Exercise 08 for MA-INF 2201 Computer Vision WS18/19 30.11.2018 Submission on 08.12.2018

- 1. **Procrustres Analysis:** We are given hands_orig_train.txt.new which contains 56 landmark points on hand contours from 39 different subjects. The underlying structure of the given data is further explained in the readme file. The goal of this task is to align the data. The rough outline of the analysis is as follows:
 - Compute the mean shape (μ_s) and fix its variance to unity $(\sigma_s = 1)$.
 - Align each shape to μ_s upto translation, scale and rotation.
 - Compute the RMS error between aligned shapes and the new mean shape.
 - Repeat above steps until $max_iter = 10^3$ or $min_error = 10^{-5}$.

Display the shapes and the mean shape before and after the alignment to verify your results.

Restriction: The entire code for task one should not contain more than two loops. Bonus point for using a single loop only.

Hint: vectorize the data and utilize the broadcasting capabilities of numpy. For the bonus point you might want to read about numpy.einsum

(8 + 1 Points)

2. Statistical Shape Modeling: Build a PCA based statistical shape model \mathcal{M} using the data in $hands_align_train.txt.new$. The data is a set of 56 corresponding landmark points on hand-contours from 39 instances that have already been aligned using Procrustres Analysis. Refer to the readme file for details about data organization. The model \mathcal{M} is to be formulated by defining the subspace model as:

$$w_i \approx \mu + \sum_{k=1}^{K} \phi_k h_{ik}$$

 $\mathcal{M} = \{\mu, \phi_1, \phi_2, \dots, \phi_N\},$

where N is the minimum number of principal components preserving 90% of the energy. Visualize μ and the effect of varying positive and negative weights of each ϕ_k .

Restriction: The entire code for task two (excluding the visualization part) should not contain more than a single loop. Implement PCA by yourself. You are allowed to utilize np.linalq.eiq or np.lingalq.svd for this task.

(8 Points)

3. **Inference:** Express the test shape in $hands_align_test.txt$ in terms of the generated model \mathcal{M} . Display the values of h_{ik} . Also, reconstruct the test shape as \hat{w}_{test} , visualize the original and the reconstructed shapes and calculate the RMS error between both shapes.

Restriction: You are not allowed to use a single loop in this task.

(4 Points)

Do not use any library except these given in the template! Happy Coding :) $\,$