
Editorial

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Biographical note: Pritish Kumar Varadwaj received PhD in Information Technology in 2009 from IIT-Allahabad, India. Currently, he is an Associate Professor at the Indian Institute of Information Technology-Allahabad. His research interests include data mining, machine learning, big data analytics and their application in various aspects of computational biology.

Special Issue: Algorithms and Applications in Computational Biology

This issue of the *International Journal of Bioinformatics Research and Applications* (IJBRA) features the extended versions of few selected papers presented at BSB-2016, the Bioinformatics and Systems Biology Conference, held at IIT-Allahabad, India on 4th to 6th of March, 2016. The goal of BSB-2016 conference was to create a platform for showcasing current research and development activities in bioinformatics, computational biology and systems biology and to further propel future interdisciplinary activity among researchers in these areas. The conference has successfully hosted with more than 100 participants across India along with participants from Israel, Russia and Singapore. Over 3 days, it featured 10 keynote speeches and 51 research presentations on various aspects of computational biology and systems biology. Further, one workshop was conducted on 'Next Generation Sequencing' with a comprehensive coverage of whole genome sequencing along with the lab session with the state-of-the-art computational facility at IIT-Allahabad. For more information on the BSB2016, you may visit <http://wbsb.iitaa.ac.in>.

We do hope that you will find this special issue as an informative compilation of recent applications and algorithms in the field of computational biology. Out of all 51 accepted submissions, the Program Committee has selected 9 relevant papers for this special issue. The articles selected in this special issue of IJBRA have undergone a thorough peer reviewing process.

The very first article by Arora et al. uses systems biology approach to understand the enzyme kinetics of Pathogenicity Island in *Salmonella* and further the establishment of the host-pathogen interaction will provide targets to develop drug against the *S. typhi* infection.

The second article by Alsmadi et al. is a comparative study which uses feature-based interaction methods in establishing the relationship among the macromolecules (*such as Protein and DNA*) modelled using social networks. The study has wide application in establishing the interaction between the genes and associated diseases.

The third article by Singh et al. emphasises on the analysis of genes associated with the Alzheimers disease using enrichment and topological examinations of network-based

information. The generated regulatory network will lead to significant gain in understanding their role in diagnosis as well as the prognosis of the disease.

The fourth article by Moazami-goodarzi et al. is a mile stone in designing a peptide-based vaccine for the infection caused by human *papilloma* virus. The study makes the use of activator-conserved epitopes which in future may enhance the immunity against infectious high-level HPV.

The fifth article by Srivastava et al. does the extensive research on human genome chromosome 11 using computational based approaches and tools. The comparative study of the chromosome 11 among the 6 different species helped in analysing the evolutionary relationship of the associated genes, categorising them in terms of sequence and structure-based information.

The next article by Kaushik et al. is *in silico*-based approach using different screening methods for identifying the peptide-based vaccine against the hepatitis C virus. The experimental validation will for sure help in completely eradicating the disease caused by the virus.

Seventh article in tow by Singh et al. utilises the data mining approaches to combat the issues related with crop production in terms of quality and quantity. The better production will help in growing high-yielding crops with better traits to overcome the shortage in food production.

The eighth article is related to the molecular docking study between the antimicrobial peptide Microcin C7 and the catalytic domain of *Diphtheria* toxin. Ojha et al. further stabilised the docked complex using simulation studies. The results in future can help in developing an alternative drug against *Diphtheria* toxin.

The last article describes the different criteria for selecting the best T cell epitope and then predicting the epitopes for hepatitis C virus.

That said, we are very much pleased to release this special issue of IJBRA with some very good research works as discussed aforementioned. We are grateful to Dr. Yi Pan, the Editor-in-Chief, IJBRA, for his kind consent and willingness to dedicate this special issue to showcase few of the selected submissions at BSB2016.

Wishing you all an excellent readership,

With warm regards

Pritish Kumar Varadwaj

Guest Editor, IJBRA Special Issue