Landmarks in Morphometrics, or the Shape and Size of Morphometrics to Come

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BOOK REVIEWS

LANDMARKS IN MORPHOMETRICS, OR THE SHAPE AND SIZE OF MORPHOMETRICS TO COME[1]

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Those of us concerned with phenotypic evolution frequently find it necessary to measure some structure and relate variation in shape or size to growth rate or age, to evolutionary hypotheses related to adaptation and geographic variation, or to questions of systematics. A poll of recent *Evolution* issues finds snout-vent length in lizards, lemma length in *Poa* inflorescences, length of widest peripheral achene in *Heterosperma pinnatum,* skull width in red-winged blackbirds, and femur length in crickets as favored measures of body size or shape. If as is sometimes the case, simple linear measures adequately represent the complex developmental events that frequently underlie the variation associated with our evolutionary hypotheses, then measurement and analysis are relatively trivial tasks. If, however, simple measures are deficient, then we are forced to delve into the complicated and often obtuse field of multivariate morphometric analysis. Such ventures, when undertaken by the uninitiated, can often confuse and sometimes obscure any underlying biological significance to the variation of interest.

Fortunately, J. Rohlf, F. Bookstein, and the morphometrics all-stars have produced what is probably the most comprehensive and diverse assemblage of discussions relating to the measurement and analysis of shape/size data ever published. In fact, there are so many complementary viewpoints contained within this volume that one cannot help but think that the NSF sponsored Michigan Workshop on which it is based must have been a very exciting event. This compilation (affectionately known as the "Blue Book" in certain numerical taxonomy circles) starts with simple overviews of the technicalities of data acquisition and image analysis and processing, continues with a broad survey of various analytical methods that can be used to analyze and graphically present multivariate morphometric data, and ends with discussions of homology in morphometrics and phylogeny.

Topics covered in the Data Acquisition section (three chapters by W. L. Fink, N. MacLeod, and F. J. Rohlf) include data acquisition devices, digital images and automated image analysis systems, adequacy of resolution in digital images, image processing and analysis, image geometry, image functions, filters, template matching, cross correlation, feature extraction, etc. In short, everything you might wish to know about digital image processing on a PC.

The Analytic Methods section starts with a long and thorough discussion of traditional multivariate morphometrics by L. Marcus. This is followed by a chapter entitled "Reification of Classical Multivariate Statistical Analysis in Morphometry," by R. Reyment. Reification means "to regard something abstract as a material thing," which in this case applies to the endowment of a morphological interpretation to multivariate statistical results. Reyment suggests that many morphometric data do not conform with the theoretical requirements of multivariate, normally distributed variables in Cartesian space, and presents several methods to deal with this problem (Reyment also has a new book of his own to be published this summer, which will presumably compete with Bookstein's recent efforts to dominate the theoretical end of the morphometrics field).

The next section of the book is concerned with the morphometrics of organisms with few or no landmarks (I will explain landmarks shortly). Lohmann and Schweitzer discuss eigenshape analysis, Rohlf discusses the art of fitting curves to outlines (including several varieties of Fourier analysis), and Straney presents an interesting discussion of median axis methods in morphometrics.

At the heart of the proceedings is a section entitled: Methods For The Analysis Of Landmark Data. What is a **LANDMARK?** According to Bookstein, landmarks are the points to which epigenetic explanations refer (!?). Alternatively, landmarks are the points at which one's explanations of biological processes are grounded. The "best" landmarks are individually recognizable points on boundaries between regions of distinct histology. The next best landmarks are local features of extended tissue boundaries, such as points of sharpest curvature, or surfaces that might serve as points of application of net biomechanical vectors even when traces of the relevant processes are not visible. The third, and worst kind of landmark, is characterized by its relationship to structures at a distance, such as the endpoints of the greatest diameter of a form. Bookstein's claim (with little humility) is that the use of landmarks will permit us "to transcend the context of classic biometry (Galton, Pearson, Wright) with its arbitrary separation of path coefficient from datum." The key ingredient to Bookstein's approach is the proposition that the proper use of landmarks will link three separate scientific thrusts of morphometrics: a) the geometry of data, b) the mathematics of deformation (i.e. change in shape and size), and c) the explanations of biology. Simply put, Bookstein suggests that landmark

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[1] *Proceedings of the Michigan Morphometrics Workshop.* F. J. Rohlf and F. L. Bookstein, editors. Special Publication Number 2, The University of Michigan Museum of Zoology, Ann Arbor, MI. 1990. viii + 380 pp. $17.50 paper without software, $25.00 paper with software.

formalism can be used to delineate explanations (developmental, evolutionary, or taxonomic), as well as to simply define locations in space.

Next are three chapters intended to provide the theoretical framework for dealing with landmark data. Rohlf discusses rotational fit (procrustes) methods (GRF), which are used to superimpose configurations of landmarks from different specimens so that differences in landmarks can be discovered. Bookstein presents his relative warps (RELWARP) and thin-plate spline methods (TPSPLINE). Chapman presents his conventional procrustes methods (LSTRA and RFTRA). These are followed by several case studies employing a variety of multivariate morphometric methods, and the proceedings end with three chapters which attempt to address the issues confronting systematists employing morphometrics to address phylogenetic questions.

Undoubtedly, the greatest strength of this book results from the inclusion of 15 software packages, which as a group might very well represent the state of the art in morphometrics data analysis and graphical presentation. Most of the software (with the exception of the Finite Scaling Analysis program, a competitor to Bookstein's RELWARP, donated to the proceedings by Jim Cheverud) are teamed with examples in the text, facilitating the use and interpretation of the results produced by a software. However, if you aren't familiar with the jargon, you may want to acquaint yourself with someone who is. Both J. Rolhf and F. Bookstein have included their email addresses for quick, informal contact. Also, many of the authors and participants at both installments of this NSF sponsored workshop are subscribers to the Morphometrics listserver, MORPHMET@CUNYVM on bitnet, established by Les Marcus of the American Museum of Natural History. The intent of this listserver (or bitnet BBS, in a manner of speaking) is to provide an informal meeting ground for morphometricians, systematists and evolutionists to discuss technical and philosophical questions relating to shape and size.

There are two significant shortcomings to the "Blue Book." First, many readers will be dismayed by the complete disregard for Macintosh based software. Similarly, most discussions of imaging hardware are oriented towards the PC platform. Second, although the primary mandate of the NSF sponsored Workshops in Morphometrics was to bring multivariate morphometric methods to the masses, there is a tendency towards spreading the gospel according to Bookstein. The first shortcoming reflects the bias of many practitioners of morphometric analysis, and the cost and availability of appropriate soft- and hardware. The second shortcoming is perhaps excusable given Bookstein's undeniable contributions to morphometric data analysis; the graphical output produced by RELWARP and TPSLINE are very appealing (thanks to F. J. Rohlf and D. Slice), and the associated statistics are extremely informative representations of morphometric variation.

To conclude, although most aspects of the "Blue Book" are broadly based, it is biased (in emphasis and philosophy) towards video image acquisition and processing on an IBM PC, the use of Bookstein's analytic methods for landmark data, and the role of morphometrics in systematic research. These biases, however, do not impair the utility of the book. The "Blue Book" contains a plethora of examples, case studies, and software which provide models for solving many problems in evolutionary biology. These case studies have been subject to intense selection—most were the successful class projects from the first workshop. When the "Blue Book" was used as the text for the second NSF Morphometric Workshop at Stony Brook, in 1990, the class project success rate was very high, vouching for the utility of this morphometrics manual. This affordable proceedings volume, and its accompanying software, could easily become a landmark in morphometrics.

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