Biological data, and DNA sequence data in particular, are accumulating at a phenomenal rate. By around 2005, it is likely that the DNA sequence of the complete human genome will have been determined. Although this achievement might seem an end in itself, in reality it is only the beginning. In order to exploit the wealth of DNA sequence and other biological data, a new science has arisen that fuses biology with mathematics and computer science – bioinformatics.

To find the genes within the genomic sequence is a massive task in itself. Once apparent, otherwise uncharacterized coding regions must be assigned a function. Thereafter, the interactions between genes and gene products must be understood at all levels, not merely in the context of the pathways within and between cells but also in terms of the evolution of gene families within and between species. These questions can all be addressed using bioinformatics. Bioinformatics touches all of biology and straightforward access to data via the Internet means that a wealth of information is available, literally at our fingertips. However, the newcomer to bioinformatics might be discouraged because of the initially daunting computational and mathematical content. Others might simply be confused by the language and terminology of bioinformatics. To help overcome these barriers, the Trends Guide to Bioinformatics examines the background to this novel and rapidly evolving scientific discipline. A series of tutorials, written by expert authors, clearly explains the concepts and provides practical examples of how the immense store of data can be exploited. Technical terms are highlighted in each article and defined in the glossary on pp. 32–33. Topics covered range from retrieving and aligning sequences, to predicting structure and function of gene products. Whether you are interested in molecular structure or taxonomy of organisms, the Trends Guide to Bioinformatics is an essential tool.