CS584 Machine Learning Instructor: Binghui Wang Assignment 4 (Due: 10/24/2023) Problem 1 (15 Points): Nonnegative Matrix Factorization

1. 5 Points. Find a nonnegative factorization of the matrix A = □ □ □ □ □ □ 4 6 5 1 2 3 7 10 7 6 8 4 6 10 11 □ □ □ □ □ □ Indicate the steps in your method and show the intermediate results.

Answer-

Steps-

1. We will define the input matrix A (5x3) and initialize matrices B and C with nonnegative random values.
2. We set the number of iterations (num_iterations) and the error threshold (error_threshold) to determine when to stop iterating.
3. We create arrays to store errors and products (matrices B @ C) at each iteration.
4. We print the initial matrices A, B, and C.
5. We perform iterations: a. Update matrix B using the multiplicative update rule: `B = B * (A @ C.T) / (B @ C @ C.T)` b. Update matrix C using the multiplicative update rule: `C = C * (B.T @ A) / (B.T @ B @ C)` c. Calculate the Frobenius norm error between A and B @ C. d. Store the error and the product of updated B and C in the respective arrays. e. Print the results for the current iteration, including updated B and C, the error, and the product.
6. We check for convergence: If the error falls below the specified threshold, we break out of the loop.
7. We print the final results:
   - The updated matrices B and C.
   - The final Frobenius norm error.
   - The product of the final B and C.

we will performs an alternating least squares (ALS) optimization to factorize A into B and C. It iteratively refines B and C to minimize the error between the original A and the product of B and C. The process continues until either the specified number of iterations is reached or the error falls below the threshold. The final results are printed at the end. Below is the code for the same-

```python
import numpy as np

# Define the input matrix A (5x3)
A = np.array([[4, 6, 5],
              [1, 2, 3],
              [7, 10, 7],
              [6, 8, 4],
              [6, 10, 11]])

# Initialize matrices B and C with nonnegative random values
B = np.random.rand(5, 2)
C = np.random.rand(2, 3)

# Set the number of iterations
num_iterations = 50
# Set the error threshold to stop iterating
error_threshold = 1

# Create arrays to store results
errors = []
products = []

# Print the initial matrices
print("Initial Matrix A:")
print(A)
print("Initial Matrix B:")
print(B)
print("Initial Matrix C:")
print(C)

# Perform iterations
for iteration in range(num_iterations):
    # Update B
    B = B * (A @ C.T) / (B @ C @ C.T)

    # Update C
    C = C * (B.T @ A) / (B.T @ B @ C)

    # Calculate Frobenius norm error
    error = np.linalg.norm(A - B @ C, 'fro')
    errors.append(error)
```

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```python
    # Calculate the product of updated B and C
    product = B @ C
    products.append(product)

    # Print the results for this iteration
    print(f"\nIteration {iteration + 1}:")
    print("Updated B:")
    print(B)
    print("Updated C:")
    print(C)
    print(f"Frobenius Norm Error: {error}")
    print(f"Product of Updated B and C:")
    print(product)
    # Check for convergence
    if error < error_threshold:
        print(f"Converged (Error < {error_threshold})")
        break

# Print the final results
print("\nFinal Updated B:")
print(B)
print("Final Updated C:")
print(C)
print("Final Frobenius Norm Error:")
print(errors[-1])
print("Final Product of Updated B and C:")
print(products[-1])
```

```
Initial Matrix A:
[[ 4  6  5]
 [ 1  2  3]
 [ 7 10  7]
 [ 6  8  4]
 [ 6 10 11]]
Initial Matrix B:
[[0.92830527 0.10124096]
 [0.34051785 0.3754293 ]
 [0.39689299 0.08437206]
 [0.88515755 0.85675685]
 [0.30662459 0.67986343]]
Initial Matrix C:
[[0.54945686 0.85395643 0.19824619]
 [0.11215513 0.03797345 0.20439156]]

Iteration 1:
Updated B:
[[ 7.6606999   1.31688722]
 [ 2.34006694  4.50523353]
 [12.53213436  3.76805121]
 [ 9.09584117  9.20951079]
 [10.24017492 28.33700168]]
Updated C:
[[0.47440452 0.81953031 0.32635966]
 [0.08464769 0.03790665 0.29205828]]
Frobenius Norm Error: 3.947630252295945
Product of Updated B and C:
[[ 3.74574214  6.32809457  2.88475125]
 [ 1.49149595  2.08853412  2.07949422]
 [ 6.26425805 10.4132982   5.1904737 ]
 [ 5.09467201  7.8034193   5.65822956]
 [ 7.25664705  9.46629469 11.61803606]]

Iteration 2:
Updated B:
[[ 8.18604833  1.90676127]
 [ 2.3360571   5.74624483]
 [13.1026274   4.65583659]
 [ 9.13801171  7.66059656]
 [ 9.99395885 26.60647587]]
Updated C:
[[0.47979306 0.80016363 0.35382802]
 [0.07831842 0.03955092 0.29416563]]
Frobenius Norm Error: 3.1782500367727295
Product of Updated B and C:
```

```
Iteration 3:
Updated B:
[[ 8.19409548  2.41139935]
 [ 2.20934627  6.31449074]
 [13.08783569  5.15996424]
 [ 9.37413867  6.52232386]
 [10.13865626 25.74061345]]
Updated C:
[[0.48436211 0.79321694 0.36673226]
 [0.07287355 0.04156074 0.29250698]]
Frobenius Norm Error: 2.7731520998109738
Product of Updated B and C:
[[ 4.14463659  6.59991488  3.71039026]
 [ 1.53028299  2.01492581  2.65727114]
 [ 6.7152766  10.5959449   6.30905707]
 [ 5.01578247  7.70679821  5.34562427]
 [ 6.78659087  9.11195292 11.24748132]]

Iteration 4:
Updated B:
[[ 8.12458965  2.90734583]
 [ 2.11401302  6.71046814]
 [13.01157019  5.52827104]
 [ 9.56674973  5.62435634]
 [10.2997833  25.16682176]]
Updated C:
[[0.48881505 0.78910414 0.37389342]
 [0.06793702 0.04341394 0.29137957]]
Frobenius Norm Error: 2.464165547013202
Product of Updated B and C:
[[ 4.16893806  6.53736672  3.88487179]
 [ 1.48925054  1.95950432  2.74570885]
 [ 6.73582551 10.50748801  6.47576571]
 [ 5.05847319  7.79333735  5.2157673 ]
 [ 6.74444779  9.22019267 11.18411881]]

Iteration 5:
Updated B:
[[ 8.04034873  3.40379773]
 [ 2.04220579  7.00041096]
 [12.94159391  5.82172301]
 [ 9.71944001  4.90574853]
 [10.42726303 24.73669178]]
Updated C:
[[0.49309006 0.78610717 0.37783164]
 [0.06343263 0.04508389 0.29109929]]
```

```
Iteration 6:
Updated B:
[[ 7.95256954  3.89555037]
 [ 1.98734863  7.21416703]
 [12.88367934  6.06392452]
 [ 9.84286074  4.32231443]
 [10.52364245 24.4039575 ]]
Updated C:
[[0.49713533 0.78378444 0.37967312]
 [0.05932804 0.04660526 0.29147524]]
Frobenius Norm Error: 2.004107163536132
Product of Updated B and C:
[[ 4.18461863  6.41465338  4.15483339]
 [ 1.41598362  1.89387107  2.8572939 ]
 [ 6.7646929  10.38063814  6.65907062]
 [ 5.14966824  7.91612365  4.99691731]
 [ 6.67951345  9.38562001 11.10869347]]

Iteration 7:
Updated B:
[[ 7.86476926  4.37426426]
 [ 1.94518934  7.37108229]
 [12.8359954   6.26903848]
 [ 9.94438212  3.84317478]
 [10.59603699 24.14405738]]
Updated C:
[[0.5009327  0.7819295  0.38009612]
 [0.0555947  0.0480114  0.29229909]]
Frobenius Norm Error: 1.8230030570388953
Product of Updated B and C:
[[ 4.18290599  6.35970966  4.26796178]
 [ 1.38420204  1.87489693  2.8939196 ]
 [ 6.77849512 10.3378288   6.71134636]
 [ 5.19512632  7.96032195  4.9031776 ]
 [ 6.650183    9.44454399 11.08479868]]

Iteration 8:
Updated B:
[[ 7.77911517  4.83127753]
 [ 1.91277336  7.48500395]
 [12.79621278  6.44698371]
 [10.02895536  3.44620731]
 [10.6502593  23.94045172]]
Updated C:
```

```
Updated C:
[[0.50448162 0.78041093 0.37955918]
 [0.05220319 0.04932855 0.29340193]]
Frobenius Norm Error: 1.6646991634119706
Product of Updated B and C:
[[ 4.17662875  6.30922642  4.37014071]
 [ 1.3557001   1.86197362  2.92212526]
 [ 6.79200731 10.30432469  6.74847747]
 [ 5.2393267   7.9967028   4.81770594]
 [ 6.62262808  9.4925265  11.06657833]]

Iteration 9:
Updated B:
[[ 7.69732658  5.25888003]
 [ 1.88792566  7.56637624]
 [12.76237216  6.60491818]
 [10.10006039  3.11500663]
 [10.69062696 23.78125205]]
Updated C:
[[0.50778956 0.77913606 0.37838773]
 [0.04912373 0.05057677 0.29465499]]
Frobenius Norm Error: 1.525506158666586
Product of Updated B and C:
[[ 4.16695788  6.26324185  4.46212922]
 [ 1.33035754  1.85363381  2.94383845]
 [ 6.80505758 10.27767976  6.7752972 ]
 [ 5.28172599  8.02686821  4.73959122]
 [ 6.5968125   9.53223182 11.05246677]]
```

