RESEARCH

Project-10

Sujan Darai (sujad96@zedat.fu-berlin.de), Matanat Mammadli (matanam94@zedat.fu-berlin.de), Samra Hamidovic (samrah96@zedat.fu-berlin.de)

Full list of author information is available at the end of the article

Abstract

Goal of the project: The project aims to use pySSAM to build 2D statistical shape models for three different object classes, following the methodology outlined in the paper [1].

Main results: We identified the common structure and primary sources of variation in the leaf shapes through Procrustes analysis and PCA. The analysis revealed that a few principal components capture 95% of the variance, highlighting the main patterns of shape variation. The shape mode with low eigenvalues seem to be similar to the mean shape because of the low variance.

Personal key learning:

1 Sujan Darai: Learned about the statistical shape model, pySSAM library, Procrustes analysis, and principal component analysis
2 Samra Hamidovic: Learned the steps of a statistical shape analysis, procrustes analysis, how to find a good dataset and how to use pySSAM
3 Matanat Mammadli: Learning about Active Shape Models, SSAM, Procrustes analysis, and how to use the pySSAM package on different datasets.

Estimated working hours:

1 Sujan Darai: 10
2 Samra Hamidovic: 10
3 Matanat Mammadli: 10

Project evaluation: 1

Number of words: 2120

Keywords: Statistical shape model, Procrustes analysis, PCA

1 Introduction

In the realm of biomedical image analysis, statistical shape modeling plays a crucial role in interpreting complex image data. The construction of 2D statistical shape models for different object classes is a key focus. By utilizing statistical shape modeling techniques, robust models are developed to capture shape variabilities within specific object classes. These models are vital for improving object localization, classification, and further analysis in biomedical imaging applications. The application of statistical shape modeling techniques aims to advance the understanding and interpretation of intricate image data in the context of biomedical research and analysis. [1]

Leveraging the advancements in this domain, the pyssam Python library emerges as a pivotal tool for creating Statistical Shape and Appearance Models (SSAMs) for diverse biological structures, including bones, lungs, and other organs. Developed by researchers at Heriot-Watt University, pyssam necessitates a point cloud representation of anatomical landmarks from each sample, enabling the integration of shape and appearance correlations into the model. [2]

This project aims to create robust models that capture shape variations within the specified object classes and delves into the theoretical underpinnings and practical applications of pyssam, shedding light on its significance in shaping the landscape of statistical modeling in biomedical research.

2 Goal of the project

The goal of the project is to utilize pySSAM to construct a 2D statistical shape model for three distinct object classes. The project aims to follow the methodology outlined in the paper [1], which involves building statistical models of shape and appearance from annotated images, defining suitable landmarks to describe the shape of the target objects, and applying techniques such as Principal Component Analysis (PCA) to reduce data dimensionality and approximate shapes in the training set. By implementing these steps, the project seeks to create robust statistical models that can effectively represent the shape variations within the three object classes for further analysis and interpretation.

3 Data and preprocessings

In the report, we used three different datasets for statistical shape modeling. I (Sujan Darai) used the hand shapes dataset with 50 training samples with varying poses of left hands. The hand shapes come from different individuals. The datasets were taken from the GitHub repository https://github.com/msrepo/. For the preprocessing of images, we have used the OpenCV Python package, and landmarks on the images have been set manually and each landmark is then converted into 2d coordinates. For each image, 55 landmarks were chosen such that the most dominant parts are included which affect the shape representation.

I (Matanat Mammadli) chose the leaf classification dataset from the Kaggle website https://www.kaggle.com/c/leaf-classification. The dataset consists of 1584 different leaf shapes with black backgrounds and white 2D leaf contours (see Figure 1). From these shapes, 50 were selected for use in the analysis. As mentioned above, I applied 55 landmarks to each image and saved the coordinates in CSV files, which were then used for Procrustes analysis and further processing steps.

