Exercise

12

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Dimensionality Reduction & Clustering

Problem 1:

exercise_12_matrix_factorization

February 2, 2020

0.1 Exporting the results to PDF

Once you complete the assignments, export the entire notebook as PDF and attach it to your homework solutions. The best way of doing that is 1. Run all the cells of the notebook. 2. Export/download the notebook as PDF (File -> Download as -> PDF via LaTeX (.pdf)). 3. Concatenate your solutions for other tasks with the output of Step 2. On linux, you can use `pdfunite`, there are similar tools for other platforms, too. You can only upload a single PDF file to Moodle.

Make sure you are using `nbconvert` version 5.5 or later by running `jupyter nbconvert --version`. Older versions clip lines that exceed page width, which makes your code harder to grade.

1 Matrix Factorization

```
In [1]: import time
        import scipy.sparse as sp
        import numpy as np
        from scipy.sparse.linalg import svds
        from sklearn.linear_model import Ridge

        import matplotlib.pyplot as plt
        %matplotlib inline
```

1.1 Restaurant recommendation

The goal of this task is to recommend restaurants to users based on the rating data in the Yelp dataset. For this, we try to predict the rating a user will give to a restaurant they have not yet rated based on a latent factor model.

Specifically, the objective function (loss) we wanted to optimize is:

$$\mathcal{L} = \min_{P,Q} \sum_{(i,x)\in W} (M_{ix} - \mathbf{q}_i^T \mathbf{p}_x)^2 + \lambda \sum_x \|\mathbf{p}_x\|^2 + \lambda \sum_i \|\mathbf{q}_i\|^2$$

where W is the set of (i, x) pairs for which the rating M_{ix} given by user i to restaurant x is known. Here we have also introduced two regularization terms to help us with overfitting where λ is hyper-parameter that control the strength of the regularization.

Hint 1: Using the closed form solution for regression might lead to singular values. To avoid this issue perform the regression step with an existing package such as scikit-learn. It is advisable to use ridge regression to account for regularization.

Hint 2: If you are using the scikit-learn package remember to set `fit_intercept = False` to only learn the coefficients of the linear regression.

1.1.1 Load and Preprocess the Data (nothing to do here)

```
In [2]: ratings = np.load("exercise_12_matrix_factorization_ratings.npy")

In [3]: # We have triplets of (user, restaurant, rating).
        ratings

Out[3]: array([[101968,   1880,      1],
               [101968,    284,      5],
               [101968,   1378,      2],
               ...,
               [ 72452,   2100,      4],
               [ 72452,   2050,      5],
               [ 74861,   3979,      5]], dtype=int64)
```

Now we transform the data into a matrix of dimension [N, D], where N is the number of users and D is the number of restaurants in the dataset. We store the data as a sparse matrix to avoid out-of-memory issues.

```
In [4]: n_users = np.max(ratings[:,0] + 1)
        n_restaurants = np.max(ratings[:,1] + 1)
        M = sp.coo_matrix((ratings[:,2], (ratings[:,0], ratings[:,1])), shape=(n_users, n_resta
        M

Out[4]: <337867x5899 sparse matrix of type '<class 'numpy.int64'>'
                with 929606 stored elements in Compressed Sparse Row format>
```

To avoid the cold start problem, in the preprocessing step, we recursively remove all users and restaurants with 10 or less ratings.

Then, we randomly select 200 data points for the validation and test sets, respectively.

After this, we subtract the mean rating for each users to account for this global effect.

