Rock Image Classification with Neural Networks

December 24, 2024

1 Rock Image Classification with Neural Networks

[2]:

```
# Import libraries
import os
import numpy as np
import pandas as pd
import time
import tensorflow as tf
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')
from PIL import Image
from matplotlib.offsetbox import OffsetImage, AnnotationBbox
from sklearn.preprocessing import StandardScaler, MinMaxScaler, LabelEncoder
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE, LocallyLinearEmbedding, MDS
from sklearn.cluster import KMeans
from sklearn.mixture import GaussianMixture
from sklearn.metrics import accuracy_score, pairwise_distances
from sklearn.model_selection import train_test_split
from scipy.spatial import procrustes
from scipy.stats import mode, pearsonr
from tensorflow.keras.preprocessing.image import load_img, img_to_array
from tensorflow.keras.utils import to_categorical
from tensorflow.keras.models import Sequential, Model
from tensorflow.keras.layers import Input, Conv2D, MaxPooling2D, Flatten, Dense
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.callbacks import EarlyStopping
```

[3]:

```
# Define the image folder path
image_folder = "360 Rocks"

# Initialize lists to store images and labels
images = []
labels = []

# Load images and labels
```

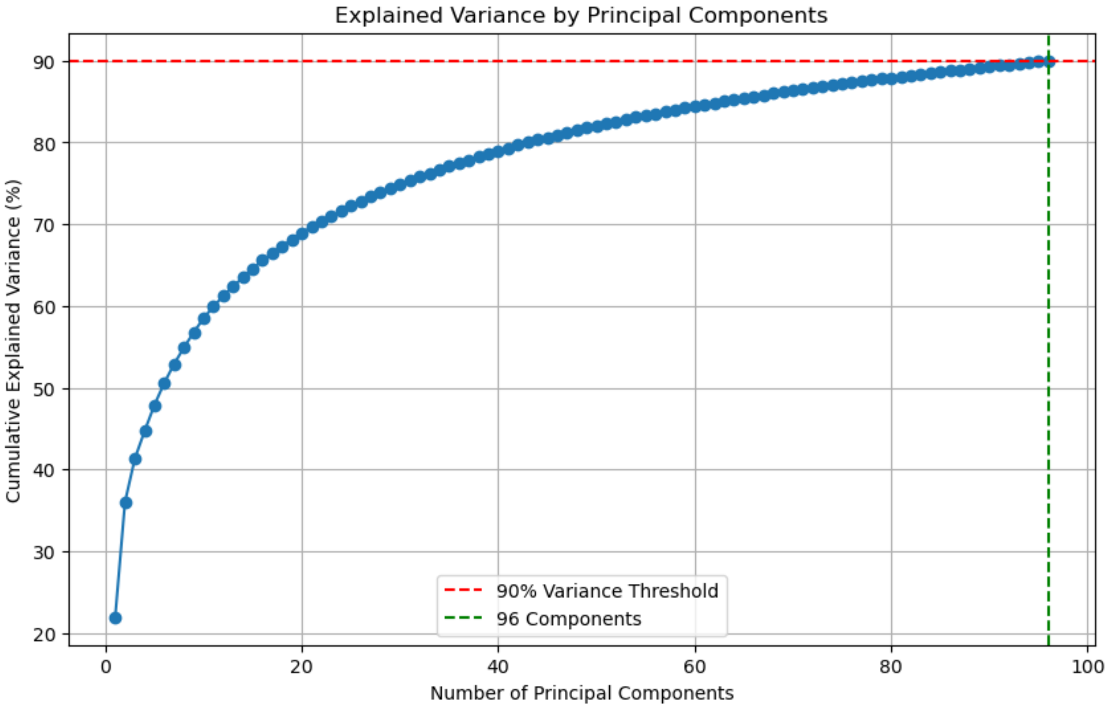
```
for filename in os.listdir(image_folder):
    if filename.lower().endswith(('.jpg', '.jpeg', '.png')):
        img = Image.open(os.path.join(image_folder, filename)).convert('L')  #␣
 ↪Convert to grayscale
        img = img.resize((64, 64))  # Resize to 64x64 pixels
        images.append(np.array(img).flatten())
        labels.append(filename[0])  # First letter indicates category

# Convert images list to a data matrix
data_matrix = np.array(images)
```

[4]:
```
# Standardize the data matrix
scaler = StandardScaler()
data_matrix_scaled = scaler.fit_transform(data_matrix)
```

2 Applied PCA to the images from the '360 Rocks' folder to determine the number of components required to preserve 90% of the variance.

[7]:
```
# Perform PCA for 90% explained variance
pca = PCA(0.90)
pca.fit(data_matrix_scaled)
n_components_90_variance = pca.n_components_
print(f"Number of components to preserve 90% variance:␣
 ↪{n_components_90_variance}")

# Transform data to reduced dimension
data_matrix_reduced = pca.transform(data_matrix_scaled)

# Plot cumulative explained variance
cumulative_variance = np.cumsum(pca.explained_variance_ratio_) * 100
plt.figure(figsize=(10, 6))
plt.plot(range(1, len(cumulative_variance) + 1), cumulative_variance,␣
 ↪marker='o', linestyle='-')
plt.axhline(y=90, color='r', linestyle='--', label="90% Variance Threshold")
plt.axvline(x=n_components_90_variance, color='g', linestyle='--',␣
 ↪label=f"{n_components_90_variance} Components")
plt.xlabel("Number of Principal Components")
plt.ylabel("Cumulative Explained Variance (%)")
plt.title("Explained Variance by Principal Components")
plt.legend()
plt.grid(True)
plt.show()
```

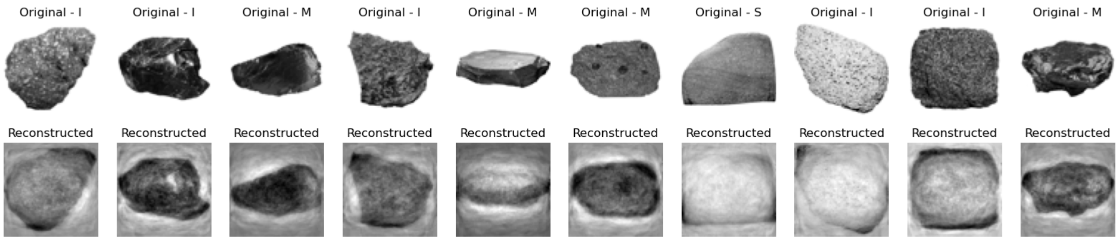
```
Number of components to preserve 90% variance: 96
```



3 Displayed 10 images from the ‘360 Rocks’ folder in their original form and then visualized their reconstruction after applying PCA to preserve 90% of the variance.

[10]:

```
# Reconstruct images with PCA preserving 90% variance
data_matrix_reconstructed = pca.inverse_transform(data_matrix_reduced)

# Select random images to plot
num_images = 10
indices = np.random.choice(len(data_matrix), num_images, replace=False)
selected_images_original = data_matrix[indices]
selected_images_reconstructed = data_matrix_reconstructed[indices]

# Plot original and reconstructed images
plt.figure(figsize=(20, 4))
for i in range(num_images):
    # Original
    plt.subplot(2, num_images, i + 1)
    plt.imshow(selected_images_original[i].reshape(64, 64), cmap="gray")
    plt.axis("off")
    plt.title(f"Original - {labels[indices[i]]}")
    # Reconstructed
    plt.subplot(2, num_images, i + 1 + num_images)
    plt.imshow(selected_images_reconstructed[i].reshape(64, 64), cmap="gray")
    plt.axis("off")
    plt.title("Reconstructed")
plt.show()
```



4 Each of the images belongs to one of three rock categories. The category is indicated by the first letter in the filename (I, M and S). We will now try to see if the visualization can help us identify different clusters.