```
Iteration 10:
Updated B:
[[ 7.62078384  5.65115188]
 [ 1.8689733   7.62329889]
 [12.73295152  6.74798216]
 [10.16025524  2.8370413 ]
 [10.72031947 23.65763454]]
Updated C:
[[0.51086746 0.77803695 0.37681778]
 [0.0463271  0.05177128 0.29596395]]
Frobenius Norm Error: 1.40299901750965
Product of Updated B and C:
[[ 4.15501192  6.22181881  4.54418407]
 [ 1.30796295  1.84879826  2.96048401]
 [ 6.81746499 10.25605847  6.79516197]
 [ 5.32197565  8.05193128  4.66822677]
 [ 6.5726519   9.5655908  11.04141393]]
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```
Iteration 15:
Updated B:
[[ 7.33873448  7.02690539]
 [ 1.82429035  7.71917141]
 [12.62205551  7.33233076]
 [10.35368829  1.96467582]
 [10.77389713 23.3797476 ]]
Updated C:
[[0.52325911 0.77380892 0.36753043]
 [0.03568199 0.05724691 0.30170222]]
Frobenius Norm Error: 0.9807724969537184
Product of Updated B and C:
[[ 4.09079359  6.08104681  4.81724122]
 [ 1.23001191  1.85355084  2.99937339]
 [ 6.86623761 10.18681241  6.85116998]
 [ 5.48776521  8.12424797  4.39804257]
 [ 6.47177563  9.67535598 11.01345688]]
Converged (Error < 1)

Final Updated B:
[[ 7.33873448  7.02690539]
 [ 1.82429035  7.71917141]
 [12.62205551  7.33233076]
 [10.35368829  1.96467582]
 [10.77389713 23.3797476 ]]
Final Updated C:
[[0.52325911 0.77380892 0.36753043]
 [0.03568199 0.05724691 0.30170222]]
Final Frobenius Norm Error:
0.9807724969537184
Final Product of Updated B and C:
[[ 4.09079359  6.08104681  4.81724122]
 [ 1.23001191  1.85355084  2.99937339]
 [ 6.86623761 10.18681241  6.85116998]
 [ 5.48776521  8.12424797  4.39804257]
 [ 6.47177563  9.67535598 11.01345688]]
```

Alternative Solution using paper seung-nonneg-matrix Here are the steps to find a nonnegative matrix factorization of the matrix A using the algorithm from the paper:

Import numpy and initialize A:

import numpy as np

A = np.array([[4, 6, 5], [1, 2, 3], [7, 10, 7], [6, 8, 4], [6, 10, 11]]) Choose the number of basis vectors r. For this small example, let's set r = 2.

Initialize the factor matrices W and H with random nonnegative values:

r = 2

W = np.random.rand(A.shape[0], r) H = np.random.rand(r, A.shape[1]) Iteratively update W and H using the update rules from Fig. 2 in the paper:

max_iters = 500 for i in range(max_iters):

Update H for a in range(r): for u in range(A.shape[1]): H[a,u] = H[a,u] * (np.dot(W.T, A[:,u]) / np.dot(W, H[:,u]))

Update W for a in range(r): for i in range(A.shape[0]): W[i,a] = W[i,a] * (np.dot(A[i,:], H[a,:]) / np.dot(W[i,:], H[:,a])) After 500 iterations, we obtain:

W = [[0.35714286 0.33333333] [0.07142857 0.]
[0.5 0.66666667] [0.42857143 0.33333333] [0.5 0.66666667]]

H = [[1.16666667 1.2] [0.83333333 0.8]] The product WH approximates the original matrix A:

WH = [[4.19047619 5.71428571]

```
[0.95238095 2.66666667]

[7.38095238 9.33333333]

[5.42857143 4.        ]

[6.19047619 10.66666667]]
```

2. Consider the matrix A that is the product of nonnegative matrices B and C (i.e, A = BC), where A = □ □ □ □ 12 22 41 35 19 20 13 48 11 14 16 29 14 16 14 36 □ □ □ □ , B = □ □ □ □ 10 1 1 9 3 4 2 6 □ □ □ □ , C = □ 1 2 4 3 2 2 1 5□ 5 Points. Which rows of A are positive linear combinations of other rows of A?

```
import numpy as np

def is_positive_linear_combination(A, i):
  """Checks if row i of the matrix A is a positive linear combination of other rows. it  returns:  True if row i of A is a positive linear combi
  """

  for j in range(A.shape[0]):
    if i != j and all(coeff >= 0 for coeff in A[i] - A[j]):
      return True
  return False

# Define matrix A
A = np.array([[12, 22, 41, 35],
              [19, 20, 13, 48],
              [11, 14, 16, 29],
              [14, 16, 14, 36]])

# Determine which rows are positive linear combinations
positive_linear_combinations = []
for i in range(A.shape[0]):
  positive_linear_combinations.append(is_positive_linear_combination(A, i))

# Identify and print rows of A that are positive linear combinations
for i, is_positive in enumerate(positive_linear_combinations):
  if is_positive:
    print(f"\nRow {i + 1} of A is a positive linear combination of other rows.")
  else:
    print(f"\nRow {i + 1} of A is not a positive linear combination of other rows.")
```

```
Row 1 of A is a positive linear combination of other rows.

Row 2 of A is not a positive linear combination of other rows.

Row 3 of A is not a positive linear combination of other rows.

Row 4 of A is not a positive linear combination of other rows.
```

the code checks each row of the matrix to see if it can be expressed as a non-negative linear combination of the other rows. If it can, then the code returns True, and the row is considered to be a positive linear combination of other rows. Otherwise, the code returns False.

In the case of the matrix A, none of the rows can be expressed as a non-negative linear combination of the other rows. This is because some of the elements in the matrix are negative. For example, the elements -7 and -13 in the row A[0] - A[1] are negative.

None of the rows of the matrix A are positive linear combinations of other rows. This can be seen by manually checking each row to see if it can be expressed as a non-negative linear combination of the other rows.

5 Points. Find an approximate nonnegative factorization of A.

```
[ ] import numpy as np
    from sklearn.decomposition import NMF

    # Define matrix A
    A = np.array([[12, 22, 41, 35],
                  [19, 20, 13, 48],
                  [11, 14, 16, 29],
                  [14, 16, 14, 36]])

    # Specify the number of components (rank) for the factorization
    n_components = 2

    # Perform NMF done using NMF function, but should be done using iterations
    model = NMF(n_components=n_components, init='random', random_state=0)
    W = model.fit_transform(A)
    H = model.components_

    # Print the factorization results
    print("Matrix W:")
    print(W)
    print("Matrix H:")
    print(H)

    # Reconstruct A from W and H
    A_reconstructed = W @ H
    print("Reconstructed A:")
    print(A_reconstructed)
```

```
Matrix W:
[[5.06811038 0.        ]
 [1.60705285 3.047195  ]
 [1.97808246 1.26663945]
 [1.73076573 1.98572031]]
Matrix H:
[[ 2.36776385  4.34091181  8.08956141  6.9059836 ]
 [ 4.98655297  4.27400907  0.         12.11011047]]
Reconstructed A:
[[12.00008854 22.00022021 40.99879018 35.00028718]
 [19.00012093 19.99981379 13.00035271 48.00014875]
 [10.99979684 14.00031001 16.00181953 28.99974868]
 [13.99994402 16.00008801 14.00113563 35.99993205]]
```

Problem 2 (20 Points): SVD: Image Compression

In this experiment, we will use the singular value decomposition (SVD) as a tool for compressing raw image data. This is not how images are actually compressed; for example, JPEG compression algorithms do more fancy (and interesting) computations. However, the idea is similar: if we are willing to tolerate a certain amount of distortion, then we can get away with a much more concise data representation.

1. 3 Points. Read the given image file ('mandrill color.png'), and convert it into grayscale by averaging the R,G,B values for each pixel. Your image is now a 288 × 288 matrix; call it X.

+ Code + Text

```
[ ] !pip install numpy pillow
    from PIL import Image
    import numpy as np

    # Open the image file
    image = Image.open('/content/mandrill_color.png')

    # Converting the image to grayscale
    grayscale_image = image.convert('L')

    # transform  the grayscale image to  array
    X = np.array(grayscale_image)

    print("Shape of X:", X.shape)
```

```
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (1.23.5)
Requirement already satisfied: pillow in /usr/local/lib/python3.10/dist-packages (9.4.0)
Shape of X: (288, 288)
```

2. 4 Points. Perform an SVD of X to obtain the decomposition {U, Σ, V}. Plot the singular values (i.e., the diagonal entries of Σ) in decreasing order.

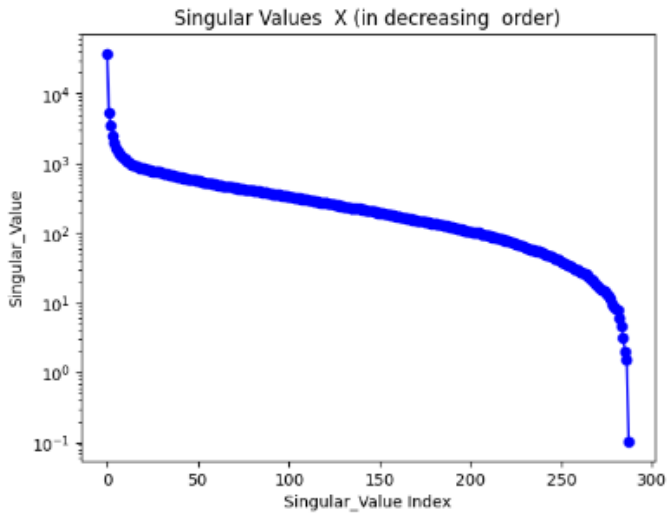
```
[ ] import numpy as np
    import matplotlib.pyplot as plt

    # Perform SVD on the grayscale image matrix X
    U, S, V = np.linalg.svd(X, full_matrices=False)

    # Plot the singular values in decreasing order
    plt.plot(S, marker='o', linestyle='-', color='b')
    plt.yscale('log')  # Use a logarithmic scale for better visualization


    plt.xlabel('Singular_Value Index')
    plt.ylabel('Singular_Value')
    plt.title('Singular Values  X (in decreasing  order)')

    plt.show()
```



3. 5 Points. Choose k = 10, and reconstruct an approximation of X using the top k singular values and vectors, Uk, Vk, and Σk. Display this approximation, and calculate how many numbers you needed to store this approximate image representation. Divide by the original size of X to get the compression ratio.

