# REI602M Machine Learning - Homework 8 (UNDER CONSTRUCTION!!!)

Due: Monday 11.3.2019

Objectives: Topic discovery with NMF, Image compression with PCA and NMF, Spectral clustering

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1. [Topic discovery with NMF, 40 points]. Here you will use non-negative matrix factorization (NMF) to analyze the content of tweets from Donald Trump. In particular, you will attempt to discover the main topics of his tweets by applying NMF to a document-term matrix derived from the tweets (or rather to a "tweet-term" matrix).

The NMF approximates a non-negative n imes p matrix X of rank r with a rank  $k \leq r$  matrix such that

$$X \approx WH$$

where W is a  $n \times k$  matrix with  $W_{ij} \ge 0$  and H is a  $k \times p$  matrix with  $H_{ij} \ge 0$ . Provided that k is appropriately chosen, the weight matrix W and coefficient matrix H can reveal interesting structures in the data. Column j of X is approximated with (see comment 1 below)

$$X_{:,j} \approx (WH)_{:,j} = H_{1j}W_{:,1} + H_{2j}W_{:,2} + \ldots + H_{kj}W_{:,k}$$

where the subscript :, j denotes column j. The columns of W in this context correspond to the main topics of Trump's tweets and column j of H contains information on how the topics are "mixed" together to form (approximately) column j of X.

- a) Download all tweets by Trump from <a href="http://www.trumptwitterarchive.com/archive">http://www.trumptwitterarchive.com/archive</a> from the period 20.1.2017 (inauguration day) to present, omitting retweets, as a CSV file (approx. 5800 tweets). Create a tweet-term matrix using word counts (see below). For a given value of k, perform NMF on the matrix and list the words corresponding to the largest  $H_{ij}$  values for columns  $j=1,\ldots,k$ . You need to experiment with different values of k (a.k.a. the *Trump-dimension*) to get interesting topic groupings. If k is too low different topics will be mixed together, when k gets large, the same subject will appear in multiple clusters. Report your results (c.a. 20 words on each topic) for the value of k that you end up picking.
- b) Select two topics of "interest" (e.g. Trump's nemesis Hillary Clinton). Identify the corresponding columns in W and list approx. 5 tweets using the largest W-values as indices. Does the content of the tweets match the selected topics?

Comments:

1) The n imes k matrix-vector product y = Ax can be interpreted as a weighted sum of the columns of A,

and matrix multiplication can be considered as multiple matrix-vector products.

- 2) Use the NMF implementation infrom sklearn.decomposition.NMF. You can use the Wikipedia data set from HW7 to test your NMF-based topic discovery code. Once you get convincing results, apply your code to the newly constructed tweet-term matrix.
- 3) Use sklearn.feature\_extraction.text.CountVectorizer to create the document-term matrix based on word counts from the raw tweets. This function performs tokenization, counting and normalization and removes stop words. Use the following parameter values max\_features=k, max\_df=0.95 (remove words that occur in at least 95% of the documents), min\_df=2 (remove words that occur in fewer than two documents), stop\_words='english'.
- 4) Use CountVectorizer.get\_feature\_names() to get the list of words that were retained. Sidenote: Rare words are downplayed by the term-frequency encoding used here but they are often found to be informative. Therefore people often encode the text using term-frequency-inverse document frequency.
- 5) Scikit's NMF function obtaines the factorization  $X \approx WH$  by minimizing the objective function  $0.5||X-WH||_F^2$  (here  $||A||_F$  denotes the Frobenius norm of a matrix A,  $||A||_F = \sqrt{\sum_{i=1}^n \sum_{j=1}^n A_{ij}^2}$ . The NMF implementation provides means to regularize the solution via parameters alpha and 11\_ratio. You may want to experiment with these parameters to see if you can improve the list of topics.
- 6) The H matrix is stored in nmf.components\_
- 7) The NMF is described briefly in section 14.6 of ESL. A more detailed account can be found in the original article <a href="http://www.columbia.edu/~jwp2128/Teaching/E4903/papers/nmf\_nature.pdf">http://www.columbia.edu/~jwp2128/Teaching/E4903/papers/nmf\_nature.pdf</a>

