

# MAT 4110 Obligatory Assignment 1

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## 1 Theory

In this assignment I will study image compression using the SVD decomposition. Grey-scale images of size  $[N \times M]$  will be studied. The images can be represented by a matrix  $\mathbf{A}_{ij}$  where  $i \in [0, N - 1]$  and  $j \in [0, M - 1]$ .

An  $[N \times M]$  matrix can be decomposed into the form

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^T \quad (1)$$

Where  $\mathbf{U}$  is an  $[N \times N]$  orthogonal matrix,  $\mathbf{V}^T$  is an  $[M \times M]$  orthogonal matrix, and  $\mathbf{\Sigma}$  is an  $[N \times M]$  matrix with the singular values of  $\mathbf{A}$  on the diagonal and zeros elsewhere. These singular values take the form

$$\sigma_1 \geq \sigma_2 \geq \sigma_3 \geq \dots \sigma_N \quad (2)$$

$\sigma_i = \sqrt{\lambda_i}$  where  $\lambda_i$  is the  $i$ th eigen value of the matrix  $\mathbf{A}^T \mathbf{A}$ . Since  $\mathbf{U}$  and  $\mathbf{V}^T$  are orthogonal, they correspond to rotations and/or reflections of the  $N$  and  $M$  dimensional spaces. This means that the singular values are solely responsible for stretching or shrinking the vectors. This can be thought of as bigger values of  $\Sigma$  explain more of the variance in  $\mathbf{A}$ , while smaller values explain less and are therefore less important.

We can find the variance explained by each singular vector of the SVD decomposition by computing

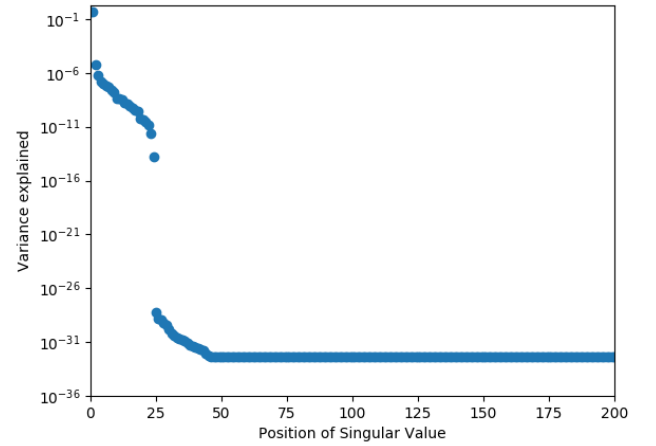
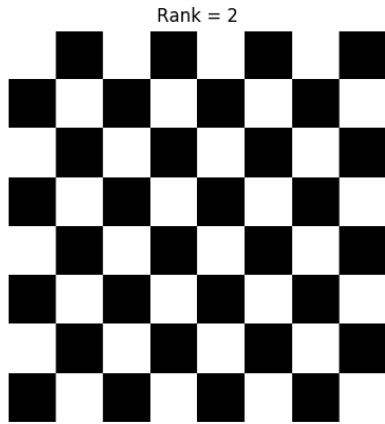
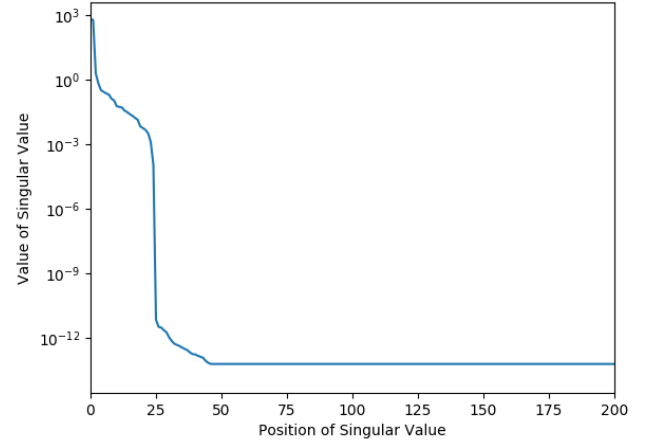
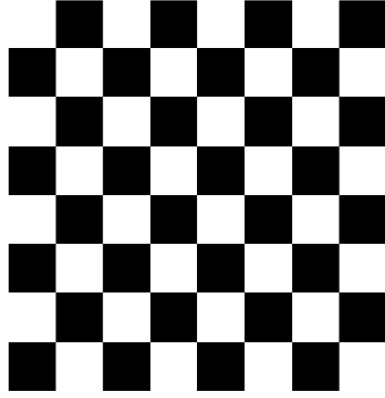
$$R_i^2 = \frac{\sigma_i^2}{\sum_j \sigma_j^2} \quad (3)$$