A. Reduced image dimensionality to 2 using PCA and calculated variance explained by the first two components.

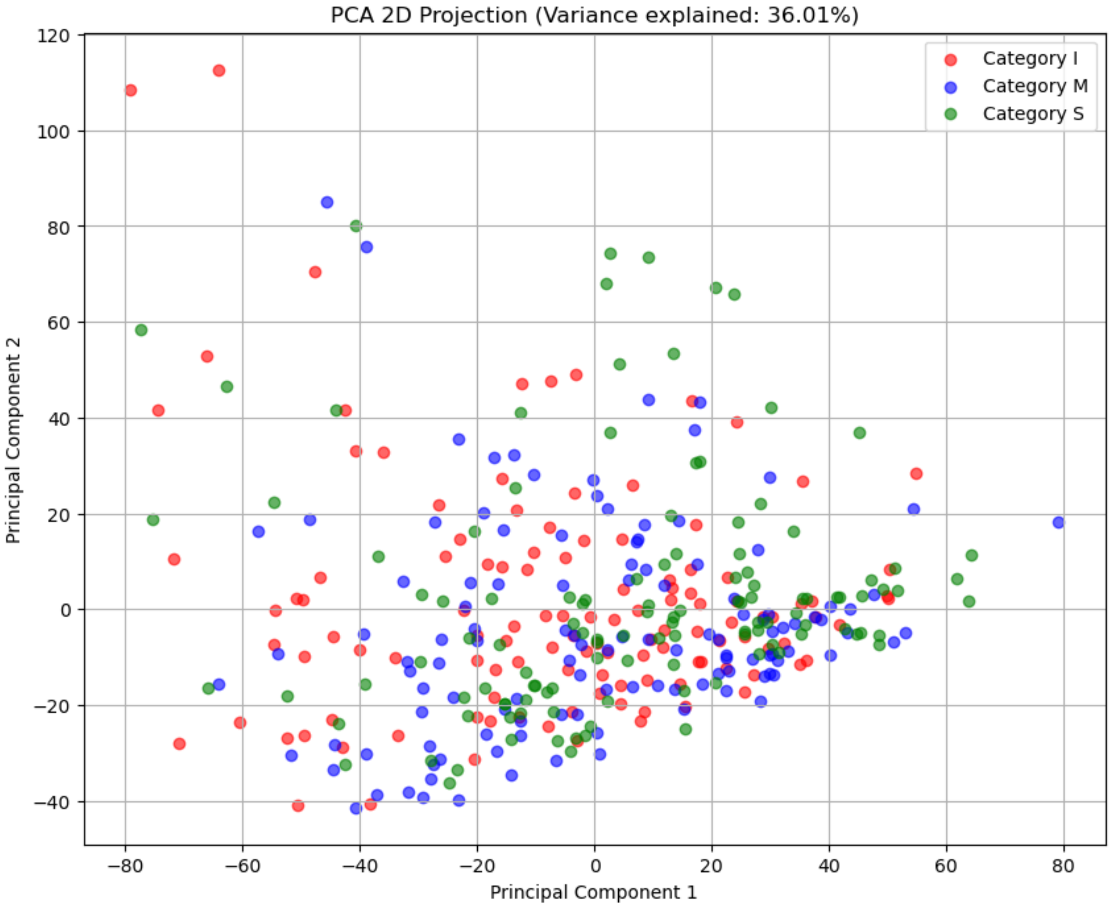
B. Plotted a 2D scatter plot with color-coded rock categories, visualizing major features with PCA, t-SNE, LLE, and MDS.

C. Discussed observations on how different dimensionality reduction techniques represented rock categories and variance.

A ->

[13]:
```
# PCA with 2 components
pca_2d = PCA(n_components=2)
data_matrix_2D_pca = pca_2d.fit_transform(data_matrix_scaled)
explained_variance_2d = np.sum(pca_2d.explained_variance_ratio_) * 100
print(f"Variance explained by the first two components: {explained_variance_2d:.
  ↪2f}%")

# Scatter plot of the 2D PCA results
categories = ['I', 'M', 'S']
colors = {'I': 'red', 'M': 'blue', 'S': 'green'}
plt.figure(figsize=(10, 8))
for category in categories:
    indices = [i for i, label in enumerate(labels) if label == category]
    plt.scatter(data_matrix_2D_pca[indices, 0], data_matrix_2D_pca[indices, 1],
                    label=f"Category {category}", color=colors[category], alpha=0.6)

plt.title(f"PCA 2D Projection (Variance explained: {explained_variance_2d:.
 ↪2f}%)")
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.legend()
plt.grid(True)
plt.show()
```

```
Variance explained by the first two components: 36.01%
```

