Worksheet 10

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Topics

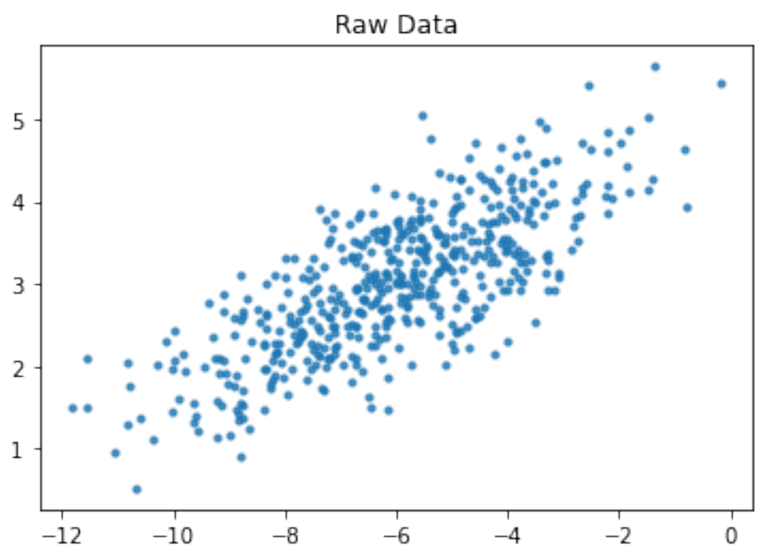
- Singular Value Decomposition

Feature Extraction

SVD finds features that are orthogonal. The Singular Values correspond to the importance of the feature or how much variance in the data it captures.

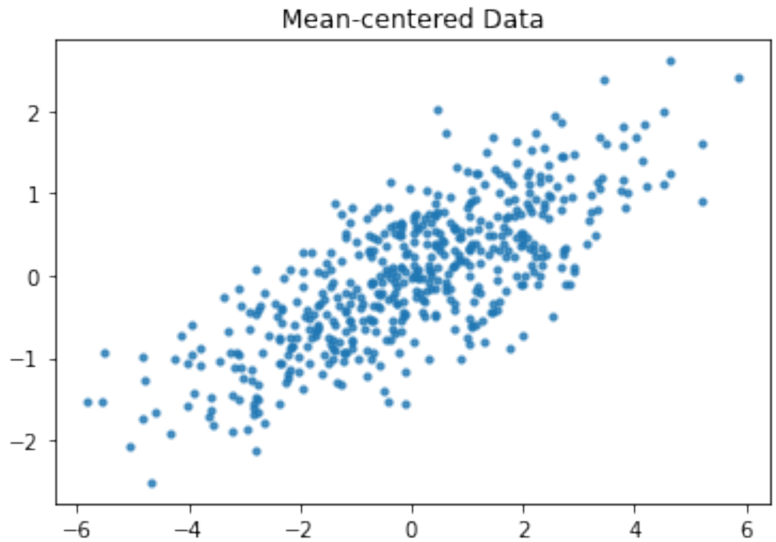
In [1]:

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

n_samples = 500
C = np.array([[0.1, 0.6], [2., .6]])
X = np.random.randn(n_samples, 2) @ C + np.array([-6, 3])
plt.scatter(X[:, 0], X[:, 1], s=10, alpha=0.8)
plt.title("Raw Data")
plt.show()
```



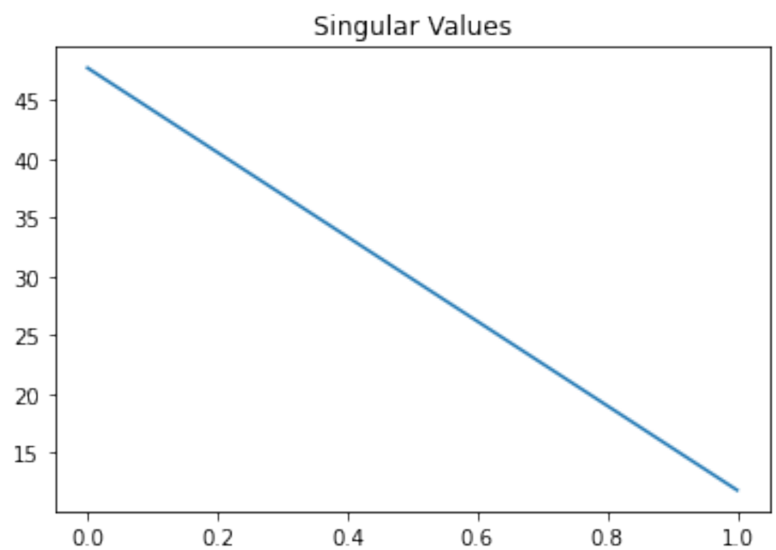
In [2]:

```
X = X - np.mean(X, axis=0)
plt.scatter(X[:, 0], X[:, 1], s=10, alpha=0.8)
plt.title("Mean-centered Data")
plt.show()
```



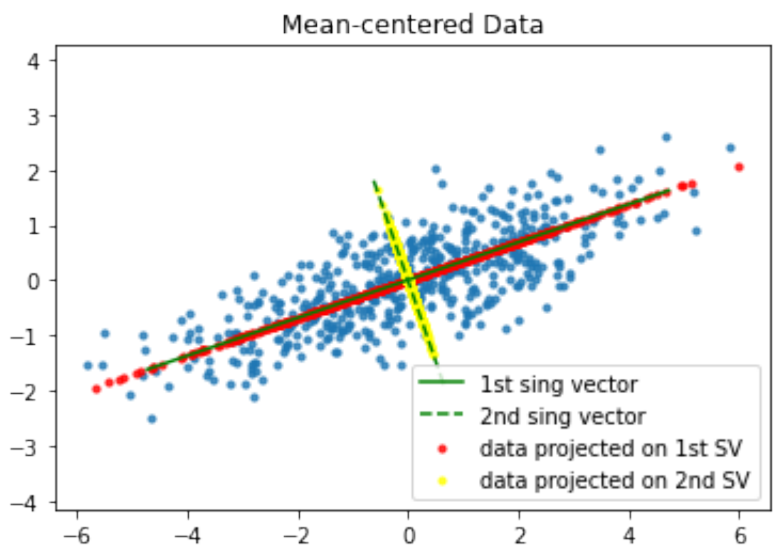
In [3]:

```
u,s,vt=np.linalg.svd(X, full_matrices=False)
plt.plot(s) # only 2 singular values
plt.title("Singular Values")
plt.show()
```



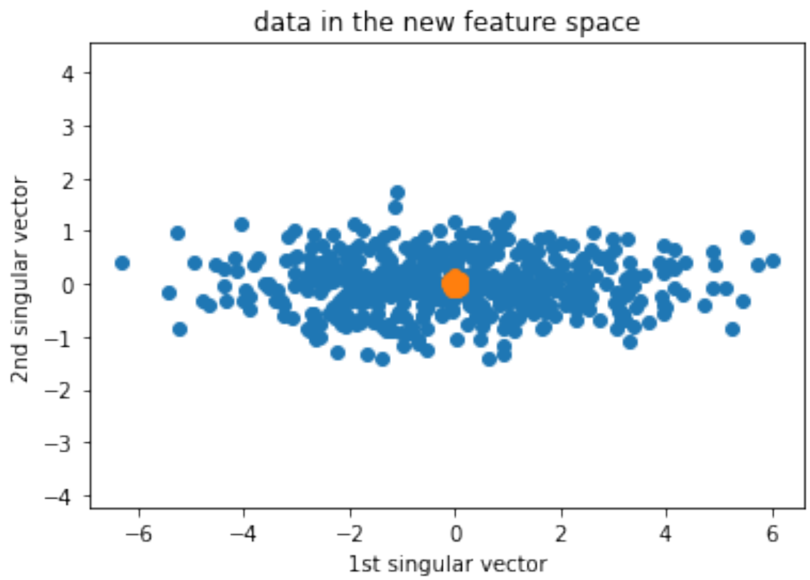
In [4]:

