



Deep Learning Assignment

Assignment 1: PCA

Mohammad Parsa Dini - Std ID: 400101204

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Introduction

This report details the implementation of Principal Component Analysis (PCA) from scratch for dimensionality reduction on a Brain Tumor dataset, as part of the Deep Learning course assignment at Sharif University of Technology. The dataset consists of MRI images categorized into two classes: "yes" (patients with tumors) and "no" (healthy individuals). The primary objectives were to pre-process the images, implement PCA without using built-in libraries, reduce the dimensionality of the data, reconstruct images from the reduced space, and evaluate the impact of dimensionality reduction on classification performance using a Support Vector Machine (SVM). The report outlines the methodology, results, and analysis of the experiments conducted.

Dataset and Preprocessing

The Brain Tumor dataset contains MRI images in two folders: "yes" (tumors) and "no" (healthy). Each image was preprocessed using a cropping function to focus on the brain region, converted to grayscale, and resized to a uniform resolution of 128×128 pixels. The preprocessing steps included:

- **Cropping:** A contour-based cropping function was applied to isolate the brain region by converting images to grayscale, applying Gaussian blur, thresholding, and extracting the largest contour to define the cropping boundaries.
- **Grayscale Conversion:** Images were converted from RGB to grayscale to reduce the feature dimensionality from three channels to one.
- **Resizing:** All images were resized to 128×128 pixels to ensure uniformity.

- **Labeling:** Images in the "yes" folder were labeled as 1 (tumor), and those in the "no" folder were labeled as 0 (healthy).

The dataset was loaded using OpenCV, resulting in 253 images, each represented as a 128×128 grayscale matrix. The images were flattened into vectors of length 16384 (i.e., 128×128) for PCA processing. The data was shuffled and split into training (80%, 202 samples) and testing (20%, 51 samples) sets using scikit-learn's `train_test_split` function with a random seed for reproducibility.

PCA Implementation

PCA was implemented from scratch using NumPy, following these steps:

1. **Centering the Data:** The mean of the training data (`X_train`) was computed and subtracted from each sample to center the data.
2. **Covariance Matrix:** The covariance matrix of the centered data was calculated.
3. **Eigenvalue Decomposition:** Eigenvalues and eigenvectors of the covariance matrix were computed using `np.linalg.eigh`. The eigenvectors were sorted by descending eigenvalues to select the top k components.
4. **Projection:** The top `n_components=20` eigenvectors were used to project the centered training and test data into a lower-dimensional space.

The PCA model was fitted on the training data (`X_train`) only, and the resulting components were used to transform both `X_train` and `X_test`. This approach was chosen to prevent information leakage from the test set, ensuring that the test data remains unseen during training, as emphasized in class lectures. Fitting PCA on `X_train` ensures that the principal components are derived solely from the training distribution, maintaining the integrity of the evaluation process.

The dimensionality of the training data was reduced from (202, 16384) to (202, 20), and the test data from (51, 16384) to (51, 20).

Image Reconstruction

To evaluate the quality of the reduced representation, a random image from the training set was reconstructed from its 20-dimensional PCA representation. The reconstruction process involved:

- Projecting the reduced data back to the original space using the transpose of the PCA components and adding the mean:

$$x_{recon} = x_{train} U_{component}^T + \mu_{mean}$$

- Reshaping the reconstructed vector to 128×128 for visualization.

The original and reconstructed images were visualized side-by-side using Matplotlib with a grayscale colormap. The plot revealed that the reconstructed image retained the general structure of the brain but exhibited some loss of fine details due to the significant dimensionality reduction (from 16384 to 20 dimensions). This loss is expected, as PCA prioritizes variance retention, potentially discarding low-variance features that contribute to fine textures.

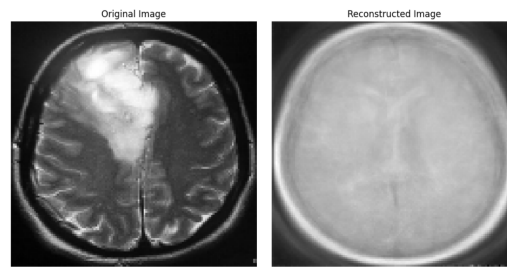


Figure 1: The image illustrates an image from the dataset(left) and also the result of reconstruction of this image(right).

Classification and Results

A linear Support Vector Machine (SVM) was trained to classify images as tumor (1) or healthy (0), and its performance was evaluated on the test set before and after dimensionality reduction.

- **Before Dimensionality Reduction:** The SVM was trained on the original X_{train} (202×16384) and tested on X_{test} (51×16384). The accuracy on the test set was approximately 74.51%.
- **After Dimensionality Reduction:** The SVM was trained on the reduced $X_{\text{train_red}}$ (202×20) and tested on $X_{\text{test_red}}$ (51×20). The accuracy on the test set was approximately 62.75%.

The classification accuracy decreased after applying PCA, suggesting that the reduction to 20 components may have discarded features critical for distinguishing between tumor and healthy images.

Analysis and Discussion

The decrease in classification accuracy after PCA (from 74.51% to 62.75%) indicates that the 20 principal components did not capture sufficient discriminative information for the SVM to effectively separate the classes. PCA, being an unsupervised method, maximizes variance without considering class labels. In this case, some features relevant to tumor detection may have had low variance and were thus excluded in the reduced representation.

The reconstruction results further support this observation. While the reconstructed image preserved the overall brain structure, the loss of fine details likely corresponds to the loss of subtle patterns that differentiate tumorous from healthy tissue. This highlights a key limitation of unsupervised dimensionality reduction: it may not prioritize features that are most relevant for the classification task.

To address the question posed in the notebook, unsupervised dimensionality reduction does not always increase accuracy. Its impact depends on the dataset's structure. If the original features contain significant noise or redundancy, PCA can improve accuracy by focusing on the most informative components. However, if critical discriminative features are discarded, as observed here, accuracy may decrease. Supervised methods, such as Linear Discriminant Analysis (LDA), might

yield better results for classification tasks by explicitly considering class labels during dimensionality reduction.

Conclusion

This assignment demonstrated the implementation of PCA from scratch for dimensionality reduction on a Brain Tumor dataset. The preprocessing steps effectively standardized the MRI images, and the PCA implementation successfully reduced the dimensionality from 16384 to 20 features. However, the classification accuracy decreased after PCA, indicating that the reduced representation lost important discriminative information. The reconstructed images showed a loss of fine details, consistent with the reduced classification performance.

Future improvements could include experimenting with different numbers of principal components to find an optimal balance between dimensionality reduction and information retention. Additionally, exploring supervised dimensionality reduction techniques or incorporating domain-specific feature engineering could enhance classification performance. This exercise underscored the importance of carefully evaluating the impact of dimensionality reduction on specific tasks, particularly in medical imaging applications where subtle details are critical.