Editorial

Highlights from the International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO) – 2015 and 2016 Editions

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ABSTRACT

The International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO) annually joint over 200 world-wide scientists in Granada (Spain) to present and discuss their most recent researches in bioinformatics and computational biology. This special issue collects a selection of the most relevant contributions in the two last editions of this conference (IWBBIO 2015 and IWBBIO 2016).

KEYWORDS

Bioinformatics; computational biology; biomedical engineering; conference; highlights

BACKGROUND

IWBBIO gathers every year a wide representation of the research community related to multidisciplinary topics like bioinformatics, computational biology and biomedical engineering. This conference aims to create a fruitful environment where the main trends in those areas are discussed, high-quality original ideas are presented and new research collaborations can be established.

During its six editions, IWBBIO has proposed a two-track session conference with around 200 contributions per edition, including over 20 oral sessions and 2-3 poster sessions. A high percentage of those were usually presented as special sessions. The special sessions allow relevant researchers to coordinate high-level discussions about very specific hot topics in the area. Contributions (both full articles and relevant abstracts) were carefully reviewed by at least two referees from our esteemed program and steering committees. The proceedings for these two editions are published and available online [1–3]. Additionally, IWBBIO provided a great opportunity to attend keynote lectures from respected researchers such as Prof. Alfonso Valencia (Centro Nacional de Investigaciones Oncológicas, CNIO, Madrid, Spain), Prof. Xavier Stivill (Centre for Genomic Regulation, CRG, Barcelona, Spain) or Prof Patrick Aloy (Institute for Research in Biomedicine, IRB, Barcelona) among others.

HIGHLIGHTS

It is well-known that the so-called NGS technologies are increasingly providing crucial knowledge to better understand genomic diseases. Additionally, NGS data is frequently combined with other sources to derive more powerful conclusions. For instance, the manuscript presented in this special issue by Vodicka et al. compares two NGS data analyses and epidemiological data in order to investigate prevalence of Parkinson’s disease in Czech Republic [4]. After integration, authors were able to highlight three statistically significant missense mutations associated to the disease. The proposed mutation can thus overcome with new insights about the genetic nature of this disease.

Another example of NGS data integration and its clinical application for disease prognosis is presented in the manuscript authored by Shao et al. [5]. In this work, authors built an epithelial mesenchymal transition (EMT) network composed of 87 molecules. This network integrates several molecular sources such as mRNA-Seq, copy number, methylation or miRNA-Seq data. A support vector machine (SVM) and logistic regression classifiers were proposed to determine potential markers in this network for the Lung Adenocarcinoma prognosis.
Nevertheless, data resulting from NGS technologies is not always easy to interpret. Expert knowledge and computational tools are usually required to facilitate interpretation. The article authored by Isabel Gonzalez-Gayte et al. presents DEgenes Hunter, a novel decision making tool to determine the most adequate R library to derive differentially expressed genes and functional interpretation from RNA-Seq data without reference genome [6]. This tool not only provides a straightforward decision making system but also quality control metrics.

Another important challenge that researchers often face in genomics is the search of accurate datasets in order to obtain significant results. For example, Marco Frasca et al. dealt in their manuscript with the need of providing guidance and prioritization for the selection of candidate genes in genetic diseases [7]. More specifically, authors propose an efficient approach to rebalance training sets and, consequently, to reduce misclassification with machine learning algorithm. This guided strategy was then applied to help in the decision-making of disease-gene associations.

Data integration has also been proved to be an excellent approach to better understand molecular and biological processes. In this sense, Bovo et al. propose in this special issue a novel gene enrichment analysis by relating both biological networks and lists of human genes/proteins to determine function-specific modules [8]. The presented system, named NET-GE, is implemented as a web server and was validated by determining functional phenotypes related to hyperactivity and obsessive-compulsive disorders.

Finally, areas such as biomedical science are reaching a complexity and heterogeneity in their researches that makes sometimes difficult to handle the constantly updated bibliography. For this reason, text mining and literature-based tools have become indispensable to assist researchers finding articles of interest. In this regard, a cross-domain knowledge discovery tool is described in this special issue by Cestnik et al. [9]. This tool implements a search space reduction by eliminating potential outlier documents and, thus, improving search efficiency. This tool also allows identifying texts with a strong relationship between different domains. A user case based on the relationship of Alzheimer and gut microbiome is shown.

CONCLUSIONS

This special issue gathers together an outstanding representation of research published and presented in IWBBIO 2015 and 2016. While the published manuscripts dealt with a wide range of challenges in bioinformatics, we can identify the following common theme: the importance of data integration for the understanding and discovery of novel insights in biomedicine and biomedical sciences. This special issue has also shown how web servers and computational applications can facilitate the data analysis process for other researchers.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

REFERENCES


