

Review of
“Fourier descriptors and their applications in biology”
edited by Pete E. Lestrel. 1997. Cambridge Univ. Press. xi+466pp.

By

F. James Rohlf
Department of Ecology and Evolution
State University of New York
Stony Brook, NY 11794-5245
rohlf@life.bio.sunysb.edu

This edited volume is concerned with the fitting of Fourier series to outlines of biological structures in order to study their variation in shape. The first five chapters present commonly used Fourier methods or discuss issues concerned with their practical application. The following twelve chapters give applications. There is also an epilogue giving a final overview, an appendix describing the EFF23 software for elliptic Fourier analysis, an extensive glossary, and a good index.

The theory chapters present the standard equations used in Fourier analyses but do not adequately cover some of the larger issues in morphometrics. Since outline contours can often be fit by a variety of functions, why is the Fourier series usually used and does it matter? Any discussion of size and shape should mention the important theorem by Mosimann as well as the special properties of the centroid size measure. Contrasts between outline methods and those based on landmark points are mentioned in several chapters (especially in the chapter by O'Higgins) but the limitations of older methods are emphasized. The point is made by several contributors that simply digitizing locations of landmarks may not capture information of the outline shape of structures. This is an empirical question that can be answered using image unwarping techniques as described by both Mardia and Bookstein (and implemented, for example, in the tpsSuper software). Other chapters argue that Fourier methods are preferable because they do not require knowledge of homologous features (yet many of these same authors use morphological landmarks to define a center for an analysis of radii, a starting point along an outline, or to orient the outlines). However, the issue is not whether it is always possible to locate a sufficient number of landmarks but whether one should ignore information on homology when one has it. Ideally, both types of information should be analyzed jointly using methods such as those recently proposed by Bookstein.

A variety of applications are included. Many of the chapters are concerned with shapes of hominoid skulls or mandibles. The chapter by Uetake gives a novel application to the study of walking patterns in humans. The chapter by Oxnard treats a very different problem – the use of optical and computed Fourier transformations to reveal information on internal structure from radiographs of thin sections of bone. The application chapters are uneven and do not always follow the advice given in the theory chapters. Several authors confuse the relation between the geometrical orthogonality of vectors and the statistical independence of variables.

Chapters 14 to 16 use an approach I find puzzling. First, several points (anatomical landmarks) were defined around a contour. The gaps were then filled in with a number of more or less equally spaced geometrically defined points. An elliptic Fourier series was then fit to these points. The predicted coordinates of selected points along the contour (usually

corresponding to the landmarks) were then used as descriptors of each specimen. The effect of the Fourier analysis was just to smooth the outline. In addition, the distances from each of the selected points to the centroid of each contour were used even though they added no additional information. The resulting data matrix was then subjected to standard multivariate analyses. However, a procedure had to be used to eliminate redundant variables since distances are, of course, a function of the coordinates from which they are computed. There also have to be singularities due to the common centering, orientation, and scaling of each specimen. If the distances were eliminated then the statistical tests for group differences should be quite similar to those one would obtain using standard geometric morphometric methods for the same points (the statistical would be identical if the configuration of points were superimposed using the generalized least-squares fitting method). The results in these chapters are discussed in terms of lists of variables that show significant differences and superimpositions of the entire contours. Advantage is not taken of the ability to directly visualize discriminant function axes as shapes to show group differences.

While the editor does not claim this book to be either an exhaustive survey or the last word on the subject, it is useful and many morphometricians will wish to have a copy on their shelves. The examples, however, must not be taken as recipes to be followed uncritically.