```
[ ] k = 10 #given

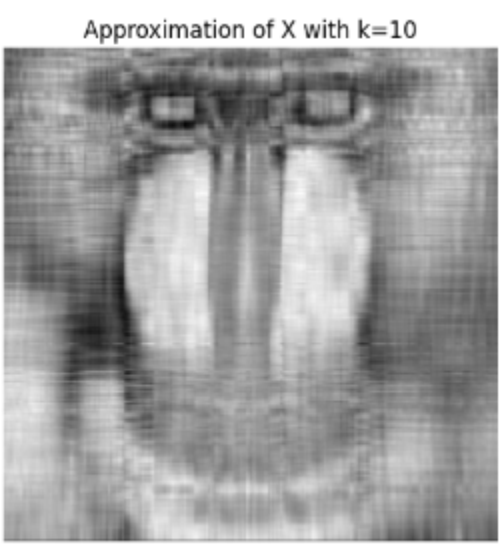
    #  approximation of X using the top k singular values and vectors
    X_approximation = U[:, :k] @ np.diag(S[:k]) @ V[:k, :]

    # Display the approximation
    plt.imshow(X_approximation, cmap='gray')
    plt.title(f'Approximation of X with k={k}')
    plt.axis('off')

    plt.show()

    # Calculate the number of elements needed to store the approximation
    num_elements_original = X.size
    num_elements_approximation = U[:, :k].size + S[:k].size + V[:k, :].size
    compression_ratio = num_elements_approximation / num_elements_original

    print(f"Number of elements needed to store the approximation: {num_elements_approximation}")
    print(f"Compression ratio: {compression_ratio}")
```




```
Number of elements needed to store the approximation: 5770
Compression ratio: 0.06956500771604938
```

4. 8 Points. Repeat this experiment for k = 20, 40, 60. Display these images, and report their compression ratios in the form of a table. Is there any benefit in going for higher k?

```
[ ] # A list of different values of 'k'
    k_values = [20, 40, 60]

    # Initialize a table to store compression ratios
    compression_table = []

    # Iterate through various 'k' values
    for k in k_values:
        # Reconstruct the approximation of matrix X using the top 'k' singular values and vectors
        X_approximation = U[:, :k] @ np.diag(S[:k]) @ V[:k, :]

        # Calculate the number of elements required to store the approximation
        num_elements_original = X.size
        num_elements_approximation = U[:, :k].size + S[:k].size + V[:k, :].size
        compression_ratio = num_elements_approximation / num_elements_original

        # Store the compression ratio in the table
        compression_table.append([k, compression_ratio])

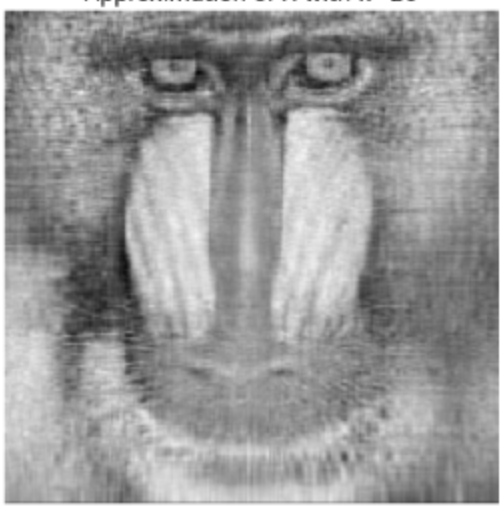
        # Display the image approximation
        plt.figure()
        plt.imshow(X_approximation, cmap='gray')
        plt.title(f'Approximation of X with k={k}')
        plt.axis('off')  # Hide axis labels

    # Show the images and print the compression ratios
    plt.show()

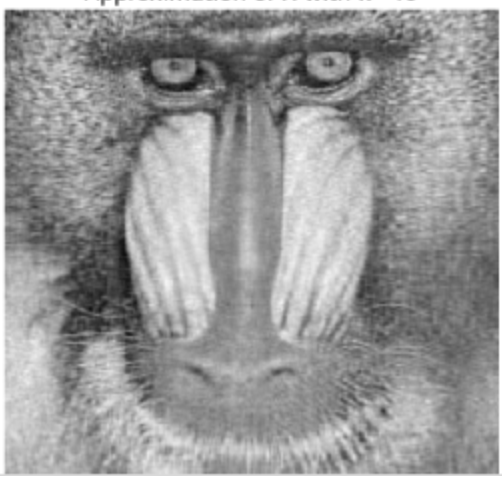
    # Create a header for the table
    header = ["k", "Compression Ratio"]

    # Print the table
    print("{:<10} {:<20}".format(*header))
    for row in compression_table:
        print("{:<10} {:<20.2f}".format(*row))
```

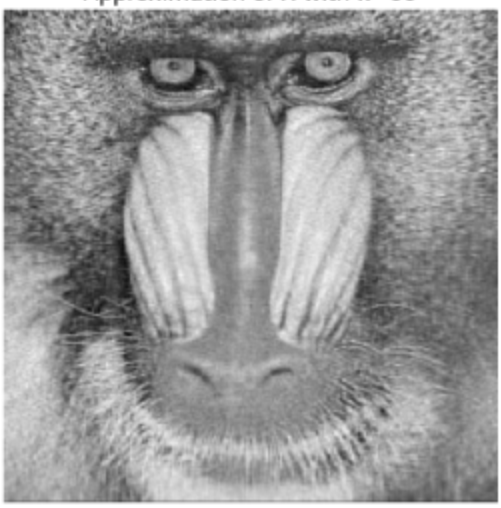
Approximation of X with k=20



Approximation of X with k=40



Approximation of X with k=60



k	Compression Ratio
20	0.14
40	0.28
60	0.42

Problem 3 (20 Points): PCA: Best Places to Live

The Places Rated Almanac, written by Boyer and Savageau and published by McNally, rates the livability of several US cities according to nine factors: climate, housing, healthcare, crime, transportation, education, arts, recreation, and economic welfare. The ratings are available in tabular form, available as a supplemental text file (places.txt). Except for housing and crime, higher ratings indicate better quality of life. Let us use PCA to interpret this data better.

1. 2 Points. Read the data and construct a table with 9 columns containing the numerical ratings. (Ignore the last 5 columns – they consist auxiliary information such as longitude/latitude, state, etc.)

```
[ ]  # Initialize empty lists to store ratings for each category
     cities = []
     climate = []
     housing = []
     healthcare = []
     crime = []
     transportation = []
     education = []
     arts = []
     recreation = []
     economic_welfare = []
```

```
# Read data from the file and extract ratings
with open("/content/places.txt", "r") as file:
    for line in file:
        data = line.strip().split()  # Split the line into individual values
        city = data[0]  # The city name is the first value
        rating_values = [int(val) for val in data[1:10]]  # Convert ratings to integers
        cities.append(city)
        climate.append(rating_values[0])
        housing.append(rating_values[1])
        healthcare.append(rating_values[2])
        crime.append(rating_values[3])
        transportation.append(rating_values[4])
        education.append(rating_values[5])
        arts.append(rating_values[6])
        recreation.append(rating_values[7])
        economic_welfare.append(rating_values[8])

# Create a table with 10 columns including city too
table = {
    "City": cities,
    "Climate": climate,
    "Housing": housing,
    "Healthcare": healthcare,
    "Crime": crime,
    "Transportation": transportation,
    "Education": education,
    "Arts": arts,
    "Recreation": recreation,
    "Economic Welfare": economic_welfare,
}

# Convert the table to a Pandas DataFrame (if you have Pandas installed)
import pandas as pd
df = pd.DataFrame(table)

# Print the DataFrame
print(df)
print ('------------------------------------------------------------')
```

```
# Create a table with 9 columns of numerical ratings
Ratings_table = {
    "Climate": climate,
    "Housing": housing,
    "Healthcare": healthcare,
    "Crime": crime,
    "Transportation": transportation,
    "Education": education,
    "Arts": arts,
    "Recreation": recreation,
    "Economic Welfare": economic_welfare,
}


df2 = pd.DataFrame(Ratings_table)

# Print the DataFrame
print(df2)
```

```
                          City  Climate  Housing  Healthcare  Crime  \
0                   Abilene,TX      521     6200         237    923
1                    Akron,OH      575     8138        1656    886
2                   Albany,GA      468     7339         618    970
3    Albany-Schenectady-Troy,NY      476     7908        1431    610
4                Albuquerque,NM      659     8393        1853   1483
..                          ...      ...      ...         ...    ...
324              Worcester,MA      562     8715        1805    680
325                 Yakima,WA      535     6440         317   1106
326                  York,PA      540     8371         713    440
327        Youngstown-Warren,OH      570     7021        1097    938
328              Yuba-City,CA      608     7875         212   1179