and plotting over the amount of singular vectors. This provides a nice visual to see when the singular values stop contributing significantly to the variance in  $\mathbf{A}$ . We can then make a choice to condense the information in the matrix by throwing out the singular values after a given  $\sigma_k$  and then reconstructing  $\mathbf{A}$  with  $\mathbf{U}^{(n \times k)}$ ,  $\mathbf{\Sigma}^{(k \times k)}$ , and  $\mathbf{V}^{T(k \times m)}$ .

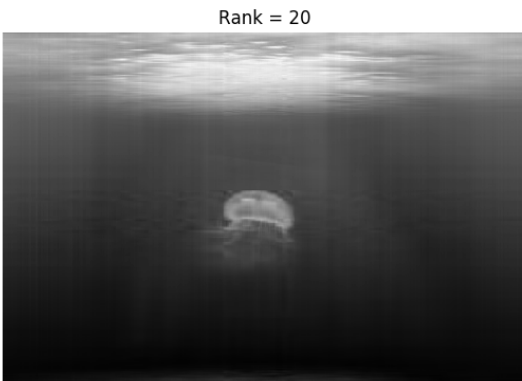
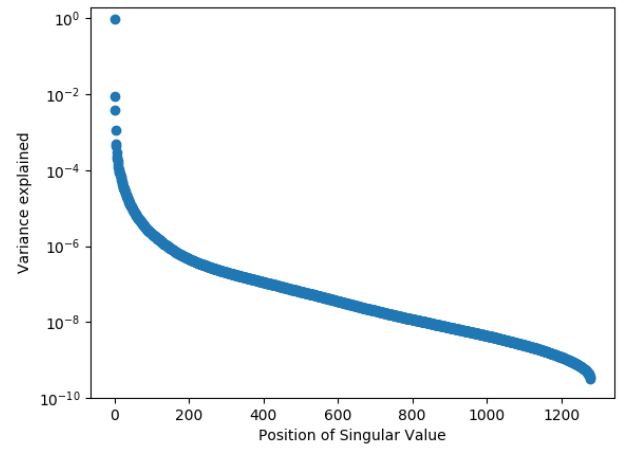
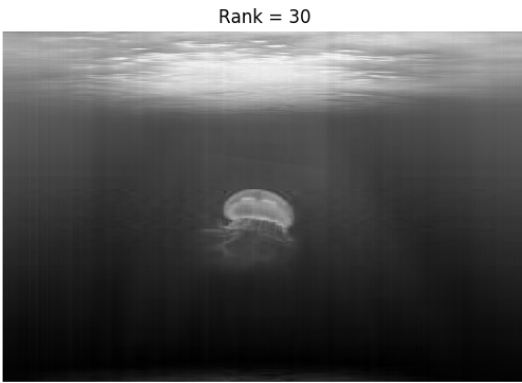
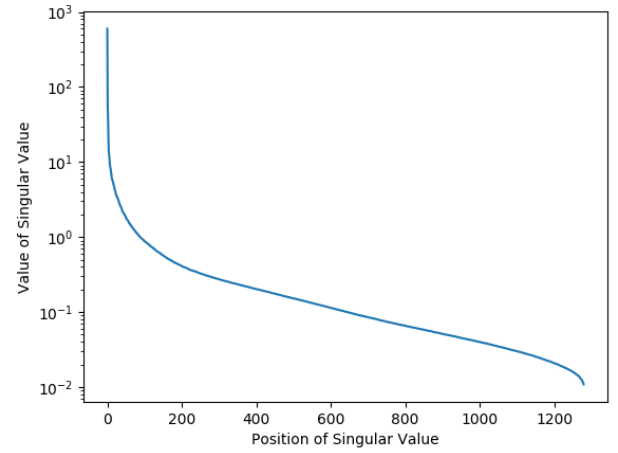
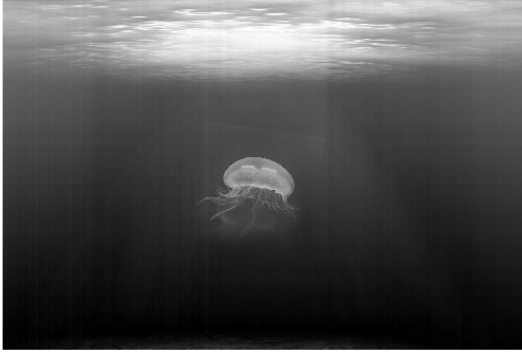
The compressed image can be characterized by the compression ratio which is give by