# In [2]:

```
from sklearn.decomposition import NMF
from sklearn.feature_extraction.text import CountVectorizer
import numpy as np
def print_top_words(nmf,feature_names, n_top_words):
   for nr, topic in enumerate(nmf.components_,1):
        top_words_indx = topic.argsort()[:-n_top_words - 1:-1]
        ordd = ''
        for i in range(n_top_words):
            if i%11==0:
                ordd += '\n'
            ordd += feature_names[top_words_indx[i]]+' '
        print('flokkur nr', nr, ':', ordd,'\n')
data = np.genfromtxt('trump_tweets.CSV',encoding="utf-8", delimiter=',',dtype=str,s
kip header=1)
k = 10
vectorizer = CountVectorizer(max df=0.95,min df=2, stop words='english')
X = vectorizer.fit transform(data)#pessi gæji heldur utan um hve oft orðin koma fyr
ir
nmf = NMF(n_components=k,init='random', random_state=0,alpha=.1, l1_ratio=.5).fit(X
)
feature_names = vectorizer.get_feature_names()
```

```
print_top_words(nmf, feature_names, 20)
flokkur nr 1:
amp military repeal replace strong loves taxes women years borders v
ets
going nation said work hard getting healthcare dems economy
flokkur nr 2:
people country american want way years enemy come like coming going
millions time working million laws let history know bad
flokkur nr 3:
news fake media cnn just story don stories bad reporting new
said dishonest enemy nbc good house like report time
flokkur nr 4:
border wall security democrats want country crime don southern immig
ration stop
need military drugs republicans laws dems mexico national open
flokkur nr 5:
fbi collusion witch hunt hillary democrats russia clinton crooked ca
mpaign comey
just russian mueller rigged election angry hoax dossier investigatio
flokkur nr 6:
president trump obama donald thank election campaign just administra
said russia american foxandfriends right day years china isis
flokkur nr 7:
trade korea united china north states just deal good country years
time tariffs countries dollars new year kim meeting long
flokkur nr 8:
great america make state job thank honor doing today new governor
military day congratulations endorsement senator night country healt
hcare meeting
flokkur nr 9:
https thank today honor america american whitehouse welcome jobs joi
national nation americans united families vote world minister melani
flokkur nr 10:
big tax vote crime win jobs cuts military strong endorsement vets
```

(b) Ég vel flokkana sem mér sýnist tengjast Border Wall(flokkur nr. 4) og Fake News(flokkur nr. 3)

borders republicans senate total amendment loves republican house go

#### In [3]:

vernor

```
W = nmf.transform(X)
bw_fn = [2,3]
```

```
n_tweets = 5
for ind in bw_fn:
    weight = W[:,ind]
    top_tweets = np.argsort(weight)[::-1]
    print('flokkur', ind+1)
    print('-'*50)
    for i in range(n_tweets):
        print('tweet',i+1,':',data[top_tweets[i]],'\n')
```

#### flokkur 3

-----

tweet 1: Google search results for "Trump News" shows only the viewin g/reporting of Fake News Media. In other words they have it RIGGED for me & Details the state of the sta

tweet 2: CNN and others in the Fake News Business keep purposely and inaccurately reporting that I said the "Media is the Enemy of the People." Wrong! I said that the "Fake News (Media) is the Enemy of the People" a very big difference. When you give out false information - not good!

tweet 3: Google search results for "Trump News" shows only the viewin g/reporting of Fake New Media. In other words they have it RIGGED for me & CNN is prominent. Republican/Conservative & CNN is prominent.

tweet 4: The Fake News refuses to talk about how Big and how Strong o ur BASE is. They show Fake Polls just like they report Fake News. Despite only negative reporting we are doing well - nobody is going to beat us. MAKE AMERICA GREAT AGAIN!

tweet 5: Last time I went to Davos the Fake News said I should not go there. This year because of the Shutdown I decided not to go and the Fake News said I should be there. The fact is that the people understand the media better than the media understands them!

