Student ID: 720027410

COMM415DA Fundamentals of Data Science ¶

Ref/Def Assessment

Question-1

Import libraries

In [1]:

```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd

%matplotlib inline
```

a)

Analyze the Exasens Data Set

From: https://archive.ics.uci.edu/ml/datasets/Exasens (https://archive.ics.uci.edu/ml/datasets/Exasens)

This repository introduces a novel dataset for the classification of 4 groups of respiratory diseases:

1. Chronic Obstructive Pulmonary Disease (COPD)
2. Asthma
3. Infected
4. Healthy Controls (HC).

The Exasens dataset includes demographic information on 4 groups of saliva samples (COPD-Asthma-Infected-HC) collected in the frame of a joint research project, at the Research Center Borstel, BioMaterialBank Nord (Borstel, Germany). The sampling procedure of the patient materials was approved by the local ethics committee of the University of Luebeck under the approval number AZ-16-167 and a written informed consent was obtained from all subjects. A permittivity biosensor, developed at IHP Microelectronics (Frankfurt Oder, Germany), was used for the dielectric characterization of the saliva samples for classification purposes

Definition of 4 sample groups included within the Exasens dataset:

1. Outpatients and hospitalized patients with COPD without acute respiratory infection (COPD).
2. Outpatients and hospitalized patients with asthma without acute respiratory infections (Asthma).

3. Patients with respiratory infections, but without COPD or asthma (Infected).
4. Healthy controls without COPD, asthma, or any respiratory infection (HC).

Attribute Information:

1. Diagnosis (COPD-HC-Asthma-Infected)
2. ID
3. Age
4. Gender (1=male, 0=female)
5. Smoking Status (1=Non-smoker, 2=Ex-smoker, 3=Active-smoker)
6. Saliva Permittivity:

a) Imaginary part (Min(Î”)=Absolute minimum value, Avg.(Î”)=Average) b) Real part (Min(Î”)=Absolute minimum value, Avg.(Î”)=Average)

Data Description:

Database is composed of 399 observations and 9 variables, among these variables we have continous variables and categorical variables

Observation:

Note that the infected observations have 0 people who smoke, the median age of people who smoke and who are affected by Asthma or are HC is less than 50 years, on the other hand the median age of people who are affected by COPD is more than 50 years old.

It is noted that the infected or HC observations are yunger than the individuals affected by COPD or by Asthma.

b)

In [2]:

```
# Load the dataset in a pandas dataframe
def load_exasens_data_set():
    path = 'https://archive.ics.uci.edu/ml/machine-learning-databases/00523/Exasens.
    df = pd.read_csv(path
                ,skiprows=3
                ,index_col=False
                ,names=  ["Diagnosis", "ID", "Imaginary_Part_Min", "Imaginary_Part_A
                ,usecols=["Diagnosis", "ID", "Imaginary_Part_Min", "Imaginary_Part_A
                )
    return df

exasens_df = load_exasens_data_set()
exasens_df.head(10)
```

Out[2]:

	Diagnosis	ID	Imaginary_Part_Min	Imaginary_Part_Avg	Real_Part_Min	Real_Part_Avg	Gend
0	COPD	301-4	-320.61	-300.563531	-495.26	-464.171991	
1	COPD	302-3	-325.39	-314.750360	-473.73	-469.263140	
2	COPD	303-3	-323.00	-317.436056	-476.12	-471.897667	
3	COPD	304-4	-327.78	-317.399670	-473.73	-468.856388	
4	COPD	305-4	-325.39	-316.155785	-478.52	-472.869783	
5	COPD	306-3	-327.78	-318.677553	-507.23	-469.024194	
6	COPD	307-3	-330.18	-320.617478	-473.73	-467.361854	
7	COPD	308	NaN	NaN	NaN	NaN	
8	COPD	309-4	-320.61	-307.599586	-476.12	-470.181633	
9	COPD	310-4	-315.82	-300.104765	-473.73	-466.378634	

c)

In [3]:

```
# Ignore the columns Diagnosis and ID
exasens_df.drop(['Diagnosis','ID'], axis=1, inplace=True)
exasens_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 399 entries, 0 to 398
Data columns (total 7 columns):
 #   Column               Non-Null Count  Dtype  
---  ------               --------------  -----  
 0   Imaginary_Part_Min   100 non-null    float64
 1   Imaginary_Part_Avg   100 non-null    float64
 2   Real_Part_Min        100 non-null    float64
 3   Real_Part_Avg        100 non-null    float64
 4   Gender               399 non-null    int64  
 5   Age                  399 non-null    int64  
 6   Smoking              399 non-null    int64  
dtypes: float64(4), int64(3)
memory usage: 21.9 KB
```

d)

In [4]:

```
# Replace missing values of each column with the average between the median and the
def replace_missing_with_average_mean_median(df, cols):
    for col in cols:
        df.loc[df[col].isnull(), col] = df[col].fillna((df[col].mean()+df[col].media
    return df

def get_had_missing(df,col):
    df['had_missing'] = df[col].isna()
    return df
```