Note: Some entries might become zero in this process -- but these entries are different than the 'unknown' zeros in the matrix. We store the indices for which we the rating data available in a separate variable.

```
In [5]: def cold_start_preprocessing(matrix, min_entries):
            """
            Recursively removes rows and columns from the input matrix which have less than mi

            Parameters
            ----------
            matrix      : sp.spmatrix, shape [N, D]
                          The input matrix to be preprocessed.
            min_entries : int
                          Minimum number of nonzero elements per row and column.
```

```
    Returns
    -------
    matrix      : sp.spmatrix, shape [N', D']
                  The pre-processed matrix, where N' <= N and D' <= D

    """
    print("Shape before: {}".format(matrix.shape))

    shape = (-1, -1)
    while matrix.shape != shape:
        shape = matrix.shape
        nnz = matrix>0
        row_ixs = nnz.sum(1).A1 > min_entries
        matrix = matrix[row_ixs]
        nnz = matrix>0
        col_ixs = nnz.sum(0).A1 > min_entries
        matrix = matrix[:,col_ixs]
    print("Shape after: {}".format(matrix.shape))
    nnz = matrix>0
    assert (nnz.sum(0).A1 > min_entries).all()
    assert (nnz.sum(1).A1 > min_entries).all()
    return matrix
```

1.1.2 Task 1: Implement a function that subtracts the mean user rating from the sparse rating matrix

```
In [6]: def shift_user_mean(matrix):
    """
    Subtract the mean rating per user from the non-zero elements in the input matrix.

    Parameters
    ----------
    matrix : sp.spmatrix, shape [N, D]
             Input sparse matrix.
    Returns
    -------
    matrix : sp.spmatrix, shape [N, D]
             The modified input matrix.

    user_means : np.array, shape [N, 1]
                 The mean rating per user that can be used to recover the absolute rat

    """

    # TODO: Compute the modified matrix and user_means
    non_zeros = (matrix>0)
    user_means = matrix.sum(1) / non_zeros.sum(1)
    matrix -= sp.csr_matrix(user_means).multiply(non_zeros)
```

```
    assert np.all(np.isclose(matrix.mean(1), 0))
    return matrix, user_means
```

1.1.3 Split the data into a train, validation and test set (nothing to do here)

```
In [7]: def split_data(matrix, n_validation, n_test):
    """
    Extract validation and test entries from the input matrix.

    Parameters
    ----------
    matrix          : sp.spmatrix, shape [N, D]
                      The input data matrix.
    n_validation    : int
                      The number of validation entries to extract.
    n_test          : int
                      The number of test entries to extract.

    Returns
    -------
    matrix_split    : sp.spmatrix, shape [N, D]
                      A copy of the input matrix in which the validation and test entr

    val_idx         : tuple, shape [2, n_validation]
                      The indices of the validation entries.

    test_idx        : tuple, shape [2, n_test]
                      The indices of the test entries.

    val_values      : np.array, shape [n_validation, ]
                      The values of the input matrix at the validation indices.

    test_values     : np.array, shape [n_test, ]
                      The values of the input matrix at the test indices.

    """

    matrix_cp = matrix.copy()
    non_zero_idx = np.argwhere(matrix_cp)
    ixs = np.random.permutation(non_zero_idx)
    val_idx = tuple(ixs[:n_validation].T)
    test_idx = tuple(ixs[n_validation:n_validation + n_test].T)

    val_values = matrix_cp[val_idx].A1
    test_values = matrix_cp[test_idx].A1

    matrix_cp[val_idx] = matrix_cp[test_idx] = 0
```

```
            matrix_cp.eliminate_zeros()

            return matrix_cp, val_idx, test_idx, val_values, test_values
```

```
In [8]: M = cold_start_preprocessing(M, 20)
```

```
Shape before: (337867, 5899)
Shape after: (3529, 2072)
```

```
In [9]: n_validation = 200
        n_test = 200
        # Split data
        M_train, val_idx, test_idx, val_values, test_values = split_data(M, n_validation, n_tes
```

```
In [10]: # Remove user means.
         nonzero_indices = np.argwhere(M_train)
         M_shifted, user_means = shift_user_mean(M_train)
         # Apply the same shift to the validation and test data.
         val_values_shifted = val_values - user_means[np.array(val_idx).T[:,0]].A1
         test_values_shifted = test_values - user_means[np.array(test_idx).T[:,0]].A1
```

