

Preface: Software Tools and Algorithms for Biological Systems

It gives us great pleasure to introduce the book entitled “Software Tools and Algorithms for Biological Systems.” This book is composed of a collection of papers received in response to an announcement that was widely distributed to academicians and practitioners in the broad area of computational biology and software tools. Also, selected authors of accepted papers of BIOCOMP’09 proceedings (International Conference on Bioinformatics and Computational Biology: July 13–16, 2009; Las Vegas, NV, USA) were invited to submit the extended versions of their papers for evaluation.

The collection of papers in Part 1 presents computational methods for microarray, gene expression analysis, and gene regulatory networks. Bioinformatics databases, data mining, and pattern discovery techniques are presented in Part 2, followed by Part 3 that is composed of a collection of papers in the areas of protein classification and structure prediction, and computational structural biology. Part 4 presents a set of chapters that discuss comparative sequence, genome analysis, genome assembly, and genome scale computational methods. Experimental medicine and analysis tools are presented in Part 5. The collection of papers in Part 6 presents computational methods for filtering, noise cancellation, and signal and image processing. Important topics in the area of computer-based medical systems appear in Part 7. Finally, Part 8 of the book presents various software packages and novel methods targeted at problems in bioinformatics.

We are very grateful to the many colleagues who helped in making this project possible. In particular, we would like to thank the members of the BIOCOMP’09 (<http://www.world-academy-of-science.org/>) Program Committee who provided their editorial services for this book project. The BIOCOMP’09 Program Committee members were:

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- *Ashu M. G. Solo (Publicity Chair), Principal/R&D Eng., Maverick Technologies America Inc.*
- *Dr Quoc-Nam Tran, Lamar University, TX, USA*
- *Prof. Alicia Troncoso, Head of CS Dept., Pablo de Olavide University, Seville, Spain*
- *Dr Mary Qu Yang (Vice Chair), National Institutes of Health, MD, USA*
- *Prof. Lotfi A. Zadeh, Member, National Academy of Engineering; IEEE Fellow, ACM Fellow, AAAS Fellow, AAAI Fellow, IFSA Fellow; Director, BISC; University of California, Berkeley, CA, USA*
- *Prof. Yanqing Zhang, Georgia State University, Atlanta, GA, USA*
- *Dr Leming Zhou, University of Pittsburgh, Pittsburgh, PA, USA*
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Last but not least, we would like to thank the editorial staff at Springer; in particular, we are indebted to Ms Melanie Wilichinsky (the editorial manager) who provided excellent professional service to us to make this project feasible.

Hamid R. Arabnia, PhD
Professor, Computer Science,
Fellow, Int'l Society of Intelligent Biological Medicine (ISIBM), Editor-in-Chief,
The Journal of Supercomputing (Springer),
Co-Editor/Board, Journal of Computational Science (Elsevier),
Member, Advisory Board, IEEE Technical Committee on Scalable Computing
(TCSC),
The University of Georgia,
Department of Computer Science,
Athens, GA 30602-7404, USA.

and

Quoc-Nam Tran, PhD
Associate Professor, Computer Science,
Vice-Chair, BIOCOMP 2010,
Lamar University,
Department of Computer Science,
Beaumont, TX 77710, USA.