In [5]:

```
exasens_df_had_missing_df = get_had_missing(exasens_df, 'Imaginary_Part_Min')
exasens_df_non_nulls_df = replace_missing_with_average_mean_median(exasens_df_had_mi
exasens_df_non_nulls_df.head(10)
```

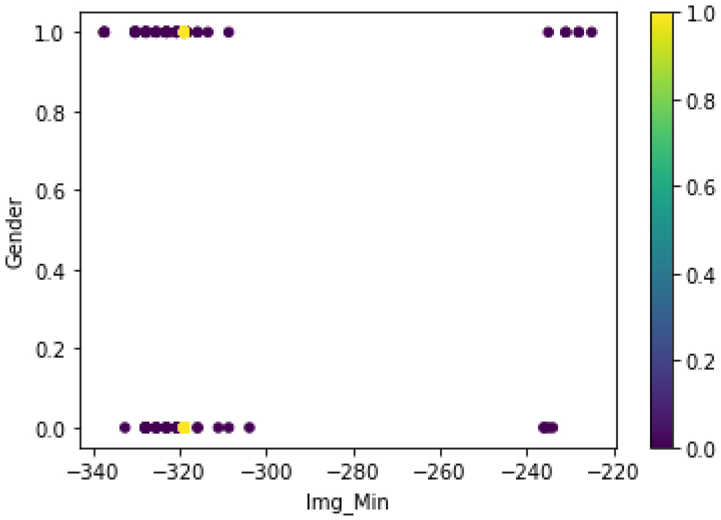
Out[5]:

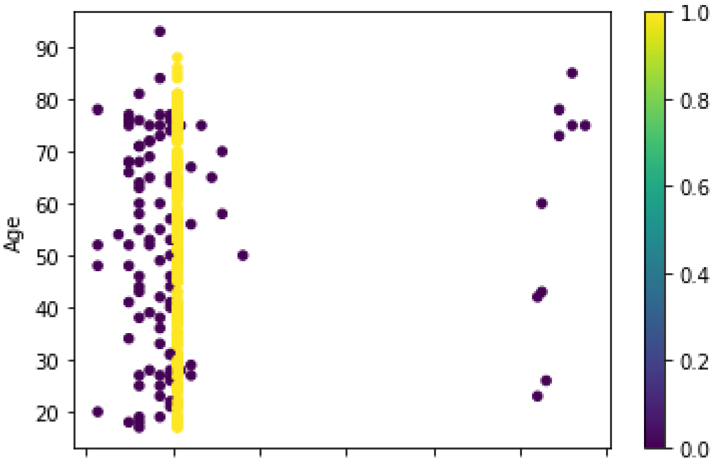
	Imaginary_Part_Min	Imaginary_Part_Avg	Real_Part_Min	Real_Part_Avg	Gender	Age	Smokin
0	-320.6100	-300.563531	-495.2600	-464.171991	1	77	
1	-325.3900	-314.750360	-473.7300	-469.263140	0	72	
2	-323.0000	-317.436056	-476.1200	-471.897667	1	73	
3	-327.7800	-317.399670	-473.7300	-468.856388	1	76	
4	-325.3900	-316.155785	-478.5200	-472.869783	0	65	
5	-327.7800	-318.677553	-507.2300	-469.024194	1	60	
6	-330.1800	-320.617478	-473.7300	-467.361854	1	76	
7	-318.9709	-309.553427	-473.3661	-462.918834	1	77	
8	-320.6100	-307.599586	-476.1200	-470.181633	1	74	
9	-315.8200	-300.104765	-473.7300	-466.378634	1	67	

e)

In [6]:

```
# Display a scatter plot for each distinct pair of columns
fig, ax = plt.subplots()
exasens_df_non_nulls_df.plot(kind='scatter',
                                  x='Imaginary_Part_Min',
                                  y='Gender',
                                  c=exasens_df_non_nulls_df['had_missing'],
                                  #color='purple',
                                  colormap='viridis',
                                  ax=ax)

plt.xlabel('Img_Min')
plt.ylabel('Gender')




exasens_df_non_nulls_df.plot(kind='scatter',
                                  x='Imaginary_Part_Min',
                                  y='Age',
                                  c=exasens_df_non_nulls_df['had_missing'],
                                  #color='purple',
                                  colormap='viridis')

plt.xlabel('Img_Min')
plt.ylabel('Age')
plt.show()
```