1.1.4 Compute the loss function (nothing to do here)

```
In [11]: def loss(values, ixs, Q, P, reg_lambda):
             """
             Compute the loss of the latent factor model (at indices ixs).
             Parameters
             ----------
             values : np.array, shape [n_ixs,]
                 The array with the ground-truth values.
             ixs : tuple, shape [2, n_ixs]
                 The indices at which we want to evaluate the loss (usually the nonzero indice
             Q : np.array, shape [N, k]
                 The matrix Q of a latent factor model.
             P : np.array, shape [k, D]
                 The matrix P of a latent factor model.
             reg_lambda : float
                 The regularization strength

             Returns
             -------
             loss : float
                    The loss of the latent factor model.

             """
             mean_sse_loss = np.sum((values - Q.dot(P)[ixs])**2)
             regularization_loss =  reg_lambda * (np.sum(np.linalg.norm(P, axis=0)**2) + np.sum

             return mean_sse_loss + regularization_loss
```

1.2 Alternating optimization

In the first step, we will approach the problem via alternating optimization, as learned in the lecture. That is, during each iteration you first update Q while having P fixed and then vice versa.

1.2.1 Task 2: Implement a function that initializes the latent factors Q and P

```
In [12]: def initialize_Q_P(matrix, k, init='random'):
             """
             Initialize the matrices Q and P for a latent factor model.

             Parameters
             ----------
             matrix : sp.spmatrix, shape [N, D]
                      The matrix to be factorized.
             k      : int
                      The number of latent dimensions.
             init   : str in ['svd', 'random'], default: 'random'
                      The initialization strategy. 'svd' means that we use SVD to initialize P
                      the entries in P and Q randomly in the interval [0, 1).

             Returns
             -------
             Q : np.array, shape [N, k]
                 The initialized matrix Q of a latent factor model.

             P : np.array, shape [k, D]
                 The initialized matrix P of a latent factor model.
             """
             np.random.seed(0)

             N, D = matrix.shape
             if init == 'svd':
                 U, s, V = svds(matrix, k=k)
                 S = np.diag(s)
                 Q = U.dot(S)
                 P = V
             else:
                 Q = np.random.random((N, k))
                 P = np.random.random((k, D))

             assert Q.shape == (matrix.shape[0], k)
             assert P.shape == (k, matrix.shape[1])
             return Q, P
```

