

# Preface

It gives us great pleasure to introduce this collection of chapters to the readers of the book series "Emerging Trends in Computer Science and Applied Computing" (Morgan Kaufmann/Elsevier). This book is entitled "Emerging Trends in Computational Biology, Bioinformatics, and Systems Biology — Systems and Applications." This is the second book in the series about the topic. We are indebted to Professor Quoc-Nam Tran (Professor and Department Chair) of the University of South Dakota for accepting our invitation to be the senior editor. His leadership and strategic plan made the implementation of this book project a wonderful experience.

Computational Biology is the science of using biological data to develop algorithms and relations among various biological systems. It involves the development and application of data-analytical and algorithms, mathematical modeling, and simulation techniques to the study of biological, behavioral, and social systems. The field is multidisciplinary in that it includes topics that are traditionally covered in computer science, mathematics, imaging science, statistics, chemistry, biophysics, genetics, genomics, ecology, evolution, anatomy, neuroscience, and visualization where computer science acts as the typical bridge between all such diverse areas (for a formal definition of Computational Biology, refer to <http://www.bisti.nih.gov/docs/compubiodef.pdf>). Many consider the area of Bioinformatics to be a subfield of Computational Biology that includes methods for acquiring, storing, retrieving, organizing, analyzing, and visualizing biological data. The area of Systems Biology is an emerging methodology applied to biomedical and biological scientific research. It is an area that overlaps with computational biology and bioinformatics. This edited book attempts to cover the emerging trends in many important areas of Computational Biology, Bioinformatics, and Systems Biology with particular emphasis on systems and applications.

The book is composed of selected papers that were accepted for the 2014 and 2015 International Conference on Bioinformatics & Computational Biology (BIOCOMP'14 and BIOCOMP'15), July, Las Vegas, USA. Selected authors were given the opportunity to submit the extended versions of their conference papers as chapters for publication consideration in this edited book. Other authors (not affiliated with BIOCOMP) were also given the opportunity to contribute to this book by submitting their chapters for evaluation. The editorial board selected 34 chapters to comprise this book.

The BIOCOMP annual conferences are held as part of the World Congress in Computer Science, Computer Engineering, and Applied Computing, WORLDCOMP (<http://www.world-academy-of-science.org/>). An important mission of WORLDCOMP includes "Providing a unique platform for a diverse community of constituents composed of scholars, researchers, developers, educators, and practitioners. The Congress makes concerted effort to reach out to participants affiliated with diverse entities (such as: universities, institutions, corporations, government agencies, and research centers/labs) from all over the world. The congress also attempts to connect participants from institutions that have **teaching** as their main mission with those who are affiliated with institutions that have **research** as their main mission. The congress uses a quota system to achieve its institution and geography diversity objectives." As this book is mainly composed of the extended versions of the accepted papers of BIOCOMP annual conferences, it is no surprise that the book has chapters from a highly qualified and diverse group of authors.

We are very grateful to the many colleagues who offered their services in organizing the BIOCAMP conferences (and its affiliated topical tracks). Their help was instrumental in the formation of this book. The members of the editorial committee included:

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We hope that you enjoy reading this book as much as we enjoyed editing it.

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