I (Samra Hamidovic) chose the butterfly shapes dataset from https://aiplanet.com/challenges/325/butterfly_identification/data. The butterfly shapes differ in size and position. The original dataset contains about 1000+ samples, which were divided in training and test set. From this amount of samples I picked 50 samples with various shapes. I also applied 55 landmarks to each image and saved the coordinates as CSV files, which were then used for Procrustes analysis and further processing steps.

4 Methods

4.1 Procrustes Analysis

A statistical shape model (SSM) is a mathematical method employed to analyze and demonstrate the variability of shapes in biomedical images. The model captures the expected shape and local grey-level structure of a target object, making it possible to catch and measure specific structures within complex images. The process involves aligning a set of training shapes into a common coordinate frame to ensure that

variations due to position, orientation, and scale are removed. Landmarks are chosen on these shapes, often at points of high curvature or junctions, which serve as reference points for alignment. The alignment of shapes to the common reference point or coordinate space can be done by Procrustes analysis. Procrustes analysis involves aligning shapes or images to minimize the sum of their distances from a central average position. To make this process smooth, restrictions are usually applied, such as centering the shapes at the origin, standardizing their scale to one, and setting a specific orientation.

4.2 Principal component analysis (PCA)

It is one of the popular dimensional reductional techniques used when sample sizes are smaller than the parameters. Principal Component Analysis (PCA) identifies the main directions (or axes) of variation in a high-dimensional dataset. It permits to approximation of the positions of points using fewer parameters. Principal Component Analysis (PCA) is applied to the aligned shapes to identify the main modes of variation, which simplifies the shape representation while retaining the essential variability observed in the training set. This statistical approach allows for the generation of new shapes that are similar to those in the training set and can be used for tasks such as object recognition and image interpretation. The model's robustness is tested through leave-one-out experiments, ensuring that it generalizes well to new shapes within the same class. SSMs are particularly useful in medical image analysis, where accurately identifying and measuring anatomical structures is critical.

4.3 pyssam

The pyssam Python library, developed by researchers at Heriot-Watt University, is founded on the principles of statistical shape and appearance modeling. At its core, pyssam enables the creation of robust statistical models that capture the shape variations and appearance characteristics present in biological structures, such as bones, lungs, or other organs. By requiring a point cloud representation of anatomical landmarks from each sample in a dataset, pyssam facilitates the incorporation of joint correlations between shape and appearance features, thereby enhancing the modeling accuracy.

Through alignment and scaling of input data, pyssam constructs a Statistical Shape and Appearance Model (SSAM) based on the covariance observed across the population. This model parameterizes and quantifies the shape changes within the dataset, offering valuable insights into the underlying variations. The SSAM generated by pyssam can be leveraged to analyze shape variations, facilitate diagnostic tools, or even reconstruct 3D structures from imaging modalities. [2]

5 Results and discussion

The leaf dataset consisted of 1584 different leaf shapes, from which 50 different shapes were chosen and added to a new folder. Some example leaf shapes can be seen in Figure 1.

We aligned a set of 2D shapes using Procrustes analysis, computed the mean shape, applied PCA to shape variations, and visualized the aligned shapes along

with the mean shape. This approach helps in understanding the common structure and variations within a set of shapes. The results can be seen in Figure 2.

We also performed Generalized Procrustes Analysis to iteratively align our set of 2D leaf shapes to a mean shape. The mean shape was updated until convergence or a maximum number of iterations was reached. The final aligned shapes and mean shape are visualized, highlighting the common structure among the shapes (as seen in Figure 3).

In Figure 4, we extracted eigenvalues and eigenvectors from a PCA object, calculated the cumulative explained variance, determined the number of principal components needed to explain 95% of the variance, and plotted the cumulative explained variance. This helps in understanding how many principal components are required to capture most of the variance in the dataset.

Lastly, we visualized three different leaf shape modes as examples (see Figure 5, Figure 6, and Figure 7). We plotted the mean shape and its variations along the specified principal component (mode of variation). This is useful for understanding the main sources of variation in the shape data and how they affect the overall shape. As a standard deviation or constraint on parameters, we chose $\pm 3\lambda_i$. As we can observe from these figures, the variance decreases with increasing modes. For shape mode 1, the variance was 0.12902; for shape mode 3, it was 0.02962; and for shape mode 4, it was 0.01663.