```
scopy0 = s.copy()
scopy1 = s.copy()
scopy0[1:] = 0.0
scopy1[:1] = 0.0
approx0 = u.dot(np.diag(scopy0)).dot(vt)
approx1 = u.dot(np.diag(scopy1)).dot(vt)
plt.scatter(X[:, 0], X[:, 1], s=10, alpha=0.8)
sv1 = np.array([[-5],[5]]) @ vt[[0],:]
sv2 = np.array([[-2],[2]]) @ vt[[1],:]
plt.plot(sv1[:,0], sv1[:,1], 'g-', label="1st sing vector")
plt.plot(sv2[:,0], sv2[:,1], 'g--', label="2nd sing vector")
plt.scatter(approx0[:, 0] , approx0[:, 1], s=10, alpha=0.8, color="red", labe
plt.scatter(approx1[:, 0] , approx1[:, 1], s=10, alpha=0.8, color="yellow", l
plt.axis('equal')
plt.legend()
plt.title("Mean-centered Data")
plt.show()
```



In [5]:

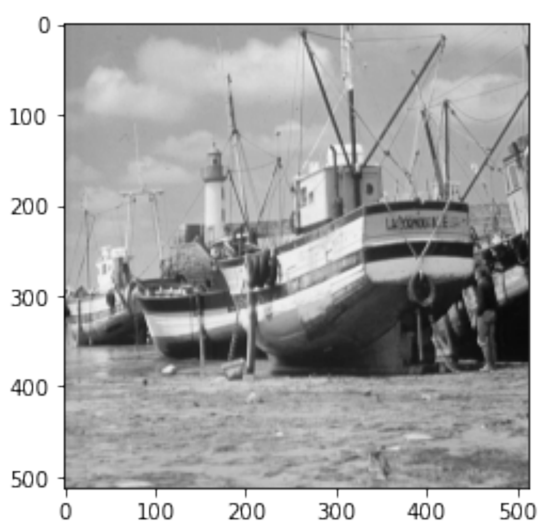
```
# show ouput from svd is the same
orthonormal_X = u
shifted_X = u.dot(np.diag(s))
plt.axis('equal')
plt.scatter(shifted_X[:,0], shifted_X[:,1])
plt.scatter(orthonormal_X[:,0], orthonormal_X[:,1])
plt.xlabel("1st singular vector")
plt.ylabel("2nd singular vector")
plt.title("data in the new feature space")
plt.show()
```



In [6]:

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

boat = np.loadtxt('./boat.dat')
plt.figure()
plt.imshow(boat, cmap = cm.Greys_r)
```

Out[6]: <matplotlib.image.AxesImage at 0x7f7c5a255be0>

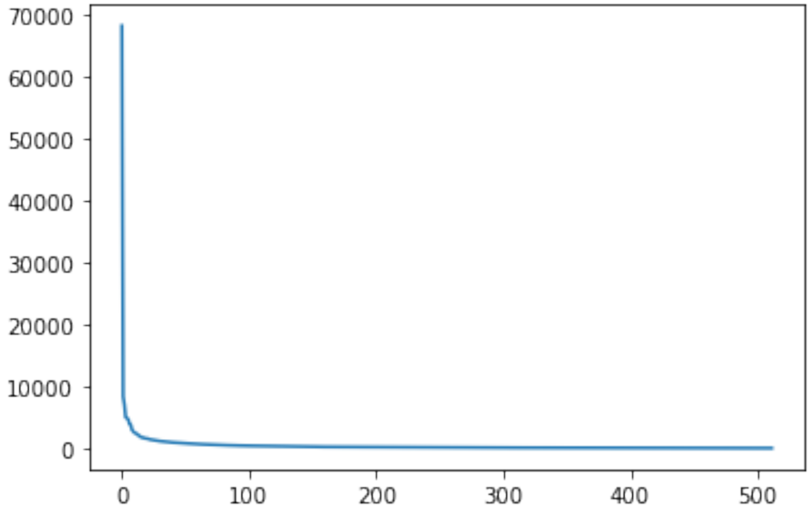


a) Plot the singular values of the image above (note: a gray scale image is just a matrix).

In [7]:

```
u,s,vt=np.linalg.svd(boat,full_matrices=False)
plt.plot(s)
```

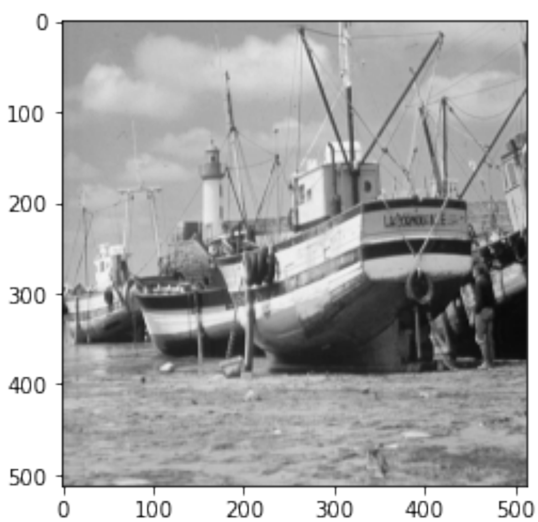
Out[7]: [<matplotlib.lines.Line2D at 0x7f7c48976850>]



Notice you can get the image back by multiplying the matrices back together:

In [8]:
```
boat_copy = u.dot(np.diag(s)).dot(vt)
plt.figure()
plt.imshow(boat_copy, cmap = cm.Greys_r)
```

Out[8]: <matplotlib.image.AxesImage at 0x7f7c5a22a220>

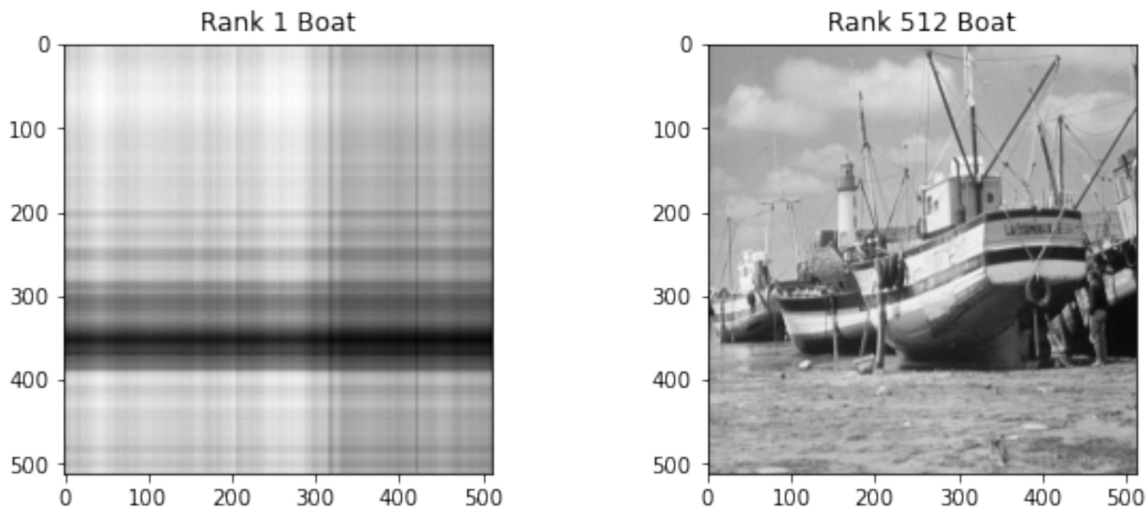


b) Create a new matrix `scopy` which is a copy of `s` with all but the first singular value set to 0.

