BIOMED - TME 2
Landmark based registration and Statistical Shape Analysis

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1 Introduction

The goal of this praticals is to implement algorithms seen in courses for landmarked based registration and statistical shape analysis.

2 Affine Registration Landmarks

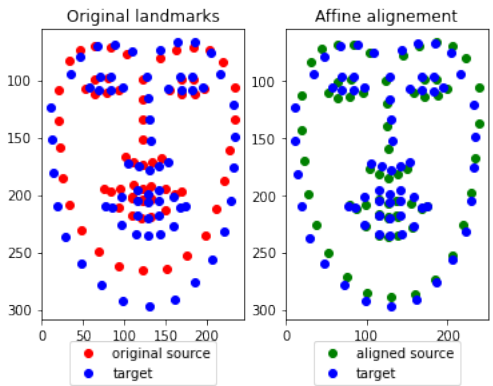

Figure 1: Affine registration landmarks

3 Procrustes Align

Procrustes Align allows to work on the analysis of shapes and therefore removes only certain types of transformations (rigids transformations) : rotation, translation, scale. At the difference of affine registration that take an acount more transformations like shear and reflection.

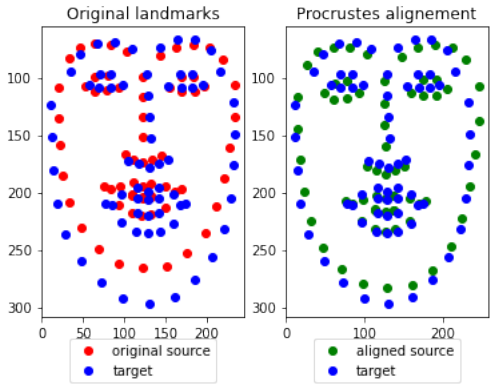

Figure 2: Procrustes Align registration

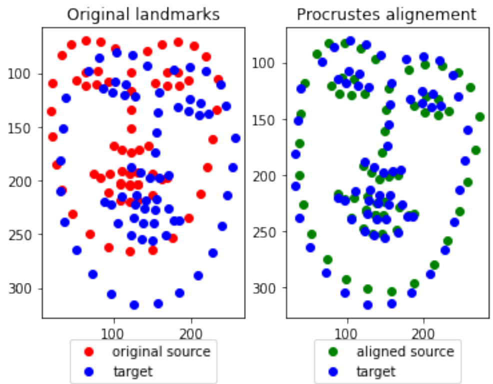

Figure 3: Procrustes Align registration with rotation and translation of landmarks

What happens if you center the configurations before the alignment ?
If we centre our data before an alignment, the optimal translation t* will be 0.

When do you expect a perfect alignment ?
A perfect alignment is expected when R*, s* and t* found and if all faces have the same shape, which is not the case.