#### flokkur 4

\_\_\_\_\_

tweet 1: The most important way to stop gangs drugs human trafficking and massive crime is at our Southern Border. We need Border Security a nd as EVERYONE knows you can't have Border Security without a Wall. The Drones & Technology are just bells and whistles. Safety for America!

tweet 2: "Border Patrol Agents want the Wall." Democrat's say they do n't want the Wall (even though they know it is really needed) and they don't want ICE. They don't have much to campaign on do they? An Open S outhern Border and the large scale crime that comes with such stupidit y!

tweet 3: Have the Democrats finally realized that we desperately need Border Security and a Wall on the Southern Border. Need to stop Drugs Human TraffickingGang Members & Criminals from coming into our Country. Do the Dems realize that most of the people not getting paid are Democrats?

tweet 4: The Border has been a big mess and problem for many years. A t some point Schumer and Pelosi who are weak on Crime and Border secur ity will be forced to do a real deal so easy that solves this long tim

e problem. Schumer used to want Border security - now he'll take Crim e!

tweet 5 : Statement by me last night in Florida: "Honestly I don't think the Democrats want to make a deal. They talk about DACA but they don't want to help. We are ready willing and able to make a deal but the y don't want to. They don't want security at the border they don't want t....

- 2. [Image compresssion with PCA and NMF, 30 points] Fit a non-negative matrix factorization model to the zero-digits in the subset of the MNIST database from the Jupyter workbook v07\_pca\_tsne\_kmeans (download from Piazza). Perform the following using 25 basis elements in the factorization:
- i) Display the W matrix as an image (see Fig. 14.33 in ESL) as well as an image for the part of H that corresponds to the first image in the data set.
- ii) Compare a reconstruction of the first image in the data set with the original image. What compression ratio is achieved with 25 basis elements?
- b) Repeat the analysis in a using 24-component (plus mean) PCA model (see Fig. 14.33 in ESL). Compare briefly with the results in a)

#### Comments:

- 1) Use the NMF implementation in sklearn.decomposition.NMF. The *columns* of the input matrix should contain the pixel values for each image (this is opposed to how we treated image data earlier). The fit\_transform function returns the W matrix and the attribute components\_ contains the H matrix.
- 2) When reconstructing images you may need to "clip" the data, i.e. set pixel values above 1.0 to 1.
- 3) Many elements of the W matrix will be zero and when you use a gray-scale color map, these elements will show up as black. You might therefore want to represent positive values with black and zeros with white.
- 4) Use scikit to perform PCA.

## (a-i)

## In [4]:

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler

# Load MNIST dataset (small subset)
data = np.loadtxt("data/mnist2500_X.txt")
labels = np.loadtxt("data/mnist2500_labels.txt")
X = data[np.where(labels==0)]
```

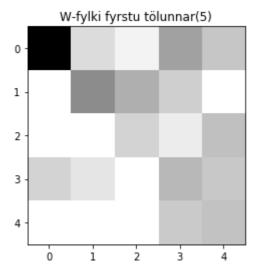
#### In [5]:

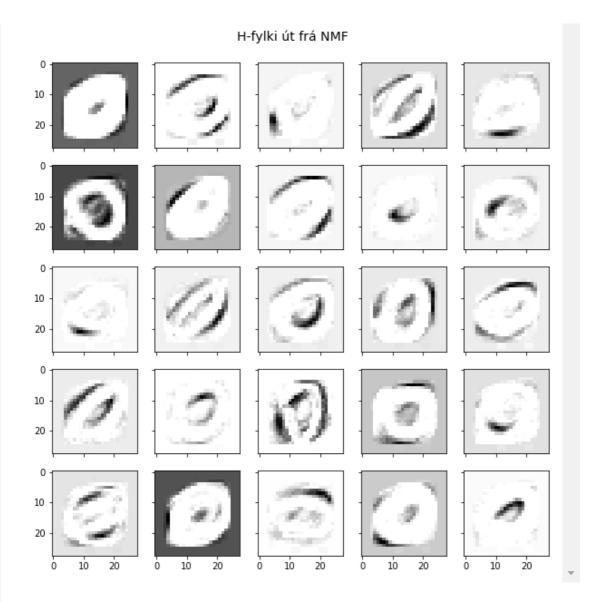
```
from sklearn.decomposition import NMF
k=25
nmf = NMF(n_components=k,init='random', random_state=0,alpha=.1, l1_ratio=.5).fit(X
```