1.2.2 Task 3: Implement the alternating optimization approach

```
In [15]: def latent_factor_alternating_optimization(M, non_zero_idx, k, val_idx, val_values,
                                                    reg_lambda, max_steps=100, init='random',
```

```
                                                log_every=1, patience=5, eval_every=1):
    """
    Perform matrix factorization using alternating optimization. Training is done via
    i.e. we stop training after we observe no improvement on the validation loss for
    amount of training steps. We then return the best values for Q and P oberved duri

    Parameters
    ----------
    M                : sp.spmatrix, shape [N, D]
                       The input matrix to be factorized.

    non_zero_idx     : np.array, shape [nnz, 2]
                       The indices of the non-zero entries of the un-shifted matrix
                       nnz refers to the number of non-zero entries. Note that this
                       from the number of non-zero entries in the input matrix M, e.
                       that all ratings by a user have the same value.

    k                : int
                       The latent factor dimension.

    val_idx          : tuple, shape [2, n_validation]
                       Tuple of the validation set indices.
                       n_validation refers to the size of the validation set.

    val_values       : np.array, shape [n_validation, ]
                       The values in the validation set.

    reg_lambda       : float
                       The regularization strength.

    max_steps        : int, optional, default: 100
                       Maximum number of training steps. Note that we will stop earl
                       no improvement on the validation error for a specified number
                       (see "patience" for details).

    init             : str in ['random', 'svd'], default 'random'
                       The initialization strategy for P and Q. See function initial

    log_every        : int, optional, default: 1
                       Log the training status every X iterations.

    patience         : int, optional, default: 5
                       Stop training after we observe no improvement of the validati
                       iterations (see eval_every for details). After we stop traini
                       observed values for Q and P (based on the validation loss) an

    eval_every       : int, optional, default: 1
                       Evaluate the training and validation loss every X steps. If w
```

```
                    of the validation error, we decrease our patience by 1, else

Returns
-------
best_Q            : np.array, shape [N, k]
                    Best value for Q (based on validation loss) observed during t

best_P            : np.array, shape [k, D]
                    Best value for P (based on validation loss) observed during t

validation_losses : list of floats
                    Validation loss for every evaluation iteration, can be used f
                    loss over time.

train_losses      : list of floats
                    Training loss for every evaluation iteration, can be used for
                    loss over time.

converged_after   : int
                    it - patience*eval_every, where it is the iteration in which
                    or -1 if we hit max_steps before converging.

"""

Q,P = initialize_Q_P(M, k, init)
best_Q = Q
best_P = P
best_loss = -1
validation_losses = []
train_losses = []
converged_after = -1
train_idx = tuple(non_zero_idx.T)

reg = Ridge(alpha=reg_lambda, fit_intercept=False)

nnz_mask = sp.coo_matrix((np.ones(len(non_zero_idx)),
                          (non_zero_idx[:,0],non_zero_idx[:,1])),
                         shape=M.shape, dtype="uint8").tocsr()
rows = nnz_mask.tolil().rows
cols = nnz_mask.T.tolil().rows

for i in range(max_steps):
    if i % eval_every == 0:
        # evaluate losses
        val_loss = loss(val_values, val_idx, Q, P, reg_lambda)
        validation_losses.append(val_loss)

        train_loss = loss(M[train_idx].A1, train_idx, Q, P, reg_lambda)
```

```
            train_losses.append(train_loss)

            if best_loss <= -1 or val_loss < best_loss:
                best_Q = Q
                best_P = P
                best_loss = val_loss
                current_patience = patience
            else:
                current_patience -= 1

            if current_patience == 0:
                converged_after = i - patience * eval_every
                break

        print("Iteration ", i)

        # fix Q
        for rating_idx in range(M.shape[1]):
            nnz_idx = cols[rating_idx]
            res = reg.fit(Q[nnz_idx], np.squeeze(M[nnz_idx, rating_idx].toarray()))
            P[:, rating_idx] = res.coef_

        # fix P
        for user_idx in range(M.shape[0]):
            nnz_idx = rows[user_idx]
            res = reg.fit(P[:, nnz_idx].T, np.squeeze(M[user_idx, nnz_idx].toarray()))
            Q[user_idx, :] = res.coef_

    return best_Q, best_P, validation_losses, train_losses, converged_after
```

1.2.3 Train the latent factor (nothing to do here)

```
In [16]: Q, P, val_loss, train_loss, converged = latent_factor_alternating_optimization(M_shif
                                                                                        k=100,
                                                                                        val_va
                                                                                        reg_la
                                                                                        max_st
```

```
Iteration  0
Iteration  1
Iteration  2
Iteration  3
Iteration  4
Iteration  5
Iteration  6
Iteration  7
Iteration  8
Iteration  9
```

```
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Iteration  99
```