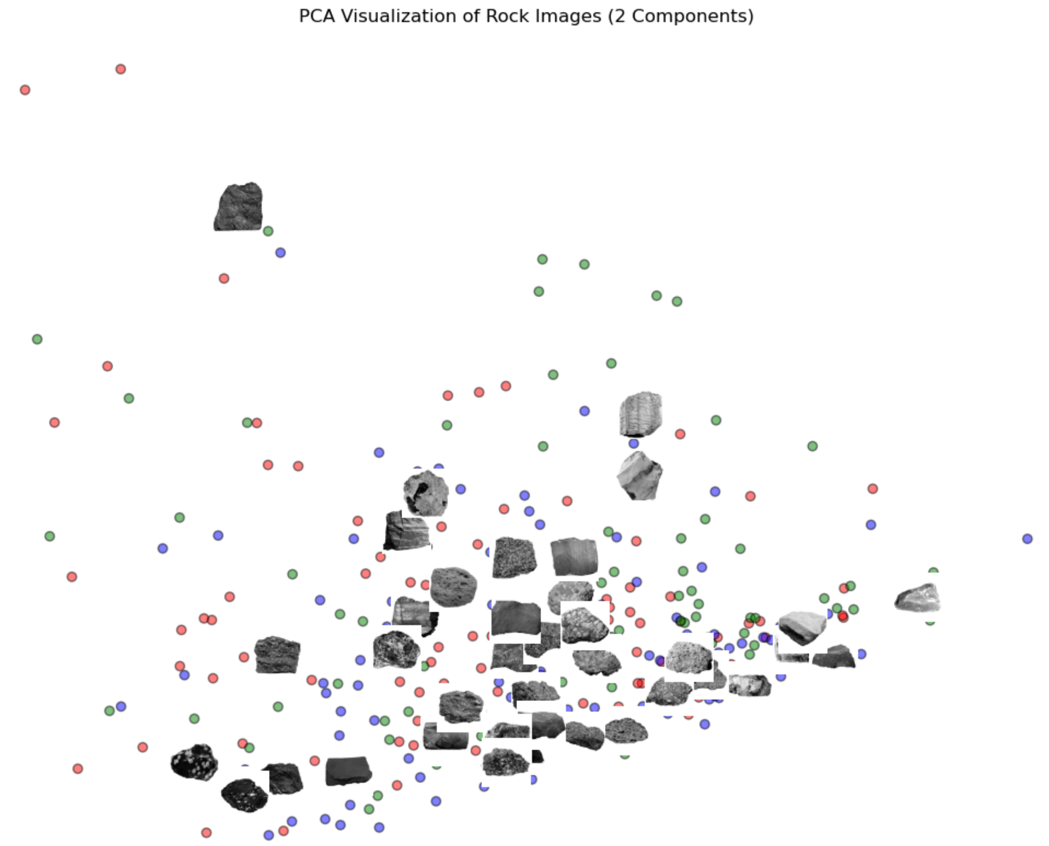


[14]:
```
# Helper function to plot with image overlays
def plot_with_images(X_2D, labels, images, title, min_distance=0.1,␣
 ↪figsize=(13, 10)):
    X_normalized = MinMaxScaler().fit_transform(X_2D)
    label_color_map = {'I': 'red', 'M': 'blue', 'S': 'green'}
    colors = [label_color_map[label] for label in labels]
    plt.figure(figsize=figsize)
    ax = plt.gca()
    plt.scatter(X_normalized[:, 0], X_normalized[:, 1], c=colors, alpha=0.5,␣
↪edgecolor='k')

    # Limit number of image overlays
    max_images = 40  # Limit the number of images
    indices = np.random.choice(len(X_normalized), size=min(max_images,␣
↪len(X_normalized)), replace=False)

    for index in indices:
        img = images[index].reshape(64, 64)
        imagebox = AnnotationBbox(OffsetImage(img, cmap="gray", zoom=0.5),␣
↪X_normalized[index], frameon=False)
        ax.add_artist(imagebox)

    plt.title(title)
    plt.axis("off")
    plt.show()
```

B ->

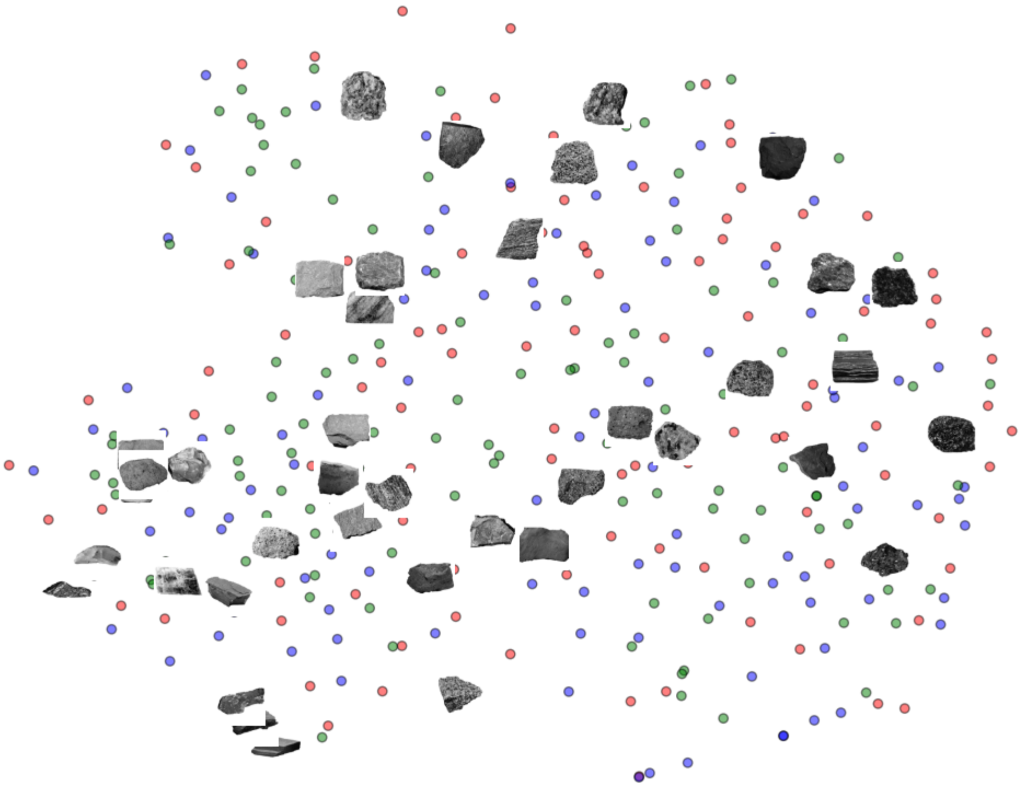
[16]:

```
# PCA 2D scatter with image overlays
plot_with_images(data_matrix_2D_pca, labels, data_matrix, "PCA Visualization of␣
↪Rock Images (2 Components)")
```

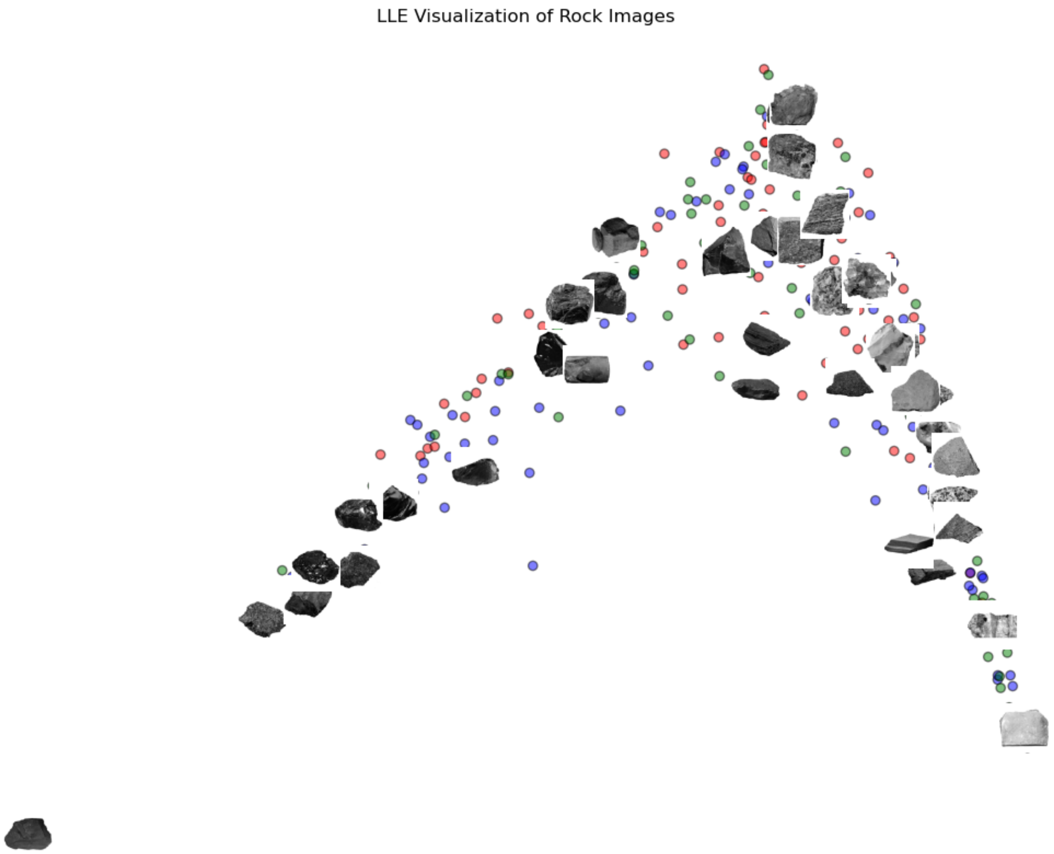


[17]:
```
# t-SNE 2D
tsne = TSNE(n_components=2, perplexity=30, random_state=42)
data_matrix_2D_tsne = tsne.fit_transform(data_matrix_scaled)
plot_with_images(data_matrix_2D_tsne, labels, data_matrix, "t-SNE Visualization␣
  ↪of Rock Images")
```

