

INTRODUCTION

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InCoB2014: Systems Biology update from the Asia-Pacific

Shoba Ranganathan^{1*}, Tin Wee Tan², Christian Schönbach^{3,4}

From Asia Pacific Bioinformatics Network (APBioNet) Thirteenth International Conference on Bioinformatics (InCoB2014)

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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 is often represented in terms of networks where biomolecules that interact

with each other are represented as interaction partners. Characterizing a complex biological network by measuring its topology using 11 parameters and identifying nodes and sub-networks, is computationally challenging. Chin *et al.* [5] have developed cytoHubba, to analyse biological networks rapidly, rank biomolecules based on their importance and provide network visualization. This tool has been constantly improved and updated since 2009 and has been used to identify networks associated with cancer metabolism, innate immunity and even complex biofilm communities. As biological networks are dynamic, Patil and Nakai [6] have developed TimeXNet to identify temporally significant sub-networks from cellular responses to stimuli. Crosstalk between different cellular compartments is essential for cellular communication and function. Gong and Feng [7] have analysed the ER-Golgi network and identified specific genes involved in the progress of diseases such as cancer and Alzheimer's disease. Barter *et al.* [8] have compared networks from two different cancers, to identify disease-specific biomarkers. Regulatory networks depend on relaying signals in a cascade, resulting in time delayed circuitry, which can be analysed with high levels of sensitivity with the novel method proposed by Chen *et al.* [9]. For systems and synthetic biology applications, a deep understanding of the complex flux in metabolic circuits is essential. Moriya *et al.* [10] have approached this problem by designing a synthetic circuit, as a model system for monitoring metabolic flux.

* Correspondence: shoba.ranganathan@mq.edu.au

¹Department of Chemistry and Biomolecular Sciences and ARC Centre of Excellence in Bioinformatics, Macquarie University, Sydney NSW 2109, Australia

Full list of author information is available at the end of the article

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 genome-wide 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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Authors' details

¹Department of Chemistry and Biomolecular Sciences and ARC Centre of Excellence in Bioinformatics, Macquarie University, Sydney NSW 2109, Australia. ²Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, 117599. ³Department of Biology, School of Science and Technology, Nazarbayev University, Astana 010000, Republic of Kazakhstan. ⁴Center for AIDS Research, Kumamoto University, Kumamoto 860-0811, Japan.

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