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Foreword to the special issue on selected papers from the 6th International Conference on Bioinformatics and Computational Biology (BICoB 2014)

The volume of experimental biological data generated using next generation sequencing technologies and high-throughput mass spectrometers is increasing at a rapid pace. With the introduction of systems biology research paradigm the amount of collected data will outpace our efforts to analyze them. Designing algorithms that could process this data in an efficient manner and gain system-wide biological insight has become a significant challenge for computational scientists. This issue is a follow-up to the 6th International Conference on Bioinformatics and Computational Biology (BICoB-2014) that took place in Las Vegas Nevada during 24–26 March 2014. The guest editors selected a few top-quality papers from the BICoB proceedings and invited the authors of these papers to submit extended versions of their proceedings papers. The papers were significantly extended by their respective authors by including more data and analysis of their methods. After a rigorous review process the guest editors have selected the papers described below for publication in this special issue.

The first paper "Analysis of evolutionary conservation pattern and their influence on identifying protein sites"[1] show that when using the evolutionary information included in position-specific scoring matrix (PSSM) for identifying protein functional sites, analyzing the detailed conservation patterns of functional sites largely facilitates and more accurately describes the prediction.

The second paper "Formal modeling of a system of chemical reactions under uncertainty"[2] describes a novel formalism representing a system of chemical reactions with imprecise rate of reactions. The formalism incorporates imprecise value of rate constants of the chemical reactions. Further two algorithms are introduced for construction of efficient model abstractions addressing uncertainty in data.

The third paper "Identification of best indicators of peptide-spectrum match using a permutation resampling approach"[3] demonstrates that the spectra match indicators Sp (Crux), hyperscore (X! Tandem) and E-value (OMSSA) with a terminal residue permutation decoy database enables effective detection of peptides compared to target database. The paper also shows that the end decoy database improves the consensus of various search programs when identifying peptides.

We would like to thank all the authors who submitted papers to this special issue. Our special thanks go to all the reviewers who devoted their professional time to

assist us in our decision process. We will also like to thank Nurit Haspel (UMass, Boston) for helping us in reviewing the manuscripts and organization of the conference.

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