

## EDITORIAL

### Selected Papers from the Annual PACBB Conference 2014: Special Issue



**Miguel Rocha**

The field of Bioinformatics has been growing fast in the recent years, prompted by research in several initiatives from distinct biological and biomedical fields. Indeed, we have assisted an exponential increase in the volume and diversity of data, including, among others, next generation sequencing data, omics data, and literature (articles, patents, etc). Systems Biology is a related field of growing interest, which requires the efforts of researchers from interdisciplinary fields, from both biological/biomedical backgrounds, and those related to computer science, data analysis/ mining, modeling, and optimization.



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The growth in the number and dimension of biological databases prompts for the development of new computational technologies, as well as for research efforts into abovementioned topics. In this scenario, several computational models and tools used in to handle these data are based on computational approaches, requiring large software development efforts, involving complex algorithmic design and intelligent systems. These systems address tasks related to knowledge discovery, modeling and optimization, seeking to develop computational models to predict the response of biological systems to perturbations.

In this context, promoting the interaction of researchers from diverse areas is of increasing relevance to boost the efforts in the Bioinformatics field and contributing towards a new generation of multidisciplinary scientists. The Practical Applications in Computational Biology and Bioinformatics (PACBB) conference has been contributing to this effort promoting this fruitful interaction over the last years. This special issue gathers four contributions, selected and significantly extended from the rich PACBB'14 technical program, which included papers from diverse sub-fields in Bioinformatics and Computational Biology.

#### CONTENT

This volume gathers four extended articles selected from the work presented at the PACBB'2014 conference, showing distinct and meaningful practical applications of Bioinformatics and Computational Biology. These range from text mining applications, to metagenomics data processing, prediction of crop yields intra-molecular tunnels in proteins or protein interactions, and network reconstruction.

Vieira *et al.* present a content-based text classifier, based on Hidden Markov Models, that is less sensitive to the text representation and the size of the corpus, and more efficient, considering running time, than previous classification techniques, demonstrating its performance in a set of well-known biomedical corpora.

Alameda *et al.* propose a multi-agent system towards the prediction of future crop yields using previous field trials and plant genetics. This agent-based approach is shown to provide best results than statistical methods being more able to handle noise and not requiring data pre-processing.

The work by Jorge *et al.* provides the first network reconstruction of antimicrobial peptides-drug combinations in *Pseudomonas aeruginosa*, which is made publicly available for the community. This represents an important step in the research related to antibiotic resistance in this important organism.

Finally, the work by Pancaroglu and Tan proposes new methods for protein interaction prediction that are able to improve on the performance of state-of-the-art classifiers in this task. The results show important improvements when compared to the existing approaches.

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