For the hand dataset, I chose one left hand with the 55 landmarks labeled manually which is shown in Figure 16. For all the hand images, the selection of landmarks has been done in the same fashion such that point-to-point correspondence can be evaluated. The mean shape of the hand was then created by taking the average of all the landmarks using the Procrustes analysis which is shown in Figure 17. From the figure, all the shapes of the hand are aligned in the same direction, and the mean shape also looks like a hand.

For the cumulative variance plot, Principal component analysis was employed. It calculates the eigenvalues and eigenvectors of the covariance matrix to determine the major axes of data and variation along the mean shape. principal components act as the shape variables/shape weights. Each eigenvalue represents the variance of the data along the direction of its associated eigenvector. The total variance is calculated by summing up all the eigenvalues which is used to measure the variations in the shape population. The amount of cumulative variance observed in the training data is plotted against the number of modes or components sorted by the eigenvalues from highest to lowest. For to overcome the variance of 95 % only three modes are sufficient which is shown in Figure 18.

The variation along the mean positions was determined with the 3 units of standard deviation with different modes 0, 1, 2, 3, 4, and 49, which are shown in Figures 20, and 21. The shape modes and shape weight describe the variation from the mean shape. With the increase in mode, less variability is observed from the mean shape. Mode 0 represents the movements of the palm while retaining the mean shape with a high eigenvalue of 0.903. Mode 49 seems to be almost similar with a mean shape with an eigenvalue of 1.781e-31. Hence, a statistical shape model has been built and analyzed using the 2d images.

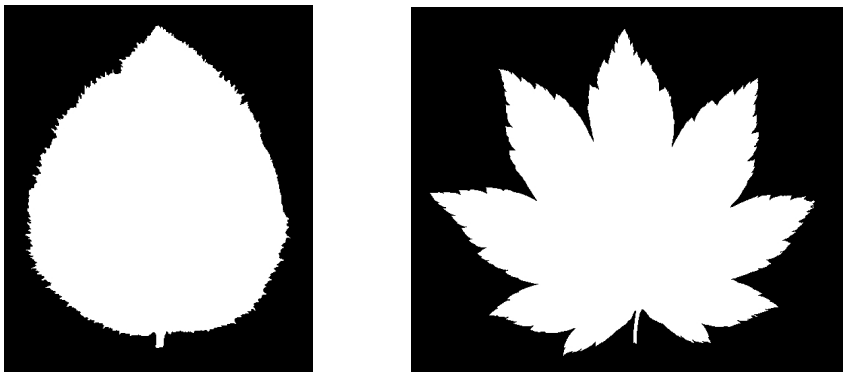
The butterfly dataset consisted of 1000+ samples, from where I chose 50 samples. The samples were labeled manually with 55 landmarks (see fig10). Mainly the samples differ in position, like some flying in left or right direction and some are shown from the side (fig. 8 & 9).

Using Procrustes analysis, we aligned the butterfly shapes to minimize differences in scale, translation, and rotation. This allowed us to compute an initial mean shape, representing the average butterfly structure in our dataset (Figure 11). We then refined this alignment using Generalized Procrustes Analysis (GPA), which iteratively updates the mean shape until convergence, providing a more accurate average shape (Figure 11b).

To analyze shape variations, we applied Principal Component Analysis (PCA) to the aligned shapes. PCA identified the main modes of variation, and the cumulative explained variance plot (Figure 13) showed that the first few principal components accounted for approximately 95% of the total variance. This indicates that a limited number of components are sufficient to capture most shape variations.

We visualized shape variations along these principal components by plotting the mean shape and its deviations (Figures 14, 15, and 16). The analysis revealed that the first few modes captured significant variations, while higher modes contributed less to the overall variability. For example, the variance for shape mode 0 was 0.70065, for mode 1 it was 0.10612, for mode 2 it was 0.04493, for mode 3 it was 0.03887, and for mode 4 it was 0.01836. Notably, the variance for mode 49 was as low as 1.3818e-31, indicating minimal deviation from the mean shape.