$$\text{ratio} = \frac{\text{uncompressed size}}{\text{compressed size}} = \frac{M \times N}{K \times (1 + M + N)} \quad (4)$$

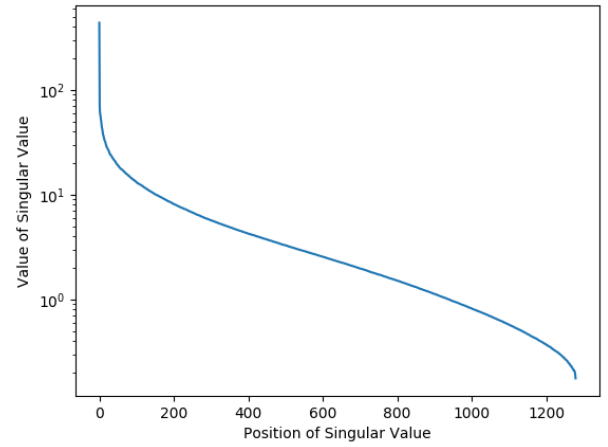
## 2 Results



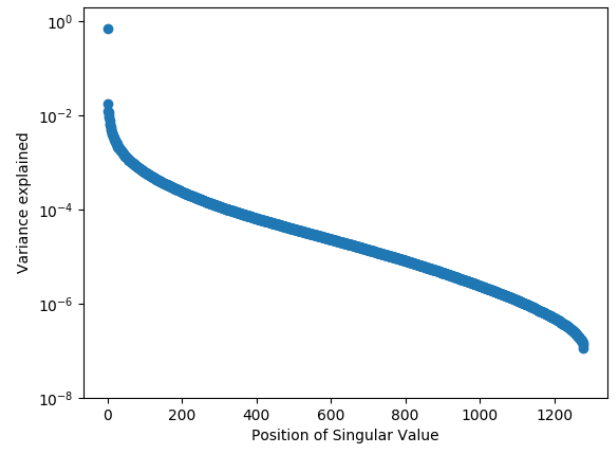
The original image is shown in the top left corner. From the two plots on the right, we see that the major first singular value is the main contributor to the variance in the image and with just using the first two singular values we reproduce the image. Here, our compression ratio for the  $1280 \times 1236$  image is 314.3



Compared to the checker board, this jellyfish has a larger number of significant singular values as the variance and singular value plot evolve more smoothly with respect to rank. For this image, I decided that rank 20 was not quite sharp enough and decided to go with rank 30. The compression ratio for the  $1280 \times 1920$  image is 25.6



Rank = 30



Rank = 100



Rank = 200



Again, we find more singular values are needed to sharply reproduce the image. The smallest singular values in this image are larger than the smallest from the other images, meaning these values have more importance in this image. I decided that rank 200 produced a sharp enough reproduction resulting in a compression ratio of 3.8. It is clear that the more complex an image is, the more singular values you need to keep to reproduce it. As a result, the compression ratio for an appropriately

