## Problem sheet 06

# Exercise 6.1: dimensionality reduction on histograms.

```
In []: import numpy as np
    import matplotlib.pyplot as plt
    from sklearn.decomposition import PCA

In []: # load npz file
    hist = np.load('hist.npz')

In []: binspec = hist['binspec']
    labels = hist['labels']
    histograms = hist['data']
```

#### 6.1) Part 1

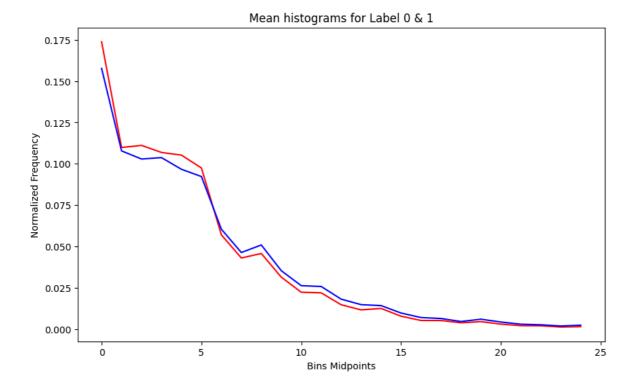
```
In []: bin_midpoints = (binspec[:-1] + binspec[1:]) / 2
    histograms_label_0 = histograms[labels == 0]
    histograms_label_1 = histograms[labels == 1]

mean_histograms_label_0 = np.mean(histograms_label_0, axis=0)

mean_histograms_label_1 = np.mean(histograms_label_1, axis=0)

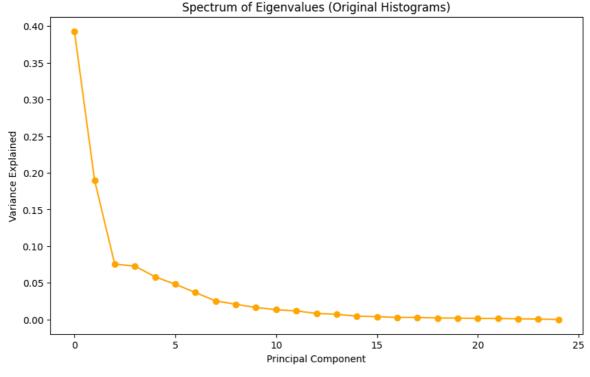
plt.figure(figsize=(10, 6))
    plt.plot(mean_histograms_label_0, alpha=1, color= 'red', label='Label 0')
    plt.plot(mean_histograms_label_1, alpha=1, color = 'blue', label='Label 1

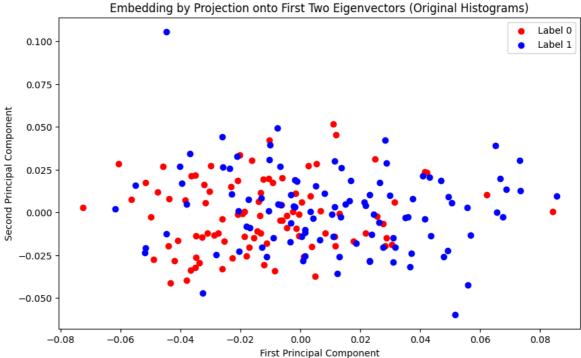
plt.title('Mean histograms for Label 0 & 1')
    plt.xlabel('Bins Midpoints')
    plt.ylabel('Normalized Frequency')
    plt.show()
```



