

Preface

The idea for *The Phylogenetic Handbook* was conceived during an early edition of the Workshop on Virus Evolution and Molecular Epidemiology. The rationale was simple: to collect the information being taught in the workshop and turn it into a comprehensive, yet simply written textbook with a strong practical component. Marco and Annemie took up this challenge, and, with the help of many experts in the field, successfully produced the First Edition in 2003. The resulting text was an excellent primer for anyone taking their first computational steps into evolutionary biology, and, on a personal note, inspired me to try out many of the techniques introduced by the book in my own research. It was therefore a great pleasure to join in the collaboration for the Second Edition of *The Phylogenetic Handbook*.

Computational molecular biology is a fast-evolving field in which new techniques are constantly emerging. A book with a strong focus on the software side of phylogenetics will therefore rapidly grow a need for updating. In this Second Edition, we hope to have satisfied this need to a large extent. We also took the opportunity to provide a structure that groups different types of sequence analyses according to the evolutionary hypothesis they focus on. Evolutionary biology has matured into a fully quantitative discipline, with phylogenies themselves having evolved from classification tools to central models in quantifying underlying evolutionary and population genetic processes. Inspired by this, the Second Edition provides a broader coverage of techniques for testing models and trees, detecting recombination, the analysis of selective pressure and genealogy-based population genetics. Changing the subtitle to *A Practical Approach to Phylogenetic Inference and Hypothesis Testing* emphasizes this shift in focus. Thanks to novel contributions, we also hope to have addressed the need for a Bayesian treatment of phylogenetic inference, which started to gain a great deal of popularity at the time the content for the First Edition was already fixed.

Following the philosophy of the First Edition, the book includes many step-by-step software tutorials using example data sets. We have not used the same data sets throughout the complete Second Edition; not only is it difficult to find data sets that

consistently meet the assumptions or reveal interesting aspects of all the methods described, but we also feel that being confronted with different data with their own characteristics adds educational value. These data sets can be retrieved from www.thephylogenetichandbook.org, where other useful links listed in the book can also be found. Furthermore, a glossary has been compiled with important terms that are indicated in italics and boldface throughout the book.

We are very grateful to the researchers who took the time to contribute to this edition, either by updating a chapter or writing a novel contribution. I hope that my persistent pestering has not affected any of these friendships. We would like to thank Eddie Holmes in particular for writing the Foreword to the book. It has been a pleasure to work with Katrina Halliday and Alison Evans of Cambridge University Press. We also wish to thank those who supported our research and the work on this book: the Flemish "Fonds voor Wetenschappelijk Onderzoek", EMBO and Marie Curie funding. Finally, we would like to express our thanks to colleagues, family and friends onto whom we undoubtedly projected some of the pressure in completing this book.

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