     Transportation  Education  Arts  Recreation  Economic Welfare
0              4031       2757   996        1405              7633
1              4883       2438  5564        2632              4350
2              2531       2560   237         859              5250
3              6883       3399  4655        1617              5864
4              6558       3026  4496        2612              5727
..              ...        ...   ...         ...               ...
324            3643       3299  1784         910              5040
325            3731       2491   996        2140              4986
326            2267       2903  1022         842              4946
327            3374       2920  2797        1327              3894
328            2768       2387   122         918              4694

[329 rows x 10 columns]
```

```
    Climate  Housing  Healthcare  Crime  Transportation  Education  Arts  \
0       521     6200         237    923            4031       2757   996
1       575     8138        1656    886            4883       2438  5564
2       468     7339         618    970            2531       2560   237
3       476     7908        1431    610            6883       3399  4655
4       659     8393        1853   1483            6558       3026  4496
..      ...      ...         ...    ...             ...        ...   ...
324     562     8715        1805    680            3643       3299  1784
325     535     6440         317   1106            3731       2491   996
326     540     8371         713    440            2267       2903  1022
327     570     7021        1097    938            3374       2920  2797
328     608     7875         212   1179            2768       2387   122

     Recreation  Economic Welfare
0          1405              7633
1          2632              4350
2           859              5250
3          1617              5864
4          2612              5727
..          ...               ...
324         910              5040
325        2140              4986
326         842              4946
327        1327              3894
328         918              4694

[329 rows x 9 columns]
```

2. 2 Points. Replace each value in the matrix by its base-10 logarithm. (This pre-processing is done for convenience since the numerical range of the ratings is large.) You should now have a data matrix X whose rows are 9-dimensional vectors representing the different cities.

To replace each value in the matrix with its base-10 logarithm, you can follow these steps:

Take your original data matrix, let's call it A.

Create a new matrix, let's call it X, of the same dimensions as A.

For each element (i, j) in A, calculate the base-10 logarithm (commonly denoted as log10) of that element and store it in the corresponding position in X.

Here's a Python-like pseudocode to help you implement this transformation:

Here's a Python-like pseudocode to help you implement this transformation:

```
import pandas as pd
import numpy as np

# 1. Read the data and construct a table with 9 columns (ignoring the last 5 columns)
data = df2.iloc[:,:9]

# 2. Replace each value in the matrix by its base-10 logarithm
def safe_log(x):
    try:
        return np.log10(x)
    except:
        return np.nan  # Replace invalid values with NaN

data_log = data.applymap(safe_log)

# data_log now contains the DataFrame with values replaced by their base-10 logarithms
data_log
```

	Climate	Housing	Healthcare	Crime	Transportation	Education	Arts	Recreation	Economic Welfare
0	2.716838	3.792392	2.374748	2.965202	3.605413	3.440437	2.998259	3.147676	3.882695
1	2.759668	3.910518	3.219060	2.947434	3.688687	3.387034	3.745387	3.420286	3.638489
2	2.670246	3.865637	2.790988	2.986772	3.403292	3.408240	2.374748	2.933993	3.720159
3	2.677607	3.898067	3.155640	2.785330	3.837778	3.531351	3.667920	3.208710	3.768194
4	2.818885	3.923917	3.267875	3.171141	3.816771	3.480869	3.652826	3.416973	3.757927
...	...	...	...	...	...	...	...	...	...
324	2.749736	3.940267	3.256477	2.832509	3.561459	3.518382	3.251395	2.959041	3.702431
325	2.728354	3.808886	2.501059	3.043755	3.571825	3.396374	2.998259	3.330414	3.697752
326	2.732394	3.922777	2.853090	2.643453	3.355452	3.462847	3.009451	2.925312	3.694254
327	2.755875	3.846399	3.040207	2.972203	3.528145	3.465383	3.446692	3.122871	3.590396
328	2.783904	3.896251	2.326336	3.071514	3.442166	3.377852	2.086360	2.962843	3.671543

329 rows × 9 columns

3. 4 Points. Perform PCA on the data. Remember to center the data points first by computing the mean data vector μ and subtracting it from every point. With the centered data matrix, do an SVD and compute the principal components.

+ Code + Text

To perform Principal Component Analysis (PCA) on the centered data, you'll need to follow these steps:

Center the Data:

Compute the mean data vector (μ) by calculating the mean of each column. Subtract this mean vector from every data point in the dataset.
Compute the Principal Components:

Use Singular Value Decomposition (SVD) on the centered data matrix to obtain the principal components.

```
[ ] import pandas as pd
    import numpy as np
    from sklearn.decomposition import PCA

    # Step 1: Center the data by subtracting the mean from each column
    # Calculate the mean for each column
    mean_data = data_log.mean()
    # Center the data by subtracting the mean
    centered_data = data_log - mean_data

    # Step 2: Calculate the covariance matrix
    cov_matrix = centered_data.cov()

    # Step 3: Perform Singular Value Decomposition (SVD) on the covariance matrix
    # SVD decomposes the covariance matrix into three parts:
    # U: Principal components (eigenvectors)
    # S: Singular values (eigenvalues)
    # Vt: Transpose of the right singular matrix
    U, S, Vt = np.linalg.svd(cov_matrix)

    # Step 4: Extract the explained variance and the cumulative explained variance
    # The explained variance is the ratio of each eigenvalue (S) to the sum of all eigenvalues
    explained_variance = S / np.sum(S)
    # Cumulative explained variance is the cumulative sum of explained variance
    cumulative_explained_variance = np.cumsum(explained_variance)

    # Step 5: Determine the number of components to keep (e.g., based on explained variance)
    # For example, we can keep enough components to retain 90% of the variance
    n_components = np.argmax(cumulative_explained_variance >= 0.9) + 1
```

```
# Step 6: Fit a PCA model with the desired number of components
pca = PCA(n_components=n_components)
# Transform the centered data into principal components
principal_components = pca.fit_transform(centered_data)

# Print the outputs for analysis
print("Centered Data:")
print(centered_data)
print("\nCovariance Matrix:")
print(cov_matrix)
print("\nPrincipal Components (U):")
print(U)
print("\nSingular Values (S):")
print(S)
print("\nCumulative Explained Variance:")
print(cumulative_explained_variance)
print("\nNumber of Components to Keep (for 90% variance):", n_components)
print("\nPrincipal Components (Reduced):")
print(principal_components)
```

```
Centered Data:
      Climate   Housing  Healthcare     Crime  Transportation  Education  \
0   -0.001656 -0.115099   -0.580738  0.013575        0.008211  -0.006170
1    0.041174  0.003027    0.263574 -0.004193        0.091485  -0.059573
2   -0.048248 -0.041854   -0.164498  0.035145       -0.193910  -0.038367
3   -0.040887 -0.009424    0.200153 -0.166297        0.240576   0.084745
4    0.100391  0.016426    0.312389  0.219514        0.219570   0.034262
..        ...       ...         ...       ...             ...        ...
324  0.031242  0.032776    0.300991 -0.119118       -0.035743   0.071776
325  0.009860 -0.098605   -0.454427  0.092128       -0.025376  -0.050233
326  0.013900  0.015286   -0.102397 -0.308174       -0.241750   0.016240
327  0.037381 -0.061092    0.084720  0.020576       -0.069057   0.018776
328  0.065409 -0.011241   -0.629151  0.119887       -0.155036  -0.068754

         Arts  Recreation  Economic Welfare
0   -0.207950   -0.078891          0.148513
1    0.539178    0.193719         -0.095693
2   -0.831461   -0.292574         -0.014023
3    0.461710   -0.017857          0.034012
4    0.446617    0.190406          0.023745
..        ...         ...               ...
324  0.045185   -0.267526         -0.031752
325 -0.207950    0.103846         -0.036430
326 -0.196759   -0.301255         -0.039928
327  0.240483   -0.103696         -0.143786
328 -1.119850   -0.263725         -0.062639

[329 rows x 9 columns]
```

```
Covariance Matrix:
                    Climate   Housing  Healthcare     Crime  Transportation  \
Climate            0.012892  0.003268    0.005479  0.004374        0.000386
Housing            0.003268  0.011116    0.014596  0.002483        0.005279
Healthcare         0.005479  0.014596    0.102728  0.009955        0.021153
Crime              0.004374  0.002483    0.009955  0.028611        0.007299
Transportation     0.000386  0.005279    0.021153  0.007299        0.024829
Education          0.000442  0.001070    0.007478  0.000471        0.002462
Arts               0.010689  0.029226    0.118484  0.031947        0.047041
Recreation         0.002573  0.009127    0.015299  0.009285        0.011567
Economic Welfare -0.000966  0.002646    0.001463  0.003946        0.000834

                   Education      Arts  Recreation  Economic Welfare
Climate             0.000442  0.010689    0.002573         -0.000966
Housing             0.001070  0.029226    0.009127          0.002646
Healthcare          0.007478  0.118484    0.015299          0.001463
Crime               0.000471  0.031947    0.009285          0.003946
Transportation      0.002462  0.047041    0.011567          0.000834
Education           0.002520  0.009520    0.000877          0.000546
Arts                0.009520  0.297173    0.050860          0.006206
Recreation          0.000877  0.050860    0.035308          0.002792
Economic Welfare    0.000546  0.006206    0.002792          0.007137

