

Tina Memo No. 2011-007
Internal Report

Bending Energy, Procrustes Distance ... or Neither?

N.A. Thacker

Last updated
21 / 9 / 2011



ISBE, Medical School,
University of Manchester,
Stopford Building, Oxford Road,
Manchester, M13 9PT, UK.

Bending Energy, Procrustes Distance ... or Neither?

N.A.Thacker 6/5/11

Abstract

This document has been written following a discussion with collaborators regarding appropriate ways to deal with non-homologous landmarks (points defined on curved surfaces) during statistical analysis. The argument constructed seems so simple and compelling that it was decided to keep a written note.

The approach to dealing with semi-landmarks in the morphometric analysis of shape currently seems to be divided between two alternatives, both of which aim to adjust the position of these landmarks by optimising a specific metric, before constructing a linear model of variation about the mean. These metrics are Bending Energy (BE) and Procrustes Distance (PD) respectively. Arguments for and against these approaches are based upon specific examples in biology.

The argument herein is that neither approach can be expected to have general validity, in fact what is needed is a third method which treats the statistics of measurement properly and incorporates the information across the entire dataset, rather than the prior selection of a metric which biases the outcome of analysis in one way or the other.

Introduction

The main issue here is one of self consistency in the scientific analysis of morphometric data when using semi-landmarks. If we have two approaches to data analysis, and they can be shown to lead to different conclusions then one of these approaches must be wrong. This leads to the inevitable debates over which must be the correct choice. If there are examples for and against each choice however, the logical conclusion must be that neither choice is correct as a basis for scientific interpretation.

We can illustrate the problem for the analysis of semi-landmarks with one simple example. Imagine that we are given only two examples of shape (Fig 1), which demonstrate the shifting of a bulge between two well located landmarks (homologous points). We seek to predict the most likely set of continuous variations which will allow us to gradually adapt (or mutate) shape 1 to shape 2. We are free to choose corresponding (semi-landmark) points between locations A and B, according to selected criteria, in order to achieve this aim.

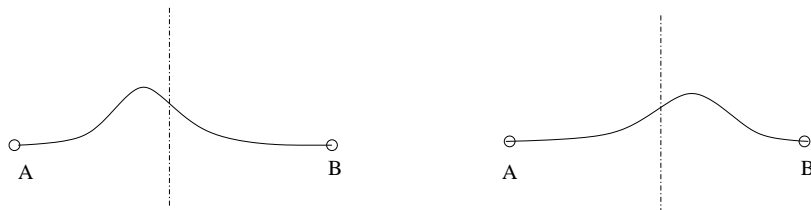


Figure 1: Two example curves fixed in position by well defined landmarks (A, B), illustrating a modified biological feature.

The argument now follows that if we seek to define the required corresponding points on these shapes using either BE or PD then different results will follow. In particular PD will generate a solution where intermediate forms see the gradual reduction in the feature and simultaneously a gradual rise in a second feature at the new position. BE on the other hand will tend to generate results which imply the shift in the position of the feature along the line between A and B. These can be described to first order as eigen vectors of morphometric deformation (Fig 2), with contradictory intermediate predicted forms as shown. We could argue that in **most** biological contexts the interpretation obtained with BE is a better description of biological variation. However the key word here is **most**. We can never exclude the possibility that for any specific system the alternative interpretation is actually a better interpretation of the biology. We thus have a situation where evidence can potentially be found for which both approaches are wrong. Faced with this observation we can only conclude that no amount of argument will prove that either is based upon a defensible principle. Those who had already noticed that Procrustes is not based upon justifiable statistical assumptions, or that it would be strange for a physical concept like bending energy to have any role in biological appearance, can now breath a sigh of relief.

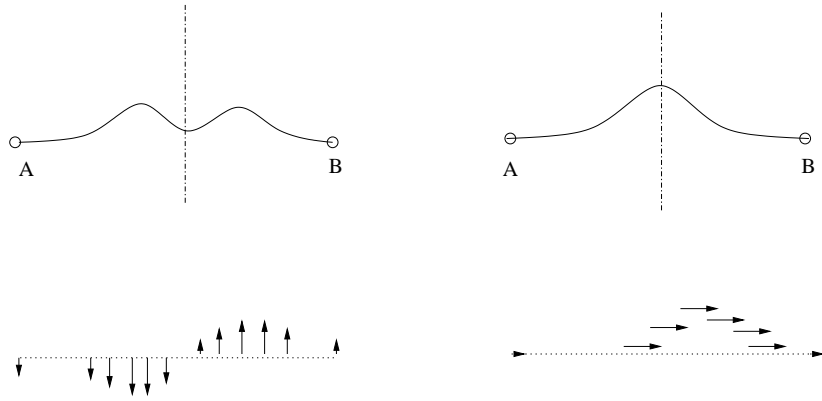


Figure 2: Two possible intermediate forms of shape data and the corresponding linear model vectors. In one case the intermediate deformation can be treated as a shift, in the other the enlargement and shrinking of two raised sections. It is said that a PD analysis will generate the result on the left, and BE that on the right.

The alternative to this is actually quite simple. If our analysis technique were to be provided with the intermediate forms we are trying to predict (Fig 2) then there would be no problem in choosing the appropriate linear model (eigen vectors) and associated correspondence locations. Although the lack of this data might be a key feature of the specific data set, we can always say that if any additional perturbations about the two indicative forms are available, then it should be possible to infer the most appropriate interpolative function by observing the allowed variations (i.e. do the features seem to grow and shrink in place or move sideways in other examples). In order to incorporate this into linear model construction, it requires the assessment of the difference between linear model prediction z' and the aligned data $z = R(w) + t$, i.e. $L_C = (z' - z)C^{-1}(z' - z)$. I would argue that it cannot be achieved using a Procrustes style $L_P = (m - z)I(m - z)$ or any approach which establishes correspondence in a way which is not influenced by the linear model.

Conclusion

When it comes to a choice of approach between minimisation of Procrustes Distance and Bending Energy for the analysis of semi-landmarks I would choose neither. In each case what we have is a method which biases the analysis of data in one way or another, without actually seeking to make use of the information which is logically required to solve the problem. Although we can find examples of biological systems which would support either approach, they cannot be generally correct. Further, it can be argued that the reason that both are wrong is that they seek to position landmarks prior to construction of the linear model, so that this model cannot be influenced by the variations observed in data.

Instead of seeing this as a simple two way choice, I would abandon approaches which require the separate steps of object alignment and linear model construction and seek the most parsimonious model which describes the dataset as a whole. This is something that the computer vision community refers to as a 'group-wise' analysis [1]. In doing so we must replace the standard Procrustes method for alignment (least-squares alignment to a mean) by an approach which instead minimises the difference between the model prediction and data (i.e. a quantitatively valid Likelihood). A simultaneous fit of both landmark positions and transformation parameters, using an appropriate statistical weighting of the evidence, is needed here to obtain the linear model parameters capable of best prediction.

On two final points, the arguments in this document are independent of any position regarding the suitability (or otherwise) of Bending Energy or other metrics as a means to place meaningful landmarks in biological systems. If you accept the logic here then such arguments become an anathema. Secondly, our arguments are entirely consistent with the conventional observation in statistics that when analysing a multi-parameter system it is wrong to expect to be able to estimate a subset of the parameters (in this case those describing transformation) without jointly estimating the rest (here the shape).

References

- [1] R. Davies, C. Twining, C. Taylor, Statistical Models of Shape (Optimisation and Evaluation), Springer, p 75, 2008.