

Selected Papers from the 16th International Conference on Bioinformatics (InCoB 2017)

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The 16th International Conference on Bioinformatics (InCoB 2017) was held at the Graduate School at Shenzhen, Tsinghua University, Shenzhen, China from September 20 to September 22, 2017. InCoB is the annual conference of the Asia-Pacific Bioinformatics Network (APBioNet) that showcases the latest research and technologies in all areas of bioinformatics. The theme for InCoB 2017 was “Big Data and Big Impact in Bioinformatics”. InCoB 2017 had several tracks for oral presentations and associated journal publications. For the track of *Journal of Bioinformatics and Computational Biology* (JBCB), there were five submissions among which three submissions were accepted for oral presentation and two were finally accepted for this special issue.

Analysis of post-transformational modification (PTM) is an important topic in bioinformatics because PTMs are closely related to various kinds of diseases. The paper by Sun *et al.*¹ presents MPTM, a tool for mining protein PTMs from the literature. MPTM (Mining Protein Post-Translational Modifications) is a text mining tool that extracts and organizes valuable knowledge on 11 common PTMs from abstracts in PubMed. Input texts are analyzed in five steps: (i) triggers filtering, (ii) named entity recognition and substitution, (iii) identification of substrates, enzymes and modification sites, (iv) identification GO terms, diseases, organisms, crosstalk, and (v) identification of diseases from OMIM (Online Mendelian Inheritance in Man). Compared with the existing tools, MPTM has comparable or better performance and much wider coverage. MPTM is a web-based tool available online and the source codes are also available via GitHub.

Biological image analysis is becoming an important subarea of bioinformatics because a lot of cell and other image data have been produced using various novel imaging techniques, especially *in vivo* imaging techniques. The paper by Shigeta *et al.*² tackled the problem of segmentation of bone marrow cavity regions from given bone image data. They developed a novel texture pattern classification method by combining support vector machines and features obtained by wavelet transforms. Furthermore, in order to consider spatial continuity, the results of texture pattern classification are integrated using a graph-cut-based segmentation method.

They showed with extensive parameter tuning that the proposed method performs very well for real image data without manual inputs.

Finally, I would like to thank the organizers and program committee members of InCoB 2017 for the successful organization of the conference and careful review. I would also like to thank Prof. Limsoon Wong who carefully checked the manuscripts for this special issue and gave useful feedback to the authors.

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Guest Editor (JBCB Track Chair of InCoB 2017)

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2. Shigeta H, Mashita T, Kikuta J, Seno S, Takemura H, Ishii M, Matsuda H, Bone marrow cavity segmentation using graph-cuts with wavelet-based texture feature, *J Bioinform Comput Biol* **15**(5):1740004, 2015.