In summary, Procrustes analysis and PCA provided a comprehensive understanding of butterfly shapes, allowing us to align and analyze shape variations effectively. The aligned shapes, mean shape, and principal components offer valuable insights into the common structure and variability within the butterfly dataset.



(a) Shape 1 (average leaf) (b) Shape 2 (maple leaf)

Figure 1: Training dataset: Different leaf shapes

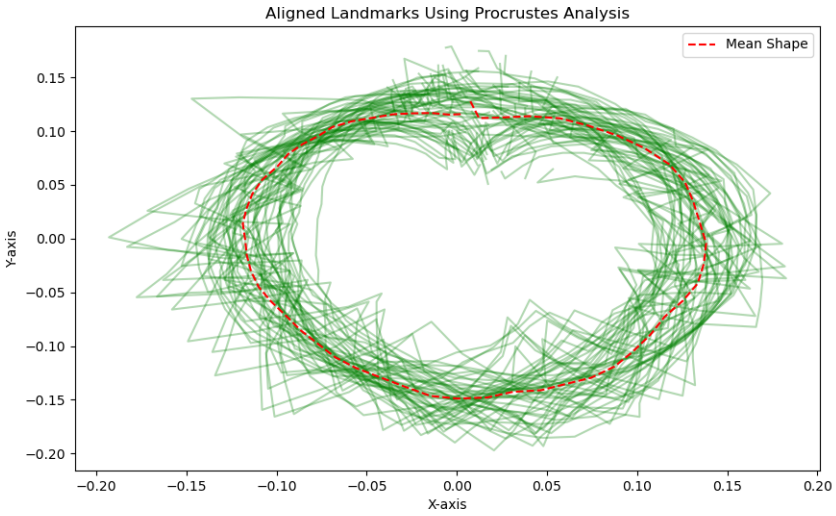


Figure 2: Aligned mean shape (leaf dataset)

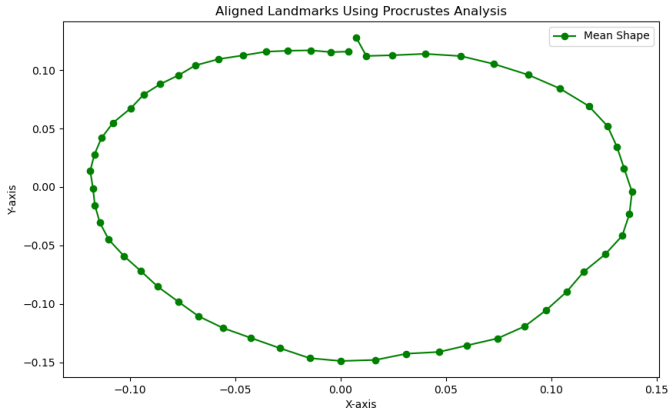


Figure 3: Mean shape (leaf dataset)

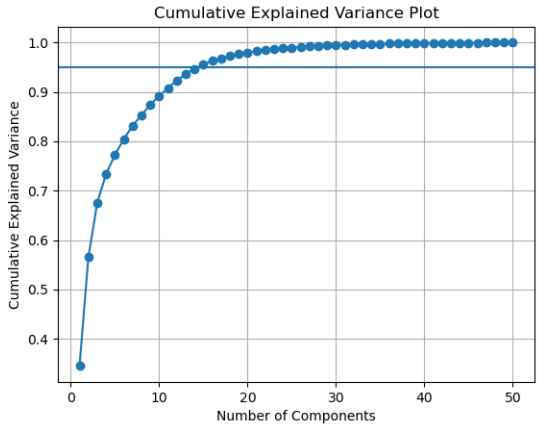


Figure 4: Cumulative Variance plot (leaf dataset)