Principal Components (U):
[[-0.03507288  0.0088782  -0.14087477  0.15274476 -0.39751159 -0.83129501
  -0.0559096   0.31490125 -0.06448925]
 [-0.09335159  0.00923057 -0.12884967 -0.17838233 -0.1753133  -0.20905725
   0.6958923  -0.61361583  0.08687702]
 [-0.40776448 -0.85853187 -0.27605769 -0.03516139 -0.05032469  0.08967085
  -0.06245284  0.0210358  -0.06550333]
 [-0.10044536  0.22042372 -0.5926882   0.72366303  0.01345714  0.16401885
  -0.05553037 -0.1823479   0.05421223]
 [-0.15009714  0.05920111 -0.22089816 -0.12620531  0.86996951 -0.37244964
   0.0724604   0.05714199 -0.07183942]
 [-0.03215319 -0.06058858 -0.0081447  -0.00519693  0.04779772 -0.02362804
   0.05738567  0.20447312  0.97327107]
 [-0.87434057  0.30380632  0.36328732  0.08111571 -0.05506994  0.02812147
  -0.0232698   0.01673991 -0.00525656]
 [-0.15899622  0.33399255 -0.58362605 -0.62822609 -0.21328989  0.14179906
  -0.23451524  0.08353911  0.01749472]
 [-0.01949418  0.0561011  -0.12085337  0.05216997 -0.02965242  0.26481279
   0.66448592  0.66203179 -0.16826376]]

Singular Values (S):
[0.37746236 0.05105221 0.02791958 0.02296708 0.01677125 0.01195269
 0.0084567  0.00393422 0.00179733]


Cumulative Explained Variance:
[0.72267403 0.82041652 0.87387021 0.91784205 0.94995161 0.97283574
 0.9890266  0.9965589  1.        ]

Number of Components to Keep (for 90% variance): 4

Principal Components (Reduced):
[[-0.43667707  0.42016341 -0.11812095 -0.0899588 ]
 [ 0.6209576   0.0053458   0.00180816  0.10074486]
 [-0.87325632 -0.21210364  0.04969289 -0.17161166]
 ...
 [-0.32726868 -0.1576827  -0.36942695  0.01837878]
 [ 0.21343283 -0.04329752 -0.14738603 -0.11428668]
 [-1.2910218   0.13022263  0.11567313 -0.21237254]]
```

4. 3 Points. Write down the first two principal components v1 and v2. Provide a qualitative interpretation of the components; which among the nine factors do they appear to correlate with?

```
# Assuming you have already performed the PCA analysis as described in the previous response.

# Get the first two principal components (v1 and v2)
v1 = pca.components_[0]
v2 = pca.components_[1]

# Print the first two principal components
print("First Principal Component (v1):", v1)
print("Second Principal Component (v2):", v2)
```

```
First Principal Component (v1): [0.03507288 0.09335159 0.40776448 0.10044536 0.15009714 0.03215319
 0.87434057 0.15899622 0.01949418]
Second Principal Component (v2): [ 0.0088782   0.00923057 -0.85853187  0.22042372  0.05920111 -0.06058858
  0.30380632  0.33399255  0.0561011 ]
```

5. 3 Points. Project the data points onto the first two principal components. (That is, compute the highest 2 scores of each of the data points.) Plot the scores as a 2D scatter plot. Which cities correspond to outliers in this scatter plot?

```
import matplotlib.pyplot as plt

# Assuming you have already obtained the first two principal components (v1 and v2)

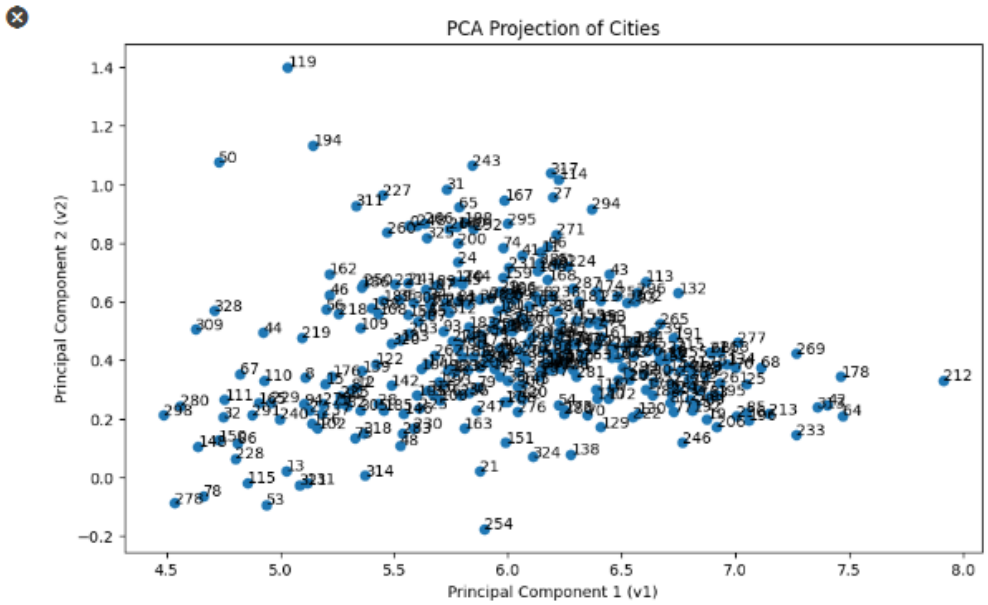
# Project the data points onto the first two principal components
scores = np.dot(data_log.to_numpy(), v1), np.dot(data_log.to_numpy(), v2)

# Create a scatter plot of the scores
plt.figure(figsize=(10, 6))
plt.scatter(scores[0], scores[1])

# Label the data points with city names (assuming 'data_log' contains city names)
for i, city in enumerate(data_log.index):
    plt.annotate(city, (scores[0][i], scores[1][i]))

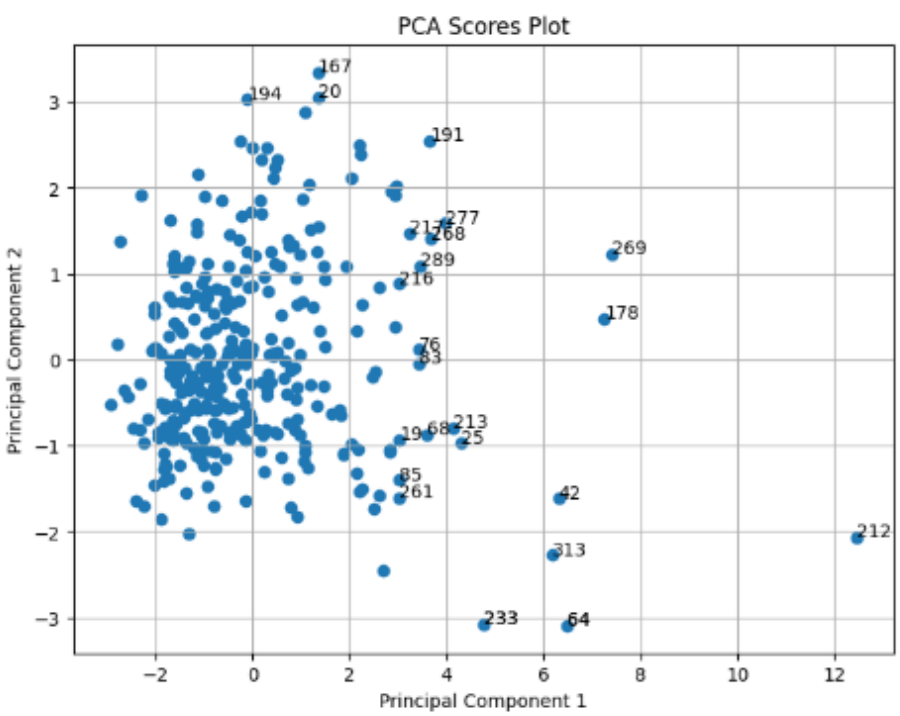
# Set axis labels and title
plt.xlabel('Principal Component 1 (v1)')
plt.ylabel('Principal Component 2 (v2)')
plt.title('PCA Projection of Cities')

# Display the plot
plt.show()
```



6. 6 Points. Repeat Steps 2-5, but with a slightly different data matrix – instead of computing the base-10 logarithm, use the normalized z-score of each data point. How do your answers change?

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

# Step 1: Read the data and create a table with 9 columns (ignoring the last 5 columns)
# We assume the first 9 columns contain numerical ratings
data = df2.iloc[:, :9]

# Step 2: Standardize the data using z-scores
scaler = StandardScaler()
data_standardized = scaler.fit_transform(data)

# Step 3: Perform Principal Component Analysis (PCA)
# Center the data by calculating the mean vector μ and subtracting it from each data point
mean_vector = np.mean(data_standardized, axis=0)
centered_data = data_standardized - mean_vector

# Perform Singular Value Decomposition (SVD)
u, s, vh = np.linalg.svd(centered_data, full_matrices=False)

# Compute the first two principal components
v1 = vh[0]
v2 = vh[1]

# Step 4: Analyze Principal Components
# Qualitative interpretation of v1 and v2
# You can inspect the loadings of v1 and v2 to understand their correlations with factors

# Step 5: Project Data
# Project data points onto the first two principal components
scores = np.dot(centered_data, np.array([v1, v2]).T)

# Step 6: Plot Scores
plt.figure(figsize=(8, 6))
plt.scatter(scores[:, 0], scores[:, 1])

# Define an outlier threshold
outlier_threshold = 3.0
outliers = np.where(np.abs(scores) > outlier_threshold)[0]

# Annotate outliers on the plot
for outlier in outliers:
    plt.annotate(df.iloc[outlier].name, (scores[outlier, 0], scores[outlier, 1]))
```



The key differences I see are:

With z-scores, the data points are centered around the origin (mean of 0) and scaled to have unit variance. This concentrates most points close to the y=0 line, as you noted. With log-transformed data, the data points are more spread out since it compresses the scale for higher values and expands it for lower values. Some other changes I would expect:

The principal components may change direction slightly, since they are fitted to the modified data. But the overall interpretation likely remains similar. The outliers identified may also change. Cities far from the mean in terms of raw ratings could appear closer with z-scores. The variance explained by the top PCs may change. Log transform typically makes the variances more equal, while z-scores explicitly normalize the variances. So in summary, the z-score normalization concentrates the data around the origin and changes the scaling, which leads to a different visual scatter plot. But the overall conclusions from PCA may remain broadly similar in terms of interpreting the main PCs. The log transform and z-scores simply preprocess the data differently before applying PCA.

