BOOK REVIEW

L.S. Kubato, L.L. Knowles (Eds): Species tree inference: a guide to methods and applications

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This book explains how to estimate and interpret species trees, but does not tell the reader why and when it is advisable to use such methods. It is immediately apparent that this volume is aimed at advanced users who are already familiar with the theory of species trees, their applications, and associated challenges. Readers should be aware that this is not a general introduction, but rather a technical, in-depth resource for practitioners. The technical aspects are thoroughly elaborated, from general considerations on the species tree estimation methods to be used to step-by-step instructions. While the volume does not provide an introduction to the theory of species trees, it offers a wide-ranging treatment in terms of methodology. In that regard, this book is likely the most comprehensive resource released to this date and will be of great value to practitioners. What is unfortunate is the considerable degree of redundancy among chapters. Coordination between the authors of individual chapters should have been emphasized more. The overall scope in terms of research questions has certain limitations, as all the applications of species trees presented pertain to either systematics or bona fide evolutionary biology. It

is a missed opportunity not to dedicate some space to the implications of species trees for disciplines beyond those immediate applications, such as macroevolution and macroecology, where the use of such approaches is still uncommon. Another notable limitation in scope that is not apparent from the title or the introductory section is that this volume focuses on the use of genomic data. Some of the analytical options presented will not be applicable to groups of organisms for which genomic data are still lacking. However, a considerable number of the analytical pipelines presented can be applied either directly or with minor changes to the analysis of datasets covering just a few genes. Some of the figures presented are too small to read comfortably and some could have been better adapted to the greyscale print. Overall, I can strongly recommend this book, provided you belong to the target audience of advanced users, and especially if you work with genomic data.

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