
Preface

DNA (deoxyribonucleic acid) acts as the information archive of most living beings. Due to the fact that a strand of DNA can be expressed as a set of four-letter character strings, so-called *string problems* have become abundant in bioinformatics and computational biology. Each year, new optimization problems dealing with DNA (or protein) sequences are being formulated that require efficient optimization techniques to arrive at solutions. From this perspective, bioinformatics is a burgeoning field for optimization experts and computer scientists in general. In this book, we will focus on a mixture of well-known and recent string optimization problems in the bioinformatics field. We will focus on problems that are combinatorial in nature.

One of the obstacles for optimization practitioners is the atypical nature of these problems, i.e. although combinatorial in nature, these problems are rather different to the classical traveling salesman problem or the quadratic assignment problem. This implies that a different type of expertise is required to efficiently solve many of these problems. Therefore, one of the main goals of this book is to pass on this kind of expertise and experience to newcomers to this field. The book provides several examples of very successful (hybrid) metaheuristics for solving specific string problems. One such example concerns the use of beam search (an incomplete branch and bound method) in solving longest common subsequence problems. The application of this algorithm in 2009 marked a breakthrough in the solution of this type of problem.

Finally, we would like to address a few words to the interested readers, especially biologists. We apologize for any imprecision in the description of biological processes, which we have tried to keep to a minimum. Keep in mind that, after all, we are only computer scientists and mathematicians.

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