4 Affine and/or Procrustes alignement for real images

5 Affine alignement

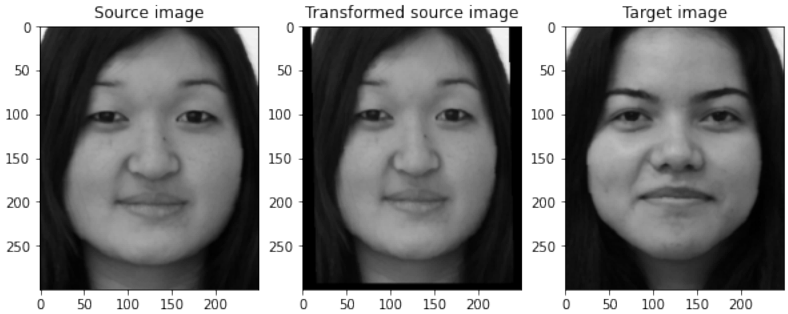

Figure 4: Affine alignement for real images

6 Procrustes alignement

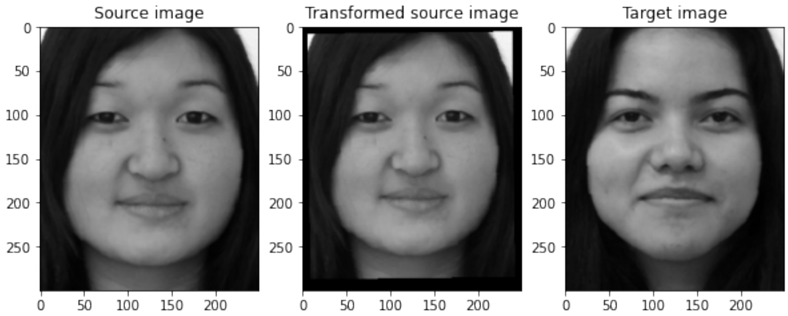

Figure 5: Procrustes alignement for real images

7 Generalized Procrustes Analysis - GPA

7.1 Results with tangent projection

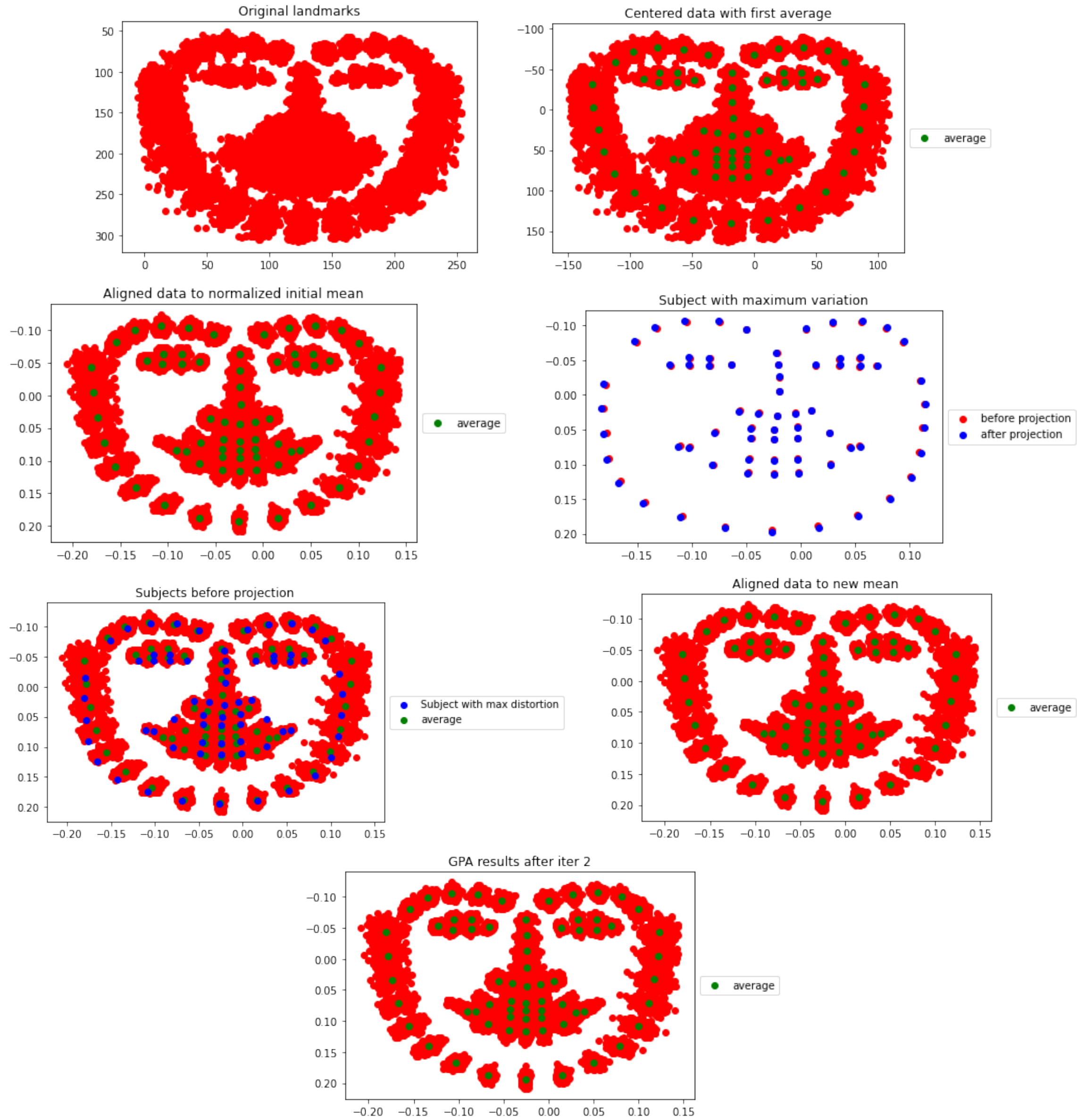

Figure 6: GPA with tangent projection

Try not to project the data onto the tangent space (i.e. tangent=0). Do the results vary ? Why in your opinion ? Hint: Look at the variability of the original data...