```
)
W = nmf.transform(X)
H = nmf.components_
```

# In [6]:

```
[[1.58170883 0.2199161 0.07983504 0.58530211 0.35511231]
[0. 0.7145099 0.49439607 0.29901622 0. ]
[0. 0. 0.2730148 0.12046098 0.39268645]
[0.27173823 0.16445356 0. 0.44348868 0.34076575]
[0. 0. 0. 0.33121117 0.38133959]]
```



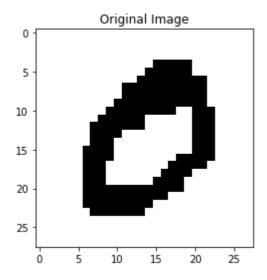


(a-ii)

# In [7]:

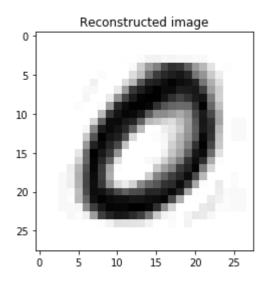
```
#Original image
mynd1 = X[0,:]
mynd1 = np.reshape(mynd1,(28,28))
plt.imshow(mynd1.T,interpolation='none',cmap='gray')
plt.title('Original Image')
plt.show()

#Reconstructed image
mynd2=np.zeros((1,784))
for i in range(784):
    mynd2[0,i] = np.minimum(1,W[0,:]@H[:,i])
mynd2 = np.reshape(mynd2,(28,28))
plt.imshow(mynd2.T,interpolation='none',cmap='gray')
plt.title('Reconstructed image')
```



## Out[7]:

Text(0.5,1,'Reconstructed image')



# In [8]:

```
print("%d bytes" % (X.nbytes))
print("%d bytes" % (H.nbytes))
print("%d bytes" % (W.nbytes))

compr_ratio = (H.nbytes + W.nbytes)/X.nbytes
print('Compression ratio:', compr_ratio)
```

1467648 bytes 156800 bytes 46800 bytes

Compression ratio: 0.13872536193964766

To store all these pictures in compressed format it only requires the H matrix and 2500 small  $5\times 5$  matrices stored within W. This takes a lot less storage than storing 2500  $28\times 28$  images. As we can see from the memory sizes of the arrays, the compression ratio  $\frac{M_{compressed}}{M_{original}}\approx 0.139$  where  $M_{compressed}$  is the memory required to store both W and H and  $M_{original}$  is the memory required to store all the 2500 pictures

```
In [9]:
```

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

data = np.loadtxt("data/mnist2500_X.txt")
labels = np.loadtxt("data/mnist2500_labels.txt")
X = data[np.where(labels==0)]
```

## In [10]:

```
from sklearn.decomposition import PCA

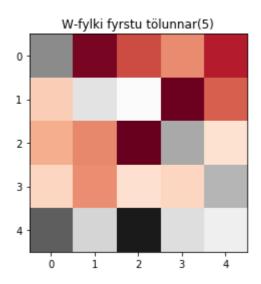
pca = PCA(n_components=24)
pca.fit(X)

W_pc = np.column_stack((np.mean(X, axis = 1), pca.transform(X)))
H_pc = np.row_stack((np.mean(X, axis = 0), pca.components_))

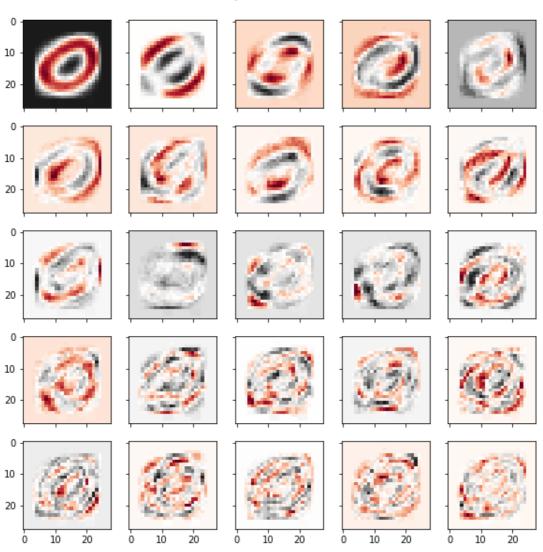
print(W_pc.shape)
print(H_pc.shape)
```