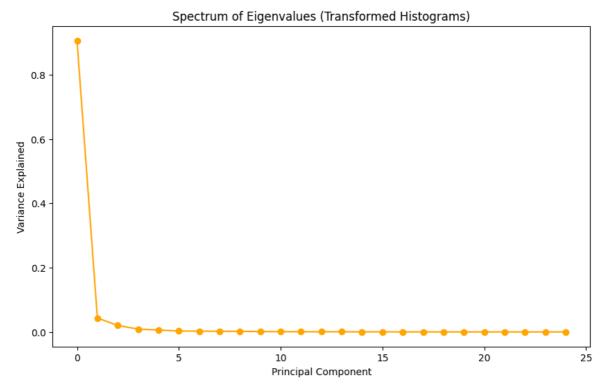
#### 6.1 Part 2

```
In [ ]: def perform_pca_and_plot(histograms, labels, title_suffix):
            pca = PCA()
            pca.fit(histograms)
            plt.figure(figsize=(10, 6))
            plt.plot(pca.explained_variance_ratio_, marker='o', color='orange')
            plt.title(f'Spectrum of Eigenvalues ({title_suffix})')
            plt.xlabel('Principal Component')
            plt.ylabel('Variance Explained')
            plt.show()
            histograms_pca = pca.transform(histograms)
            histograms_pca_2d = histograms_pca[:, :2]
            plt.figure(figsize=(10, 6))
            plt.scatter(histograms_pca_2d[labels == 0, 0], histograms_pca_2d[labe
            plt.scatter(histograms_pca_2d[labels == 1, 0], histograms_pca_2d[labe
            plt.title(f'Embedding by Projection onto First Two Eigenvectors ({tit
            plt.xlabel('First Principal Component')
            plt.ylabel('Second Principal Component')
            plt.legend()
            plt.show()
            return pca, histograms_pca
        pca_original, histograms_pca_original = perform_pca_and_plot(histograms,
```

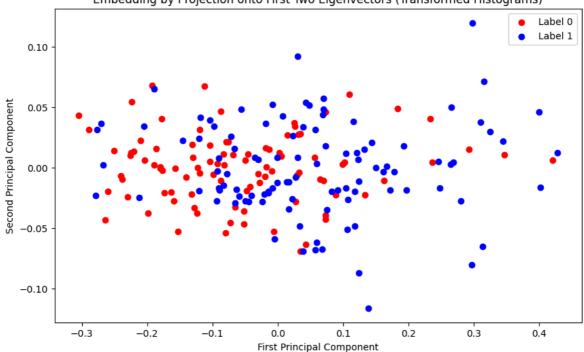




## 6.1) Part 3







### 6.1) Part 4

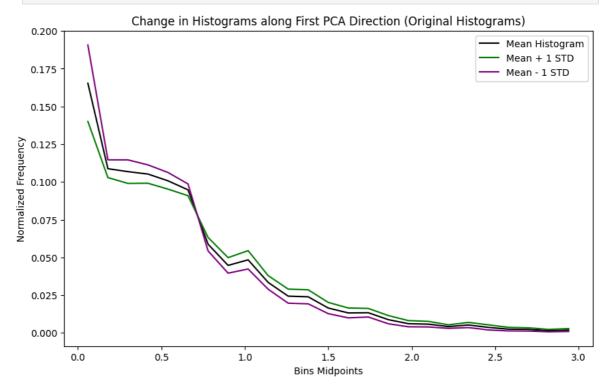
```
In []: def visualize_pca_changes(histograms, pca, histograms_pca, title_suffix):
    mean_histogram = np.mean(histograms, axis=0)
    first_pc = pca.components_[0]
    std_dev_first_pc = np.std(histograms_pca[:, 0])

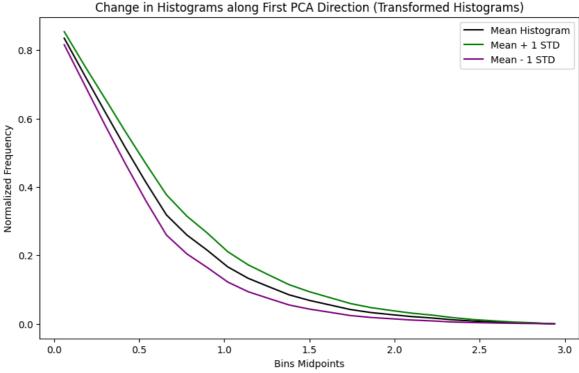
histogram_plus = mean_histogram + std_dev_first_pc * first_pc
    histogram_minus = mean_histogram - std_dev_first_pc * first_pc

plt.figure(figsize=(10, 6))
    plt.plot(bin_midpoints, mean_histogram, label='Mean Histogram', color
    plt.plot(bin_midpoints, histogram_plus, label='Mean + 1 STD', color='
    plt.plot(bin_midpoints, histogram_minus, label='Mean - 1 STD', color='
    plt.plot(bin_m
```

```
plt.title(f'Change in Histograms along First PCA Direction ({title_su
plt.xlabel('Bins Midpoints')
plt.ylabel('Normalized Frequency')
plt.legend()
plt.show()

visualize_pca_changes(histograms, pca_original, histograms_pca_original,
visualize_pca_changes(transformed_histograms, pca_transformed, histograms
```