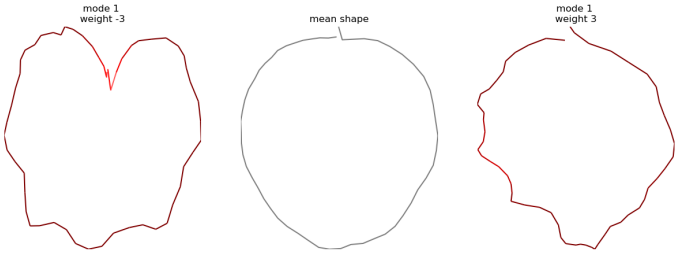


Figure 5: Shape mode 1 (leaf dataset)

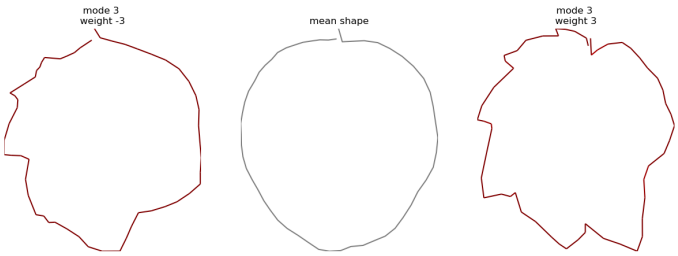


Figure 6: Shape mode 3 (leaf dataset)

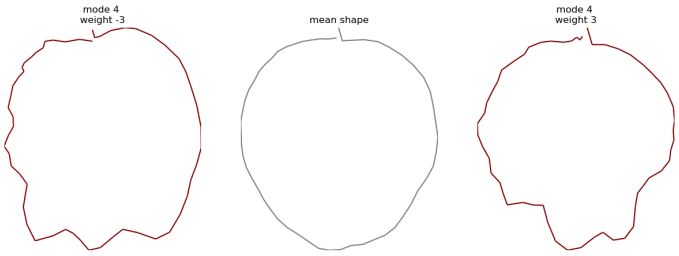


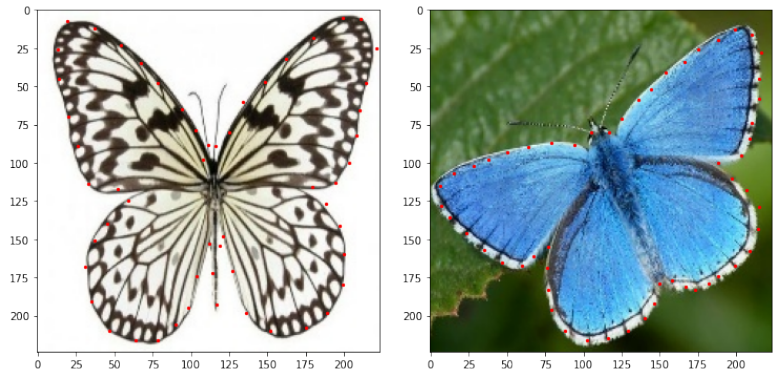
Figure 7: Shape mode 4 (leaf dataset)

(a) Shape 1 (b) Shape 2 (c) Shape 3

Figure 8: Training dataset: Different butterfly shapes

(a) Shape 4 (b) Shape 5 (c) Shape 6

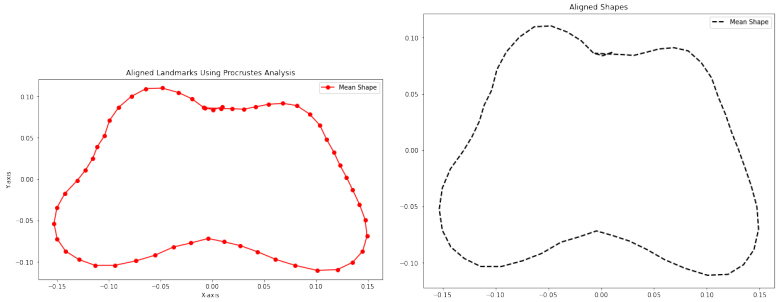
Figure 9: Training dataset: Different butterfly shapes



