mlxtend
```

```
Requirement already satisfied: mlxtend in c:\users\byju\anaconda3\lib\site-pack
ages (0.19.0)
Requirement already satisfied: numpy>=1.16.2 in c:\users\byju\anaconda3\lib\sit
e-packages (from mlxtend) (1.20.1)
Requirement already satisfied: scikit-learn>=0.20.3 in c:\users\byju\anaconda3
\lib\site-packages (from mlxtend) (0.24.1)
Requirement already satisfied: matplotlib>=3.0.0 in c:\users\byju\anaconda3\lib
\site-packages (from mlxtend) (3.3.4)
Requirement already satisfied: setuptools in c:\users\byju\anaconda3\lib\site-p
ackages (from mlxtend) (52.0.0.post20210125)
Requirement already satisfied: pandas>=0.24.2 in c:\users\byju\anaconda3\lib\si
te-packages (from mlxtend) (1.2.4)
Requirement already satisfied: scipy>=1.2.1 in c:\users\byju\anaconda3\lib\site
-packages (from mlxtend) (1.6.2)
Requirement already satisfied: joblib>=0.13.2 in c:\users\byju\anaconda3\lib\si
te-packages (from mlxtend) (1.0.1)
Requirement already satisfied: cycler>=0.10 in c:\users\byju\anaconda3\lib\site
-packages (from matplotlib>=3.0.0->mlxtend) (0.10.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.3 in c:\u
sers\byju\anaconda3\lib\site-packages (from matplotlib>=3.0.0->mlxtend) (2.4.7)
Requirement already satisfied: python-dateutil>=2.1 in c:\users\byju\anaconda3
\lib\site-packages (from matplotlib>=3.0.0->mlxtend) (2.7.5)
Requirement already satisfied: pillow>=6.2.0 in c:\users\byju\anaconda3\lib\sit
e-packages (from matplotlib>=3.0.0->mlxtend) (8.2.0)
Requirement already satisfied: kiwisolver>=1.0.1 in c:\users\byju\anaconda3\lib
\site-packages (from matplotlib>=3.0.0->mlxtend) (1.3.1)
Requirement already satisfied: six in c:\users\byju\anaconda3\lib\site-packages
(from cycler>=0.10->matplotlib>=3.0.0->mlxtend) (1.15.0)
Requirement already satisfied: pytz>=2017.3 in c:\users\byju\anaconda3\lib\site
-packages (from pandas>=0.24.2->mlxtend) (2021.1)
Requirement already satisfied: threadpoolctl>=2.0.0 in c:\users\byju\anaconda3
\lib\site-packages (from scikit-learn>=0.20.3->mlxtend) (2.1.0)
```

In [108]:
```
# import SequentialFeatureSelector from mlextend and DecisionTreeClassifier from
from mlxtend.feature_selection import SequentialFeatureSelector as sfs
#from sklearn.tree import DecisionTreeClassifier
```

In [109]:
```
# calling the decision tree model

dtc1 = DecisionTreeClassifier()
sfs1 = sfs(dtc1, k_features=4, forward=True, verbose=2, scoring='accuracy')
```

```
# In the Feature Selector Model, The first parameter is the model name, dtc,
which is basically our decision tree classification model.

k_features tells us how many features should be selected. We've it set to 4 so
the model will train until 4 features are selected.

For the Forward Feature Selection method, the parameter forward is set to True.
This means training the forward feature selection model. We set it as False for
the backward feature elimination technique.
```

```
Next, verbose = 2 allow us to bring the model summary at each iteration.

And finally, since it is a decision tree model , we set scoring = 'accuracy'
```

In [110]:
```
X = X_pca_99point5
y = merged_data['Class']
sfs1 = sfs1.fit(X, y)
```

```
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worker
s.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0s
[Parallel(n_jobs=1)]: Done 747 out of 747 | elapsed:    6.4s finished

[2022-06-30 19:52:12] Features: 1/4 -- score: 0.7190916149068324[Parallel(n_job
s=1)]: Using backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0s
[Parallel(n_jobs=1)]: Done 746 out of 746 | elapsed:    6.1s finished

[2022-06-30 19:52:18] Features: 2/4 -- score: 0.9700621118012422[Parallel(n_job
s=1)]: Using backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0s
[Parallel(n_jobs=1)]: Done 745 out of 745 | elapsed:    5.6s finished

[2022-06-30 19:52:23] Features: 3/4 -- score: 0.9787732919254658[Parallel(n_job
s=1)]: Using backend SequentialBackend with 1 concurrent workers.
[Parallel(n_jobs=1)]: Done   1 out of   1 | elapsed:    0.0s remaining:    0.0s
[Parallel(n_jobs=1)]: Done 744 out of 744 | elapsed:    6.0s finished