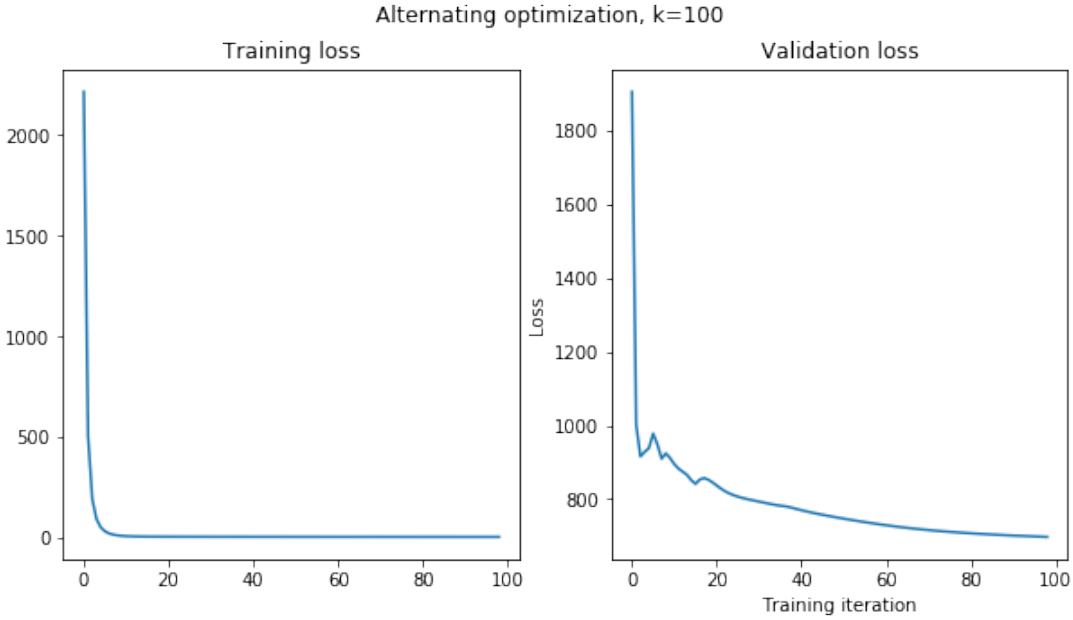
1.2.4 Plot the validation and training losses over for each iteration (nothing to do here)

```
In [17]: fig, ax = plt.subplots(1, 2, figsize=[10, 5])
         fig.suptitle("Alternating optimization, k=100")
```

```
ax[0].plot(train_loss[1::])
ax[0].set_title('Training loss')
plt.xlabel("Training iteration")
plt.ylabel("Loss")


ax[1].plot(val_loss[1::])
ax[1].set_title('Validation loss')
plt.xlabel("Training iteration")
plt.ylabel("Loss")

plt.show()
```



In [ ]:

Problem 2:

(Linear) Autoencoder:

Input data X: D-dimensional

Hidden layer: K-dimensional

No biases, activations = identity.

This results in a linear transformation: $f(x) = f_{dec}(f_{enc}(x)) = XW_1W_2$

With dimensions: $X : N \times D, W_1 : D \times K, W_2 : K \times D$

With $K < D, XW_1$ forces X into a K dimensional5 subspace.

Since this transformation is not the identity ($K < D$) perfect reconstruction is not achievable unless the input data X is already in a K-dimensional subspace despite being D-dimensional data.

Problem 3:

K Gaussians:

Intuition: Expected value of Gaussian is the mean.

$\implies$ Expected value of K Gaussians should be the K means added up (each cluster z).

$$p(x) = \sum_k \pi_k \mathcal{N}(x|\mu_k, \Sigma_k)$$

$$\mathbb{E}[x] = \mathbb{E}_{p(z)}[\mathbb{E}_{p(x|z)}[x|z]]$$

$\mathbb{E}_{p(x|z)}[x|z]$ is the expected value of x in cluster z which is the mean of cluster z.

This implies $\mathbb{E}_{p(x|z)}[x|z] = \mu_k$.

$\mathbb{E}_{p(z)}$ is the prior probability π_z of z, also have to consider all clusters.

This implies $\mathbb{E}_{p(z)} = \sum_{k=1}^{K} \pi_k$.

Simply filling into the equation yields: $\mathbb{E}[x] = \sum_{k=1}^{K} \pi_k \mu_k$

Now $Cov[x]$:

$\mathbb{E}[x]$ and $\mathbb{E}[x]^T$ respectivly are already known.

$$Cov[x] = \mathbb{E}[xx^T] - \mathbb{E}[x]\mathbb{E}[x]^T$$

So only $\mathbb{E}[xx^T]$ is still missing:

Filling into $\mathbb{E}[x] = \mathbb{E}_{p(z)}[\mathbb{E}_{p(x|z)}[x|z]]$:

$$\mathbb{E}[xx^T] = \mathbb{E}_{p(z)}[\mathbb{E}_{p(x|z)}[xx^T|z]]$$

$$\mathbb{E}[xx^T] = \sum_{k=1}^{K} \pi_k \mathbb{E}_{p(x|z)}[xx^T|z]$$

With $\Sigma = \mathbb{E}[(X-\mu)(X-\mu)^T] = \mathbb{E}[XX^T] - \mu\mu^T$

$\implies \mathbb{E}[XX^T] = \Sigma + \mu\mu^T$

$$\mathbb{E}[xx^T] = \sum_{k=1}^{K} \pi_k(\Sigma_k + \mu_k\mu_k^T)$$

$$\implies Cov[x] = \sum_{k=1}^{K} \pi_k(\Sigma_k + \mu_k\mu_k^T) - \sum_{k=1}^{K}\sum_{l=1}^{K} \pi_k\pi_l\mu_k\mu_l^T$$