(a) Example 1 with landmarks of butterfly

(b) Example 2 with landmarks of butterfly

Figure 10: Butterflies with landmarks in a coordinate system



(a) butterfly mean shape

(b) improved butterfly mean shape

Figure 11: Mean shapes of butterfly

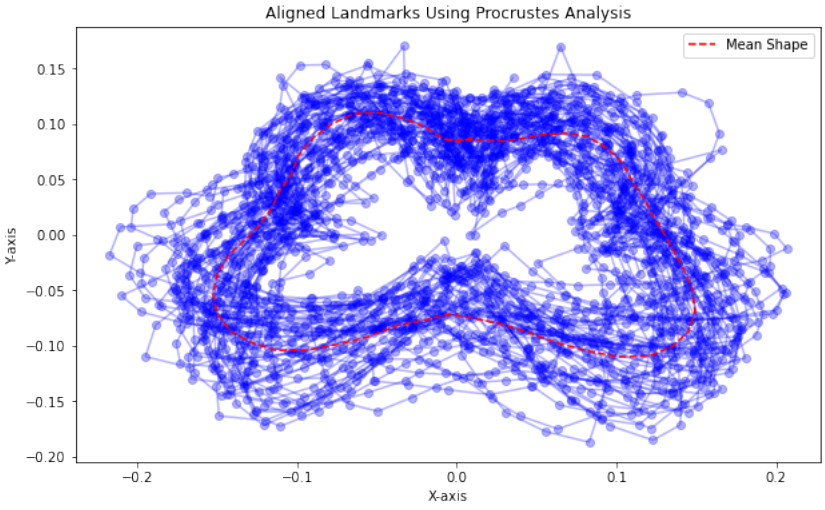


Figure 12: Procrustes alignment of shapes (butterfly dataset)

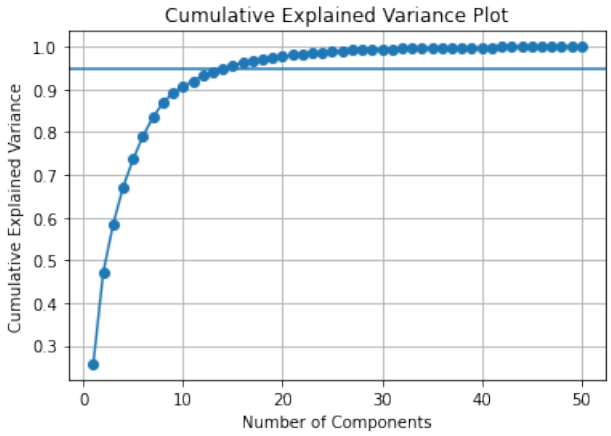
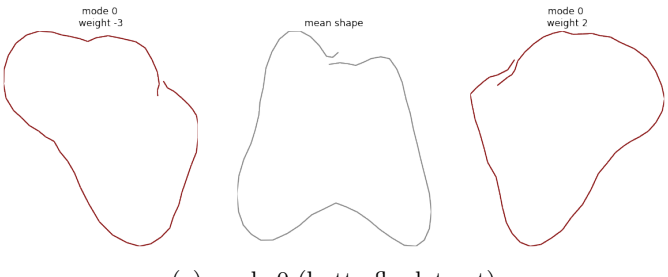
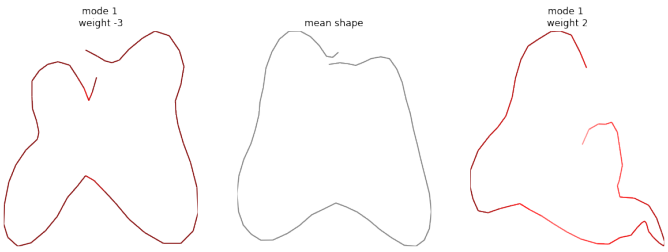


Figure 13: Cumulative Variance plot (butterfly dataset)