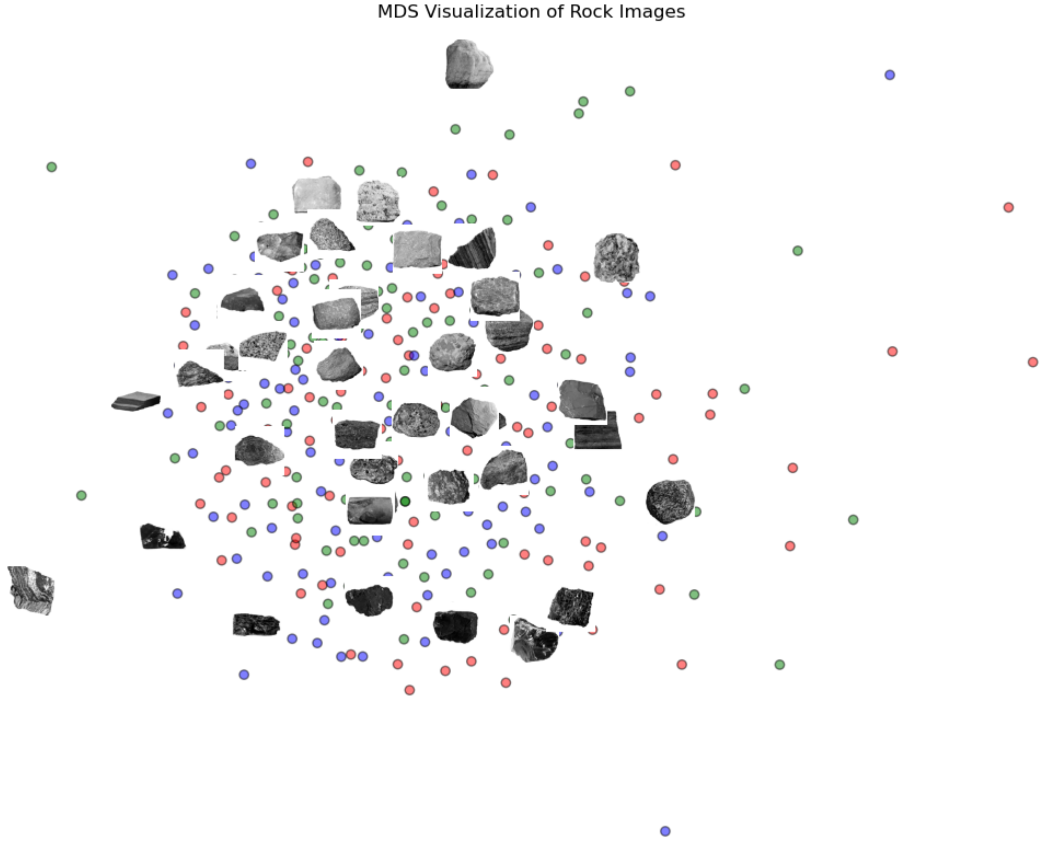
t-SNE Visualization of Rock Images



[18]:
```
# LLE 2D
lle = LocallyLinearEmbedding(n_components=2, random_state=42)
data_matrix_2D_lle = lle.fit_transform(data_matrix_scaled)
plot_with_images(data_matrix_2D_lle, labels, data_matrix, "LLE Visualization of␣
 ↪Rock Images")
```



```
[19]: # MDS 2D
mds = MDS(n_components=2, random_state=42)
data_matrix_2D_mds = mds.fit_transform(data_matrix_scaled)
plot_with_images(data_matrix_2D_mds, labels, data_matrix, "MDS Visualization of Rock Images")
```



C ->

Discussion on the visualizations.

1. PCA Visualization

In the PCA visualization, the rocks are spread out across the plot without forming clear clusters. PCA is a method that shows the main patterns in the data using a straightforward, linear approach. This spread means that PCA captures the overall variation in the data but doesn't highlight strong groupings among the rocks. The scattered arrangement suggests that PCA might not be the best method for finding clusters of similar rocks.

2. t-SNE Visualization

The t-SNE visualization shows rocks grouped into tighter clusters. This method is good at capturing complex relationships, so rocks that look similar are placed close together. Compared to PCA, the t-SNE layout has more defined clusters, making it easier to see differences between groups of rocks. However, t-SNE sometimes creates clusters that may not be accurate for larger datasets, as it focuses more on local patterns rather than the global structure.

3. LLE (Locally Linear Embedding) Visualization

The LLE visualization arranges the rocks in an elongated, curved shape, showing a possible continuous pattern in the dataset. This arrangement suggests that LLE found a hidden structure within the rock images. Rocks with similar textures or features are placed close to each other along the curve. LLE works well for datasets that follow gradual changes, so the shape may reflect a progression in features like texture, size, or shape.

4. MDS (Multi-Dimensional Scaling) Visualization

In the MDS visualization, most of the rocks are clustered in a circular shape, with some scattered along the edges. MDS focuses on preserving the distances between data points, showing how similar or different the rocks are. The central cluster suggests that many rocks share common features, while the scattered points on the edges represent rocks that are different. While MDS gives a good overall view, it may not reveal small, detailed patterns as well as t-SNE or LLE.

5 We will apply PCA, LLE, and MDS to reduce the dimensionality of 360 rock images to 8 features, and then compare these reduced embeddings with human data from mds_360.txt using Procrustes analysis. The disparity between the image embeddings and human data will be reported for each of the three dimensionality reduction methods, and the correlation coefficients between corresponding dimensions of the embeddings will be computed and displayed in a table.

[23]:

```
# Load human rankings from mds_360.txt
human_data = np.loadtxt("mds_360.txt")
print("Shape of human data:", human_data.shape)
```

```
Shape of human data: (360, 8)
```

[24]:

