EDITORIAL

Advanced Practical Applications of Computational Biology & Bioinformatics: PACBB'15

The success of Bioinformatics in recent years has been prompted by research in Molecular Biology and Molecular Medicine in several initiatives. These initiatives gave rise to an exponential increase in the volume and diversification of data, including next generation sequencing data and their annotations, high-throughput experimental (omics) data, biomedical literature, among many others. Systems Biology is a related research area that has been replacing the reductionist" view that dominated Biology research in the last decades, requiring the coordinated efforts of biological researchers with those related to data analysis, mathematical modeling, computer simulation and optimization.

The accumulation and exploitation of large-scale databases prompt the development of new computational technology and research on these issues. In this context, many widely successful computational models and tools used by biologists in these initiatives, such as clustering and classification methods for omics data, are based on Computer Science/ Artificial Intelligence (CS/AI) techniques. In fact, these methods have been helping in tasks related to knowledge discovery, modeling and optimization tasks, aiming at the development of computational models so that the response of biological complex systems to any perturbation can be predicted.

In this context, the interaction of researchers from different scientific fields is, more than ever, of foremost importance, boosting the research efforts in the field and contributing to the education of a new generation of bioinformatics scientists. The Practical Applications in Computational Biology and Bioinformatics (PACBB) conference has been contributing to this effort, promoting this fruitful interaction over the last 7 years. This special issue gathers four contributions, selected and significantly extended from the rich PACBB'15 technical program, which included papers spanning many different sub-fields in bioinformatics and computational biology.

This volume gathers four extended articles selected from the work presented at the PACBB'2015 conference, showing distinct and meaningful practical applications of bioinformatics and computational biology. These range from text mining, to next generation sequencing and gene expression data applications.

Calderon-Mantilla *et al.* propose a pipeline architecture for inferring and visualizing gene networks from expression data, applied to the specific case of coffee plants [1]. Rodriguez-Gonzalez *et al.* present a comparison of two distinct text mining approaches for extracting diagnostic related knowledge from MedLine Plus articles [2]. The work by Graña *et al.* proposes nextpresso, a pipeline for the analysis of next generation sequencing (RNA-seq) data that covers the most common requirements of these experimental data [3]. Finally, the work by Fernandez-Gonzalez *et al.* addresses a relevant problem in text retrieval, namely the influence of class imbalance when developing classifier models for assessing relevant biomedical literature [4].

REFERENCES

[1]   Calderón-Mantilla G, Gaitan-Bustamante A, Castillo-Ossa LF. A pipeline architecture for inferring and visualizing gene networks from cDNA microarray expression data in crop plants. Curr Bioinform 2018; 13: 566-72.
[2]   Rodríguez-González A, Costumero R, Martinez-Romero M, Wilkinson MD, Menasalvas-Ruiz E. Extracting diagnostic knowledge from MedLine Plus: a comparison between MetaMap and cTAKES approaches. Curr Bioinform 2018; 13: 573-82.
[3]   Graña O, Rubio-Camarillo M, Fdez-Riverola F, Pisano DG, Glez-Peña D. Nextpresso: next generation sequencing expression analysis pipeline. Curr Bioinform 2018; 13: 583-91.
[4]   Fdez-Glez J, Ruano-Ordás D, Méndez JR, Fdez-Riverola F, Laza R, Pavón R. Determining the influence of class imbalance for the triage of biomedical documents. Curr Bioinform 2018; 13: 592-605.

Miguel Rocha
(Guest Editor)
University of Minho
Braga
Portugal

Florentino Fdez-Riverola
(Co-Guest Editor)
University of Vigo
Vigo
Spain