In [9]:
```
scopy = s.copy() #copy singular values
scopy[1:] = 0.0 #first columns reperesent the most variants in data, loosing
```

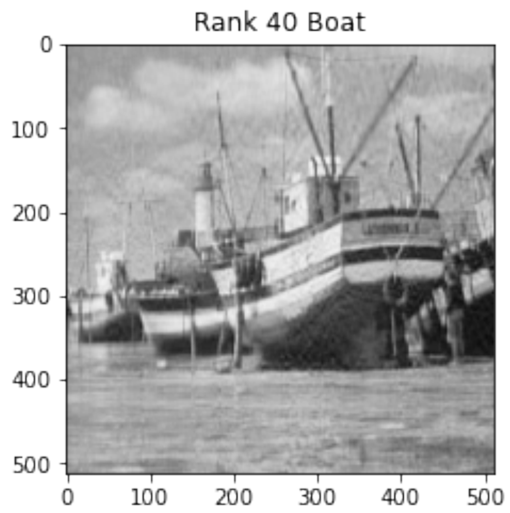
c) Create an approximation of the boat image by multiplying `u`, `scopy`, and `v` transpose. Plot them side by side.

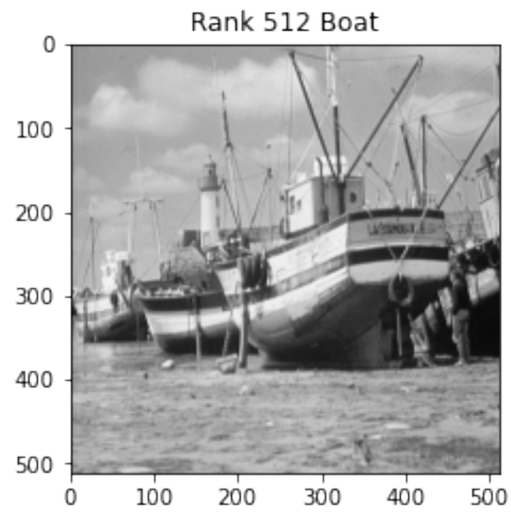
In [10]:
```
boat_app = u.dot(np.diag(scopy)).dot(vt)

plt.figure(figsize=(9,6))
plt.subplot(1,2,1)
plt.imshow(boat_app, cmap = cm.Greys_r)
plt.title('Rank 1 Boat')
plt.subplot(1,2,2)
plt.imshow(boat, cmap = cm.Greys_r)
plt.title('Rank 512 Boat')
_ = plt.subplots_adjust(wspace=0.5)
plt.show()
```



d) Repeat c) with 40 singular values instead of just 1.

In [11]:
```
scopy = s.copy() #copy singular values
scopy[40:] = 0.0

boat_app = u.dot(np.diag(scopy)).dot(vt)

plt.figure(figsize=(9,6))
plt.subplot(1,2,1)
plt.imshow(boat_app, cmap = cm.Greys_r)
plt.title('Rank 40 Boat')
plt.subplot(1,2,2)
plt.imshow(boat, cmap = cm.Greys_r)
plt.title('Rank 512 Boat')
_ = plt.subplots_adjust(wspace=0.5)
plt.show()
```





Why you should care

a) By using an approximation of the data, you can improve the performance of classification tasks since:

1. there is less noise interfering with classification
2. no relationship between features after SVD
3. the algorithm is sped up when reducing the dimension of the dataset

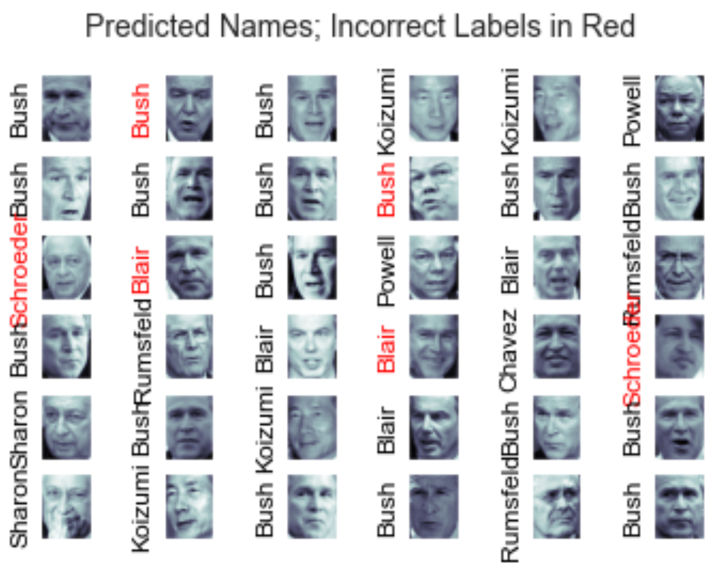
Below is some code to perform facial recognition on a dataset. Notice that, applied blindly, it does not perform well:

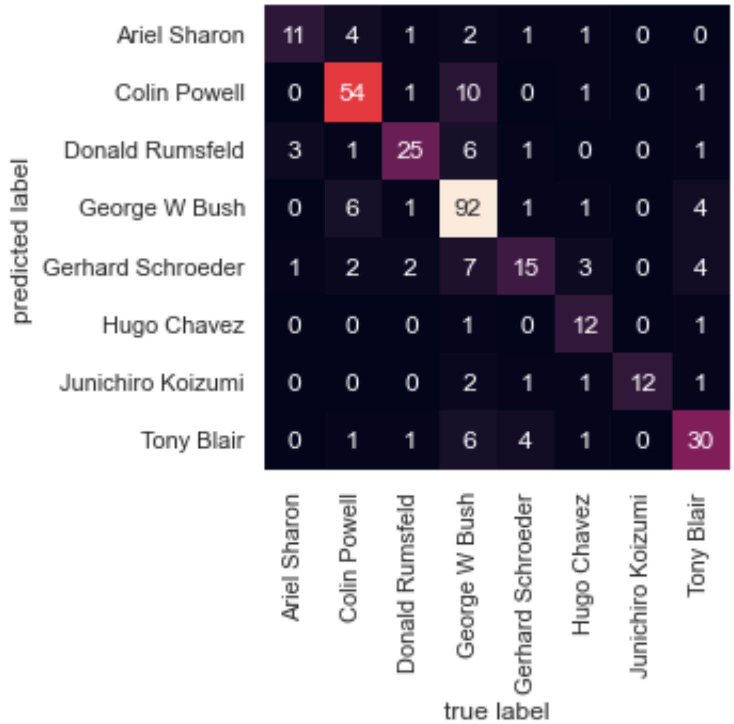
In [12]:
```
# %pip install seaborn
# %pip install scikit-learn
import numpy as np
from PIL import Image
import seaborn as sns
from sklearn.svm import SVC
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.pipeline import make_pipeline
from sklearn.metrics import confusion_matrix, accuracy_score
from sklearn.datasets import fetch_lfw_people
from sklearn.ensemble import BaggingClassifier
from sklearn.model_selection import GridSearchCV, train_test_split

sns.set()

# Get face data
faces = fetch_lfw_people(min_faces_per_person=60)

# plot face data
fig, ax = plt.subplots(3, 5)
```

```
for i, axi in enumerate(ax.flat):
    axi.imshow(faces.images[i], cmap='bone')
    axi.set(xticks=[], yticks=[],
            xlabel=faces.target_names[faces.target[i]])
plt.show()

# split train test set
Xtrain, Xtest, ytrain, ytest = train_test_split(faces.data, faces.target, ran

# blindly fit svm
svc = SVC(kernel='rbf', class_weight='balanced', C=5, gamma=0.001)

# fit model
model = svc.fit(Xtrain, ytrain)
yfit = model.predict(Xtest)

fig, ax = plt.subplots(6, 6)
for i, axi in enumerate(ax.flat):
    axi.imshow(Xtest[i].reshape(62, 47), cmap='bone')
    axi.set(xticks=[], yticks=[])
    axi.set_ylabel(faces.target_names[yfit[i]].split()[-1],
                   color='black' if yfit[i] == ytest[i] else 'red')
fig.suptitle('Predicted Names; Incorrect Labels in Red', size=14)
plt.show()

mat = confusion_matrix(ytest, yfit)
sns.heatmap(mat.T, square=True, annot=True, fmt='d', cbar=False,
            xticklabels=faces.target_names,
            yticklabels=faces.target_names)
plt.xlabel('true label')
plt.ylabel('predicted label')
plt.show()

print("Accuracy = ", accuracy_score(ytest, yfit))
```

```
/Users/nyx/opt/anaconda3/lib/python3.9/site-packages/pandas/core/computation/e
xpressions.py:21: UserWarning: Pandas requires version '2.8.0' or newer of 'nu
mexpr' (version '2.7.3' currently installed).
  from pandas.core.computation.check import NUMEXPR_INSTALLED
/Users/nyx/opt/anaconda3/lib/python3.9/site-packages/pandas/core/arrays/maske
d.py:62: UserWarning: Pandas requires version '1.3.4' or newer of 'bottleneck'
(version '1.3.2' currently installed).
  from pandas.core import (
```


