

Faust

Then shall I see, with vision clear,
How secret elements cohere,
And what the universe engirds,
And give up huckstering with words.

Johann Wolfgang von Goethe

Preface

This second edition contains three new chapters covering (a) the high resolution of the folding pathways of six proteins by using the powerful method of Φ -value analysis (Chap. 11; Nölting and Andert, 2000), (b) the structural determinants of protein folding kinetics (Chap. 12; Nölting 2003; Nölting et al., 2003), and finally (c) presenting a novel method called “evolutionary computer programming” (Chap. 13; Nölting et al., 2004). The latter method involves the self-evolution of computer programs that can lead to highly advanced programs which are able to calculate protein folding and structure with unprecedented efficiency. The scope of such self-evolving computer programs is far beyond protein folding and biophysics. Section 13.3 outlines some possible future applications of self-evolving computer programs which can yield systems smarter than humans in fulfilling certain technological tasks. For further information on biophysics methods in general, the reader may refer also to the textbook “Methods in Modern Biophysics”.

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