
PREFACE

In 2004 we compiled the *Dictionary of Bioinformatics and Computational Biology* to 'provide clear definitions of the fundamental concepts of bioinformatics and computational biology'. We wrote then, 'The entries were written and edited to enhance the book's utility for newcomers to the field, particularly undergraduate and postgraduate students. Those already working in the field should also find it handy as a source for quick introductions to topics with which they are not too familiar' and this applies equally to this new edition, the *Concise Encyclopaedia of Bioinformatics and Computational Biology*, which is a follow-up edition to the Dictionary.

Over the last decade bioinformatics has undergone largely evolutionary change. This is reflected in the *Concise Encyclopaedia* by turnover in the description of popular software programs, many of which have changed although the most popular remain. Probably the area of most revolutionary change has been in the technology, and associated bioinformatics, of DNA sequencing with the advent of High-Throughput (Next-Generation) sequencing (NGS). This is reflected in this edition by a number of new entries relating to NGS. Although NGS is replacing microarray technology in many applications, we have retained entries on microarray techniques as they are still current and highly used.

Apart from the changes, the *Concise Encyclopaedia* has been enhanced by expanding coverage in some of the more computer science-derived areas of the subject, as these are becoming increasingly important. To keep the book's length within reasonable limits, we have removed some entries that apply to what on reflection we consider to be purely biological concepts that are not in themselves necessary for an understanding of bioinformatics applications.

We hope that this new edition will be a welcome addition to bookshelves and electronic libraries and that it will continue to perform a useful function for the community.

As always, we thank our contributors for their efforts in writing the vast majority of the entries in this book, although as editors we accept responsibility for their accuracy.

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