[2022-06-30 19:52:29] Features: 4/4 -- score: 0.9812810559006211
```

In [111]:
```
# merged_data.Class.values # converts the class column to an array
```

In [112]:
```
#The model is trained until four features were selected. Print the feature names:

feat_names = list(sfs1.k_feature_names_)
print(feat_names) #numeric string
feat_names = [int(x) for x in feat_names]
#feat_names =[0, 1, 2, 5]
feat_names # numeric
```

```
['0', '1', '2', '5']
```

Out[112]:
```
[0, 1, 2, 5]
```

In [113]:
```
X.shape
```

Out[113]:
```
(801, 747)
```

In [114]:
```
X_pca_99point5
```

Out[114]:
```
array([[-6.27554152e+01, -9.40719735e+01,  8.95198311e+01, ...,
         3.09258084e+00,  7.13597730e-01, -8.21221710e-02],
       [-2.43289636e+00,  9.05858418e+01, -1.06730787e+00, ...,
         1.39674724e-02, -3.95175744e-01, -9.49947250e-01],
       [-7.12668528e+01, -8.06460774e+00,  6.61124549e+01, ...,
         1.28898532e-01, -2.64530262e-01,  3.84594189e-01],
       ...,
       [ 1.04862615e+01,  2.15705946e+01,  4.13458784e+01, ...,
        -6.47882986e-01, -2.07256774e-01,  1.38942922e-01],
       [-5.50636049e+01, -9.23947780e+01,  8.00500394e+01, ...,
         1.74673062e+00,  2.02232239e+00, -1.92708948e+00],
       [-4.91030338e+01, -5.09976391e+01,  4.05037544e+01, ...,
         1.80367340e+00,  2.22994027e+00, -8.07255452e-01]])
```

In [115]:
```
Xnew = pd.DataFrame(X_pca_99point5)
Xnew
```

Out[115]:

	0	1	2	3	4	5	6	7
0	-62.755415	-94.071973	89.519831	-15.942567	81.423539	-13.998292	7.716073	-22.936551
1	-2.432896	90.585842	-1.067308	-53.083120	-15.676684	60.842472	10.257369	-48.822959
2	-71.266853	-8.064608	66.112455	81.381475	-7.525685	109.824273	5.519407	-13.364480
3	-84.770785	-73.244566	74.181000	27.022697	-18.044895	50.116433	-3.495197	-11.318520
4	-69.560171	-9.612940	-67.497549	34.868543	-1.795849	-6.676780	-2.840781	16.780157
...	...	...	...	...	...	...	...	...
796	-60.861882	-22.278633	-80.927167	42.670292	7.843763	-4.545218	-27.602910	-8.840676
797	-14.465433	53.392194	38.153904	-63.217345	22.799082	39.543441	-47.899401	39.925172
798	10.486261	21.570595	41.345878	-59.639929	-2.163066	-96.453878	38.375897	46.997294
799	-55.063605	-92.394778	80.050039	-7.782015	15.180574	2.563620	8.487660	10.571657
800	-49.103034	-50.997639	40.503754	-31.495505	-10.361908	-1.272555	9.185948	-31.629661

801 rows × 747 columns

In [116]:
```
df_pca_995['cancer_class']
```

Out[116]:
```
0      1
1      2
2      1
3      1
4      3
      ..
796    3
797    2
798    5
799    1
800    1
Name: cancer_class, Length: 801, dtype: int64
```

In [117]:
```
X[feat_names]
```

Out[117]:
```
array([[-6.27554152e+01, -9.40719735e+01,  8.95198311e+01, ...,
         3.09258084e+00,  7.13597730e-01, -8.21221710e-02],
       [-2.43289636e+00,  9.05858418e+01, -1.06730787e+00, ...,
         1.39674724e-02, -3.95175744e-01, -9.49947250e-01],
       [-7.12668528e+01, -8.06460774e+00,  6.61124549e+01, ...,
         1.28898532e-01, -2.64530262e-01,  3.84594189e-01],
       [-3.63753197e+01, -1.01351157e+02,  5.39319731e+01, ...,
         6.68428454e-01,  1.61936138e+00, -1.02884726e+00]])
```

In [118]:
```
# creating a new dataframe using the above variables and adding the target variab

new_data_fs = X[feat_names]
new_data_fs = pd.DataFrame(new_data_fs)
new_data_fs['class'] = df_pca_995['cancer_class']


# first five rows of the new data
print(new_data_fs.head(5))

# shape of new and original data
new_data_fs.shape, data.shape
```

```
           0           1          2          3          4           5  \
0 -62.755415  -94.071973  89.519831 -15.942567  81.423539  -13.998292
1  -2.432896   90.585842  -1.067308 -53.083120 -15.676684   60.842472
2 -71.266853   -8.064608  66.112455  81.381475  -7.525685  109.824273
3 -36.375320 -101.351157  53.931973  -1.738138   3.940702   -8.232349