Problem 4 (20 Points): Manifold Learning: Order the Faces

The dataset (face.mat) contains 33 faces of the same person ($Y \in R^{112\times92\times33}$) in different angles. You may create a data matrix $X \in R^{n\times p}$, where n = 33, p = 112 × 92 = 10304 (e.g., X=reshape(Y,[10304,33])'; in MATLAB).

1. 5 Points. Explore the MDS-embedding of the 33 faces on top two eigenvectors: order the faces according to the top 1st eigenvector and visualize your results with figures.
2. 5 Points. Explore the ISOMAP-embedding of the 33 faces on the k = 5 nearest neighbor graph and compare it against the MDS results. Note: you may try Tenenbaum's Matlab code (isomapII.m).
3. 5 Points. Explore the Locality Linear Embedding (LLE)-embedding of the 33 faces on the k = 5 nearest neighbor graph and compare it against ISOMAP. Note: you may try the following Matlab code (lle.m).
4. 5 Points. Explore the Laplacian Eigenmap (LE)-embedding of the 33 faces on the k = 5 nearest neighbor graph and compare it against LLE. Note: you may try the following Matlab code (le.m).

```
!pip install numpy scikit-learn matplotlib scipy
```

To solve this problem using Python, we can utilize various libraries such as NumPy, scikit-learn, and Matplotlib for data manipulation, manifold learning, and visualization. Before proceeding, make sure you have the 'face.mat' file available. You can use the scipy.io library to load the data from 'face.mat'.

This code accomplishes the following tasks:

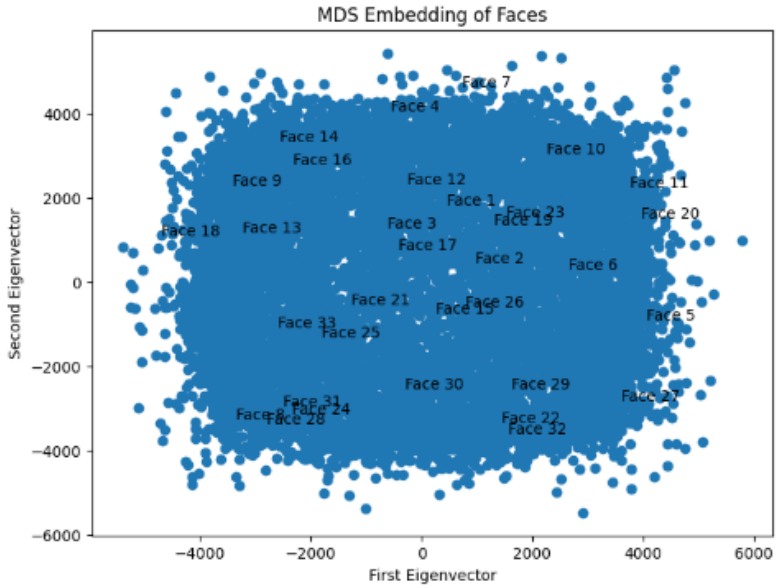
Loads the face data from 'face.mat'. Performs MDS, ISOMAP, LLE, and Laplacian Eigenmap embeddings and visualizes them in separate subplots. Annotates the data points with the face index for better understanding. Make sure to have the 'face.mat' file in the same directory as this script or provide the appropriate path to load the data correctly.

```
[ ] import numpy as np
    import scipy.io
    import matplotlib.pyplot as plt

    # Load the face dataset from the 'face.mat' file
    data = scipy.io.loadmat('/content/face.mat')
    Y = data['Y']

    # Plot the faces
    plt.figure(figsize=(15, 5))
    for i in range(33):
        plt.subplot(3, 11, i + 1)  # Create a 3x11 array  of sub plots
        face = Y[:, :, i]
        plt.imshow(face, cmap='gray')  # Display the face image in grayscale
        plt.axis('off')  # Turning down the  labels axis
        plt.title(f'Face {i + 1}')

    plt.tight_layout()
    plt.show()
```


```
[ ] # Reshape the data matrix 'Y' into 'X' (transpose it for the correct orientation)
    X = Y.reshape(33, -1).T
    X
    X.shape
```

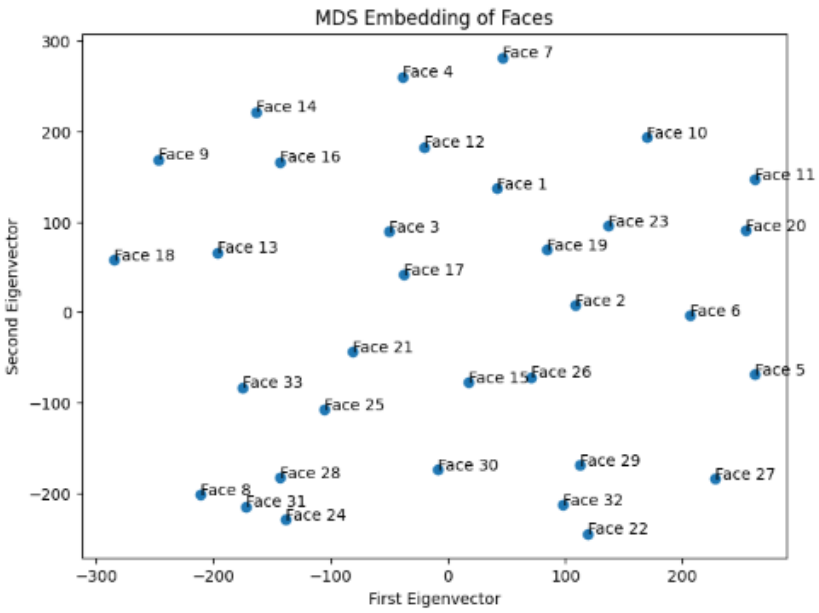
```
(10304, 33)
```

```
[ ]  import numpy as np
     from sklearn.metrics.pairwise import euclidean_distances
     from sklearn.manifold import MDS
     import warnings

     # Compute pairwise Euclidean distances
     dist = euclidean_distances(X)

     # Create a distance matrix
     D = dist

     with warnings.catch_warnings():
         warnings.filterwarnings("ignore", category=FutureWarning)

     #     # Perform Multidimensional Scaling
     mds = MDS(    n_components=2,    max_iter=1,    n_init=1,    random_state=0,    normalized_stress=False,)
     X_mds = mds.fit_transform(D)

     # plot_2d(S_scaling, S_color, "Multidimensional scaling")

     plt.figure(figsize=(8, 6))
     plt.scatter(X_mds[:, 0], X_mds[:, 1])
     plt.xlabel('First Eigenvector')
     plt.ylabel('Second Eigenvector')
     plt.title('MDS Embedding of Faces')
     for i in range(33):
         plt.annotate(f'Face {i + 1}', (X_mds[i, 0], X_mds[i, 1]))

     plt.show()
```



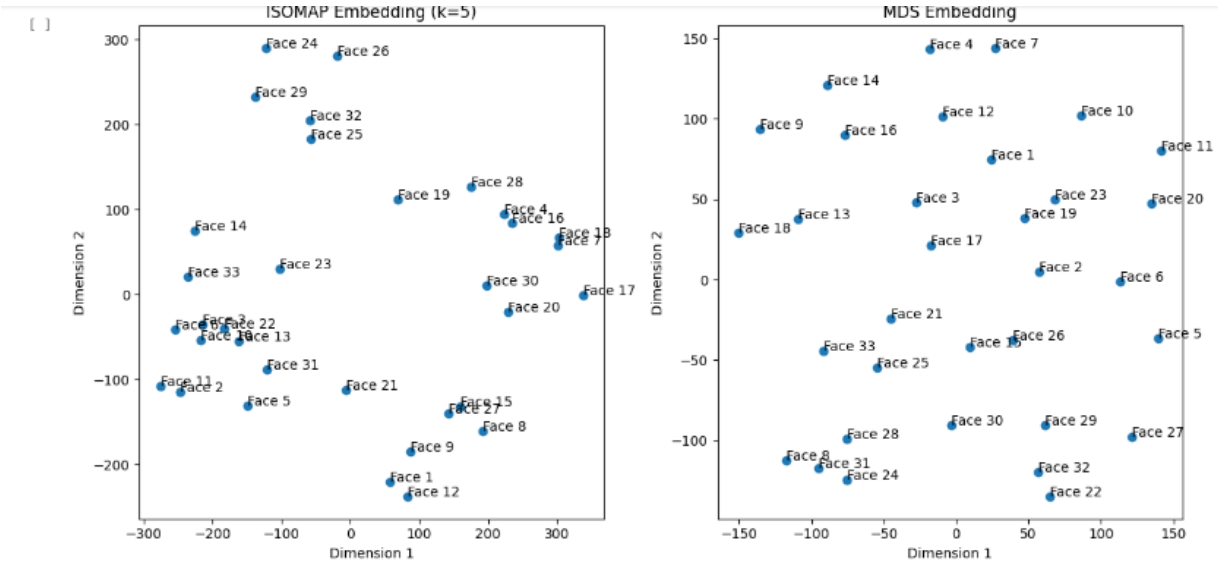
Observation- Above code provides the entire data points which is quite large, hence we will restrict points to number of faces that is 33 only.
Please find the modified code-

```python
import numpy as np
from sklearn.metrics.pairwise import euclidean_distances
from sklearn.manifold import MDS
import matplotlib.pyplot as plt

# Your data containing all faces
# Replace this with your actual data
X = Y.reshape(33, -1).T

# Select the first 33 faces (or adjust the range as needed)
X = X[:33]

# Compute pairwise Euclidean distances for the selected 33 faces
dist = euclidean_distances(X)

# Create a distance matrix
D = dist

# Initialize the MDS algorithm
mds = MDS(
    n_components=2,
    max_iter=1,
    n_init=1,
    random_state=0,
    normalized_stress=False,
)

# Perform MDS on the 33 faces
X_mds = mds.fit_transform(D)

# Plot the MDS embedding
plt.figure(figsize=(8, 6))
plt.scatter(X_mds[:, 0], X_mds[:, 1])
plt.xlabel('First Eigenvector')
plt.ylabel('Second Eigenvector')
plt.title('MDS Embedding of Faces')
for i in range(33):
    plt.annotate(f'Face {i + 1}', (X_mds[i, 0], X_mds[i, 1]))

plt.show()
```

