Morphometrics with R
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Monografía

Quantifying shape and size variation is essential in evolutionary biology and in many other disciplines. Since the "morphometric revolution of the 90s," an increasing number of publications in applied and theoretical morphometrics emerged in the new discipline of statistical shape analysis. The R language and environment offers a single platform to perform a multitude of analyses from the acquisition of data to the production of static and interactive graphs. This offers an ideal environment to analyze shape variation and shape change. This open-source language is accessible for novices and for experienced users. Adopting R gives the user and developer several advantages for performing morphometrics: evolvability, adaptability, interactivity, a single and comprehensive platform, possibility of interfacing with other languages and software, custom analyses, and graphs. The book explains how to use R for morphometrics and provides a series of examples of codes and displays covering approaches ranging from traditional morphometrics to modern statistical shape analysis such as the analysis of landmark data, Thin Plate Splines, and Fourier analysis of outlines. The book fills two gaps: The gap between theoreticians and students by providing worked examples from the acquisition of data to analyses and hypothesis testing. The gap between user and developers by providing and explaining codes for performing all the steps necessary for morphometrics rather than providing a manual for a given software or package. Students and scientists interested in shape analysis can use the book as a reference for performing applied morphometrics, while prospective researchers will learn how to implement algorithms or interfacing R for new methods. In addition, adopting the "R" philosophy will enhance exchanges within and outside the morphometrics community. Julien Claude is evolutionary biologist and palaeontologist at the University of Montpellier 2 where he got his Ph.D. in 2003. He works on biodiversity and phenotypic evolution of a variety of organisms, especially vertebrates. He teaches evolutionary biology and biostatistics to undergraduate and graduate students and has developed several functions in R for the package APE

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Contenido: Contributors -- Abbreviations and notations -- Introduction -- Acquiring and manipulating morphometric data -- Traditional statistics for morphometrics -- Modern morphometrics based on configurations of landmarks -- Statistical analysis of shape using modern morphometrics -- Going further with R -- Appendix

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