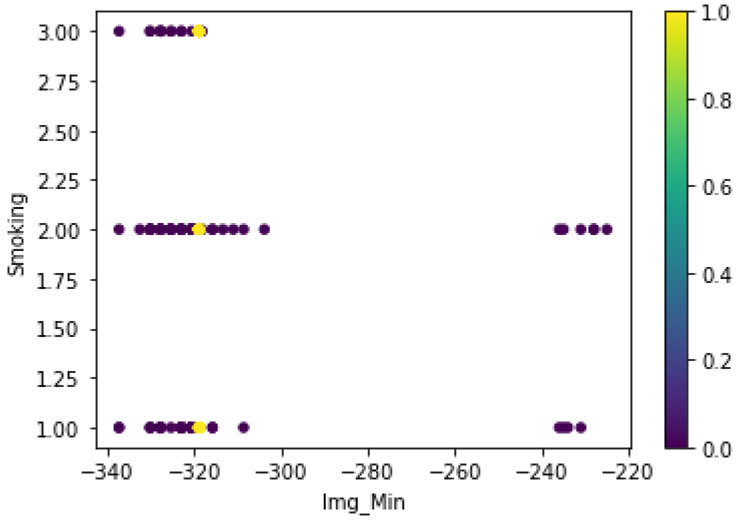


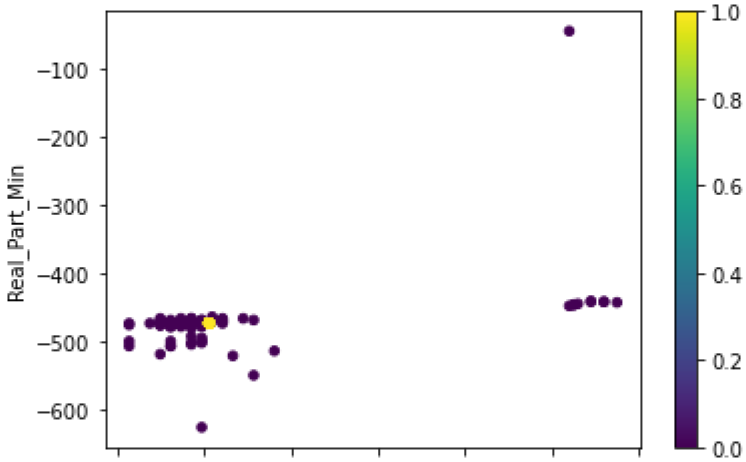
Note: Here the label of colormap/c (had_missing) is not being printed and ylabel is getting missed due to the bug of the pandas version - 1.4.2 I'm using.

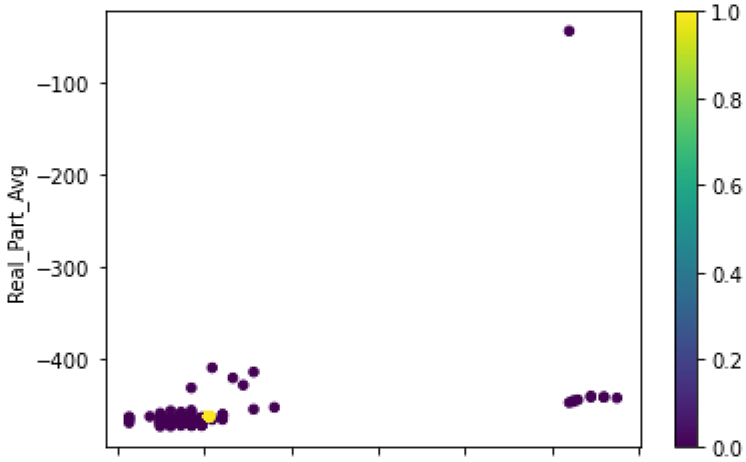
Extras from 'e' with different combinations with 'Imaginary_Part_Min'

In [7]:

```
fig, ax = plt.subplots()
exasens_df_non_nulls_df.plot(kind='scatter',
                                  x='Imaginary_Part_Min',
                                  y='Smoking',
                                  c=exasens_df_non_nulls_df['had_missing'],
                                  #color='purple',
                                  colormap='viridis',
                                  ax=ax)

plt.xlabel('Img_Min')
plt.ylabel('Smoking')




exasens_df_non_nulls_df.plot(kind='scatter',
                                  x='Imaginary_Part_Min',
                                  y='Real_Part_Min',
                                  c=exasens_df_non_nulls_df['had_missing'],
                                  #color='purple',
                                  colormap='viridis')

plt.xlabel('Img_Min')
plt.ylabel('Real_Part_Min')
plt.show()

exasens_df_non_nulls_df.plot(kind='scatter',
                                  x='Imaginary_Part_Min',
                                  y='Real_Part_Avg',
                                  c=exasens_df_non_nulls_df['had_missing'],
                                  #color='purple',
                                  colormap='viridis')

plt.xlabel('Img_Min')
plt.ylabel('Real_Part_Avg')
plt.show()
```







Question-2

Demonstrate an understanding of PCA and matrix factorization using SVD

In [3]:

```
# import library and dataset
from sklearn.datasets import load_iris
X,y = load_iris(return_X_y=True)
```

a)