Problem 4:

a) According to slide 12-19, we first need to draw the cluster indicators k, l from categorical distribution given the probabilities π_k^x, π_l^y

$$k \sim Cat(\pi_k^x)$$
$$l \sim Cat(\pi_l^y)$$

and then sample from their respective normal distributions:

$$x \sim \mathcal{N}(\mu_k^x, \Sigma_k^x)$$
$$y \sim \mathcal{N}(\mu_k^x, \Sigma_k^x)$$

z is then given by $z := x + y$

b) Since x and y are i.i.d and $x \sim \mathcal{N}(\mu_k^x, \Sigma_k^x)$ and $y \sim \mathcal{N}(\mu_k^y, \Sigma_k^y)$, the sum of two Gaussian distributions is again Gaussian. Therefore $p(z \mid \theta^x, \theta^y)$ is a mixture of Gaussians.

c)

$$p(z \mid \theta^x, \theta^y) = \sum_{k=1}^{K_x}\sum_{l=1}^{K_y} \pi_k^x\pi_l^y \; \mathcal{N}(z \mid \mu_k^x + \mu_l^y, \Sigma_k^x + \Sigma_l^y)$$

Problem 5:

exercise_12_clustering

February 2, 2020

0.1 Exporting the results to PDF

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```
In [2]: import matplotlib.pyplot as plt
        import numpy as np
        from PIL import Image
        from sklearn.datasets import load_sample_image

        %matplotlib inline

        def compare_images(img, img_compressed, k):
            """Show the compressed and uncompressed image side by side.
            """

            fig, axes = plt.subplots(1, 2, figsize=(16, 12))
            axes[0].set_axis_off()
            if isinstance(k, str):
                axes[0].set_title(k)
            else:
                axes[0].set_title(f"Compressed to {k} colors")
            axes[0].imshow(img_compressed)
            axes[1].set_axis_off()
            axes[1].set_title("Original")
            axes[1].imshow(img)
```

1 K-Means

In this first section you will implement the image compression algorithm from Bishop, chapter 9.1.1. Take an RGB image $X \in \mathbb{R}^{h \times w \times 3}$ and interpret it as a data matrix $X \in \mathbb{R}^{N \times 3}$. Now apply

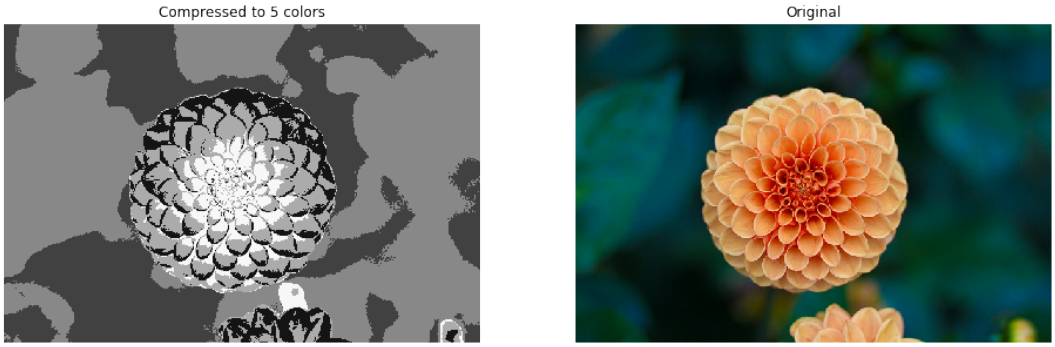
k-means clustering to find k colors that describe the image well and replace each pixel with its associated cluster.

