

Book review

R. S. LELE and J. & T. RICHTSMEIER: An invariant approach to statistical analysis of shapes. Chapman and Hall/CRC, Boca Raton, 2001, pp. viii + 308. GBP 46.69, ISBN 0-8493-0319-2.

Shape statistics is an important task in morphometry, which studies shape and form of preferably biological objects. So it is of great interest for biologists and paleontologists, who study forms in order to understand processes that underlie variations in form and shape, such as disease, growth and evolution.

While traditional techniques use shape indices such as ratios of linear distances, modern methods use landmark coordinate data and analyse them as multivariate data.

There are several mathematical approaches to shape statistics, which is rather complicated since shape has to be considered as a statistic that is maximally invariant under Euclidean motions and homothetics. In the last years, a series of books have been published on the topic, namely those by Bookstein (1991), Dryden and Mardia (1998), Small (1996) and Kendall et al. (1999), which are all difficult to read for non-mathematicians. The present book is an interesting attempt to come closer to the needs and taste of biological readers. As most of the other books, it presents many biological examples with real data. Very helpful is also the extensive discussion of the nature of morphometric data. Additionally, "most chapters have two parts. Part 1 is intended to be accessible to biologists", while part 2 "contains fully rigorous mathematical arguments". However, it is a regrettable shortcoming that shape-statistical software is only marginally discussed; only once WinEDMA is mentioned.

The main idea of the authors is Euclidean Distance Matrix Analysis (EDMA). It starts from the location- and orientation-independent matrix of linear inter-landmark distances. The main statistical model is the matrix normal distribution. The book presents methods for estimating the corresponding parameters and also describes how to generate matrix normal random variates. Tests are presented for the comparison of mean shapes of samples of biological objects, where of course within-population variability is not ignored. It is valuable that the book says clearly what is possible in shape statistics and what not, in particular in the context of estimation of mean shapes and variability. Finally, the authors show several times that their approach has better statistical properties than Bookstein's method of shape coordinates and Goodall's Procrustean superposition estimation.

D. Stoyan