Colin Powell
George W Bush
George W Bush
George W Bush
Hugo Chavez
George W Bush
Junichiro Koizumi
George W Bush
Tony Blair
Ariel Sharon
George W Bush
Donald Rumsfeld
George W Bush
George W Bush
George W Bush


Predicted Names; Incorrect Labels in Red
Bush
Bush
Schroeder
Bush
Sharon
Sharon
Bush
Bush
Blair
Rumsfeld
Bush
Koizumi
Bush
Bush
Bush
Blair
Koizumi
Bush
Koizumi
Bush
Powell
Blair
Blair
Bush
Koizumi
Bush
Blair
Chavez
Bush
Rumsfeld
Powell
Bush
Rumsfeld
Schroeder
Bush
Bush

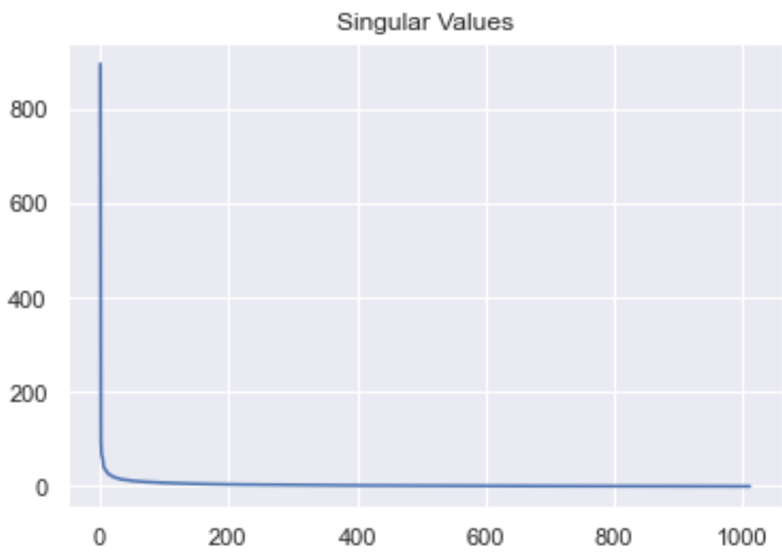


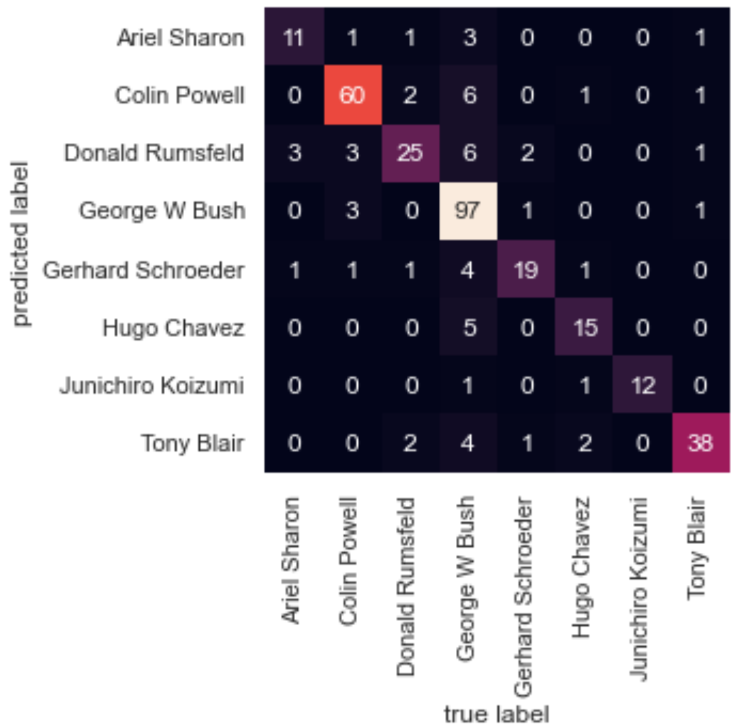

```
Accuracy =  0.744807121661721
```

By performing SVD before applying the classification tool, we can reduce the dimension of the dataset.

In [13]:

```
# look at singular values
_, s, _ = np.linalg.svd(Xtrain, full_matrices=False)
plt.plot(range(1,len(s)+1),s)
plt.title("Singular Values")
plt.show()

# extract principal components
pca = PCA(n_components=100, whiten=True)
svc = SVC(kernel='rbf', class_weight='balanced', C=5, gamma=0.001)
svcpca = make_pipeline(pca, svc)
model = svcpca.fit(Xtrain, ytrain)
yfit = model.predict(Xtest)

fig, ax = plt.subplots(6, 6)
for i, axi in enumerate(ax.flat):
    axi.imshow(Xtest[i].reshape(62, 47), cmap='bone')
    axi.set(xticks=[], yticks=[])
    axi.set_ylabel(faces.target_names[yfit[i]].split()[-1],
                   color='black' if yfit[i] == ytest[i] else 'red')
fig.suptitle('Predicted Names; Incorrect Labels in Red', size=14)
plt.show()

mat = confusion_matrix(ytest, yfit)
sns.heatmap(mat.T, square=True, annot=True, fmt='d', cbar=False,
            xticklabels=faces.target_names,
            yticklabels=faces.target_names)
plt.xlabel('true label')
plt.ylabel('predicted label')
plt.show()

print("Accuracy = ", accuracy_score(ytest, yfit))
```