(234, 25) (25, 784)

#### In [11]:



H-fylki út frá PCA

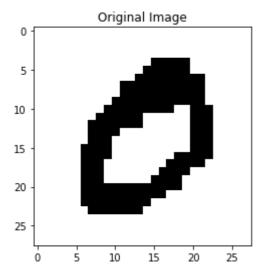


# In [12]:

```
#Original image
mynd1b = X[0,:]
mynd1b = np.reshape(mynd1b,(28,28))
plt.imshow(mynd1b.T,interpolation='none',cmap='gray')
plt.title('Original Image')
plt.show()

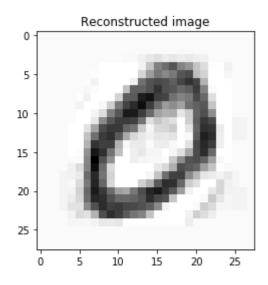
#Reconstructed image
```

```
mynd2b=np.zeros((1,784))
for i in range(784):
    mynd2b[0,i] = np.minimum(0.8,W_pc[0,:]@H_pc[:,i])
mynd2b = np.reshape(mynd2b,(28,28))
plt.imshow(mynd2b.T,interpolation='none',cmap='gray')
plt.title('Reconstructed image')
```



#### Out[12]:

Text(0.5,1,'Reconstructed image')



Við fáum í báðum tilvikum ( ${f a}$  og  ${f b}$ ) góðar niðurstöður. Það er áhugavert að sjá hvernig H og W fylkin eru uppbyggð og hve mikið þau eru frábrugðin hver öðrum í lið  ${f b}$  miðað við lið  ${f a}$ . Út frá mynd af H í PCA má sjá að stökin í H eru ekki jafn látlaus og í NMF.

3. [Spectral clustering, 30 points] In spectral clustering the clustering problem is transformed to a graph partitioning problem. The input data  $\mathbb{X} = \{x^{(1)}, \dots, x^{(n)}\}$  is used to construct a *similarity graph* of pair-wise similarities between data points. The graph is then partitioned into disjoint sets of connected vertices which correspond to clusters in  $\mathbb{X}$ . While many clustering algorithm such as k-means impose strict assumptions on the cluster shape, spectral clustering makes no such assumptions which makes it applicable in many situations. Spectral clustering is fairly computationally demanding which limits its use on large data sets.

The following algorithm (NCUT) can be used to partition the data into two groups A and B:

- 1) Construct an  $n \times n$  similarity matrix W with  $W_{ij} = e^{-\gamma ||x^{(i)}, \dots, x^{(j)}||^2}$  for  $i, j = 1, \dots, n$  (note that the matrix is symmetric). Note that  $\gamma$  is a hyperparameter that you need to specify.
- 2) Compute the *degree* of node  $i,\ d_i=\sum_{j=1}^n w_{ij},\ j=1,\dots,n$  and form the diagonal matrix D with  $D_{ii}=d_i$  and  $D_{ij}=0$  for  $i\neq j$ .
- 3) Compute the *unnormalized graph Laplacian* L=D-W.
- 4) Solve the *generalized eigenvalue problem*  $Lu=\lambda Du$ . The *second smallest* eigenvector (in terms of corresponding eigenvalue)  $u_2$  gives a partition of the data into groups A and B as follows. If element i of  $u_2$  is negative then  $x^{(i)}$  belongs to group A and B otherwise.

For k > 2 groups add the following extra step:

- 5) Form the  $n \times k$  matrix Z with the k eigenvectors  $u_2, \ldots, u_{k+1}$ . Apply k-means to this matrix and return the resulting clustering (the rows of Z corresponds to derived features).
- a) Implement steps 1 4 of the above algorithm and cluster the 2D data in hw8\_toy\_data.txt. The data has two clusters so the k-means step (5) is not needed. You should present i) a scatterplot of the original data, ii) a graph of the elements of the second-smallest eigenvector (in ascending order) and iii) a scatterplot of the data with different colors indicating the two clusters that you find. You need to experiment with to find a good value of  $\gamma$  (look for a jump in the eigenvector plot).
- b) Add the k-means step to your code from a). Apply the code to the image data in hw8\_fruit.jpg after reducing it in size to make the computations more managable (see comment 5 below). You should present i) the reduced image, ii) an image illustrating the clustering obtained with your algorithm, and iii) results of running k-means directly on the (reduced) image.