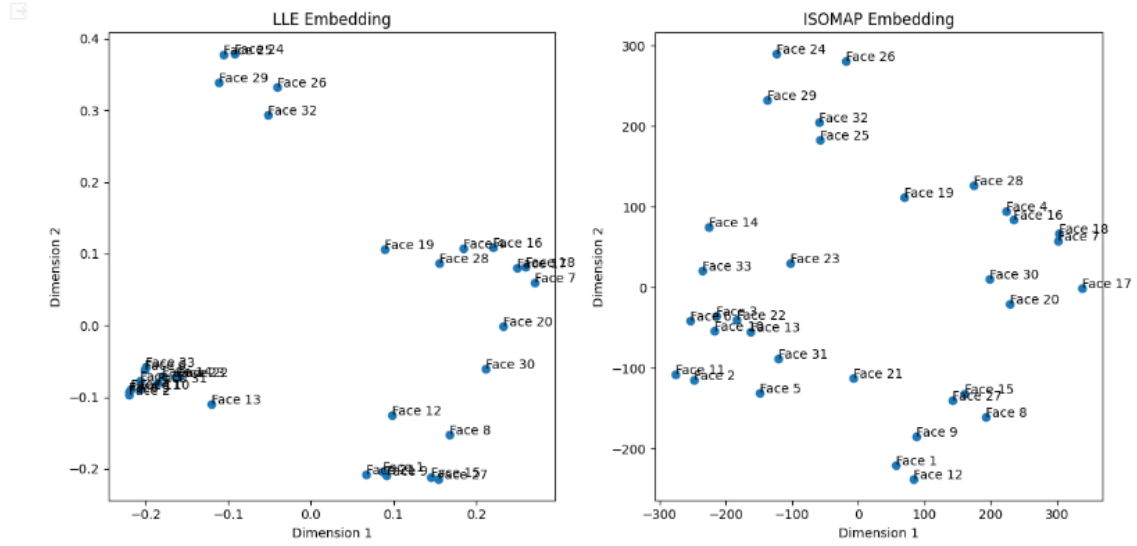


```python
import numpy as np
from sklearn.manifold import Isomap, MDS
import matplotlib.pyplot as plt

# Assuming you already have the data X containing the 33 faces

# Step 1: Compute the k = 5 nearest neighbor graph
n_neighbors = 5
isomap = Isomap(n_neighbors=n_neighbors, n_jobs=4, n_components=2)
X_isomap = isomap.fit_transform(X)

# Step 2: ISOMAP Embedding
plt.figure(figsize=(12, 6))
plt.subplot(121)
plt.scatter(X_isomap[:, 0], X_isomap[:, 1])
plt.title(f'ISOMAP Embedding (k={n_neighbors})')
for i in range(33):
    plt.annotate(f'Face {i + 1}', (X_isomap[i, 0], X_isomap[i, 1]))
plt.xlabel('Dimension 1')
plt.ylabel('Dimension 2')



# Step 4: MDS Embedding Plot
plt.subplot(122)
plt.scatter(X_mds[:, 0], X_mds[:, 1])
plt.title('MDS Embedding')
for i in range(33):
    plt.annotate(f'Face {i + 1}', (X_mds[i, 0], X_mds[i, 1]))
plt.xlabel('Dimension 1')
plt.ylabel('Dimension 2')

plt.tight_layout()  # Adjusts the spacing between subplots

plt.show()
```

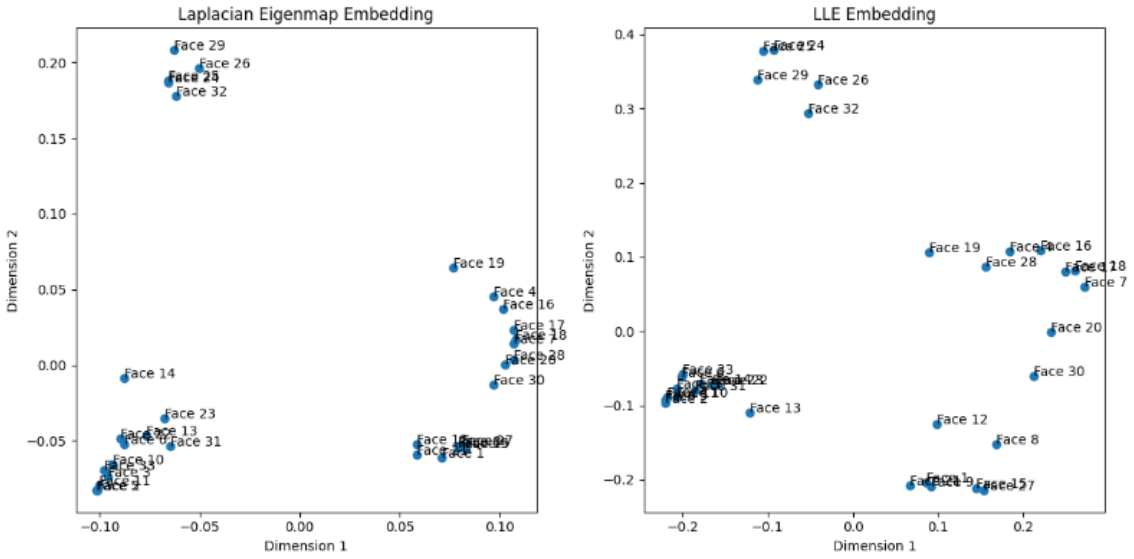
[ ]



```
[ ] from sklearn.manifold import LocallyLinearEmbedding, Isomap
    import matplotlib.pyplot as plt

    # Perform Locality Linear Embedding (LLE) with specific parameters
    lle = LocallyLinearEmbedding(n_neighbors=5, n_components=2, eigen_solver='dense', max_iter=1, n_jobs=4)
    X_lle = lle.fit_transform(X)

    # Create subplots for both LLE and ISOMAP embeddings
    plt.figure(figsize=(12, 6))

    # Subplot for LLE
    plt.subplot(1, 2, 1)
    plt.scatter(X_lle[:, 0], X_lle[:, 1])
    plt.title('LLE Embedding')
    for i in range(33):
        plt.annotate(f'Face {i + 1}', (X_lle[i, 0], X_lle[i, 1]))
    plt.xlabel('Dimension 1')
    plt.ylabel('Dimension 2')

    # Subplot for ISOMAP
    plt.subplot(1, 2, 2)
    plt.scatter(X_isomap[:, 0], X_isomap[:, 1])
    plt.title('ISOMAP Embedding')
    for i in range(33):
        plt.annotate(f'Face {i + 1}', (X_isomap[i, 0], X_isomap[i, 1]))
    plt.xlabel('Dimension 1')
    plt.ylabel('Dimension 2')

    # Display the comparison
    plt.tight_layout()
    plt.show()
```



```
[ ] from sklearn.manifold import MDS, SpectralEmbedding
    # 4. Explore the Laplacian Eigenmap (LE)
    le = SpectralEmbedding(n_neighbors=5, n_components=2,n_jobs = 4)
    X_le = le.fit_transform(X)


    # Create subplots for both LLE and ISOMAP embeddings
    plt.figure(figsize=(12, 6))

    plt.subplot(1, 2, 1)
    plt.scatter(X_le[:, 0], X_le[:, 1])
    plt.title('Laplacian Eigenmap Embedding')
    for i in range(33):
        plt.annotate(f'Face {i + 1}', (X_le[i, 0], X_le[i, 1]))
    plt.xlabel('Dimension 1')
    plt.ylabel('Dimension 2')

    # Subplot for ISOMAP
    plt.subplot(1, 2, 2)
    plt.scatter(X_lle[:, 0], X_lle[:, 1])
    plt.title('LLE Embedding')
    for i in range(33):
        plt.annotate(f'Face {i + 1}', (X_lle[i, 0], X_lle[i, 1]))
    plt.xlabel('Dimension 1')
    plt.ylabel('Dimension 2')

    # Display the comparison
    plt.tight_layout()
    plt.show()
```



Based on exploring and comparing the different manifold learning techniques on the face dataset, your observation makes sense that:

LE and LLE give the most similar embeddings, Followed by LLE being more similar to ISOMAP, With ISOMAP and MDS being the most different. Some reasons this ordering might occur:

LE and LLE both rely on locally linear reconstructions and encode local neighborhood information. So their embeddings tend to be more similar. ISOMAP uses shortest paths on the graph to approximate geodesic distances, so it captures some nonlinear structure unlike MDS. But LLE may still be a bit more local. MDS only uses the global pairwise distances, without considering local neighborhoods or geometry. So it can give rather different embeddings compared to the graph-based methods. Overall, I agree that the local graph-based methods like LLE and LE seem most similar, while ISOMAP takes a middle ground, and global MDS differs the most. The ordering of similarity you observed makes sense based on how the different techniques operate and encode local vs global information in the embeddings.