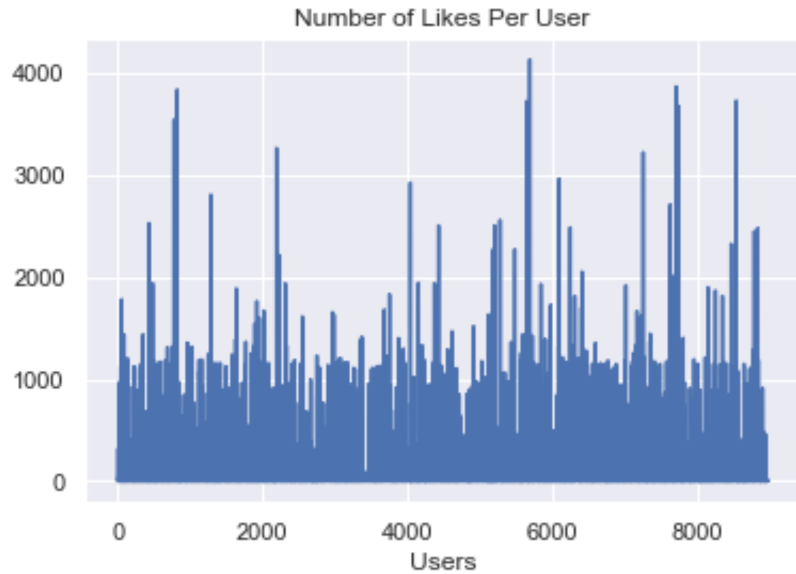

```
Accuracy =  0.8219584569732937
```

Similar to finding k in K-means, we're trying to find the point of diminishing returns when picking the number of singular vectors (also called principal components).

b) SVD can be used for anomaly detection.

The data below consists of the number of 'Likes' during a six month period, for each of 9000 users across the 210 content categories that Facebook assigns to pages.

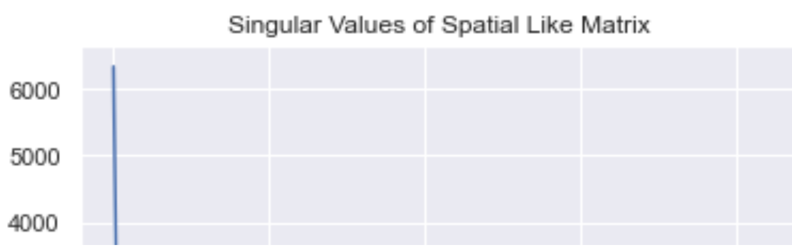
In [14]:
```
data = np.loadtxt('spatial_data.txt')

FBSpatial = data[:,1:]
FBSnorm = np.linalg.norm(FBSpatial,axis=1,ord=1)
plt.plot(FBSnorm)
plt.title('Number of Likes Per User')
_ = plt.xlabel('Users')
plt.show()
```

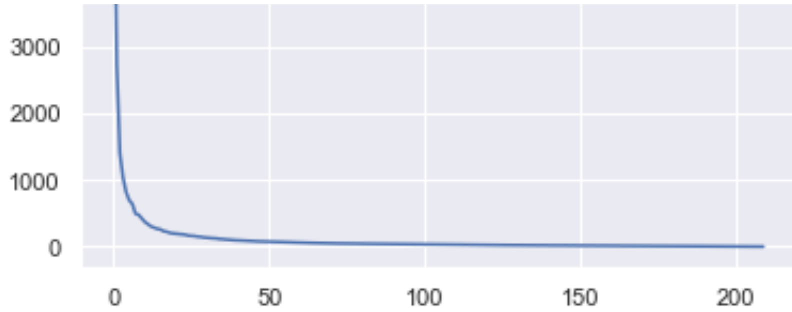


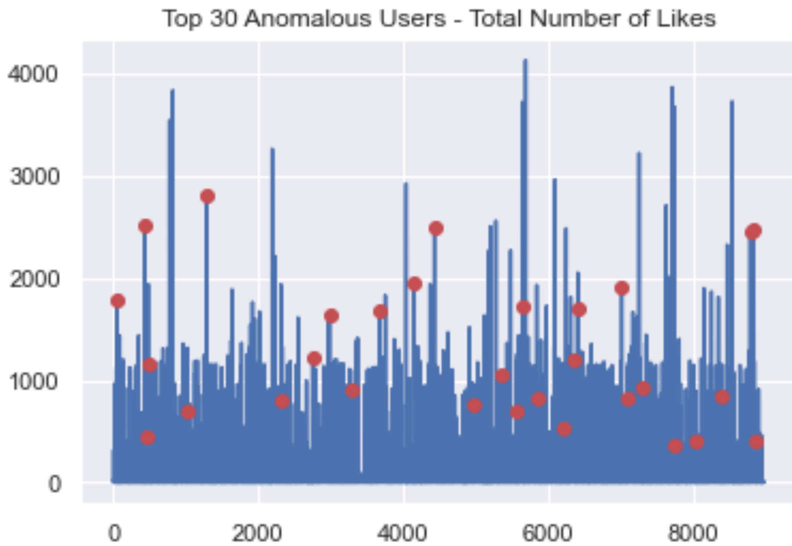
How users distribute likes across categories follows a general pattern that most users follow. This behavior can be captured using few singular vectors. And anomalous users can be easily identified.

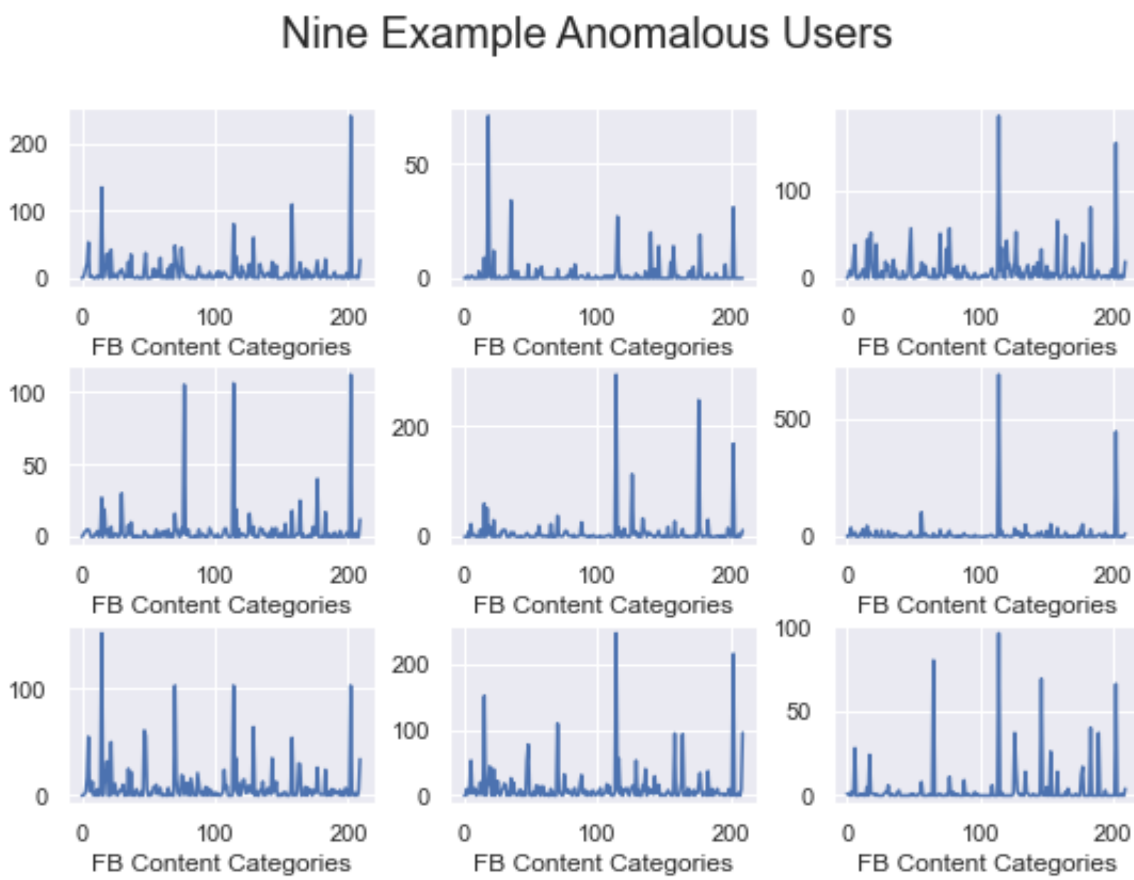
In [15]:

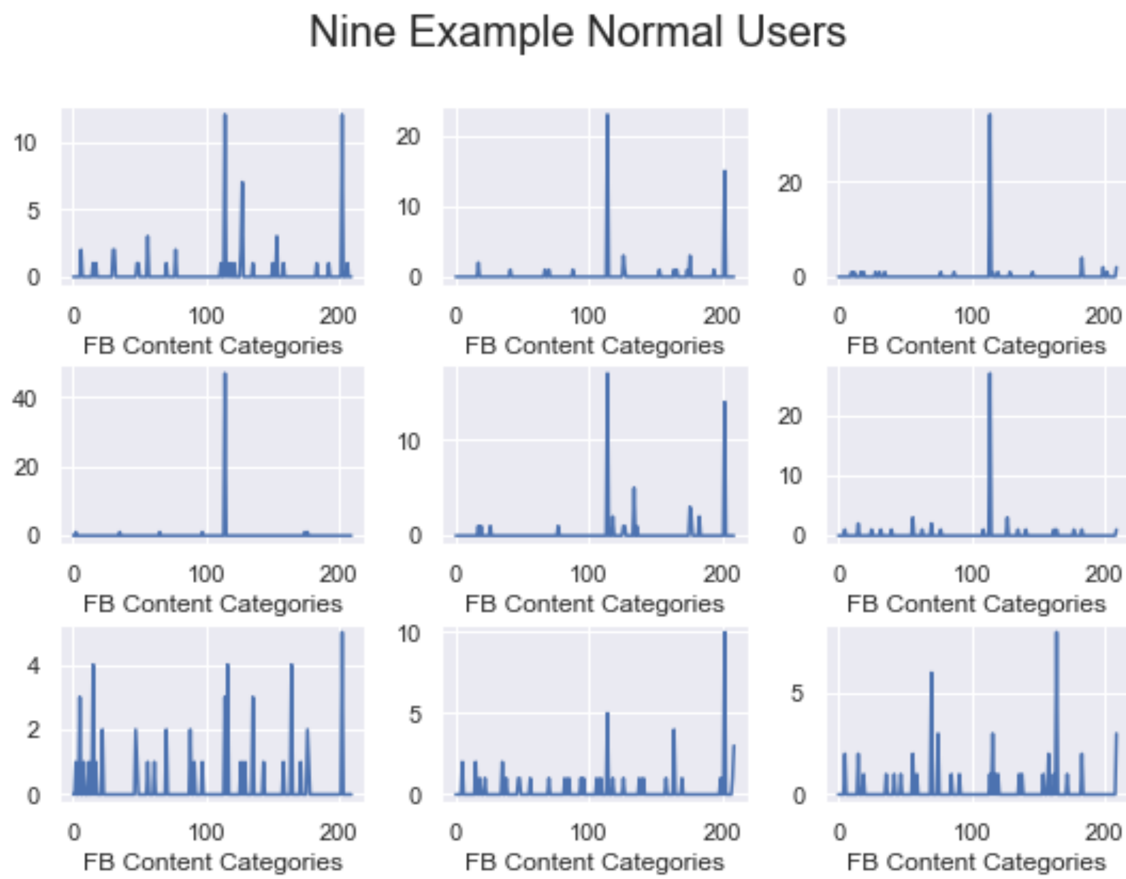
```
u,s,vt = np.linalg.svd(FBSpatial,full_matrices=False)
plt.plot(s)
_ = plt.title('Singular Values of Spatial Like Matrix')
plt.show()

RANK = 10
scopy = s.copy()
scopy[RANK:] = 0.
N = u @ np.diag(scopy) @ vt
O = FBSpatial - N
Onorm = np.linalg.norm(O, axis=1)
anomSet = np.argsort(Onorm)[-30:]
# plt.plot(Onorm)
# plt.plot(anomSet, Onorm[anomSet],'ro')
# _ = plt.title('Norm of Residual (rows of O)')
# plt.show()

plt.plot(FBSnorm)
plt.plot(anomSet, FBSnorm[anomSet],'ro')
_ = plt.title('Top 30 Anomalous Users - Total Number of Likes')
plt.show()

# anomalous users
plt.figure(figsize=(9,6))
for i in range(1,10):
    ax = plt.subplot(3,3,i)
    plt.plot(FBSpatial[anomSet[i-1],:])
    plt.xlabel('FB Content Categories')
plt.subplots_adjust(wspace=0.25,hspace=0.45)
_ = plt.suptitle('Nine Example Anomalous Users',size=20)
plt.show()

# normal users
set = np.argsort(Onorm)[0:7000]
# that have high overall volume
max = np.argsort(FBSnorm[set])[::-1]
plt.figure(figsize=(9,6))
for i in range(1,10):
    ax = plt.subplot(3,3,i)
    plt.plot(FBSpatial[set[max[i-1]],:])
    plt.xlabel('FB Content Categories')
plt.subplots_adjust(wspace=0.25,hspace=0.45)
_ = plt.suptitle('Nine Example Normal Users',size=20)
plt.show()
```






Top 30 Anomalous Users - Total Number of Likes

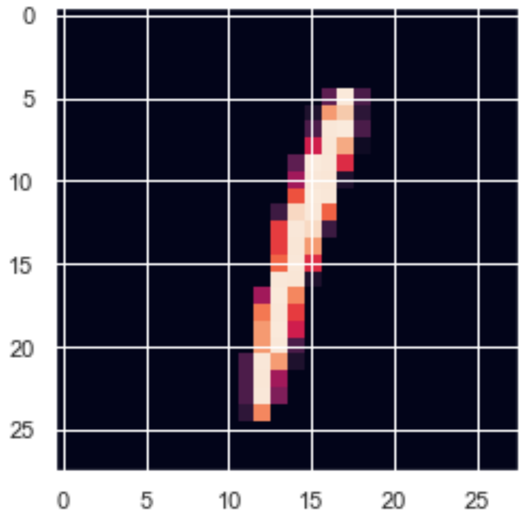

Nine Example Anomalous Users
FB Content Categories



Challenge Problem

a) Fetch the "mnist_784" data. Pick an image of a digit at random and plot it.