           6          7          8          9  ...       738       739  \
0   7.716073 -22.936551 -32.837892  -2.202680  ... -4.081064 -0.626193
1  10.257369 -48.822959  14.257400 -12.214352  ...  0.215619 -0.593678
2   5.519407 -13.364480  38.415728  -5.124731  ...  0.263786  0.328453
3  17.651078 -17.763020  15.129324  36.070017  ...  0.217054  2.243980

        740       741       742       743       744       745       746  class
0 -1.265756 -0.017984 -2.740860  0.944037  3.092581  0.713598 -0.082122      1
1 -0.403462  1.181537  0.490910  0.197768  0.013967 -0.395176 -0.949947      2
2  0.004078  0.363928 -1.109210  0.331488  0.128899 -0.264530  0.384594      1
3  1.703770 -0.077690  1.474417  1.533704  0.668428  1.619361 -1.028847      1

[4 rows x 748 columns]
```

Out[118]: ((4, 748), (801, 20532))

Backward Feature Elimination

In [119]:
```
# calling the decision tree model

dtc2 = DecisionTreeClassifier()
sfs2 = sfs(dtc2, k_features=4, forward=False, verbose=2, scoring='accuracy')
X = X_pca_99point5
y = merged_data['Class']
sfs2 = sfs2.fit(X, y)

#The model is trained until four features were selected. Print the feature names:

feat_names = list(sfs2.k_feature_names_)
print(feat_names)

# Taking enormous run time...
```

In [ ]:
```
feat_names = [int(x) for x in feat_names]
```

In [ ]:
```
# feat_names
# creating a new dataframe using the above variables and adding the target variab
new_data_be = X[feat_names]
new_data_be = pd.DataFrame(new_data_fs)
new_data_be['class'] = df_pca_995['cancer_class']

# first five rows of the new data
print(new_data_be.head(5))

# shape of new and original data
new_data_be.shape, data.shape
```

In [ ]:
```
```

Deep Neural Network

In [120]:
```
features=merged_data.drop(['Unnamed: 0'],axis=1)
features=features.drop(['Class'],axis=1)
target=merged_data['Class']
features.head()
```

Out[120]:

	gene_0	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7	gene_8	gene_9
0	0.0	2.017209	3.265527	5.478487	10.431999	0.0	7.175175	0.591871	0.0	0.0
1	0.0	0.592732	1.588421	7.586157	9.623011	0.0	6.816049	0.000000	0.0	0.0
2	0.0	3.511759	4.327199	6.881787	9.870730	0.0	6.972130	0.452595	0.0	0.0
3	0.0	3.663618	4.507649	6.659068	10.196184	0.0	7.843375	0.434882	0.0	0.0
4	0.0	2.655741	2.821547	6.539454	9.738265	0.0	6.566967	0.360982	0.0	0.0

5 rows × 20531 columns

In [121]:
```
target.head()
```

Out[121]:
```
0    1
1    2
2    1
3    1
4    3
Name: Class, dtype: int64
```

In [122]:
```
x1=features.values
y1 = pd.get_dummies(y_lda)
```

In [123]:
```
from sklearn.model_selection import train_test_split

X1_train, X1_test, y1_train, y1_test = train_test_split(x1,y1, test_size = 0.10,
X1_train.shape,X1_test.shape,y1_test.shape,y1_train.shape
```

Out[123]:
```
((720, 20531), (81, 20531), (81, 5), (720, 5))
```

In [124]:
```
import tensorflow as tf
```

In [125]:
```
#Initialize Sequential model
model = tf.keras.models.Sequential()

#adding layers of inout
model.add(tf.keras.layers.Dense(10000, input_dim=20531, activation='relu', kernel

#Normalize the data
model.add(tf.keras.layers.BatchNormalization())

#Add 1st hidden layer
model.add(tf.keras.layers.Dense(5000, activation='relu'))

#Add 2nd hidden layer
model.add(tf.keras.layers.Dense(2000, activation='relu'))

#Add 3rd hidden layer
model.add(tf.keras.layers.Dense(1000, activation='relu'))

#Add 4th hidden layer
model.add(tf.keras.layers.Dense(500, activation='relu'))

#Add 5th hidden layer
model.add(tf.keras.layers.Dense(200, activation='relu'))

#Add 6th hidden layer
model.add(tf.keras.layers.Dense(100, activation='relu'))

#Add OUTPUT layer
model.add(tf.keras.layers.Dense(5, activation='softmax'))