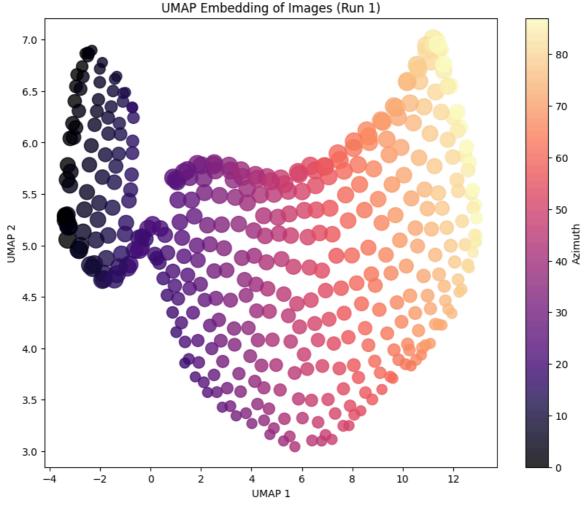
#### **Description of Induced Changes:**

 Original Data: Moving along the first PCA direction tends to adjust the histogram's shape, highlighting the most significant variance captured by PCA. The changes can represent shifts in peaks and valleys or overall spread. Transformed Data: The transformed histograms display similar adjustments, but
these changes now reflect the cumulative distribution differences captured by
PCA. The inverse cumulative distance transform might smooth or amplify
specific histogram features, leading to different visual patterns compared to the
original histograms. The transformations highlight different aspects of data
variance and can provide insights into the underlying structure of the data based
on PCA's most significant components.

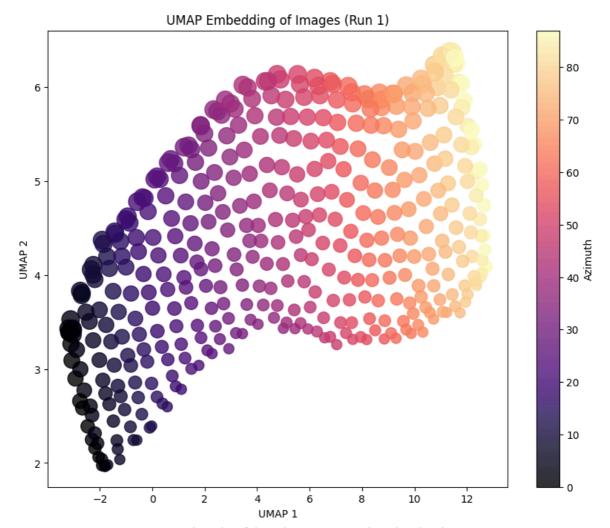
## Exercise 6.2: nonlinear manifold learning with UMAP

#### Part 1

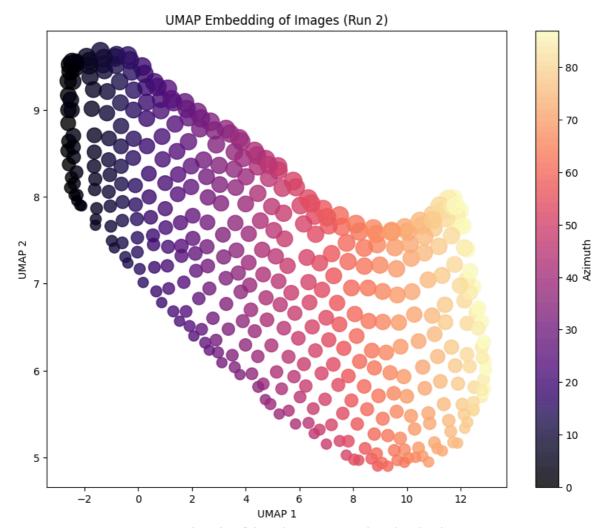
```
In [ ]: import glob
        import imageio.v2 as imageio
        import re
        import numpy as np
        import umap
        image files = glob.glob("imgs/*")
        elevations = []
        azimuths = []
        image_vectors = []
        for file in image_files:
            match = re.search(r'e(\d+)_a(\d+)', file)
            if match:
                elevation = int(match.group(1))
                azimuth = int(match.group(2))
                elevations.append(elevation)
                azimuths.append(azimuth)
            image = imageio.imread(file)
            flattened_image = image.flatten()
            image_vectors.append(flattened_image)
        elevation_range = (min(elevations), max(elevations))
        azimuth_range = (min(azimuths), max(azimuths))
        elevation_range, azimuth_range
Out[]: ((20, 59), (0, 87))
In [ ]: image_vectors = np.array(image_vectors)
        umap_embedding = umap.UMAP(n_components=2)
        embedding = umap_embedding.fit_transform(image_vectors)
        def create_umap_plot(run_number):
            umap_embedding = umap.UMAP(n_components=2, random_state=None)
            embedding = umap_embedding.fit_transform(image_vectors)
```