In [3]:

```
#Collect all instances belonging to the same class in distinct data matrices
setosa_array = X[y==0]
versicolour_array = X[y==1]
virginica_array = X[y==2]

print(setosa_array[:5])
print("---------------------------------------------------")
print(versicolour_array[:5])
print("---------------------------------------------------")
print(virginica_array[:5])
```

```
[[5.1 3.5 1.4 0.2]
 [4.9 3.  1.4 0.2]
 [4.7 3.2 1.3 0.2]
 [4.6 3.1 1.5 0.2]
 [5.  3.6 1.4 0.2]]
---------------------------------------------------
[[7.  3.2 4.7 1.4]
 [6.4 3.2 4.5 1.5]
 [6.9 3.1 4.9 1.5]
 [5.5 2.3 4.  1.3]
 [6.5 2.8 4.6 1.5]]
---------------------------------------------------
[[6.3 3.3 6.  2.5]
 [5.8 2.7 5.1 1.9]
 [7.1 3.  5.9 2.1]
 [6.3 2.9 5.6 1.8]
 [6.5 3.  5.8 2.2]]
```

b)

In [4]:

```
#PCA Algorithm
def PCA(X, n_dim=2):
    # mean Centering the data
    X_meaned = X - np.mean(X , axis = 0)

    # calculating the covariance matrix of the mean-centered data.
    cov_mat = np.cov(X_meaned , rowvar = False)

    #Calculating Eigenvalues and Eigenvectors of the covariance matrix
    eigen_values , eigen_vectors = np.linalg.eigh(cov_mat)

    #sort the eigenvalues in descending order
    sorted_index = np.argsort(eigen_values)[::-1]
    sorted_eigenvalue = eigen_values[sorted_index]

    #similarly sort the eigenvectors
    sorted_eigenvectors = eigen_vectors[:,sorted_index]

    # select the first n eigenvectors, n is desired dimension of our final reduced d
    eigenvector_subset = sorted_eigenvectors[:,0:n_dim]

    #Transform the data
    X_reduced = np.dot(eigenvector_subset.transpose() , X_meaned.transpose() ).trans

    return X_reduced
```

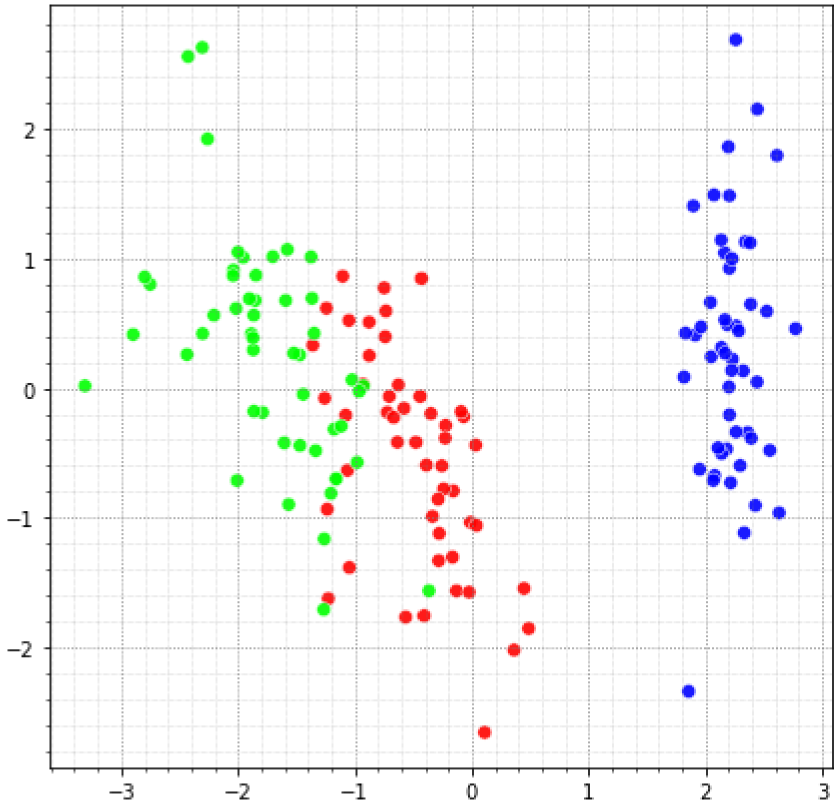
c)

In [5]:

```
# Plot 2D scatter of the iris dataset using PCA for x1 and x2
def plot(X,y=None):
    X_PCA = PCA(X , 2)
    assert(X_PCA.shape[1]==2)
    x1,x2 = X_PCA.T
    plt.figure(figsize=(7,7))
    #plt.axvline(x=0, c='r', lw=.5)
    #plt.axhline(y=0, c='r', lw=.5)
    #plt.scatter(x1,x2, c=y, alpha=.9, linewidths=0.5, edgecolors='w', cmap='viridis
    plt.scatter(x1,x2, c=y, alpha=.9, s=50, linewidths=0.5, edgecolors='w', cmap='br
    plt.grid(which='major', color='grey', linestyle=':')
    plt.minorticks_on()
    plt.grid(which='minor', color='grey', alpha=.6,  linestyle=':', lw=.5)
    plt.show()
```

