

# Statistical Shape Analysis

## BIOMED

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This TP is about statistical shape analysis. You will have to answer some theoretical questions and code some parts of the algorithms using *Python 3*.

You will use a data-set composed of 400 configurations of 68 anatomical landmarks automatically annotated on frontal face images from both men and women aged between 19 and 40 years old. Faces have variable size, shape and orientation. You will code the Procrustes alignment and Generalized Procrustes Analysis (GPA) algorithm to estimate an average configuration and align all configurations onto it. You will then code Principal Component Analysis (PCA) to analyze the shape variability.

If you use the computers of Télécom, please use Anaconda 3. Just open a terminal and type 'export PATH=/cal/softs/anaconda/anaconda3/bin:\$PATH' and then, on the same terminal, type 'spyder' or 'jupyter-notebook'.

If you use your own computer, I strongly suggest that you use Anaconda. You can create a new environment with the following command: '*conda create -n BIOMED python=3.7 numpy matplotlib spyder notebook*', then '*conda activate BIOMED*' and on the same terminal you should type either 'spyder' or 'jupyter-notebook'.

Download and unzip the folder '*TP.zip*'. You should find a file '*.npz*' with the data and 4 functions:

- *main\_exam* is the main function of the exam
- *Procrustes\_alignement* is the function where you will implement the Procrustes alignment
- *GPA* is the function where you will implement the Generalized Procrustes Analysis
- *pca\_exam* is the function where you will implement the Principal Component Analysis

**You will have to complete these functions, by changing the lines showing *XXXXXXXX*, and answer some questions.**

Do not change the inputs and outputs of the functions.

You can answer in English or French (or Italian if you prefer ...).

**Remember that this TP is evaluated. Please send the code and the answers to [pietro.gori@telecom-paris.fr](mailto:pietro.gori@telecom-paris.fr) before the 16th of October 23:59.**

You should put everything (code and answers) in a jupyter notebook or in a zip file.

## 1 Data

Open *main\_exam*. Set the parameters and the *working\_folder* to the absolute path of the folder where you downloaded the data and the functions. Use the first part of the code to look at the configurations. They have been automatically annotated as shown in Fig. 1.

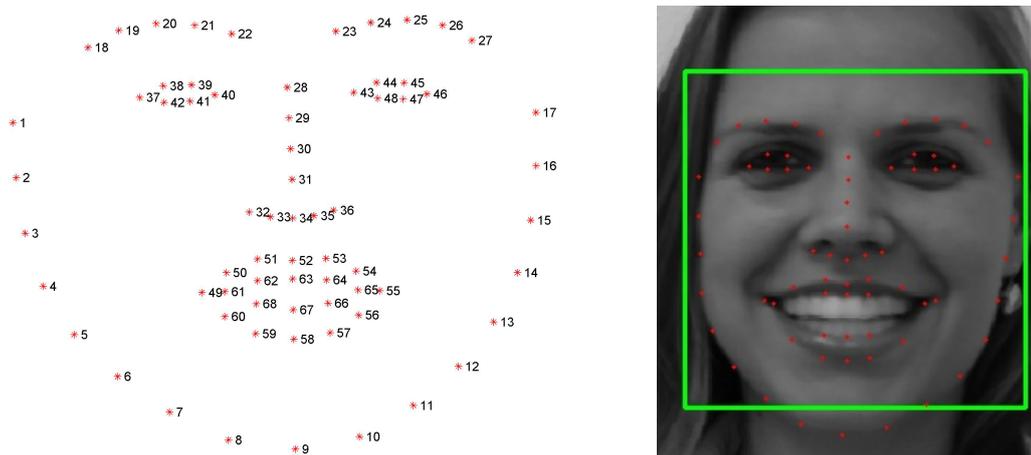


Figure 1: Example of landmark annotation

## 2 Procrustes alignment of two configurations

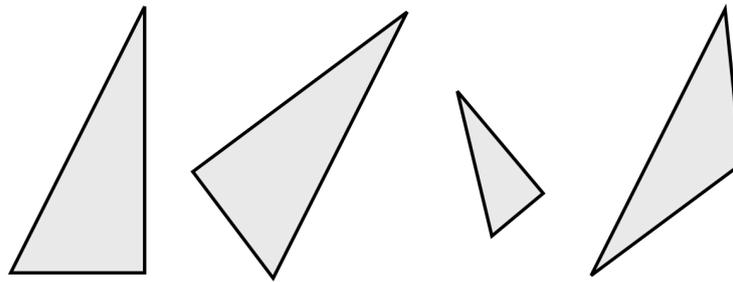
Choose two configurations and implement the Procrustes alignment in the function *Procrustes\_alignment*. This means computing the optimal scaling  $s$ , rotation/reflection  $R$  and translation  $t$ , the aligned source configuration  $Xp$  and the SSR (sum of squared of residuals).

1. What happens if you center the configurations before the alignment ?
2. When do you expect a perfect alignment ?

## 3 Generalized Procrustes Analysis (GPA)

Implement GPA in the function *GPA*. Test it on the data and answer the following questions:

1. Try not to project the data onto the tangent space. Do the results vary ? Do they vary in the same way for all subjects ? Why ? Hint: look at the configuration that varies the most after the projection.
2. Do the following four triangles have the same shape ? Explain why ?



## 4 Shape variations

Complete the function `pca_exam`. Use it to compute the first two modes of variation of the landmarks in `main_exam`.

Questions:

1. How many modes do you need to explain 90% of the variability ?
2. Show the first two modes at  $\pm 3\sqrt{\lambda}$  with the average in the middle. Comment the results. What are the main anatomical variations ?
3. Do they show an anatomically plausible deformation ? If not, which kind of deformation would you use instead ?