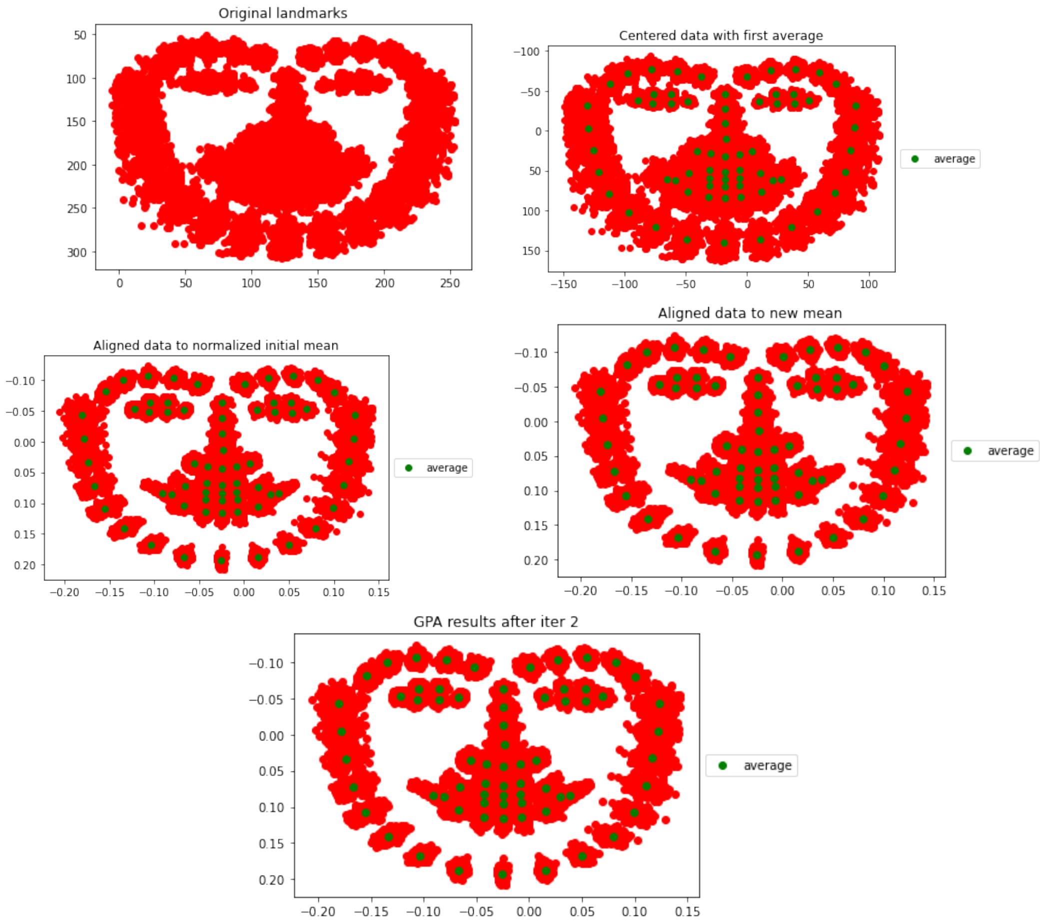

Figure 7: GPA without tangent projection

The results are very similar and there seems to be no difference in this case. In fact we can see from the previous diagram that the result of the subject's projection with maximum variability is actually very low. Indeed the variability of the original data is very low, the average subject is then very close to the others and the projection is therefore relatively low.