#### Comments:

- 1) To speed up computation of the similarity matrix, use you can use scipy.spatial.distance.cdist.
- 2) We call a scalar  $\lambda$  and an n-vector u that satisfy the equation  $Lu=\lambda Du$  an eigenvalue/eigenvector pair. There are n such pairs.
- 3) It is assumed that the eigenvalues are in ascending order and when werefer to the j-th smallest eigenvector we refer to the eigenvector that corresponds to the j-th smallest eigenvalue. It can be shown that all eigenvalues of L are non-negative. Since L1=(D-W)1=D1-W1=0 (1 denotes a vector of all 1's) we see that  $u_1=1$  is an eigenvector corresponding to  $\lambda=0$  and is therefore not relvant to the clustering. The second smallest (and onwards) eigenvector however contains information about the clustering (see section 14.5.3 in ESL for details).
- 4) You only need the k smallest eigenvalues and corresponding eigenvectors. You can use scipy.linalg.eigh to obtain them efficiently (using the eig function to find all the pairs requires  $O(n^3)$  operations which quickly becomes prohibitive).
- 5) Use skimage.data.load to load the image file into a matrix, skimage.transform.resize to reduce it in size by factor 4 and matplotlib.pyplot.imshow to display the image.
- 6) A detailed review of spectral clustering is given in "A Tutorial on Spectral Clustering" by Ulrike von Luxburg.

#### In [30]:

```
from scipy.spatial import distance
from scipy.linalg import eigh
```

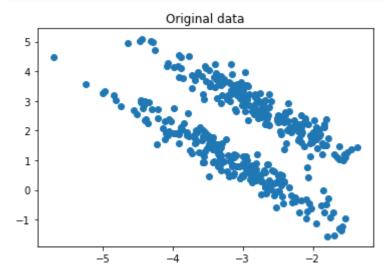
```
X = np.loadtxt('hw8_toy_data.txt')
n,p = X.shape

gamma=5
W = np.exp(-gamma*distance.cdist(X, X, 'euclidean')**2)
d = np.zeros(n)
for i in range(n):
    d[i] = np.sum(W[i,:])
D = np.eye(n)*d
L=D-W
lam, u = eigh(L, D, eigvals_only=False,eigvals=(0,1))
sec_small = u[:,1]
```

# In [31]:

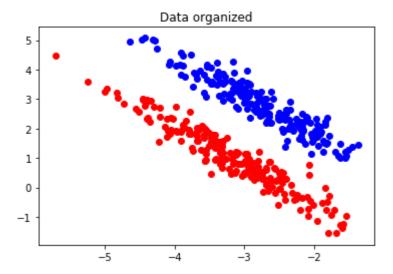
```
#original data
plt.scatter(X[:,0],X[:,1])
plt.title('Original data')
plt.show()
#eigvector
X1 = X[np.where(sec_small<0)]
X2 = X[np.where(sec_small>0)]

plt.scatter(X1[:,0],X1[:,1],c='b')
plt.scatter(X2[:,0],X2[:,1],c='r')
plt.title('Data organized')
```



## Out[31]:

Text(0.5,1,'Data organized')

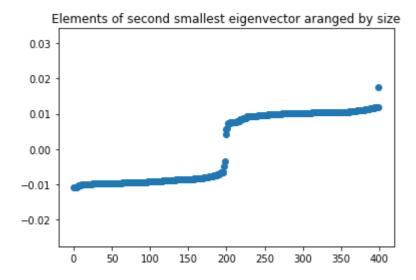


# In [32]:

```
#graph of the elements of the second-smallest eigenvector (in ascending order)
plt.scatter(np.arange(n),sec_small[sec_small.argsort()])
plt.title('Elements of second smallest eigenvector aranged by size')
```

## Out[32]:

Text(0.5,1,'Elements of second smallest eigenvector aranged by size')



(b)

