FOREWORD

Our understanding of biology has undergone a revolution in the past 20 years, driven by our ability to capture, store, and interrogate ever-increasing volumes of data. The monumental strides are best illustrated and most visible in the world of genetics and molecular biology in which the power of the discovery of the structure of DNA – for which the Nobel Prize was awarded to Watson, Crick, and Wilkins in 1962 – was only fully unleashed in the late 1990s, when high-performance computers were made available to unlock the secrets of the entire human genome. However, this only heralded the beginning: genomics is only one of a growing number of enormous data sets in biology that requires substantial computing power to realize their full potential. New disciplines have evolved: transcriptomics, proteomics, lipidomics, metabolomics, systems biology, epigenomics, and data analytics are all exponents of this brave new, biological world of "Computational Biology".

This book draws together many of the latest cutting-edge developments in the field of Computational Biology. Each chapter draws on the expertise of world leaders in the field to highlight the utility and potential importance of specific technologies. The breadth of the text is impressive: from Integrative Biology in human diseases through the various branches of metabolomics and proteomics to sequencing and deep learning are all covered. In addition, the key role of statistics in large data set analysis is discussed in a dedicated chapter.

This book would have broad appeal to anybody with an interest in cutting-edge biology. It is important that the computational power that is now available to us to help unravel the seemingly impenetrable complexity of biological systems is fully utilized. The benefits of these technologies are boundless in biology and have yet to be fully realized; precision medicine represents an excellent example of an aspiration in medical development that would be simply unachievable without computational biology at its core.

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