

Beyond Phylogeny Reconstruction—Tree-Based Analyses in Paleontology

FOREWORD

The reconstruction of phylogenies using cladistic methods is a powerful and well-established tool for evolutionary biologists and paleobiologists. Indeed, the construction of rigorous phylogenetic hypotheses has become widely accepted as an essential first step in the analysis of historical patterns for both extant and extinct organisms. In the past few years, there has arisen a healthy and constructive debate as to the exact methods that will lead to the most accurate tree (for example whether statistical inference or stratigraphic information has any part to play in phylogenetic reconstruction). Although important, this debate has tended to focus on the problems of tree construction and divert attention away from the applications of tree-based research. The construction of a phylogeny is, after all, only a first step, and phylogenetic trees provide the starting point from which to address a wide range of interesting biological and geological topics.

The following seven papers, guest-edited by the two of us, represent a compilation of contributions originating from a topical session (sponsored by the Paleontological Society) entitled "Beyond Phylogeny Reconstruction: Tree-based Analyses in Paleontology" that we organized for the Geological Society of America national meeting (Denver) in 1999. This session and the resultant papers in this volume emphasize just some of the diverse questions that can be addressed once a phylogenetic working hypothesis is established, and present studies that utilize tree-based approaches to paleobiological questions. This is by no means exhaustive and there are obvious omissions, such as the use of tree-based methods for interpreting biogeographic patterns; nevertheless, the contributions that follow show phylogenetic trees being used in con-

structive and novel ways across much of contemporary paleobiological research.

Because the potential application of phylogenetic trees beyond just discovering taxic sister-groups still remains underexploited, it was and is our hope that this collection of papers will provide stimulus to those who have not appreciated the wide application of tree-based approaches, and to encourage workers in groups traditionally thought of as "difficult" for the cladistic approach (e.g., protists, gastropods) to consider using phylogenetic methods. Through these efforts, we ultimately hope to help bridge the gap between biology and paleontology by showing that many key biological questions can be addressed with the help of fossil data.

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