#Create optimizer with non-default learning rate
sgd_optimizer = tf.keras.optimizers.SGD(learning_rate=0.03)

#Compile the model
model.compile(optimizer=sgd_optimizer, loss='categorical_crossentropy', metrics=[
```

In [126]:
```
model.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 dense (Dense)               (None, 10000)             205320000

 batch_normalization (BatchN  (None, 10000)            40000
 ormalization)

 dense_1 (Dense)             (None, 5000)              50005000

 dense_2 (Dense)             (None, 2000)              10002000

 dense_3 (Dense)             (None, 1000)              2001000

 dense_4 (Dense)             (None, 500)               500500

 dense_5 (Dense)             (None, 200)               100200

 dense_6 (Dense)             (None, 100)               20100

 dense_7 (Dense)             (None, 5)                 505

=================================================================
Total params: 267,989,305
Trainable params: 267,969,305
Non-trainable params: 20,000
_________________________________________________________________
```

In [127]:
```
history = model.fit(X1_train,y1_train,
          validation_data=(X1_test,y1_test),
          epochs=5,
          batch_size=32)
```

```
Epoch 1/5
23/23 [==============================] - 11s 456ms/step - loss: 0.2387 - accura
cy: 0.9417 - val_loss: 7.0087 - val_accuracy: 0.3827
Epoch 2/5
23/23 [==============================] - 10s 439ms/step - loss: 0.0076 - accura
cy: 1.0000 - val_loss: 4.1834 - val_accuracy: 0.4444
Epoch 3/5
23/23 [==============================] - 10s 438ms/step - loss: 0.0046 - accura
cy: 0.9986 - val_loss: 0.2827 - val_accuracy: 0.8889
Epoch 4/5
23/23 [==============================] - 10s 442ms/step - loss: 0.0024 - accura
cy: 1.0000 - val_loss: 0.1068 - val_accuracy: 0.9877
Epoch 5/5
23/23 [==============================] - 16s 715ms/step - loss: 0.0016 - accura
cy: 1.0000 - val_loss: 0.0445 - val_accuracy: 0.9877
```

In [128]:
```
test_mod_out = model.predict(X1_test)
```

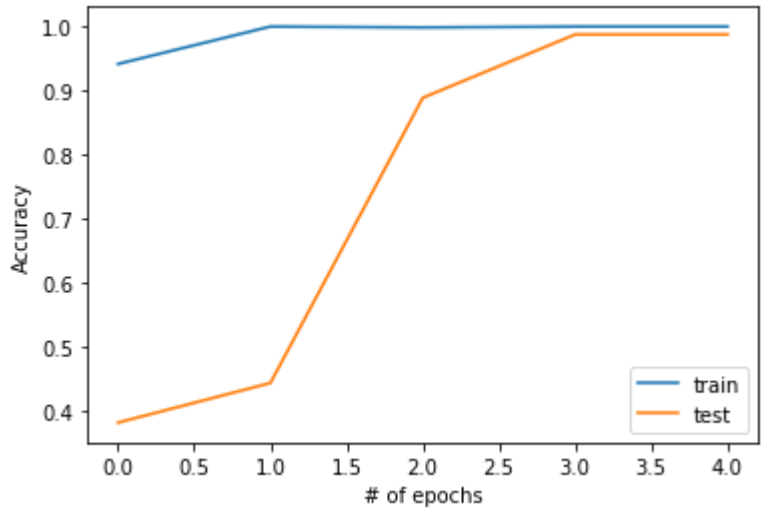
In [129]:
```
y_predict=[]
for k in test_mod_out:
    #np.argmax(k)
    #print(np.argmax(k))
    y_predict.append(np.argmax(k))

y_val=[]
for k in y1_test.values:
    #np.argmax(k)
    #print(np.argmax(k))
    y_val.append(np.argmax(k))

# Making the Confusion Matrix
from sklearn.metrics import confusion_matrix
confusion_matrix(y_val, y_predict)
```

Out[129]:
```
array([[14,  0,  0,  0,  0],
       [ 0, 17,  0,  0,  0],
       [ 0,  0, 31,  0,  0],
       [ 0,  0,  1, 11,  0],
       [ 0,  0,  0,  0,  7]], dtype=int64)
```

In [130]:
```
_, train_acc = model.evaluate(X1_train, y1_train, verbose=0)
_, test_acc = model.evaluate(X1_test, y1_test, verbose=0)
print('Train: %.3f, Test: %.3f' % (train_acc, test_acc))
```

```
Train: 0.986, Test: 0.988
```

In [131]:
```
plt.plot(history.history['accuracy'], label='train')
plt.plot(history.history['val_accuracy'], label='test')
plt.xlabel('# of epochs')
plt.ylabel('Accuracy')
plt.legend()
plt.show()
```



In [ ]: