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Systematists, comparative biologists, taxonomists and evolutionary biologists all concern themselves with the evolutionary relationships between animals and plants. Homology is the principle underlying these disciplines. When looking at groups of organisms, shared positional similarities (homologues) provide the raw data from which hypotheses of common ancestry (homology) may be suggested. In order to explore the relationship between homologues (characters) and particular hypotheses of common ancestry, complex matrices are devised, where homologues are coded, allowing theories of homology to be developed and tested. Practically nothing has been written about this matrix-building process and yet it is of fundamental importance to our understanding of diversity and evolutionary history. This book fills the gap by discussing the different ways observations are coded and the consequences for the resulting hypotheses. It takes a pragmatic approach and uses case studies as well as theoretical examples to offer practical solutions.

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