```
In [4]: # Alternatively try china.jpg
        X = load_sample_image("flower.jpg")

        # or load your own image
        # X = np.array(Image.open("/home/user/path/to/some.jpg"))
```

```
In [3]: def kmeans(X, k):
            """Compute a k-means clustering for the data X.

            Parameters
            ----------
            X : np.array of size N x D
                where N is the number of samples and D is the data dimensionality
            k : int
                Number of clusters

            Returns
            -------
            mu : np.array of size k x D
                Cluster centers
            z : np.array of size N
                Cluster indicators, i.e. a number in 0..k - 1, for each data point in X
            """

            # TODO: Compute mu and z

            N, D = X.shape

            # 1. Initialize the centroids at random
            #mu = X.max() * np.random.random((k, D)) + X.min()
            mu = np.array([ X[np.random.randint(0, N)] for _ in range(k) ])
            z = np.zeros(N, dtype=np.int8)

            # 1. Initialize the centroids with K-means++
            mu = np.empty((k, D))
            # 1.1 Choose random centroid mu_1
            mu[0] = X[np.random.randint(N)]
            # 1.2 For each x_i compute Distance D_i^2
            Di2 = np.linalg.norm(X - mu[0], axis=1) ** 2
            for i in range(1, k):
                # 1.3 Sample the next centrouid mu_i from {x_i} with probability proportional
                potential = Di2.sum()
                sample = np.random.random_sample(1) * potential # only 1 but could be multiple
                candidate = np.searchsorted(np.cumsum(Di2), sample)
                mu[i] = X[candidate]
```

```
            # 1.4 Recompute distance Di2
            Di2 = np.minimum(Di2, np.linalg.norm(X - mu[i], axis=1) ** 2)
        # 1.5 Continue Steps 3 and 4 und all k have been chosen

        # 2. Update cluster indicators
        for i, x in enumerate(X):
            cluster = np.argmin(np.linalg.norm(x - mu, axis=1) ** 2)
            z[i] = int(cluster)

        # 3. Update centroids
        for i in range(k):
            mask = z == i
            N_k = np.sum(mask)
            mu[i] = (1 / N_k) * np.sum(X[mask])

        # 4. Has objective converged
        if np.isnan(mu).any():
            print("Contained empty clouds")
            print(mu)
            #return kmeans(X, k)

        return mu, z
```

In [4]:
```
# Cluster the color values
k = 5
mu, z = kmeans(X.reshape((-1, 3)), k)

# Replace each pixel with its cluster color
X_compressed = mu[z].reshape(X.shape).astype(np.uint8)

# Show the images side by side
compare_images(X, X_compressed, k)
```



2 Gaussian Mixture Models & EM

Now you will repeat the same exercise with GMMs.

```
In [1]: def gmm_log_probability(X, pi, mu, sigma):
            """Compute the joint log-probabilities for each data point and component.

            Parameters
            ----------
            X : np.array of size N x D
                where N is the number of samples and D is the data dimensionality
            pi : np.array of size k
                Prior weight of each component
            mu : np.array of size k x D
                Mean vectors of the k Gaussian component distributions
            sigma : np.array of size k x D x D
                Covariance matrices of the k Gaussian component distributions

            Returns
            -------
            P : np.array of shape N x k
                P[i, j] is the joint log-probability of data point i under component j
            """

            # TODO: Compute P

            # log p(X, Z | , ţ, )
            N, D = X.shape
            k = pi.shape[0]


            #s1 = 1 / (np.sqrt( 2 * np.pi * sigma))
            #s2 = np.exp(-(np.square(X - mu) / (2 * sigma)))
            #P = pi * s1 * s2
            #print(P.shape)

            from scipy.stats import multivariate_normal
            P = np.empty((N, k))
            for i in range(k):
                P[i] = np.log(pi[i] * multivariate_normal.pdf(X, mu[i], sigma[i]))

            return P


        def em(X, k, tol=0.001):
            """Fit a Gaussian mixture model with k components to X.