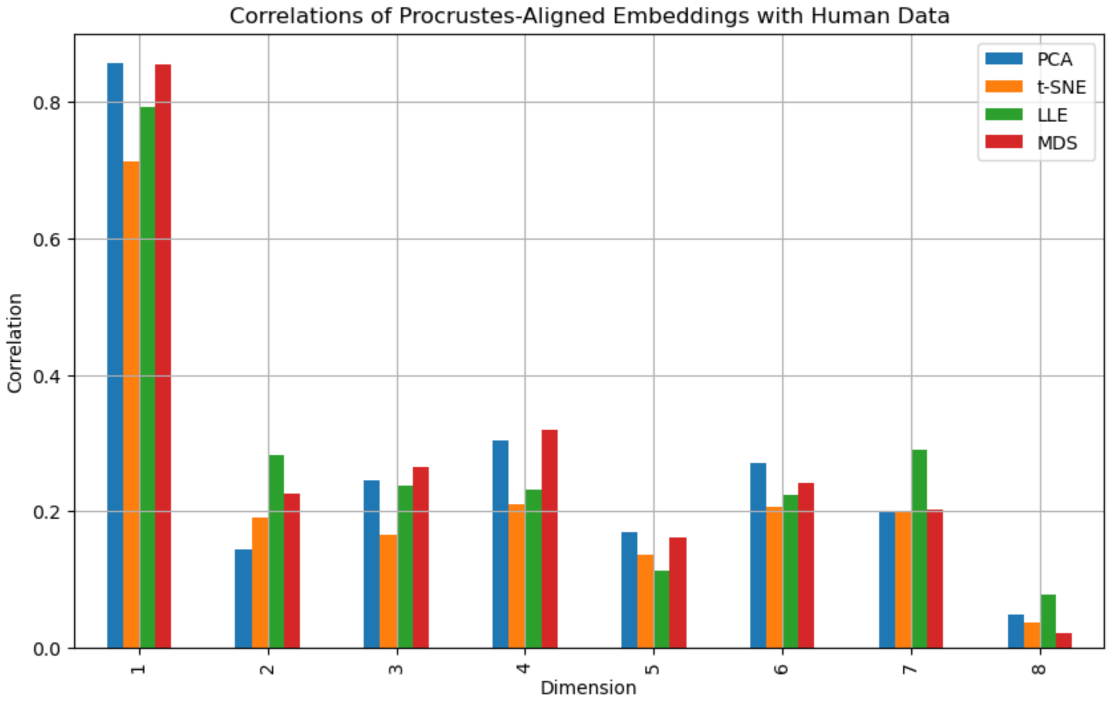
```
# Dimensionality Reduction to 8 Dimensions on Image Data
embeddings = {
    'PCA': PCA(n_components=8).fit_transform(data_matrix_scaled),
    't-SNE': TSNE(n_components=8, random_state=42, method="exact").
 ↪fit_transform(data_matrix_scaled),
    'LLE': LocallyLinearEmbedding(n_components=8, random_state=42).
 ↪fit_transform(data_matrix_scaled),
    'MDS': MDS(n_components=8, random_state=42).
 ↪fit_transform(data_matrix_scaled)
}

# Procrustes Analysis
disparities = {}
aligned_matrices = {}
for method, embed in embeddings.items():
    mtx1, mtx2, disparity = procrustes(human_data, embed)
    disparities[method] = disparity
    aligned_matrices[method] = (mtx1, mtx2)
    print(f"{method} embedding shape:", embed.shape)
    print(f"{method} disparity with human data: {disparity:.4f}")
```

```
PCA embedding shape: (360, 8)
PCA disparity with human data: 0.8674
t-SNE embedding shape: (360, 8)
t-SNE disparity with human data: 0.9296
LLE embedding shape: (360, 8)
LLE disparity with human data: 0.9078
MDS embedding shape: (360, 8)
MDS disparity with human data: 0.8814
```

[25]:

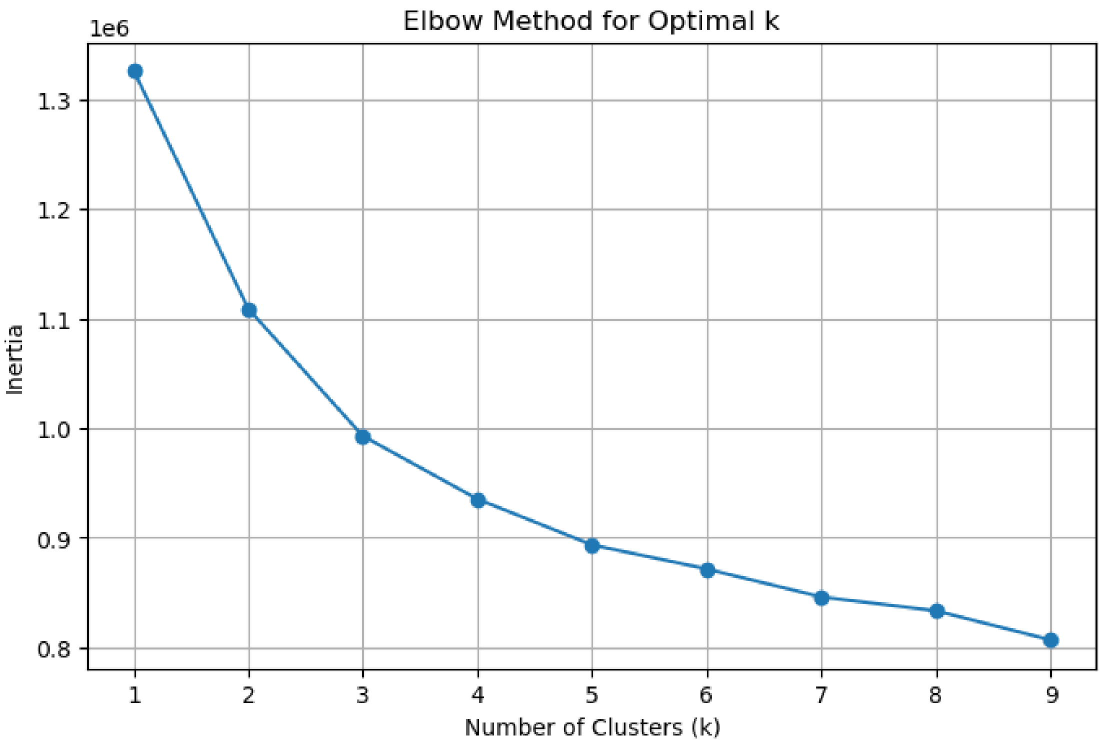
```
# Correlation between mtx1 and mtx2 for each method
correlation_results = {}
for method, (mtx1, mtx2) in aligned_matrices.items():
    correlations = [np.corrcoef(mtx1[:, i], mtx2[:, i])[0, 1] for i in range(8)]
    correlation_results[method] = correlations

# Convert results to DataFrame for better readability
correlation_df = pd.DataFrame(correlation_results, index=[f"Dimension {i+1}"␣
 ↪for i in range(8)])
print("Correlation coefficients between each dimension of mtx1 and mtx2:")
print(correlation_df)

# Display correlation results
correlation_df = pd.DataFrame(correlation_results)
correlation_df.index = correlation_df.index + 1
correlation_df.plot(kind="bar", figsize=(10, 6))
plt.title("Correlations of Procrustes-Aligned Embeddings with Human Data")
plt.xlabel("Dimension")
plt.ylabel("Correlation")
plt.grid(True)
plt.show()
```

```
Correlation coefficients between each dimension of mtx1 and mtx2:
                  PCA     t-SNE       LLE       MDS
Dimension 1  0.857580  0.712250  0.793314  0.854693
Dimension 2  0.144730  0.190087  0.281389  0.225030
Dimension 3  0.244418  0.165790  0.237586  0.264437
Dimension 4  0.304410  0.209424  0.232424  0.319460
Dimension 5  0.169693  0.135868  0.112935  0.161852
Dimension 6  0.270861  0.206371  0.223721  0.241874
Dimension 7  0.198097  0.200900  0.290112  0.202135
Dimension 8  0.047837  0.037266  0.077815  0.020447
```



6 We will cluster the 360 rock images using K-Means, reducing the dimensionality with PCA to retain at least 90% of the variance if desired.

