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Morphometrics is the statistical study of biological shape and shape change. Its richest data are landmarks, points such as “the bridge of the nose” that have biological names as well as geometric locations. This book is the first systematic survey of morphometric methods for landmark data. The methods presented here combine conventional multivariate statistical analysis with themes from plane and solid geometry and from biomathematics to support biological insights into the features of many different organs and organisms.

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MORPHOMETRIC TOOLS FOR  
LANDMARK DATA

*Morphometric tools  
for landmark data*  
*Geometry and biology*

FRED L. BOOKSTEIN  
*Center for Human Growth and Development  
The University of Michigan*



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## *Preface*

No book about methodology is ever finished, really. But after 10 years of major developments in morphometrics, each published (or unpublished) as a separate article, it was time for a coherent overview. My “introductory lecture,” for which there was no text available, would take four hours at the podium. Students complained that my lecture notes, even when not handwritten, were unreadable. I was beginning to mislay some of the explanations of lovely patterns from the earliest examples, while other early work needed triage: Certain changes of position were so blatant as to be embarrassing. And I had grown weary of the endless cross-referencing between papers: Bookstein (1989*q*) citing (1986*x*), (1987*w*, *y*, *z*), and (1990*v*, *k*, and forthcoming) – many of which cited each other incestuously as well.

Yes, it was time for a 10-year retrospective, if only to simplify the indexing. Yet the principal stimulus for the writing of this book was none of these general intellectual aches and urges, but instead a specific crisis. In 1987 the National Science Foundation instituted a series of workshops on morphometrics for systematic and evolutionary biology. The first took place in Ann Arbor, Michigan, in May 1988. Each instructor was to distribute a text in advance of his lecture. (Most of these are collected in Rohlf and Bookstein, eds., 1993.) As they arrived at Michigan through the spring of 1988, these notes ranged from 15 to 40 pages in length; but mine ran to 224. It was thus relabeled the “zeroth edition” of the manuscript for this book. Only a partial draft, it covered Chapters 4 through 7 of this text, without *any* of the introductory material – without even a bibliography. “That’s all right,” I quipped, “most of the references are to my own work anyway.”

In other words, by 1988 there existed a synthesis of the landmark-based morphometric methods, but no associated pedagogy. For this teaching task there is simply no substitute for a bound volume. I have endlessly shuffled too many slides into the 20- to 40-minute versions of the obviously necessary “four-hour introduction” without ever quite managing to set these techniques in

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an accessible context. My apologies to any of my listeners who were baffled by my experimental lectures at AAAS, AAPA, AIBS, ASA, ENAR, ICSEB, IMS, IPMI, or ISM meetings; apparently the expositions were uniformly more obscure than these initials. This experimentation might have continued indefinitely except that (1) another NSF workshop was approaching (Stony Brook, New York, June 1990), for which I needed another text to distribute, this time one that would be self-contained, and (2) Cambridge University Press had accepted this volume for publication, “pending satisfactory completion.”

Hence the edition you hold in your hand. The newest material is found in the simpler Chapters 1 through 3, while the more technical expositions in Chapters 4 through 7 date from up to eight years ago. Historically, the statistics of simple tensors were developed first, in 1982; then the shape coordinates that linearize them (1983); then the critique of distance-based analyses (1984); then the serious pursuit of feature spaces, both the uniform and the nonuniform (1985); then underlayment of the statistical and geometrical points of view by the spectrum of bending energy of the thin-plate spline model (1987); finally, only yesterday, the language of Chapters 1 through 3 and 8, which speak directly to this unification.

The publication of this book is intended to declare the existence of a new specialty: *morphometrics*, the biometry of shape (for a more focused definition, see the beginning of Chapter 1). Morphometrics as a discipline should be of interest to anyone in statistics, image analysis, or quantitative biology whose work involves the contemplation of living or fossil form, its causes or its effects. Those are also the fields from which I expect readers to come: professionals and preprofessionals in any of these areas whose problems bear them broadly across the boundary of their own discipline toward one of the other two. Biologists interested in the processes regulating shape over ontogeny or phylogeny need tools for coherent quantitative reports that do not waste data. Computer scientists pursuing features of solid medical images ought to use quantitative form comparisons to guide their parameterizations. Statisticians who have always suspected there might be more structure to some sets of variables than their names and covariances will be challenged by a style of data for which that suspicion is justified. Surgeons, cardiologists, and neurologists need to test and understand covariates of the disproportions they see or correct. All these research purposes, and many, many others, can benefit from the tools taught here.

The new discipline thus deserves a place in several graduate curricula. In biology, it should be required of the student proposing a dissertation in any aspect of morphology. In statistics, it should be offered, like psychometrics, econometrics, or log-linear modeling of tables, as an elective in applied multivariate analysis. In image processing, it should be strongly urged upon anyone

proposing to specialize in medical imaging. In paleobiology, it should be required, period. This book is intended as a main text and reference for such courses in morphometrics and as a supplemental text for lower-level surveys of biomathematics, biometric statistics, quantitative paleobiology, and the like. The examples are not restricted to any single field, but draw widely from medical studies of normal growth and of congenital syndromes and from comparative and evolutionary studies.