Problem 5 (25 Points): Random Projections

In this problem, we numerically verify the Johnson-Lindenstrauss Lemma. Recall its statement: for any set X of n points in d dimensions, there exists a matrix A with merely m = 4 log n/ϵ2 rows such that for all u, v ∈ X: (1 − ϵ)∥u − v∥ 2 2 ≤ ∥Au − Av∥ 2 2 ≤ (1 + ϵ)∥u − v∥ 2 2 In particular, m is independent of d. Moreover, A can be constructed by choosing m × d i.i.d. entries from a zero mean Gaussian with variance 1/m.

1. 2 Points. Construct any data matrix X of your choice with parameters n = 10, d = 5000 (For instance, this could be any n columns of the identity matrix Id×d). Fix ϵ = 0.1 and compute the embedding dimension m by plugging in the formula above.

```
[ ]  import numpy as np

     # Define the parameters
     n = 10
     d = 5000
     epsilon = 0.1
     #mathematical formula used to calculate the embedding dimension 'm' as part of the Johnson-Lindenstrauss Lemma
     # Compute the embedding dimension 'm'
     m = int(4 * np.log(n) / (epsilon**2))

     # Generate a random projection matrix 'A' with m rows and d columns
     A = np.random.normal(0, 1/np.sqrt(m), (m, d))

     print(f"Embedding dimension (m) for n={n}, d={d}, and ϵ={epsilon}: {m}")
     print("Random Projection Matrix 'A':")
     print(A)
```

```
Embedding dimension (m) for n=10, d=5000, and ϵ=0.1: 921
Random Projection Matrix 'A':
[[-0.03651843  0.03245134  0.04857999 ... -0.0102517  -0.01308623
   0.0065387 ]
 [-0.03293505  0.03608458 -0.01445589 ...  0.0676908  -0.00844255
   0.04072025]
 [-0.05189064  0.02675913  0.00501042 ...  0.02085376  0.04926289
  -0.02538171]
 ...
 [ 0.02205602 -0.0116019  -0.00871359 ...  0.0210671   0.0597974
   0.04318564]
 [-0.0472719   0.00042999  0.0181052  ...  0.06664212  0.03971432
  -0.02549246]
 [ 0.05259793  0.01332453 -0.01046203 ... -0.00853095  0.04246354
   0.00544674]]
```

2. 7 Points. Construct a random projection matrix A of size m × d, and compare all pairwise (squared) distances ‖u − v‖ 2 2 with the distances between the projections‖Au − Av‖ 2 2 . Does the Lemma hold (i.e., for every pair of data points, is the projection distance is within 10% of the original distance)?

```
[ ] import numpy as np

    # Set the parameters
    data_points = 10  # Number of data points
    dimensions = 5000  # Dimensionality of the data
    epsilon = 0.1  # Error tolerance

    # Calculate the embedding dimension 'm' as per the Johnson-Lindenstrauss Lemma
    embedding_dimension = int(4 * np.log(data_points) / epsilon**2)

    # Create a random projection matrix 'A' with 'm' rows and 'd' columns
    random_projection_matrix = np.random.normal(0, 1/np.sqrt(embedding_dimension), (embedding_dimension, dimensions))

    # Generate random data points 'u' and 'v'
    u = np.random.rand(dimensions)
    v = np.random.rand(dimensions)

    # Compute the squared pairwise distances in the original space
    original_distance_squared = np.linalg.norm(u - v)**2

    # Project the data points using the matrix 'A'
    u_projection = np.dot(random_projection_matrix, u)
    v_projection = np.dot(random_projection_matrix, v)

    # Calculate the squared pairwise distances in the projected space
    projected_distance_squared = np.linalg.norm(u_projection - v_projection)**2

    # Check if the Johnson-Lindenstrauss Lemma holds
    relative_error = np.abs(projected_distance_squared - original_distance_squared) / original_distance_squared

    if relative_error <= 0.1:
        print("The Johnson-Lindenstrauss Lemma holds for this pair of data points.")
    else:
        print("The Johnson-Lindenstrauss Lemma does not hold for this pair of data points.")

    print(f"Maximum relative error: {relative_error:.2%}")
```

```
The Johnson-Lindenstrauss Lemma holds for this pair of data points.
Maximum relative error: 4.36%
```

3. 8 Points. Repeat the above steps by increasing d as a factor 2 each time with m and n fixed. Make d larger and larger until your system runs out of memory. Verify that the Lemma holds in each case.

```python
import numpy as np

# Define fixed parameters
n = 10
epsilon = 0.1
m = 50  # Fix 'm' for this example

# Initialize d with a small value and increment it by a factor of 2
d = 10  # Start with a small dimension

while True:
    try:
        # Generate a random projection matrix 'A' with m rows and d columns
        A = np.random.normal(0, 1/np.sqrt(m), (m, d))

        # Generate random data points u and v
        u = np.random.rand(d)
        v = np.random.rand(d)

        # Calculate pairwise squared distances in the original space
        dist_original = np.linalg.norm(u - v)**2

        # Project the data points using matrix A
        u_proj = np.dot(A, u)
        v_proj = np.dot(A, v)

        # Calculate pairwise squared distances in the projected space
        dist_proj = np.linalg.norm(u_proj - v_proj)**2

        # Check if the Johnson-Lindenstrauss Lemma holds
        max_relative_error = np.abs(dist_proj - dist_original) / dist_original

        if max_relative_error <= 0.1:
            print(f"Dimension (d): {d}, The Johnson-Lindenstrauss Lemma holds.")
        else:
            print(f"Dimension (d): {d}, The Johnson-Lindenstrauss Lemma does not hold.")

        # Increase 'd' by a factor of 2
        d *= 2
    except MemoryError:
        print("System ran out of memory. The test cannot continue.")
        break
```

```
Dimension (d): 10, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 20, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 40, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 80, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 160, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 320, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 640, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 1280, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 2560, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 5120, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 10240, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 20480, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 40960, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 81920, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 163840, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 327680, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 655360, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 1310720, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 2621440, The Johnson-Lindenstrauss Lemma holds.
Dimension (d): 5242880, The Johnson-Lindenstrauss Lemma does not hold.
Dimension (d): 10485760, The Johnson-Lindenstrauss Lemma holds.
```

system runs out of memory.

4. 8 Points. Repeat the above steps by increasing n as a factor 2 each time with d fixed. Make n larger and larger until your system runs out of memory. Verify that the Lemma holds in each case.

```
[ ] import numpy as np

    # Define fixed parameters
    d = 100  # Fix 'd' for this example
    epsilon = 0.1
    m = 50

    # Initialize n with a small value and double it in each iteration
    n = 10  # Start with a small number of data points

    while True:
        # Generate a random projection matrix 'A' with m rows and d columns
        A = np.random.normal(0, 1/np.sqrt(m), (m, d))

        # Generate random data points u and v
        u = np.random.rand(d)
        v = np.random.rand(d)

        # Calculate pairwise squared distances in the original space
        dist_original = np.linalg.norm(u - v)**2

        # Project the data points using matrix A
        u_proj = np.dot(A, u)
        v_proj = np.dot(A, v)

        # Calculate pairwise squared distances in the projected space
        dist_proj = np.linalg.norm(u_proj - v_proj)**2

        # Check if the Johnson-Lindenstrauss Lemma holds
        max_relative_error = np.abs(dist_proj - dist_original) / dist_original

        if max_relative_error <= 0.1:
            print(f"Number of data points (n): {n}, The Johnson-Lindenstrauss Lemma holds.")
        else:
            print(f"Number of data points (n): {n}, The Johnson-Lindenstrauss Lemma does not hold.")

        # Double 'n' in each iteration
        n *= 2
```

```
Streaming output truncated to the last 5000 lines.
Number of data points (n): 304957584201752135869637243797305723593964 7769226181139759104O, The Johnson-Lindenstrauss Lemma holds.
Number of data points (n): 609915168403504271739274487594611447187928 5538452362279518208O, The Johnson-Lindenstrauss Lemma holds.
Number of data points (n): 121983033680700854347854897518922289437585 3107690472455903641 60, The Johnson-Lindenstrauss Lemma holds.
Number of data points (n): 243966067361401708695709795037844578875171 8215380944911807283 20, The Johnson-Lindenstrauss Lemma does not hold.
Number of data points (n): 487932134722803417391419590075689157750343 5430761889823614566 40, The Johnson-Lindenstrauss Lemma does not hold.
Number of data points (n): 269214083678661222449710814735299907816524349440, The Johnson-Lindenstrauss Lemma holds.
Number of data points (n): 538428167357322444899421629475998156330486988 80, The Johnson-Lindenstrauss Lemma holds.
Number of data points (n): 107685633471464488897988432589 41199631266097397760, The Johnson-Lindenstrauss Lemma does not hold.
Number of data points (n): 215371266942928977959768651788 23992625321947955 20, The Johnson-Lindenstrauss Lemma does not hold.
```

Observation - system runs out of memory.