[28]:
```
inertia = []
K_range = range(1, 10)

for k in K_range:
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(data_matrix_reduced)
    inertia.append(kmeans.inertia_)

# Plot the Elbow curve
plt.figure(figsize=(8, 5))
plt.plot(K_range, inertia, marker='o')
plt.xlabel("Number of Clusters (k)")
plt.ylabel("Inertia")
plt.title("Elbow Method for Optimal k")
plt.grid(True)
plt.show()
```



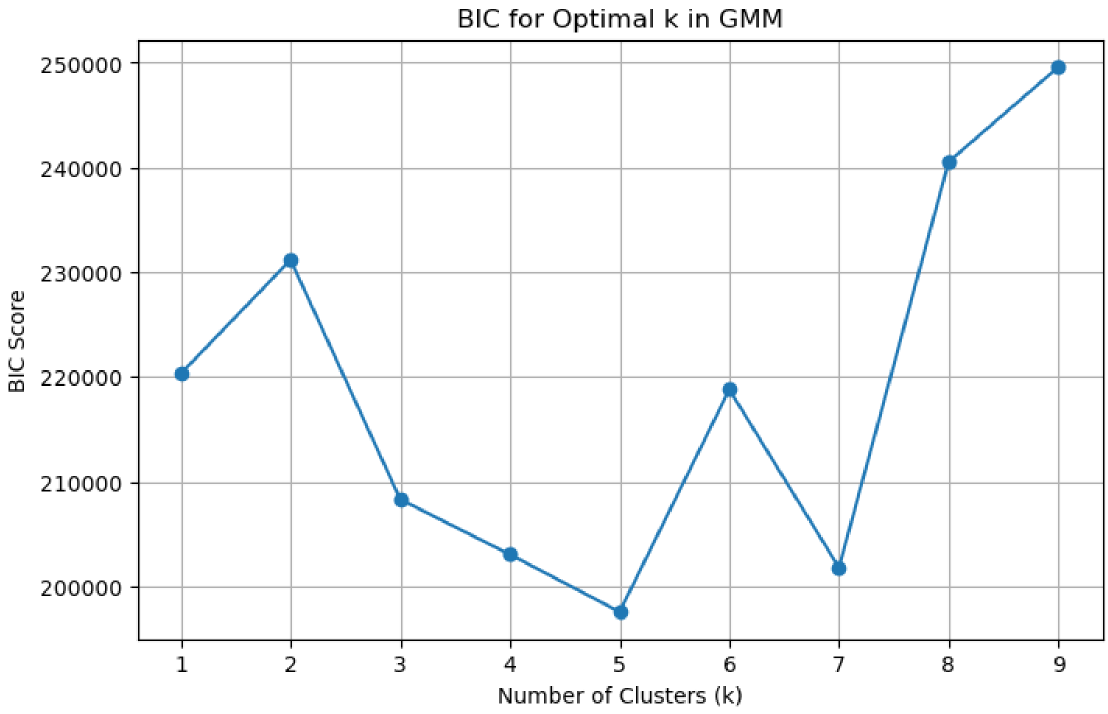
Based on the Elbow Method plot, the optimal number of clusters for this dataset appears to be k = 3.

[30]:
```
# Apply K-Means clustering with k=3
kmeans = KMeans(n_clusters=3, random_state=42)
cluster_labels_kmeans = kmeans.fit_predict(data_matrix_reduced)

# Convert true labels to numerical format
label_mapping = {'I': 0, 'M': 1, 'S': 2}
true_labels = np.array([label_mapping[label] for label in labels])

# Map each cluster label to true label using majority voting
mapped_labels_kmeans = np.zeros_like(cluster_labels_kmeans)
for i in range(3):
    mask = (cluster_labels_kmeans == i)
    mapped_labels_kmeans[mask] = mode(true_labels[mask])[0]

# Calculate accuracy
accuracy_kmeans = accuracy_score(true_labels, mapped_labels_kmeans)
print(f"K-Means Clustering Accuracy with k=3: {accuracy_kmeans * 100:.2f}%")
```

```
K-Means Clustering Accuracy with k=3: 36.11%
```

7 We will cluster the 360 rock images using Expectation Maximization (EM), reducing the dimensionality with PCA to retain at least 90% of the variance if desired. Additionally, the model will be used to generate 20 new rocks using the sample() method, and these new rocks will be visualized in the original image space using the inverse transform method from PCA.

[33]:
```
bic_scores = []
K_range = range(1, 10)

for k in K_range:
    gmm = GaussianMixture(n_components=k, random_state=42)
    gmm.fit(data_matrix_reduced)
    bic_scores.append(gmm.bic(data_matrix_reduced))

# Plot BIC scores
plt.figure(figsize=(8, 5))
plt.plot(K_range, bic_scores, marker='o')
plt.xlabel("Number of Clusters (k)")
plt.ylabel("BIC Score")
plt.title("BIC for Optimal k in GMM")
plt.grid(True)
plt.show()
```



Based on the BIC plot, k=5 appears to be the optimal number of clusters.

[35]:

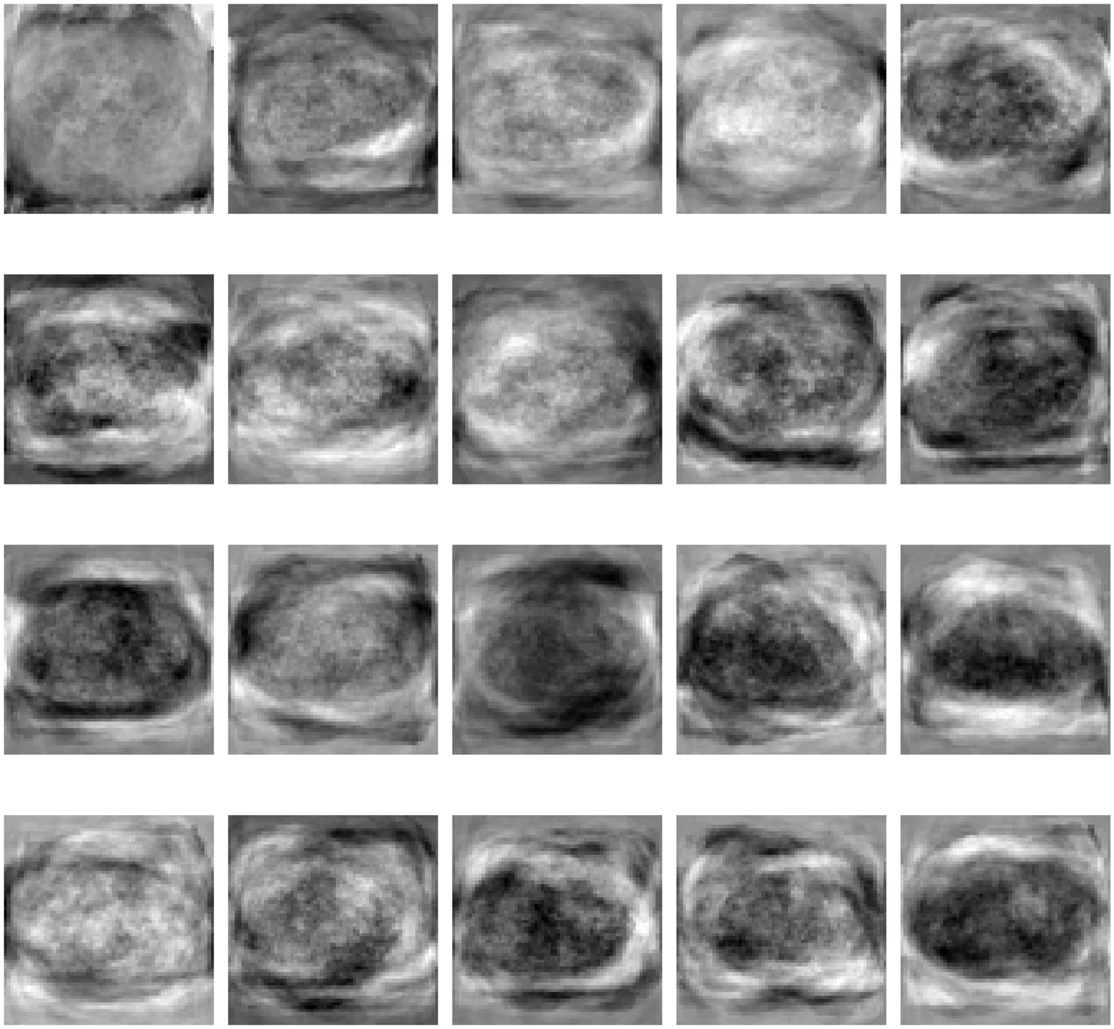
```
# Fit GMM with k=3
gmm = GaussianMixture(n_components=3, random_state=42)
gmm_labels = gmm.fit_predict(data_matrix_reduced)

# Map GMM cluster labels to true labels using majority voting
mapped_labels_gmm = np.zeros_like(gmm_labels)
for i in range(3):
    mask = (gmm_labels == i)
    mapped_labels_gmm[mask] = mode(true_labels[mask])[0]

# Calculate accuracy
accuracy_gmm = accuracy_score(true_labels, mapped_labels_gmm)
print(f"GMM Clustering Accuracy with k=3: {accuracy_gmm * 100:.2f}%")
```

```
GMM Clustering Accuracy with k=3: 35.56%
```