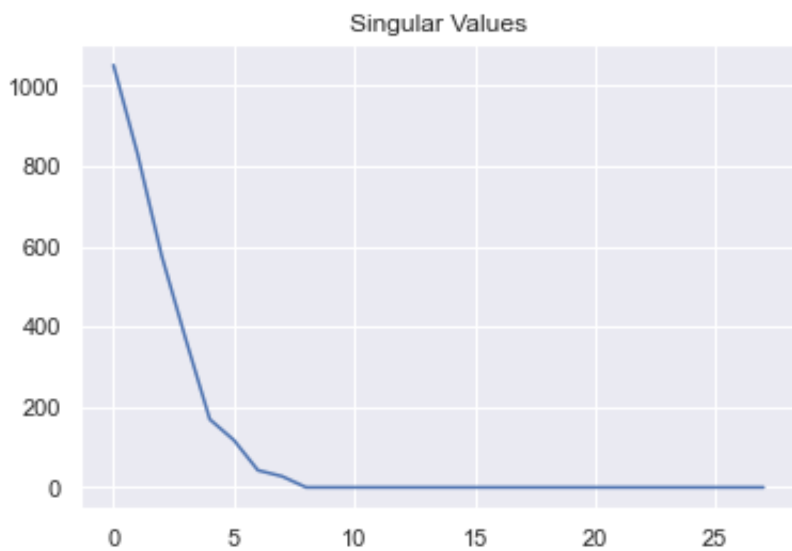
In [16]:
```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.datasets import fetch_openml
import matplotlib.cm as cm

X, y = fetch_openml(name="mnist_784", version=1, return_X_y=True, as_frame=Fa

# your code here
#get random image
random_index = np.random.randint(0, X.shape[0])
digit_img = X[random_index].reshape(28, 28)

plt.imshow(digit_img)
plt.show()
```



b) Plot its singular value plot.

In [17]:

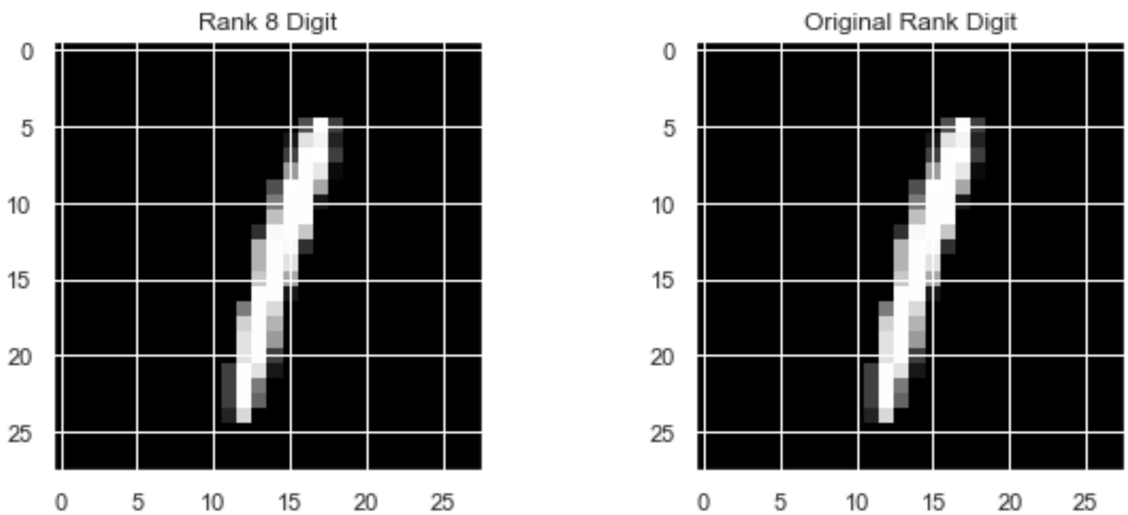
```
u,s,vt = np.linalg.svd(digit_img,full_matrices=False)
plt.plot(s)
_ = plt.title('Singular Values')
plt.show()
```



c) By setting some singular values to 0, plot the approximation of the image next to the original image

In [18]:

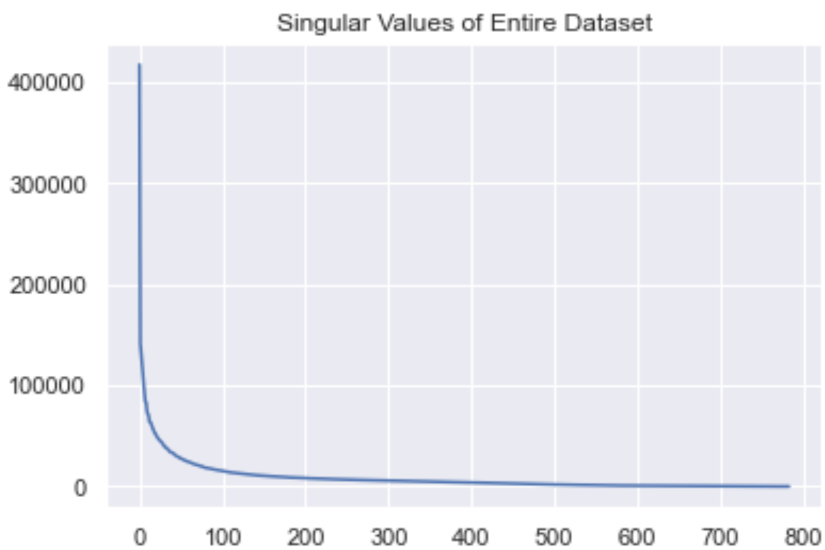
```
scopy = s.copy() #copy singular values
scopy[8:] = 0.0

digit_app = u.dot(np.diag(scopy)).dot(vt)

plt.figure(figsize=(9,6))
plt.subplot(1,2,1)
plt.imshow(digit_app, cmap = cm.Greys_r)
plt.title('Rank 8 Digit')
plt.subplot(1,2,2)
plt.imshow(digit_img, cmap = cm.Greys_r)
plt.title('Original Rank Digit')
_ = plt.subplots_adjust(wspace=0.5)
plt.show()
```

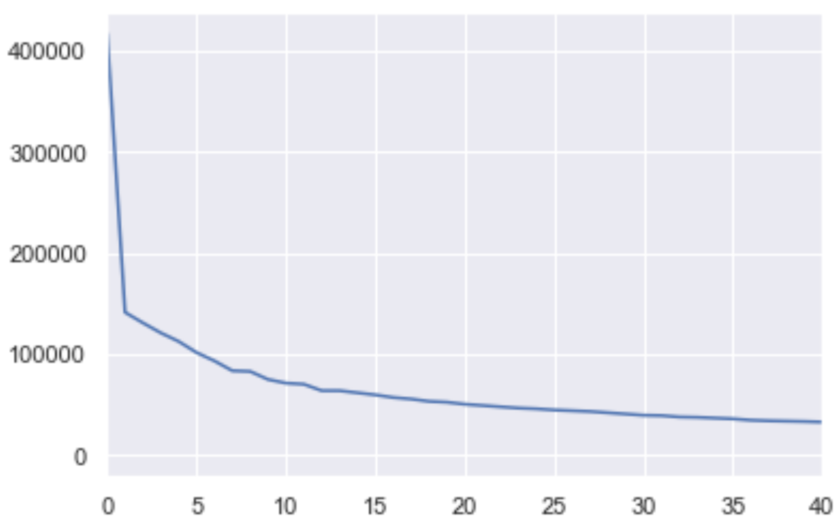


d) Consider the entire dataset as a matrix. Perform SVD and explain why / how you chose a particular rank. Note: you may not be able to run this on the entire dataset in a reasonable amount of time so you may take a small random sample for this and the following questions.