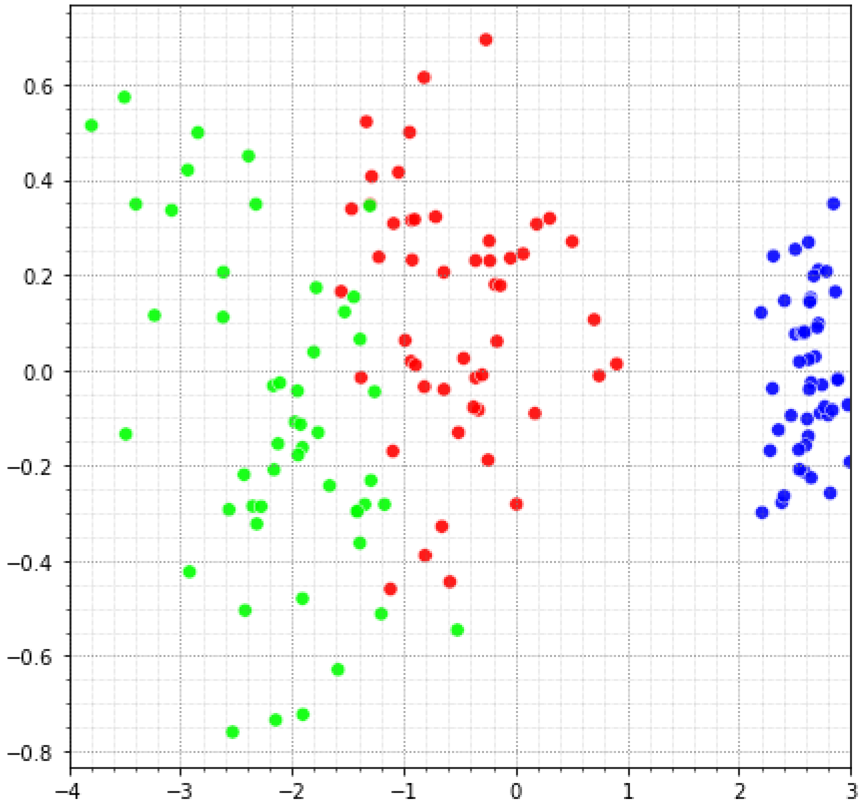
In [301]:

```
plot(X,y=y)
```



In [43]:

```
# Plot 2D scatter of the iris dataset using PCA for x1 and x3
def plot(X,y=None):
    X_PCA = PCA(X , 4)
    assert(X_PCA.shape[1]==4)
    x1,x2,x3,x4 = X_PCA.T
    plt.figure(figsize=(7,7))
    #plt.axvline(x=0, c='r', lw=.5)
    #plt.axhline(y=0, c='r', lw=.5)
    #plt.scatter(x1,x2, c=y, alpha=.9, linewidths=0.5, edgecolors='w', cmap='viridis
    plt.scatter(x1,x3, c=y, alpha=.9, s=50, linewidths=0.5, edgecolors='w', cmap='br
    plt.grid(which='major', color='grey', linestyle=':')
    plt.minorticks_on()
    plt.grid(which='minor', color='grey', alpha=.6,  linestyle=':', lw=.5)
    plt.xlim(-4,3)
    #plt.ylim(-1.5,2.0)
    plt.show()

plot(X, y=y)
```



d)

In [6]:

```
# Perform a low rank reconsruction of a data matrix
def low_rank_reconstruction(X, r):
    Dn = X
    #Dn = np.mat(X - np.mean(X,axis=0))

    # Compute truncated SVD
    U, S, Vt = np.linalg.svd(Dn)
    Z = U[:, :r] @ np.diag(S[:r]) @ Vt[:r, :]

    V = Vt.T
    #Z = Dn * V

    U, S, Vt = np.linalg.svd(X)
    Z = U[:, :r] @ np.diag(S[:r]) @ Vt[:r, :]

    #print('approx matrix: \n', Z[:10])
    #print ('Rank of Output Matrix: ', r)
    return Z
```

e)

In [7]:

```
def reconstruction_error(X,r):
    orig_n = X
    #orig_n = np.mat(X - np.mean(X,axis=0))

    approx = low_rank_reconstruction(X, r)

    #diff = np.subtract(X,approx)
    diff = np.sum(X,axis=1) - np.sum(approx,axis=1)

    #print('Diff:\n',diff)
    err = np.array(diff.flat)
    return err
```

