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coordinate data and standard multivariate statistical analyses which are available in most major statistical packages. At the University of Washington we have found it especially convenient to carry out our analyses using an interactive statistical programming language such as "S" (Becker and Chambers, 1984), or "ISP" (Dunlap, 1985), both of which have facilities for user-defined special purpose macros. In this interactive macro environment we easily extract shape coordinates (using the simple expressions of complex arithmetic given by Bookstein) for arbitrary sets of landmarks, compute the usual statistical analyses, and generate various graphical displays of the results.

One of Bookstein's most important contributions to the field of morphometrics was the method of biorthogonal grids which he introduced in 1978. We are finding biorthogonal grids very useful for graphically synthesizing the findings from the discrete analyses of multiple triangles (as Bookstein describes in Section 6). However, to our knowledge no one but Bookstein himself at the University of Michigan has ever had software to generate a biorthogonal grid. This is probably due to the complexity of the algorithms originally described. We have recently implemented (with Bookstein), in the "S" environment, new and simpler algorithms for the computation of biorthogonal grids. The computed homology which maps and smoothly interpolates one set of landmarks onto another is derived from easily programmed "thinplate" spline interpolators (Meinguet, 1979). This algorithm does not constrain the mapping to be linear on a specified boundary as does Bookstein's

original algorithm. Our algorithm for drawing out the biorthogonal grids, the integral curves of the symmetric tensor field (Figure 15b), is based on a widely available differential equation solver. A report describing this new biorthogonal grid software and applications is in preparation.

ACKNOWLEDGMENTS

I would like to thank Dr. Sterling Clarren and Deborah Donnell, colleagues on the Pregnancy and Health Study at the University of Washington, for their contributions to the analysis cited above. This research was supported in part by Grant AA01455-10 from the National Institute of Alcoholism and Alcohol Abuse.

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Comment

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Fred Bookstein's energy, enthusiasm, leadership, and innovative thinking about morphometrics are highly valued, greatly appreciated, and a spur to further work. The present paper is a major advance in multivariate morphometrics, and contains some of the few substantive results available. The linear spaces for size and shape statistics are derived, however, at the cost of restrictive assumptions, including a simple error structure (the null model), almost uniform deformation (negligible curvature), and small errors

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(linearized, normally distributed, statistics). This discussion looks at a broader approach, and, while lacking the detail and rigor of Bookstein's paper, suggests that statistical machinery, centered on function estimation, is mostly available.

The author has convincingly demonstrated how to move back and forth between deformations and multivariate statistics. These statistics are based directly on linear combinations of landmarks. I prefer to emphasize a two-stage procedure, in which estimation of the biological process, namely the deformation (strain) tensor field varying in space and time, is primary. Only at the second stage statistics that summarize (are functionals of) the deformation tensor field are used in multivariate comparisons. As Bookstein