In [19]:

```
u, s, vt = np.linalg.svd(X, full_matrices=False)
_ = plt.title('Singular Values of Entire Dataset')
plt.plot(s)
plt.show()
plt.xlim(0, 40)
plt.plot(s)
plt.show()

scopy = s.copy() #copy singular values
scopy[10:] = 0.0
data_approx = u.dot(np.diag(scopy)).dot(vt)

#Based upon the singular values, we can perform the elbow method and
#pick the rank just before the point where the singular values/number of clus
#I would pick a rank around 10, as this point (see zoomed in graph below)
#indicates that adding more singular values does not significantly contribute
```



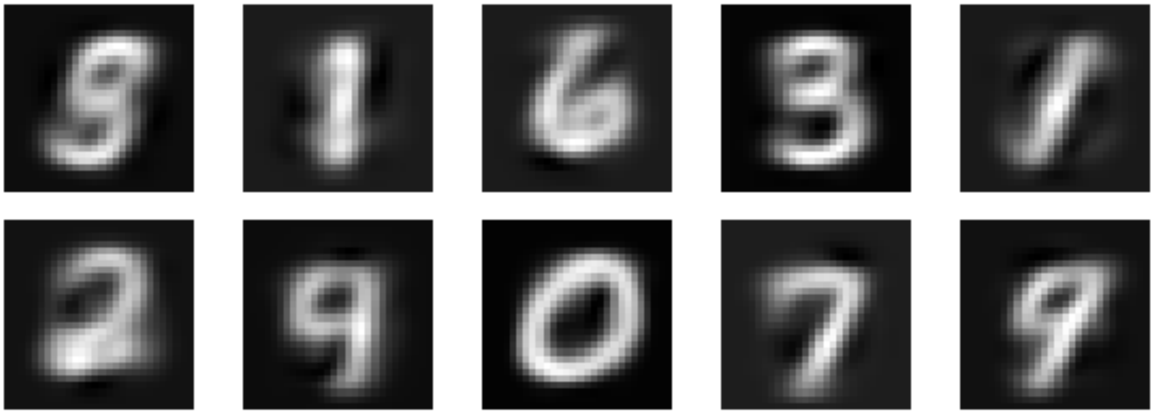


e) Using Kmeans on this new dataset, cluster the images from d) using 10 clusters and plot the centroid of each cluster. Note: the centroids should be represented as images.

In [20]:
```
!pip install --upgrade scikit-learn numpy
```

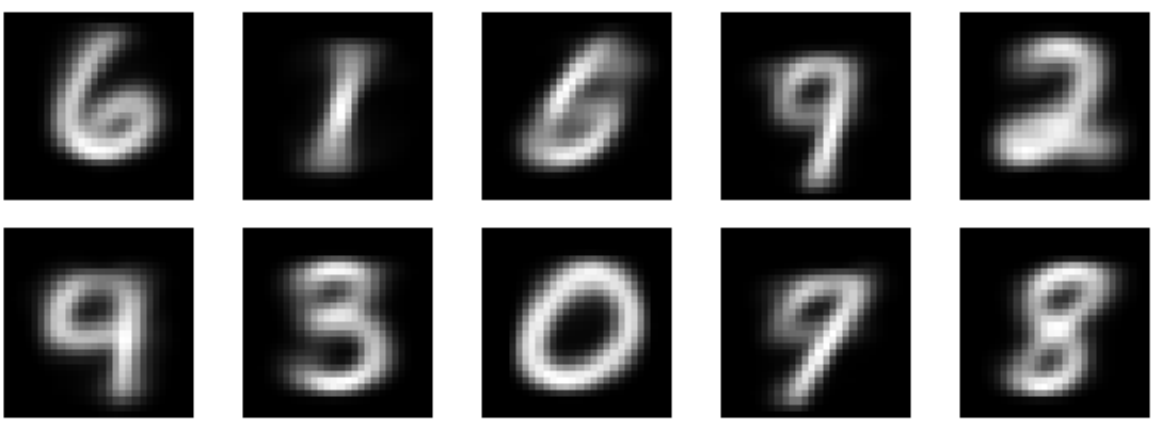
```
Requirement already satisfied: scikit-learn in /Users/nyx/opt/anaconda3/lib/py
thon3.9/site-packages (1.4.1.post1)
Requirement already satisfied: numpy in /Users/nyx/opt/anaconda3/lib/python3.
9/site-packages (1.22.4)
Collecting numpy
  Using cached numpy-1.26.4-cp39-cp39-macosx_10_9_x86_64.whl.metadata (61 kB)
Requirement already satisfied: scipy>=1.6.0 in /Users/nyx/opt/anaconda3/lib/py
thon3.9/site-packages (from scikit-learn) (1.7.1)
Requirement already satisfied: joblib>=1.2.0 in /Users/nyx/opt/anaconda3/lib/p
ython3.9/site-packages (from scikit-learn) (1.3.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in /Users/nyx/opt/anaconda
3/lib/python3.9/site-packages (from scikit-learn) (3.3.0)
DEPRECATION: pyodbc 4.0.0-unsupported has a non-standard version number. pip 2
4.1 will enforce this behaviour change. A possible replacement is to upgrade t
o a newer version of pyodbc or contact the author to suggest that they release
a version with a conforming version number. Discussion can be found at http
s://github.com/pypa/pip/issues/12063
```

In [21]:
```
from sklearn.cluster import KMeans


kmeans = KMeans(n_clusters=10, init='k-means++')
kmeans.fit_predict(data_approx)

centroids = kmeans.cluster_centers_

plt.figure(figsize=(8, 3))
for i in range(10):
    plt.subplot(2, 5, i + 1)
    centroid_image = centroids[i].reshape(28, 28)  # Reshape centroid to imag
    plt.imshow(centroid_image, cmap='gray')
    plt.axis('off')
plt.tight_layout()
plt.show()

# plt.figure(figsize=(9,6))
# plt.subplot(1,2,1)
# plt.imshow(digit_app, cmap = cm.Greys_r)
# plt.title('Rank 1 Digit')
# plt.subplot(1,2,2)
# plt.imshow(digit_img, cmap = cm.Greys_r)
# plt.title('Original Rank Digit')
# _ = plt.subplots_adjust(wspace=0.5)
# plt.show()
```



f) Repeat e) on the original dataset (if you used a subset of the dataset, keep using that same subset). Comment on any differences (or lack thereof) you observe between the centroids created here vs the ones you created in e).

In [22]:
```
from sklearn.cluster import KMeans


kmeans = KMeans(n_clusters=10, init='k-means++')
kmeans.fit_predict(X)

centroids = kmeans.cluster_centers_

plt.figure(figsize=(8, 3))
for i in range(10):
    plt.subplot(2, 5, i + 1)
    centroid_image = centroids[i].reshape(28, 28)  # Reshape centroid to imag
    plt.imshow(centroid_image, cmap='gray')
    plt.axis('off')
plt.tight_layout()
plt.show()
```



g) Create a matrix (let's call it 0) that is the difference between the original dataset and the rank-10 approximation of the dataset. i.e. if the original dataset is A and the rank-10 approximation is B, then $0 = A - B$

In [23]:

```
O = X - data_approx
```

h) The largest (using euclidean distance from the origin) rows of the matrix 0 could be considered anomalous data points. Briefly explain why. Plot the 10 images (by finding them in the original dataset) responsible for the 10 largest rows of that matrix 0.

In [25]:

```
Onorm = np.linalg.norm(O, axis=1)
anomSet = np.argsort(Onorm)[-10:]

fig, axs = plt.subplots(1, 10, figsize=(20, 2))
for i, ax in enumerate(axs.flat):
    img = X[anomSet[i]].reshape(28, 28)
    ax.imshow(img, cmap='gray')
    ax.axis('off')
plt.suptitle('Top 10 Anomalous Images Based on Approximation Error Difference
plt.show()

#The largest rows of matrix O could be considered anomalous data points becau
#we are essentially identifying instances where the approximation model devia
#Larger errors imply greater divergence from the original dataset, suggesting
```