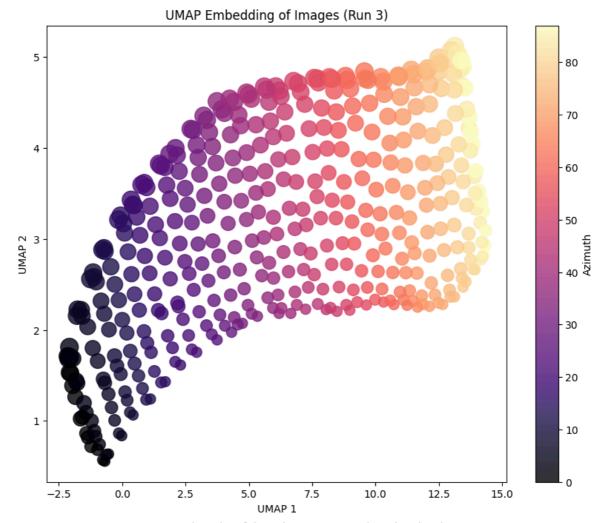
The color of the points represents the azimuth values. The size of the points represents the elevation values, scaled by a factor of 5 for better visibility.



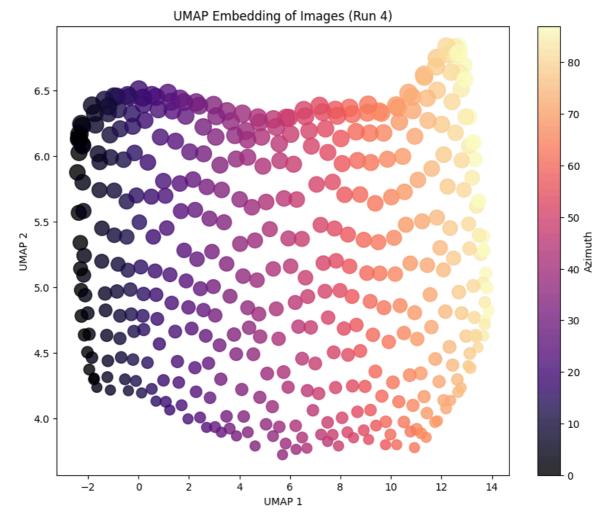
The color of the points represents the azimuth values. The size of the points represents the elevation values, scaled by a factor of 5 for better visibility.



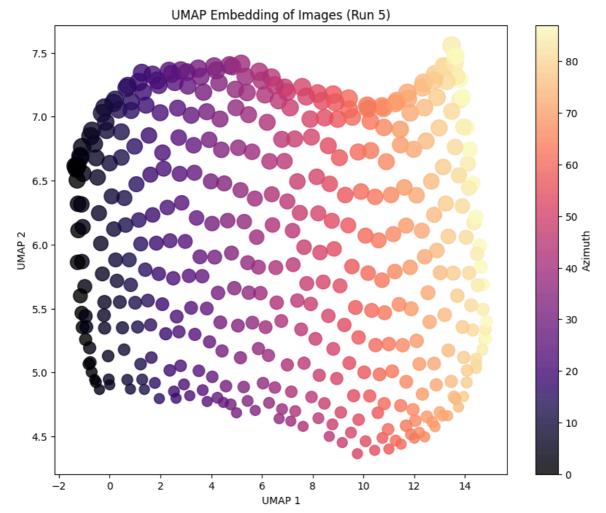
The color of the points represents the azimuth values. The size of the points represents the elevation values, scaled by a factor of 5 for better visibility.



 $The color of the points represents the azimuth values. \\ The size of the points represents the elevation values, scaled by a factor of 5 for better visibility. \\$ 



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The color of the points represents the azimuth values. The size of the points represents the elevation values, scaled by a factor of 5 for better visibility.

Despite the stochastic nature, the overall structure and layout of the embeddings remain somewhat consistent across the different runs. This indicates that UMAP is able to capture the underlying manifold reliably.