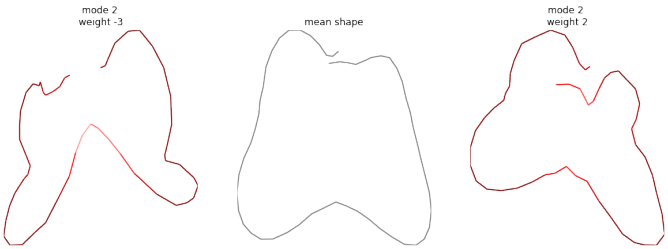


(a) mode 0 (butterfly dataset)

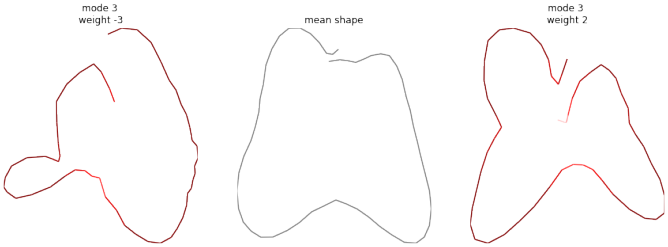


(b) mode 1 (butterfly dataset)

Figure 14: mode 0 and 1 with weight -3 on buterfly dataset

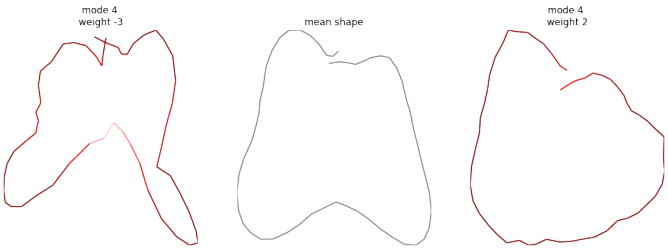


(a) mode 2 (butterfly dataset)

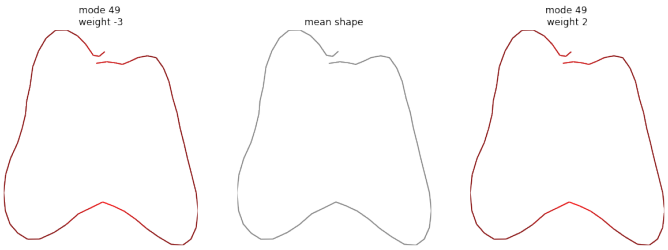


(b) mode 3 (butterfly dataset)

Figure 15: mode 2 and 3 with weight -3 on buterfly dataset



(a) mode 4 (butterfly dataset)



(b) mode 49 (butterfly dataset)

Figure 16: mode 4 and 49 with weight -3 on buterfly dataset

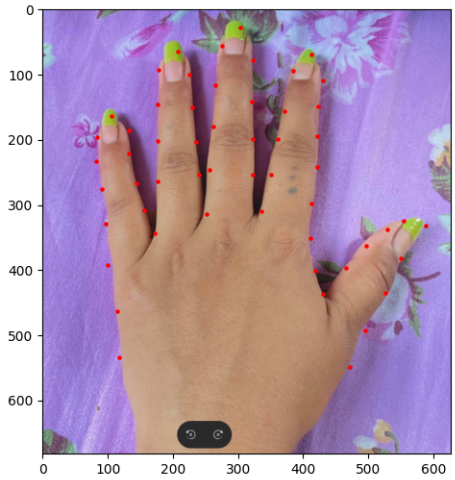
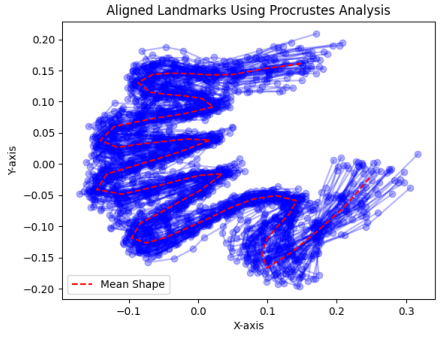
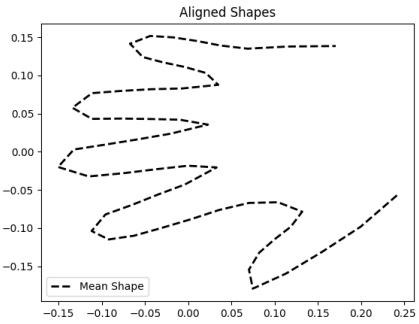