[37]:

```
# Generate 20 new samples using the GMM model
num_samples = 20
new_samples_reduced, _ = gmm.sample(num_samples)

# Inverse transform the reduced samples back to the original image space
new_samples_original = pca.inverse_transform(new_samples_reduced)

# Check the shape of new_samples_original
print(f"Shape of new_samples_original: {new_samples_original.shape}")

# Visualize the 20 new "rocks"
fig, axes = plt.subplots(4, 5, figsize=(12, 12))  # 4 rows, 5 columns for 20␣
  ↪images
axes = axes.flatten()

# Loop through and visualize the new samples
for i in range(num_samples):
    axes[i].imshow(new_samples_original[i].reshape(64, 64), cmap='gray')
    axes[i].axis('off')

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

```
Shape of new_samples_original: (20, 4096)
```



8 We will build a feedforward neural network using Keras (within TensorFlow) or PyTorch with dense and/or CNN layers and a few hidden layers. The network will be trained to classify 360 rock images, with the rock category indicated by the first letter in the filename (I, M, and S). Images from the ‘120 Rocks’ folder will be used as validation data. The number of neurons will be chosen for efficiency, ensuring the last layer before the softmax activation has 8 neurons. Hidden layers will use the ReLU activation function. The network will be trained for multiple epochs until convergence, with the learning rate adjusted if necessary. The performance will be evaluated based on decreasing training and validation loss and increasing accuracy.

[39]:

```
# Paths for training and validation datasets
train_folder = "360 Rocks"
val_folder = "120 Rocks"

# Function to load and preprocess images
def load_images(image_folder, image_size=(64, 64)):
    images = []
    labels = []

    for filename in os.listdir(image_folder):
        if filename.endswith(".jpg") or filename.endswith(".png"):
            img = load_img(os.path.join(image_folder, filename),␣
 ↪target_size=image_size, color_mode='grayscale')
            img_array = img_to_array(img)
            images.append(img_array)

            label = filename[0].upper()  # Use the first character as label
            labels.append(label)

    images = np.array(images).astype('float32') / 255.0  # Normalize images
    labels = np.array(labels)

    # Encode labels
    label_encoder = LabelEncoder()
    labels = label_encoder.fit_transform(labels)
    labels = to_categorical(labels)  # One-hot encoding for categorical labels

    return images, labels

# Load the data
```

```
train_images, train_labels = load_images(train_folder)
val_images, val_labels = load_images(val_folder)
```

[41]:

```
# Build the feedforward neural network using Functional API
input_shape = (64, 64, 1)
num_classes = 3

inputs = Input(shape=input_shape)
x = Conv2D(32, (3, 3), activation='relu')(inputs)
x = MaxPooling2D((2, 2))(x)
x = Conv2D(64, (3, 3), activation='relu')(x)
x = MaxPooling2D((2, 2))(x)
x = Conv2D(128, (3, 3), activation='relu')(x)
x = MaxPooling2D((2, 2))(x)
x = Flatten()(x)
x = Dense(128, activation='relu')(x)
x = Dense(64, activation='relu')(x)
x = Dense(8, activation='relu')(x)  # Next-to-last layer with 8 neurons
outputs = Dense(num_classes, activation='softmax')(x)

model = Model(inputs=inputs, outputs=outputs)
model.compile(optimizer=Adam(learning_rate=0.001),␣
 ↪loss='categorical_crossentropy', metrics=['accuracy'])

# Display the model summary
model.summary()

# Early stopping callback to stop training when validation loss stops improving
early_stopping = EarlyStopping(monitor='val_loss', patience=5,␣
 ↪restore_best_weights=True)

# Train the model with early stopping
start_time = time.time()
history = model.fit(
    train_images,
    train_labels,
    epochs=30,
    batch_size=32,
    validation_data=(val_images, val_labels),
    callbacks=[early_stopping]  # Add early stopping here
)
end_time = time.time()
training_time = end_time - start_time
print(f"Training Time with Early Stopping: {training_time:.2f} seconds")
```

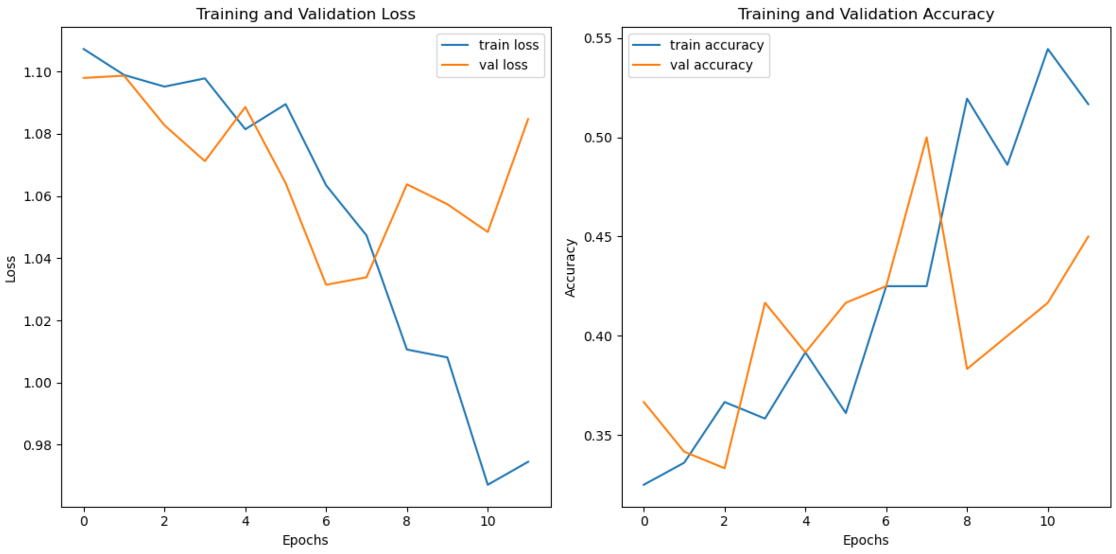
```
Model: "functional"
```