            Parameters
```

```
    ----------
    X : np.array of size N x D
        where N is the number of samples and D is the data dimensionality
    k : int
        Number of clusters
    tol : float
        Converge when the increase in the mean of the expected joint log-likelihood
        is lower than this

    The algorithm should stop when the relative improvement in the optimization
    objective is less than rtol.

    Returns
    -------
    pi : np.array of size k
        Prior weight of each component
    mu : np.array of size k x D
        Mean vectors of the k Gaussian component distributions
    sigma : np.array of size k x D x D
        Covariance matrices of the k Gaussian component distributions
    """

    # https://github.com/scikit-learn/scikit-learn/blob/a95203b/sklearn/mixture/gmm.py

    # TODO: Compute pi, mu, sigma
    N, D = X.shape

    # 1. Initialize model parameters
    pi = np.ones(k)
    mu = np.random.random((k, D))
    sigma = np.array([np.identity(D) for i in range(k)])

    from scipy.stats import multivariate_normal

    num_iters = 0
    converged = False
    #while not(converged):
    while num_iters < 5:
        # 2. E step. Evaluate the responsibilities
        gamma = np.zeros((N, k), dtype=float)
        for i in range(k):
            gamma[:,i] = pi[i] * multivariate_normal.pdf(X, mu[i,:], sigma[i])
        gamma_norm = np.sum(gamma, axis=1)[:,np.newaxis]
        gamma /= gamma_norm

        # 3. M step. Re-estimate the parameters
        pi = np.mean(gamma, axis=0)
        mu = np.dot(gamma.T, X) / np.sum(gamma, axis=0)[:,np.newaxis]
```

```
                for i in range(k):
                    x = X - mu[i,:]
                    x_mu = np.matrix(x)
                    gamma_diag = np.diag(gamma[:,i])
                    gamma_diag = np.matrix(gamma_diag)
                    sigma_i = x.T * gamma_diag * x
                    sigma[i,:,:] = (sigma_i) / np.sum(gamma, axis=0)[:,np.newaxis]
                    #sigma[i] = (1 / N_k) * np.sum(gamma[i] * np.square(X - mu[i]).T)

                print(gamma)
                print(mu)
                print(sigma)
                print(pi)
                #likelihood = gmm_log_probability(X, pi, mu, sigma)
                #if likelihood <= tol:
                #    converged = True

                print(likelihoods.shape)
                print(np.mean(likelihoods))
                # test
                converged = True

                num_iters += 1

            return pi, mu, sigma
```

In [ ]:
```
# Fit the GMM
k = 5
pi, mu, sigma = em(X.reshape((-1, 3)), k)

# Determine the most likely cluster of each pixel
log_p = gmm_log_probability(X.reshape((-1, 3)), pi, mu, sigma)
z = log_p.argmax(axis=1)

# Replace each pixel with its cluster mean
X_compressed = mu[z].reshape(X.shape).astype(np.uint8)

# Show the images side by side
compare_images(X, X_compressed, k)
```

```
/Users/lilith/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:88: RuntimeWarning:
```

3 Sampling Unseen Datapoints

You have trained a generative model which allows you to sample from the learned distribution. In this section, you sample new images.

```
In [ ]: def gmm_sample(N, pi, mu, sigma):
            """Sample N data points from a Gaussian mixture model.

            Parameters
            ----------
            N : int
                Number of data points to sample
            pi : np.array of size k
                Prior weight of each component
            mu : np.array of size k x D
                Mean vectors of the k Gaussian component distributions
            sigma : np.array of size k x D x D
                Covariance matrices of the k Gaussian component distributions

            Returns
            -------
            X : np.array of shape N x D
            """

            # TODO: Sample X

            return X
```

```
In [ ]: # Sample pixels and reshape them into the size of the original image
        X_sampled = gmm_sample(np.prod(X.shape[:-1]), pi, mu, sigma).reshape(X.shape).astype(np

        # Compare the original and the sampled image
        compare_images(X, X_sampled, "Sampled")
```

Explain what you see in the generated images. (1-3 sentences)

Appendix

We confirm that the submitted solution is original work and was written by us without further assistance. Appropriate credit has been given where reference has been made to the work of others.

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