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Biometrics, biomathematics and the morphometric synthesis. (English) Zbl 0855.92002
Bull. Math. Biol. 58, No. 2, 313-365 (1996).

Summary: At the core of contemporary morphometrics – the quantitative study of biological shape variation – is a synthesis of two originally divergent methodological styles. One contributory tradition is the multivariate analysis of covariance matrices originally developed as biometrics and now dominant across a broad expanse of applied statistics. This approach, couched solely in the linear geometry of covariance structures, ignores biomathematical aspects of the original measurements. The other tributary emphasizes the direct visualization of changes in biological form. However, making objective the biological meaning of the features seen in those diagrams was always problematical; also, the representation of variation, as distinct from pairwise difference, proved infeasible.

To combine these two variants of biomathematical modeling into a valid praxis for quantitative studies of biological shape was a goal earnestly sought through most of this century. That goal was finally achieved in the 1980s when techniques from mathematical statistics, multivariate biometrics, non-Euclidean geometry and computer graphics were combined in a coherent new system of tools for the complete regionalized quantitative analysis of landmark points together with the biomedical images in which they are seen.

In this morphometric synthesis, correspondence of landmarks (biologically labeled geometric points, like “bridge of the nose”) across specimens is taken as a biomathematical primitive. The shapes of configurations of landmarks are defined as equivalence classes with respect to the Euclidean similarity group and then represented as single points in *D. G. Kendall’s* shape space [*Bull. Lond. Math. Soc.* 16, 81-121 (1984; [Zbl 0579.62100](#))], a Riemannian manifold with Procrustes distance as metric. All conventional multivariate strategies carry over to the study of shape variation and covariation when shapes are interpreted in the tangent space to the shape manifold at an average shape. For biomathematical interpretation of such analyses, one needs a basis for the tangent space compatible with the reality of local biotheoretical processes and explanations at many different geometric scales, and one needs graphics for visualizing average shape differences and other statistical contrasts there. Both of these needs are managed by the thin-plate spline, a deformation function that has an unusually helpful linear algebra. The spline also links the biometrics of landmarks to deformation analysis of the images from which the landmarks originally arose.

This article reviews the history and principal tools of this synthesis in their biomathematical and biometrical context and demonstrates their usefulness in a study of focal neuroanatomical anomalies in schizophrenia.

MSC:

[92B05](#) General biology and biomathematics
[62P10](#) Applications of statistics to biology and medical sciences; meta analysis

Cited in 10 Documents

Keywords:

[morphometrics](#); [biological shape variation](#); [multivariate analysis of covariance matrices](#); [landmarks](#); [shape space](#); [thin-plate spline](#); [focal neuroanatomical anomalies](#); [schizophrenia](#)

Software:

[Edgewarp](#)

Full Text: [DOI](#)

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