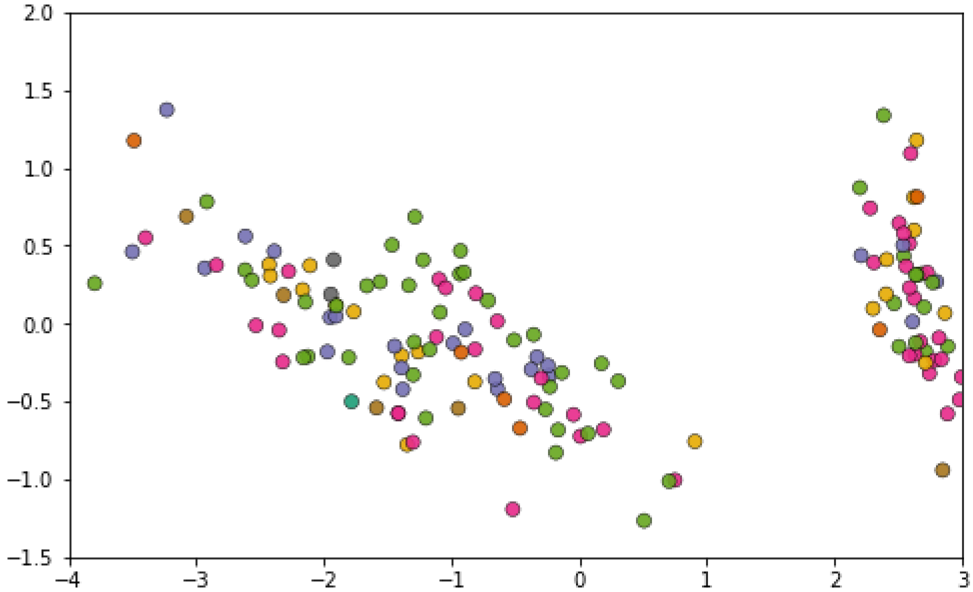
In [8]:

```
err = reconstruction_error(X, r=3)
```

f)

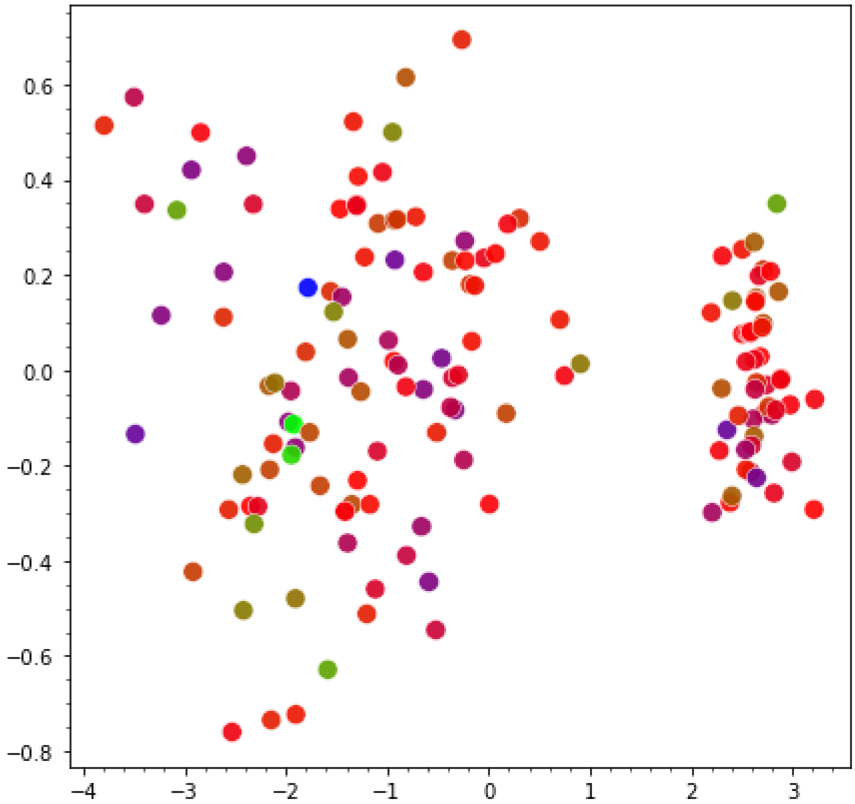
In [9]:

```
# Plot 2D scatter of the iris dataset using PCA for x1 and x2
def plot(X,y=None):
    X_PCA = PCA(X , 2)
    assert(X_PCA.shape[1]==2)
    x1,x2 = X_PCA.T
    plt.figure(figsize=(8,5))
    plt.scatter(x1,x2, c=y, alpha=.9, s=50, linewidths=0.5, edgecolors='black', cmap
    plt.xlim(-4,3)
    plt.ylim(-1.5,2.0)
    plt.show()
plot(X,y=err)
```