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To the breadth of coverage intrinsic to the morphometric theme corresponds a commensurate breadth of background. Mastering the material in this book requires that the reader have at least moderate expertise in three different subject areas – geometry, statistics, and mathematical biology. A short course in morphometrics, for which some of this background might be waived, would include Chapters 1 through 3 (except for Section 1.3) and about half the rest of the book: Sections 4.1–4.3, 5.1, 5.3–5.5, 6.1–6.5, 7.2–7.3, 7.5.1, and 7.6. For the remainder of the text, the background needed is perhaps the equivalent of a two-semester upper-level undergraduate sequence in multivariate statistics or biomathematics, or the equivalent of a one-semester course in advanced analytic geometry. Of these, only the first, the statistics sequence, is at all common in the American college curriculum. Selections from the reading lists in Section 2.5 can substitute for the syllabus of any of these prerequisites that the aspiring morphometrician has unaccountably missed, but in that case two or three of the books must be *read*, not browsed, not skimmed.

Beyond this background, the way to learn morphometrics is to think closely and skeptically through dozens of applications, as varied as one can find. Whether beginner or advanced, the student of morphometrics should be careful never to specialize in a particular organism or human organ or particular form of question, but should instead master a large number of specific techniques, such as those emphasized in this book. New morphometric methods introduced for particular applications, like the landmark methods that arose in roentgenographic cephalometrics, usually apply broadly to make sense of data in a variety of biological contexts. It is a good tactic to tailor a method for a particular problem, then see how far afield it can be pushed. In the effort to understand which attempts at generalization succeed and which fail, one may arrive at a clear statement of the tacit assumptions that actually bore responsibility for success in the original context. Exceptions to this metastatic pattern – D’Arcy Thompson’s notion of transformation grids, or Blum’s invention of the medial axis, each proposed as a general method right from the start – have hitherto not found many specific applications to problems of measurement. Rather, methods carefully developed for particular contexts (growth gradients, for example, or the rubber-sheet techniques for recognizing chromosomes) have proved quite protean. Any model that leads to verifiably meaningful biological explana-

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tions in any morphometric application should be tentatively considered for every morphometric application, no matter what the literature of the subject finds respectable; but a model must work first in *some* application, must improve on the routine use of the methods currently “standard” there, before it is worth considering anywhere else.

Many colleagues inadvertently helped me write this book. Those who collaborated on the projects or expositions here include Bernard Crespi, Court Cutting, Barry Grayson, Lewis Holmes, Robert Moyers, Richard Reyment, F. James Rohlf, Paul Sampson, and Elena Tabachnick. Among the many others who asked good questions or supplied good answers are Miriam Zelditch, Richard Skalak, David Ragozin, Stephen Pizer, James Mosimann, Kanti Mardia, Pat Lohmann, William D. K. Green, Colin Goodall, and the late Harry Blum. It is time for me to thank Stephen Jay Gould and Joel Cohen for suggesting, way back in 1973, that it might be possible to be an academic morphometrician. (That phrasing is anachronistic, of course – the vocation of “morphometrician” had not yet been invented.) Two editors – James Tanner of *Annals of Human Biology* and the late Morris deGroot of *Statistical Science* – invited me to publish large chunks of not terribly well digested morphometrics when it was still quite unprecedented to do so. Elena Tabachnick made hundreds of suggestions to improve the comprehensibility of the manuscript. When figures show evidence of balance, the hand is usually Teryl Lynn’s, my illustrator since my dissertation days.

Besides the NSF workshops, two other small groups have borne the brunt of my early attempts at explaining the more technical parts of this material: the Ninth, Tenth, and Eleventh International Conferences on Information Processing in Medical Imaging (Bethesda, Maryland, 1985; Zeist, The Netherlands, 1987; Berkeley, California, 1989), and the two Wilks Workshops on Shape Theory organized by Colin Goodall at Princeton University in 1987 and again in 1990. Thanks to all of you for your patience during the question periods dealing with the thin-plate splines, and special thanks to Goodall and to Kanti Mardia for answering some of the questions, especially those dealing with the ties to Kendall’s shape space, more adeptly than I could. I am grateful to Mardia, also, for so elegantly and expeditiously working out the exact distribution of the complex normal model, Section 5.6, in collaboration with his student Ian Dryden, and yet graciously naming the coordinates after me anyway.

Principal support for the development of the methods reported here has come from NIH grants DE-05410 and GM-37251 to the University of Michigan, each for the explicit purpose of such development. Other support has derived from NIH grants DE-03610 and NS-26529 to the University of Michigan and DE-03568 to New York University and from NIAAA grant AA-01455 to the University of Washington. The two morphometric workshops at



which earlier “editions” of this text were first distributed were due entirely to the enthusiasm of David Schindel of the Systematic Biology Program at the National Science Foundation. Jennifer Kitchell and Bill Fink urged me to prepare that monstrous hand-out for the 1988 meeting, and F. James Rohlf was similarly tolerant of an inordinate Xeroxing bill in 1990. My own computer programs run mainly on MTS, the Michigan mainframe. Rohlf has devoted too much time to packaging the spline routines for easy access by the ordinarily perseverant quantitative biologist (see the program TPSPLINE in the disk pack of Rohlf and Bookstein, 1990, and also Rohlf’s 1991 program TPSRW); Paul Sampson, the same for the statistician; and Leslie Marcus and Richard Reyment have been spreading the word that there is something in landmark-based morphometrics worth the frustrations of learning it early in its evolution. I thank all of you for your trust that someday these ideas would be not only demonstrated but also explained.

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*Ann Arbor, Michigan  
June 10, 1991*