Do the following four triangles have the same shape ? Explain why ?
Yes, the triangles have the same shape because if we remove all rotations, scaling and translations we would obtain the same shape with only small possible differences corresponding to residues that correspond to the variability of the shapes of objects.

8 Shape variability

How many modes do you need to explain 90% of the variability ?
A mode corresponds to a model allowing to represent the variations on an axis. This axis corresponds to the principal component containing the maximum variance after projection of the points on this axis (for mode 1). If we assume that data follow a Gaussian distribution, by recovering the data in -3 et +3 σ we can represent the shapes with the opposite variabilities on an axis.

To find the number of modes that explain 90% of the variance, we need to find the number of eigenvectors necessary to obtain at least 90% of the variance.
The explained variance of u_j :

$$\frac{\lambda_j}{\sum_{t=1}^{M} \lambda_t}$$

with M the number of dimension of U
So,

```
var_expl=0
i=0
while var_expl < 0.9:
  var_expl+= D[i] / D.sum()
  i+=1
print(i)
```

We obtain 9 vectors, so 9 modes are necessary to explain 90% of the variability.

Which anatomical variability do the first three modes show ? Was it expected ?

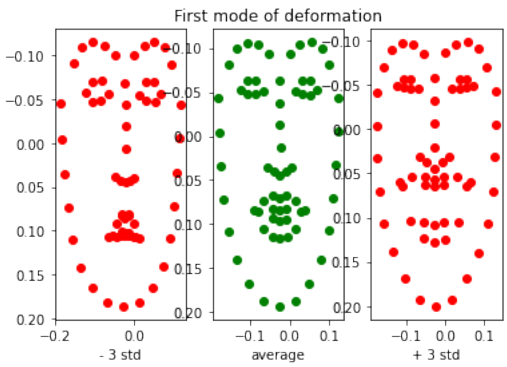

Figure 8: Mode 1

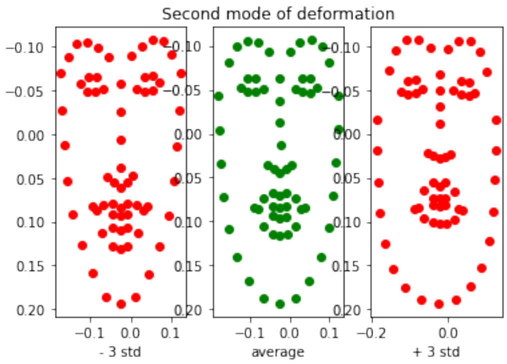

Figure 9: Mode 2

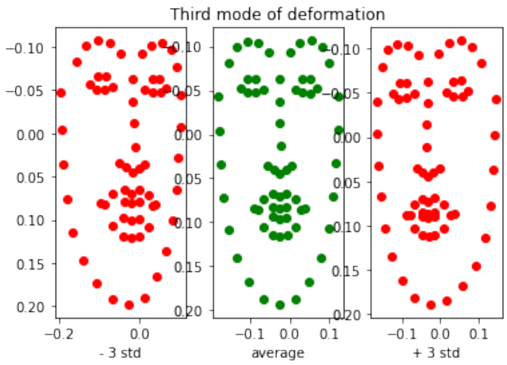

Figure 10: Mode 3

- 1 Mode
  The first mode/axis corresponds to a variability on the smile. On the left you can see a subject who does not smile, who even looks sad, and on the right a subject who smiles a lot.
- 2 Mode
  The second mode/axis corresponds to a variability on the size of the face. On the left you can see a subject with a very thin face and on the right a subject with a much larger face.
- 3 Mode
  The last mode/axis corresponds to a variability in the rotation of the subjects. On the left you can see a subject that is turned to the right and on the right a subject that is turned to the left.

How could you check whether they show an anatomically plausible deformation ?
By comparing to an atlas where all subject have only variations in shape (only residual informations). An atlas gives a common coordinate system for the whole population where anatomical prior information can be mapped. So if our subjects (with only shape variations) differs to much from the atlas then they don't show an anatomically plausible deformation.

Let's say that the anatomical deformation is not anatomically plausible, which kind of deformation would you use instead ? Why ?
We could use diffeomorphic transformation, we can preserve the topology and spatial organization.