Figure 17: Training hand sample with landmarks



(a) Aligned hand shapes with Procrusts analysis



(b) Mean shape of hand

Figure 18: Procrustes alignment of hands with mean shape

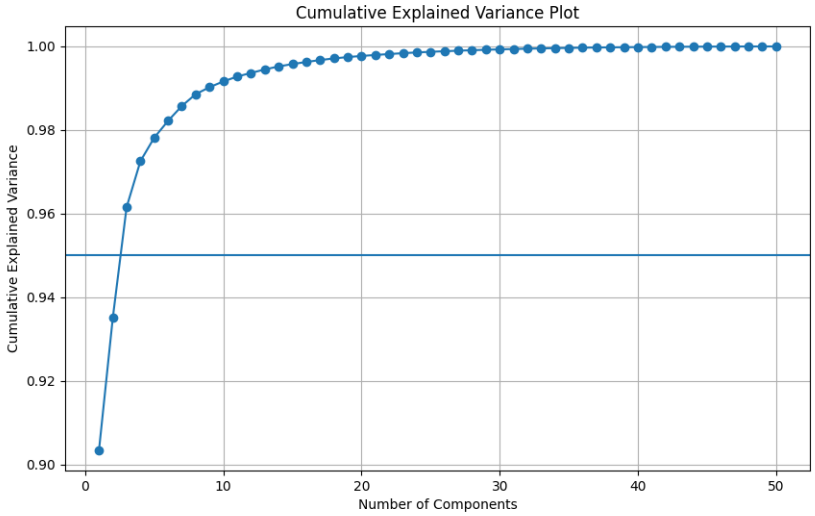
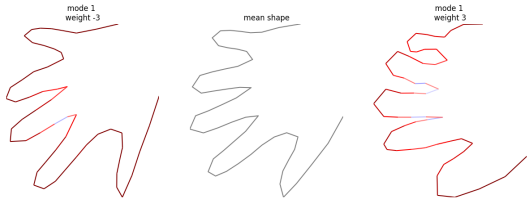
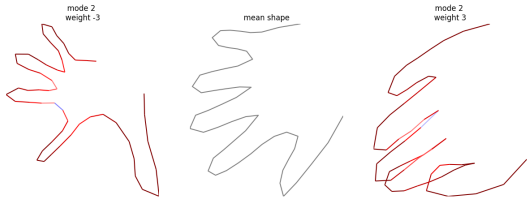


Figure 19: Cumulative variance plot of hand

(a) mode 0



(b) mode 1

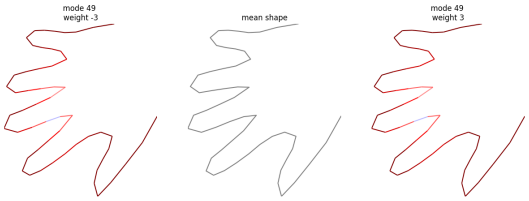


(c) mode 2

Figure 20: Training dataset: Different modes of hand shapes

(a) mode 3 (hand dataset)

(b) mode 4 (hand dataset)



(c) mode 49 (hand dataset)

Figure 21: Training dataset: Different modes of hand shapes

6 Contributions

Sujan Darai: Implemented the codes, Writing data & preprocessings, methods, results and discussion.
Matanat Mammadli: Running analysis on Leaf dataset, Writing data & preprocessing, Results & Discussion
Samra Hamidovic: Running analysis on butterfly dataset, Writing introduction, goal of the project, methods, data & preprocessing, Results & Discussion

7 Appendix

References

1. Tim Cootes. An Introduction to Active Shape Models. 2000.
2. Josh Williams, Ali Ozel, and Uwe Wolfram. pyssam – a Python library for statistical modelling of biomedical shape and appearance, January 2023. arXiv:2301.04416 [cs, eess, q-bio].