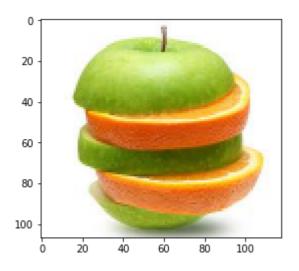
## In [468]:

```
from skimage import data
from matplotlib.image import imread
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans

def ncut(X,k,gamma):
    n,p = X.shape
    gamma=1
    W = np.exp(-gamma*distance.cdist(X, X, 'euclidean')**2)
    d = np.zeros(n)
    for i in range(n):
        d[i] = np.sum(W[i,:])
    D = np.eye(n)*d
```

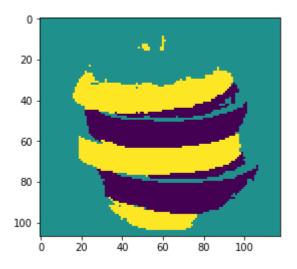
```
L=D-W
    lam, u = eigh(L, D, eigvals_only=False,eigvals=(1,k+1))
    return(lam,u)
k=3
gamma=0.2
A = imread('fruit.jpg')
n,p,tmp = A.shape #Upphafleg stærð myndar
A = skimage.transform.resize(A,(int(n/2),int(p/2)))#minnkum myndina
n,p,tmp=A.shape
plt.imshow(A)
plt.show()
A_rgb = A.reshape(A.shape[0]*A.shape[1],3)#rgb transform
lam, u = ncut(A_rgb,k,gamma)
#K-means flokkun
A_km = KMeans(n_clusters=k)
A_km.fit(u)
clusters = A_km.cluster_centers_ #Litir i rgb
labels = A_km.labels_ #vigur
labels = labels.reshape(n,p); #n X p fylki með labels
plt.imshow(labels)
```

C:\Users\snati\Anaconda3\lib\site-packages\skimage\transform\\_warps.p
y:84: UserWarning: The default mode, 'constant', will be changed to 'r
eflect' in skimage 0.15.
 warn("The default mode, 'constant', will be changed to 'reflect' in



#### Out[468]:

<matplotlib.image.AxesImage at 0x1b6804787f0>



Ég ákvað út frá upphaflegu myndinni að hafa k=3 sem sagt flokkarnir appelsína, epli og bakgrunnur. Með góðu gildi á  $\gamma$  fæst síðan ágætis skipting á myndinni. Það má líklega fínstilla  $\gamma$  svo toppurinn á eplinu flokkist ekki í bakgrunninn.

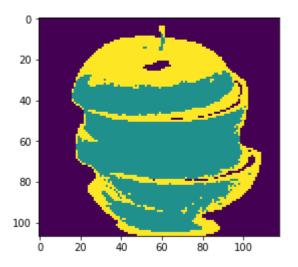
## In [39]:

```
#notum K-means á upprunalegu myndina og sleppum öllu með eiginvigrum
import skimage
from matplotlib.image import imread
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
k=3
A = imread('fruit.jpg')
n,p,tmp = A.shape #Upphafleg stærð myndar
A = skimage.transform.resize(A,(int(n/2),int(p/2)))#minnkum myndina
n,p,tmp=A.shape
A_rgb = A.reshape(A.shape[0]*A.shape[1],3)#rgb transform
#K-means flokkun
A_km2 = KMeans(n_clusters=k)
A_km2.fit(A_rgb)
clusters2 = A_km2.cluster_centers_ #Litir i rgb
labels2 = A_km2.labels_ #vigur
labels2 = labels2.reshape(n,p); #n X p fylki með labels
plt.imshow(labels2)
C:\Users\snati\Anaconda3\lib\site-packages\skimage\transform\_warps.p
```

```
C:\Users\snati\Anaconda3\lib\site-packages\skimage\transform\_warps.p
y:84: UserWarning: The default mode, 'constant', will be changed to 'r
eflect' in skimage 0.15.
  warn("The default mode, 'constant', will be changed to 'reflect' in
"
```

#### Out[39]:

<matplotlib.image.AxesImage at 0x279ef7282e8>



Fáum ekki nálægt því jafn góða skiptingu og í úrvinnslunni hér á undan.(Ef takmarkið er að flokka epli frá appelsínum)