

Preface

Bioinformatics can be defined as research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral, or health data, including those to acquire, store, organize, archive, analyze, or visualize such data. Bioinformatics is a recent scientific discipline that combines biology, computer science, mathematics, and statistics into a broad-based field with profound impacts on all fields of biology and industrial application. Biological data sets have several common problems: They are typically large, have inherent biological complexity, may have significant amounts of noise, and may change with time. These challenges require computer scientists to rethink and adapt modeling approaches. Due to limitations of traditional algorithms, computational intelligence (CI) has been applied to bioinformatics recently and with promising results. This book serves to highlight the importance and recent success of computational intelligence methods over a diverse range of bioinformatics problems. It will encourage others to apply these methods to their research, while simultaneously serving as an introduction to CI methods and their application. The objective of this book is to facilitate collaboration between the CI community, bioinformaticians, and biochemists by presenting cutting edge research topics and methodologies in the area of CI in bioinformatics.

The book is organized as a number of stand-alone chapters developed and edited by leading educators that explain and apply CI methods to problem areas such as gene expression analysis and system biology, sequence analysis and feature detection, RNA and protein structure prediction and phylogenetics, and medicine. This book aims to highlight some of the important applications of CI in bioinformatics and identify how CI can be used to better implement these applications. Therefore, this book represents the unification of two fields (biology and computer science) with CI as a common theme.

Computational intelligence has been defined typically as biologically and linguistically motivated computational paradigms such as artificial neural networks, evolutionary algorithms, fuzzy systems, and hybridizations/extensions thereof. While each of these methods has its own significant history, their hybridization and application to bioinformatics problems remains a recent development. In addition, it is important to note that each problem may require a unique hybridization of CI methods, and it is hoped that part of the education that results from this book is the diversity of ways in which CI methods can be applied for problem solving so that the reader will have a better appreciation of how to solve similar problems in the future.