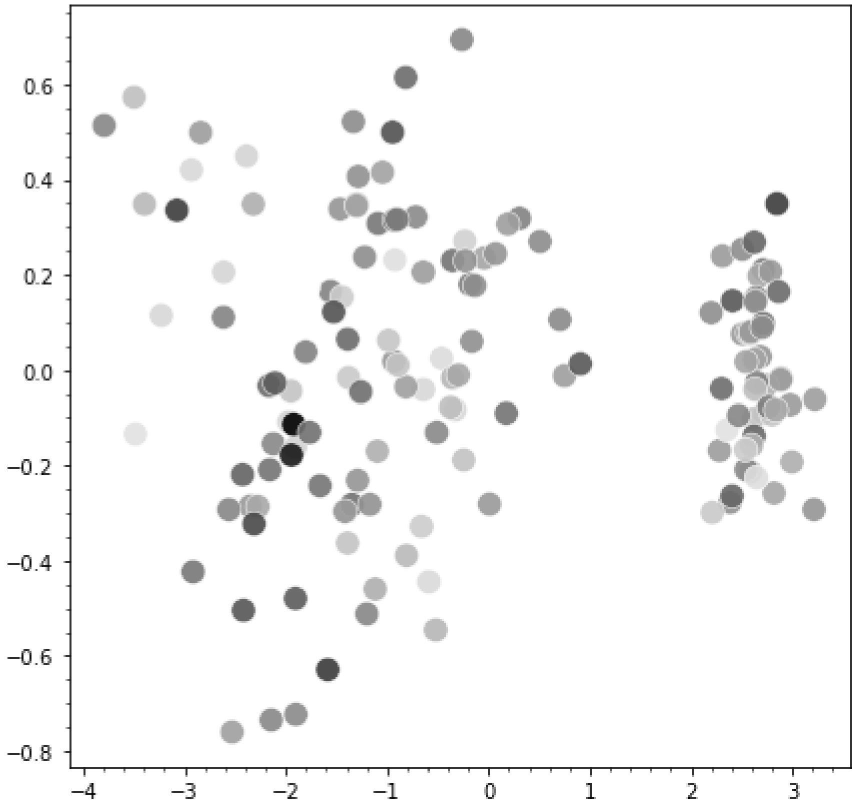
In [10]:

```
# Plot 2D scatter of the iris dataset using PCA for x1 and x3
def plot(X,y=None):
    X_PCA = PCA(X, 4)
    x1,x2,x3,x4 = X_PCA.T
    plt.figure(figsize=(7,7))
    plt.scatter(x1,x3, c=y, alpha=.9, s=100, linewidths=0.5, edgecolors='w', cmap='b
    plt.minorticks_on()
    plt.show()
plot(X,y=err)
```



In [11]:

```
# Plot 2D scatter of the iris dataset using PCA for x1 and x3 in Greys
def plot(X,y=None):
    X_PCA = PCA(X, 4)
    x1,x2,x3,x4 = X_PCA.T
    plt.figure(figsize=(7,7))
    plt.scatter(x1,x3, c=y, alpha=.9, s=150, linewidths=0.5, edgecolors='w', cmap='G
    plt.minorticks_on()
    plt.show()
plot(X,y=err)
```



Question-3

Demonstrate an understanding of LDA

a)

In [2]:

```
def make_means(k, radius):
    mu = (np.random.rand(k)*2-1)*radius
    return mu
```

b)

In [3]:

```
def make_covariance(ratio, rotation):
    theta = np.radians(rotation)
    c, s = np.cos(theta), np.sin(theta)
    R = np.array([[c, -s], [s, c]])
    S = np.diag([ratio, 1])
    L = S**2
    return R@L@R.T
```

In [94]:

```
var = make_covariance(2, 45)
var
```

Out[94]:

```
array([[2.5, 1.5],
       [1.5, 2.5]])
```

c)

In [5]:

```
def make_mean_and_cov(n, scale=2):
    #mu = (np.random.rand(n)*2-1)*scale
    mu = make_means(n,scale)
    return mu, make_covariance(n, scale)

def make_data(k=5, n_instances=500, radius=10, ratio=2):
    Ds = [np.random.multivariate_normal(*make_mean_and_cov(radius, ratio), n_instanc
    X = np.vstack(Ds)
    y = np.hstack([[i]*D.shape[0] for i, D in enumerate(Ds)])
    return np.mat(X),y.reshape(-1)
```

