Introductory note for BGRS\SB-2014 special issue

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The international conference series Bioinformatics of Genome Regulation and Structure\Systems Biology, known as “BGRS\SB” or just “BGRS”, is a traditional biennial event that gets together biologists, computer scientists, mathematicians and biochemists working in an interdisciplinary field of systems biology biotechnology and genetics. Initiated by Prof. Nikolay A. Kolchanov in 1998, BGRS\SB has been held every two years in Novosibirsk, Russia, organized by the Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences. The ninth conference BGRS\SB-2014 held 23–28 June 2014 (<http://conf.nsc.ru/BGRSSB2014>) was associated with the multi-conference “Bioinformatics and System Biology” and the traditional Young Scientists’ School “Systems Biology and Bioinformatics” (SBB-2014). The BGRS\SB-2014 event hosted more than 400 participants from more than 20 countries, confirming the conference as largest international system biology meeting series in Russia and in Northern Asia. Next year, the jubilee tenth BGRS-2016 conference will be held in summer 2016, again in Novosibirsk Akademgorodok. BGRS series has long traditions of special post-conference issue publications in the Journal of Bioinformatics and Computational Biology (JBCB), starting from 2006.

Selected materials presented at the multi-conference were recommended for full-text publications in several special journal issues, besides JBCB. BioMed Central journals publishing BGRS-2014 supplements include BMC Genomics, BMC Syst Biol, BMC Evol Biol, and BMC Genetics. A special issue on bioinformatics using BGRS\SB-2014 presentations was printed in 2014 in “Vavilov Journal of Genetics and Breeding” in Russian (published in English as “Russian Journal of Genetics: Applied Research”). Additionally, some separate papers related to the conference materials have been submitted for publications in JBSD (Journal of Biomolecular Structure and Dynamics) and JIB (Journal of Integrative Bioinformatics). Due to the multi-disciplinary nature of the conference, the organizing committees decided to diversify post-conference publications in different journals covering wider bioinformatics areas.

This JBCB special issue contains 9 papers based on selected presentations at the conference, focusing mainly on algorithmic problems in bioinformatics. The papers were chosen from as much as twice more submissions for this journal. We believe that

these selected publications cover different aspects of the multi-conference and should be enjoyable to many readers.

The paper by Alban Shoshi *et al.* “Identifying adverse drug reactions and drug-induced diseases using network-based drug mapping”¹ describes computer modeling of gene networks in pharmacology applications. The work by Vitaly Likhoshvai *et al.* “Alternative splicing can lead to chaos”² considers fundamental problems of transcription network structures based on alternative splicing.

The paper by Sergey Matvienko *et al.* “Interaction sorting method for molecular dynamics on multi-core SIMD CPU architecture”³ deals with computer aspects of molecular modeling. Vladimir Golubyatnikov and co-authors consider practical application of theoretical gene network model in their paper “A model study of the morphogenesis of *D. melanogaster* mechanoreceptors: the central regulatory circuit”.⁴ The paper by Krasnobaeva and Yakushevich “Rotational dynamics of bases in the gene coding interferon alpha 17 (IFNA17)”⁵ also presents application of theoretical model of rotational dynamics of nucleotide sequence. Eduard Fomin presents an algorithmic solution of the cyclic sequence reconstruction problem in “Reconstruction of sequence from its circular partial sums for cyclopeptide sequencing problem”.⁶

The paper by Petr Ponomarenko and Mikhail Ponomarenko “Sequence-based prediction of transcription up-regulation by auxin in plants”⁷ describes nucleotide sequence analysis in genome scale in plants. The topic of plant development modeling continues in the paper “A computational model of the effect of symplastic growth on cell mechanics in a linear leaf blade”⁸ by Ulyana Zubairova *et al.* The paper by Irina M. Larina “Permanent proteins in the urine of healthy humans during the MARS-500 experiment”⁹ presents application of bioinformatics to medical problems in unique proteomics experiment.

Thus, this special issue reflects modern trends in bioinformatics highlighted at the recent BGRS\SB-2014 conference in Novosibirsk.

References

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4. Vladimir Golubyatnikov *et al.*, A model study of the morphogenesis of *D. melanogaster* mechanoreceptors: The central regulatory circuit, *J Bioinform Comput Biol* **13**(1):1540006, 2015.
5. Larisa Krasnobaeva and Ludmila Yakushevich, Rotational dynamics of bases in the gene coding interferon alpha 17 (IFNA17), *J Bioinform Comput Biol* **13**(1):1540002, 2015.
6. Eduard Fomin, Reconstruction of sequence from its circular partial sums for cyclopeptide sequencing problem, *J Bioinform Comput Biol* **13**(1):1540008, 2015.

7. Petr Ponomarenko and Mikhail Ponomarenko, Sequence-based prediction of transcription up-regulation by auxin in plants, *J Bioinform Comput Biol* **13**(1):1540009, 2015.
8. Ulyana Zubairova *et al.*, A computational model of the effect of symplastic growth on cell mechanics in a linear leaf blade, *J Bioinform Comput Biol* **13**(1):1540005, 2015.
9. Irina Larina *et al.*, Permanent proteins in the urine of healthy humans during the MARS-500 experiment, *J Bioinform Comput Biol* **13**(1):1540001, 2015.

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