condensed complex image is much smaller than that for a simple image.

```
1 from skimage import io
2 from skimage.color import rgb2gray
3 import numpy as np
4 from sklearn.preprocessing import MinMaxScaler
5 import matplotlib.pyplot as plt
6
7 # import and scale data
8 chess = io.imread('chess.png')
9 chess_g = rgb2gray(chess)
10
11 scaler = MinMaxScaler()
12 jelly = io.imread('jellyfish.jpg')
13 jelly_g = rgb2gray(jelly)
14 scaler.fit(jelly_g)
15 jelly_g = scaler.transform(jelly_g)
16
17 scaler1 = MinMaxScaler()
18 ny = io.imread('newyork.jpg')
19 ny_g = rgb2gray(ny)
20 scaler1.fit(ny_g)
21 ny_g = scaler1.transform(ny_g)
22
23 print(chess_g.shape, jelly_g.shape, ny_g.shape)
24
25 # show images
26 fig1, axes1 = plt.subplots()
27 axes1.imshow(jelly_g, cmap = plt.cm.gray)
28 axes1.axis('off')
29 plt.savefig('jelly_g')
30
31 fig2, axes2 = plt.subplots()
32 axes2.imshow(chess_g, cmap = plt.cm.gray)
33 axes2.axis('off')
34 plt.savefig('chess_g')
35
36 fig3, axes3 = plt.subplots()
37 axes3.imshow(ny_g, cmap = plt.cm.gray)
38 axes3.axis('off')
39 plt.savefig('ny_g')
40
41 def singular_val_study(image):
42     u, s, vT = np.linalg.svd(image)
43     val_vec = np.arange(s.shape[0])
44     var = np.zeros_like(s)
45     var = (s*s)/np.sum(s*s)
46     return val_vec, s, var
47
48
49 def svd_compress(image, rank):
50     u, s, vT = np.linalg.svd(image)
51     s = s[:rank]
52     u = u[:, :rank]
53     vT = vT[:rank, :]
54     print(u.shape)
55     print(s.shape)
```

```

56     print(vT.shape)
57     compress = (u @ np.diag(s)) @ vT
58     return rank, compress
59
60 # CHECKERS
61 range, s, var = singular_val_study(chess_g)
62 fig1 = plt.figure()
63 plt.semilogy(range,s)
64 plt.xlabel('Position of Singular Value')
65 plt.ylabel('Value of Singular Value')
66 plt.xlim(0,200)
67 plt.savefig('checker_sv')
68
69 fig2 = plt.figure()
70 plt.scatter(range,var)
71 plt.xlabel('Position of Singular Value')
72 plt.ylabel('Variance explained')
73 plt.yscale('log')
74 plt.xlim(0,200)
75 plt.ylim(1e-36,2*1e0)
76 plt.savefig('checker_var')
77 plt.show()
78
79 rank, n_checker = svd_compress(chess_g, 2)
80 fig = plt.figure()
81 plt.imshow(n_checker, cmap=plt.cm.gray)
82 plt.axis('off')
83 plt.title('Rank = 2')
84 plt.savefig('checker_compress')
85 plt.show()
86
87 # JELLY FISH
88 range, s, var = singular_val_study(jelly_g)
89 fig1 = plt.figure()
90 plt.semilogy(range,s)
91 plt.xlabel('Position of Singular Value')
92 plt.ylabel('Value of Singular Value')
93 plt.savefig('jelly_sv')
94
95 fig2 = plt.figure()
96 plt.scatter(range,var)
97 plt.xlabel('Position of Singular Value')
98 plt.ylabel('Variance explained')
99 plt.yscale('log')
100 plt.ylim(1e-10,2*1e0)
101 plt.savefig('jelly_var')
102 plt.show()
103
104 rank, n_jelly = svd_compress(jelly_g, 30)
105 fig = plt.figure()
106 plt.imshow(n_jelly, cmap=plt.cm.gray)
107 plt.axis('off')
108 plt.title('Rank = 30')
109 plt.savefig('jelly_compress_30')
110 plt.show()
111
112 #NYC
113 range, s, var = singular_val_study(ny_g)
114 fig1 = plt.figure()

```

```

115 plt.semilogy(range,s)
116 plt.xlabel('Position of Singular Value')
117 plt.ylabel('Value of Singular Value')
118 plt.savefig('ny_sv')
119
120 fig2 = plt.figure()
121 plt.scatter(range,var)
122 plt.xlabel('Position of Singular Value')
123 plt.ylabel('Variance explained')
124 plt.yscale('log')
125 plt.ylim(1e-8,2*1e0)
126 plt.savefig('ny_var')
127 plt.show()
128
129 rank, n_ny = svd_compress(ny_g, 200)
130 fig = plt.figure()
131 plt.imshow(n_ny, cmap=plt.cm.gray)
132 plt.axis('off')
133 plt.title('Rank = 200')
134 plt.savefig('ny_compress_200')
135 plt.show()

```