INTRODUCTION



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InCoB2014: Systems Biology update from the Asia-Pacific

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From Asia Pacific Bioinformatics Network (APBioNet) Thirteenth International Conference on Bioinformatics (InCoB2014) Sydney, Australia. 31 July - 2 August 2014

Abstract

Selected papers from the 13th International Conference on Bioinformatics (InCoB2014), July 31-2 August, 2014 in Sydney, Australia have been compiled in this supplement. These range from network analysis and gene regulatory networks to systems level biological analysis, providing the 2014 update to InCoB's computational systems biology research.

Introduction

Sydney, Australia hosted the 13th InCoB (International Conference on Bioinformatics), the official conference of the Asia-Pacific Bioinformatics Network (APBioNet) [1]. Since 2006, the best InCoB papers have been published as supplements in BMC Bioinformatics, with an additional supplement in BMC Genomics since 2009. With rising interest in systems biology and holistic analysis of biological data, InCoB published its first BMC Systems Biology supplement last year [2]. This introduction provides an update to the 2014 research in systems biology from the APBioNet community.

Manuscript submission and review

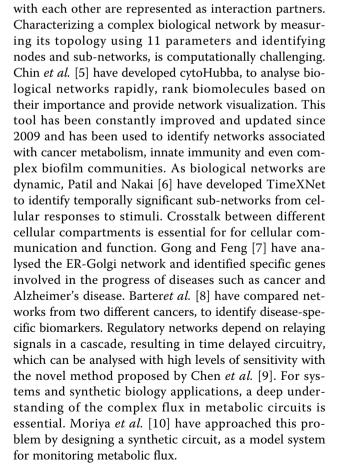
Authors were offered the BMC track (supplement issues of BMC Bioinformatics, BMC Systems Biology or BMC Genomics) and PeerJ [3]. The details of acceptance rates and the reviewing process are available from our BMC Genomics overview [4]. Eleven articles with a "systems" theme briefly described in the following sections.

Network analysis

The complexity of biological systems of often represented in terms of networks where biomolecules that interact

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Regulatory networks

Understanding transcriptional regulation of genes remains a challenging problem, dependent on the binding of several transcription factors as well as epigenetic changes. Given the sparseness of experimental genomewide epigenetic profiles, Yang *et al.* [11] have developed the *cis*MEP database comprising predicted *cis*-regulatory modules integrated with available epigenetic data, as a first step to support research in this area. Approaching the transcription regulation problem from another angle, Yan and Wang [12] propose a new graph theoretical method to predict DNA binding sites from protein structures.

Systems analysis

A comprehensive understanding of the symbiosis between the human microbiome and the host organism is essential for defining its role in human health and disease. Yang *et al.* [13] have applied an ensemble clustering framework to delineate the structure of human microbiome and provide a new insight to the pathological role of microbes within the host organism. Srihari *et al.* [14] have analysed complexes in core cellular processes to decipher cancer mechanisms, by data integration at the protein-protein interaction and gene expression levels, across all cancer conditions.

Conclusion

The articles in this supplement span network analysis, regulatory networks as well as systems-level analysis. With ongoing NIH Big Data to Knowledge (DB2K) [15] and other similar global initiatives, we expect to see more extensive computational studies at our 2015 InCoB meeting to be held jointly with the Genome Informatics Workshop (GIW) in Tokyo, Japan [16].

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

SR wrote the introduction. CS and SR (Program Committee Co-chairs) managed the review and editorial processes, respectively. TWT supported the post-acceptance manuscript processing.

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