

The growing success of molecular methods has challenged traditional views of animal evolution and a large number of alternative hypotheses are hotly debated today. For the deep metazoan phylogeny project, data sets of hitherto unmatched quality and quantity were compiled and analysed with innovative bioinformatics tools. The book begins at the base of the tree of life to discuss the origin of animals and early branches of the phylogenetic tree. The following chapters present special data sets and hypotheses gained from genomes and from morphology. The final section is dedicated to theoretical aspects of data analysis and new bioinformatics tools. Sources of error that cause contradictions between published analyses are discussed and the reader is encouraged to more critical thinking. This work provides the most comprehensive overview available of the state of the art in this exciting field of evolutionary research.

- Combination of theoretical molecular systematics and innovative bioinformatics tools applied to deep phylogenetic problems
- Collaboration of over 30 research groups with expertise in a variety of taxa and methods
- Extensive treatment of molecular data and modern morphological information



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