```
Layout (type)                          Output Shape                      ␣
↪Param #

input_layer (InputLayer)               (None, 64, 64, 1)                     ␣
↪   0

conv2d (Conv2D)                        (None, 62, 62, 32)                    ␣
↪320

max_pooling2d (MaxPooling2D)           (None, 31, 31, 32)                    ␣
↪   0

conv2d_1 (Conv2D)                      (None, 29, 29, 64)                 ␣
↪18,496

max_pooling2d_1 (MaxPooling2D)         (None, 14, 14, 64)                    ␣
↪   0

conv2d_2 (Conv2D)                      (None, 12, 12, 128)                ␣
↪73,856

max_pooling2d_2 (MaxPooling2D)         (None, 6, 6, 128)                     ␣
↪   0

flatten (Flatten)                      (None, 4608)                          ␣
↪   0

dense (Dense)                          (None, 128)                       ␣
↪589,952

dense_1 (Dense)                        (None, 64)                          ␣
↪8,256

dense_2 (Dense)                        (None, 8)                             ␣
↪520

dense_3 (Dense)                        (None, 3)                             ␣
↪ 27


Total params: 691,427 (2.64 MB)

Trainable params: 691,427 (2.64 MB)
```

```
 Non-trainable params: 0 (0.00 B)


Epoch 1/30
12/12                 4s 90ms/step -
accuracy: 0.3141 - loss: 1.1139 - val_accuracy: 0.3667 - val_loss: 1.0979
Epoch 2/30
12/12                 1s 63ms/step -
accuracy: 0.3349 - loss: 1.0986 - val_accuracy: 0.3417 - val_loss: 1.0987
Epoch 3/30
12/12                 1s 40ms/step -
accuracy: 0.3469 - loss: 1.0971 - val_accuracy: 0.3333 - val_loss: 1.0827
Epoch 4/30
12/12                 1s 71ms/step -
accuracy: 0.3324 - loss: 1.1052 - val_accuracy: 0.4167 - val_loss: 1.0712
Epoch 5/30
12/12                 1s 69ms/step -
accuracy: 0.4078 - loss: 1.0725 - val_accuracy: 0.3917 - val_loss: 1.0886
Epoch 6/30
12/12                 1s 67ms/step -
accuracy: 0.3201 - loss: 1.0968 - val_accuracy: 0.4167 - val_loss: 1.0641
Epoch 7/30
12/12                 1s 73ms/step -
accuracy: 0.4181 - loss: 1.0682 - val_accuracy: 0.4250 - val_loss: 1.0314
Epoch 8/30
12/12                 2s 86ms/step -
accuracy: 0.4333 - loss: 1.0433 - val_accuracy: 0.5000 - val_loss: 1.0338
Epoch 9/30
12/12                 1s 72ms/step -
accuracy: 0.5552 - loss: 0.9875 - val_accuracy: 0.3833 - val_loss: 1.0637
Epoch 10/30
12/12                 1s 64ms/step -
accuracy: 0.4949 - loss: 0.9983 - val_accuracy: 0.4000 - val_loss: 1.0573
Epoch 11/30
12/12                 1s 57ms/step -
accuracy: 0.5974 - loss: 0.9499 - val_accuracy: 0.4167 - val_loss: 1.0484
Epoch 12/30
12/12                 1s 53ms/step -
accuracy: 0.5349 - loss: 0.9609 - val_accuracy: 0.4500 - val_loss: 1.0847
Training Time with Early Stopping: 16.80 seconds
```

[42]:

```python
# Plot training and validation loss and accuracy
def plot_training_history(history):
    plt.figure(figsize=(12, 6))

    # Plot Loss
    plt.subplot(1, 2, 1)
    plt.plot(history.history['loss'], label='train loss')
    plt.plot(history.history['val_loss'], label='val loss')
    plt.title('Training and Validation Loss')
    plt.xlabel('Epochs')
    plt.ylabel('Loss')
    plt.legend()

    # Plot Accuracy
    plt.subplot(1, 2, 2)
    plt.plot(history.history['accuracy'], label='train accuracy')
    plt.plot(history.history['val_accuracy'], label='val accuracy')
    plt.title('Training and Validation Accuracy')
    plt.xlabel('Epochs')
    plt.ylabel('Accuracy')
    plt.legend()

    plt.tight_layout()
    plt.show()

plot_training_history(history)
```



[44]:
```
# Calculate the total number of parameters
total_params = model.count_params()

# Calculate the number of bias parameters
bias_params = sum(np.prod(p.shape) for p in model.trainable_weights if 'bias'␣
 ↪in p.name)

print(f"Total parameters: {total_params}")
print(f"Bias parameters: {bias_params}")
```

```
Total parameters: 691427
Bias parameters: 427
```

[46]:

```
# Procrustes Analysis on Next-to-Last Layer
human_train_data = np.loadtxt("mds_360.txt")
human_val_data = np.loadtxt("mds_120.txt")

def get_activations(model, data):
    intermediate_layer_model = Model(inputs=model.input, outputs=model.
 ↪layers[-2].output)
    return intermediate_layer_model.predict(data)

# Get activations for training and validation
train_activations = get_activations(model, train_images)
val_activations = get_activations(model, val_images)

def procrustes_analysis_and_correlation(human_data, activations):
    min_dim = min(human_data.shape[0], activations.shape[0])
    mtx1, mtx2, disparity = procrustes(human_data[:min_dim], activations[:
 ↪min_dim])

    correlations = [pearsonr(mtx1[:, i], mtx2[:, i])[0] for i in range(mtx1.
 ↪shape[1])]
    return disparity, correlations

train_disparity, train_correlations =␣
 ↪procrustes_analysis_and_correlation(human_train_data, train_activations)
val_disparity, val_correlations =␣
 ↪procrustes_analysis_and_correlation(human_val_data, val_activations)

# Create a DataFrame for disparity
disparity_df = pd.DataFrame({
    'Metric': ['Disparity'],
    'Training': [train_disparity],
    'Validation': [val_disparity]
})

# Create a DataFrame for correlation dimensions
correlation_df = pd.DataFrame({
    'Metric': [f'Correlation Dim {i+1}' for i in range(8)],
    'Training': train_correlations,
    'Validation': val_correlations
})

# Combine the disparity and correlation DataFrames
```

```python
results = pd.concat([disparity_df, correlation_df], ignore_index=True)

# Display the table
print(results)
```

```
12/12             1s 30ms/step
4/4             0s 62ms/step
              Metric  Training  Validation
0          Disparity  0.833837    0.864805
1  Correlation Dim 1  0.676757    0.678401
2  Correlation Dim 2  0.424282    0.346546
3  Correlation Dim 3  0.309967    0.381740
4  Correlation Dim 4  0.448410    0.290289
5  Correlation Dim 5  0.149592    0.134752
6  Correlation Dim 6  0.237217    0.124047
7  Correlation Dim 7  0.272559    0.063004
8  Correlation Dim 8  0.265294    0.468478
```

The model aligns well with human data in Dimension 1 but performs poorly in other dimensions. Overall, the disparity values show a significant gap between the model and human data.