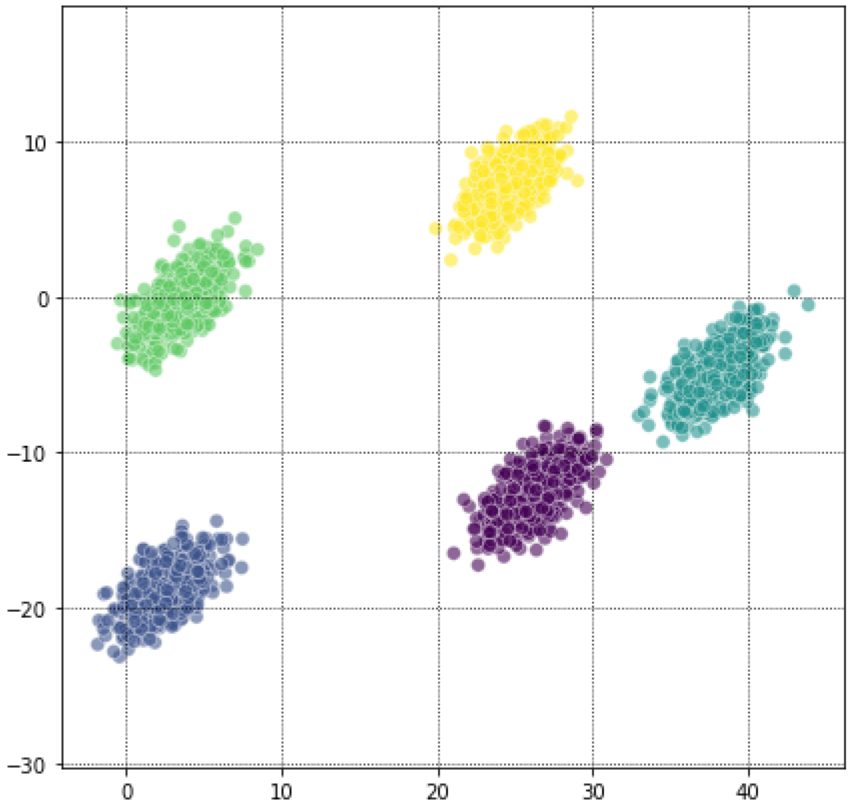
d)

In [6]:

```
def plot(M,y=None):
    #assert(M.shape[1]==2)
    x1,x2 = M.A.T
    plt.figure(figsize=(7,7))
    #plt.axvline(x=0, c='r', lw=.5)
    #plt.axhline(y=0, c='r', lw=.5)
    if y is None:
        plt.scatter(x1,x2, alpha=.6, s=200, linewidths=0.5, edgecolors='w', cmap='vi
    else:
        plt.scatter(x1,x2, c=y, alpha=.6, s=50,  linewidths=0.5, edgecolors='w', cma
    plt.grid(which='major', color='black', linestyle=':')
    #plt.minorticks_on()
    plt.grid(which='minor', color='black', alpha=.3,  linestyle=':', lw=.5)
    plt.axis('equal')
    #plt.xlim(-15, 15)
    #plt.ylim(-15, 10)
    plt.show()
```

In [156]:

```
data_matrix,targets = make_data(k=5, n_instances=500, radius=2, ratio=45)
plot(data_matrix,targets)
```



e)

LDA Model

In [8]:

```
def covariance_matrix(D):
    n = D.shape[0]-1
    C = np.mat(D-np.mean(D,axis=0))
    S = C.T*C/n
    return S

def mean(D):
    return np.mat(np.mean(D,axis=0)).reshape(-1,1)

def LDA_factors(D,N):
    pi = D.shape[0]/N
    mu = mean(D)
    S = covariance_matrix(D)
    return pi,mu,S

def fit_LDA(data_matrix, targets):
    #assert y[y==0].shape[0] + y[y==1].shape[0] == y.shape[0], 'Expecting 2 classes

    D0 = data_matrix[targets==0]
    D1 = data_matrix[targets==1]

    pi0,mu0,S0 = LDA_factors(D0,data_matrix.shape[0])
    pi1,mu1,S1 = LDA_factors(D1,data_matrix.shape[0])

    S = np.mat((S0+S1)/2)
    SI = S.I
    w = SI*(mu0-mu1)
    c = np.log(pi0/pi1) -0.5 *mu0.T * SI * mu0 +0.5 *mu1.T * SI * mu1

    return w,c
```

f)

In [9]:

```
def test_LDA(data_matrix, params):
    return 1 - (data_matrix * params > -c).astype(int).A.reshape(-1)
```

g)

In [10]:

```
def make_grid(D, n=10):
    mn = np.min(D.A,axis=0).reshape(-1)
    mx = np.max(D.A,axis=0).reshape(-1)
    dat1 = np.linspace(mn[0],mx[0],n)
    dat2 = np.linspace(mn[1],mx[1],n)
    #dat3 = np.linspace(mn[2],mx[2],n)
    #grid = [(x1,x2, x3) for x1 in dat1 for x2 in dat2 for x3 in dat3]
    grid = [(x1,x2) for x1 in dat1 for x2 in dat2]
    grid = np.mat(grid)
    return grid
```

h)

Generating 500 instances with 2D Model

In [93]:

```
# Generating datasets
data_matrix,targets = make_data(k=5, n_instances=500, radius=2, ratio=2)

#Fitting LDA
params,c = fit_LDA(data_matrix,targets)

#Making Grid
G = make_grid(data_matrix, n=30)

#Testing LDA
p = test_LDA(G, params)

#Merging
X2 = np.vstack([data_matrix,G])
y2 = np.hstack([targets,p])

#plot
plot(X2,y2)
```