
Guest Editorial

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Biographical notes: Swetha Sunkar, Assistant Professor, is currently heading the Department of Bioinformatics, Sathyabama Institute of Science and Technology, Chennai India. She has pursued her graduation in life sciences and double post-graduation in Zoology and Bioinformatics with PhD in Bioengineering. Her research began by exploring endophytes for their bioactivities followed by biodegradation of dyes. With her Bioinformatics and Cheminformatics background, she is currently studying genetic polymorphisms related to oral cancer and Vitamin D metabolism. She has 40 papers to her credit in impact journals and has been an active member in organising and participating various workshops and conferences. She is also a reviewer for Elsevier and Springer journals.

Universe is infinite. Exploring the unexpected is an unending process in this world. Genomics and proteomics are not an exception and the data we are accumulating presents us immense knowledge that can be implemented in the current healthcare research. This scientific congregation “National Conference in Computational Biology and Medical Biotechnology in Healthcare (CBMH)” attempted to explore the newer and relevant approaches to decipher the biological data simultaneously adding research information to the existing data resources thereby establishing evidence based application in the genomic technologies. Bioinformatics addresses the issues of data acquisition, accumulation, analysis, integration and storage of genomic and proteomic data. Cellular behaviour in the role of health and disease is very intricate and critical and understanding its natural path is a herculean task. But with bioinformatics tools and approaches, it is possible to arrive at a reasonable good conclusion that would aid in achieving better healthcare. Research is not an individual effort. It requires teams of scholars across the globe with continuous sharing, discussing and debating at different forums and levels that includes students, scholars, and academician and healthcare professionals. Our national conference provided a platform to such research minds for collaborating their views and ideas and contribute to better healthcare to the society.

The conference witnessed a variety of participants from different fields of research-biology to computer science. There were papers related to drug discovery, gene expression analysis, SNP studies and their functional significance, image processing, neural networks in biological data interpretation etc covering wide areas of biological research. This special issue titled *CBMH 18: Special Issue on: “Computational Approaches in Biology And Medicine”* in *International Journal of Computational Biology and Drug Design* would therefore comprise papers related to diverse

bioinformatics approaches in biodata analysis there by providing clues to further research.

I was honoured when I was invited to be the Guest Editor for this special issue as this gave me an opportunity to interact with research community for which I would like to thank Editor. With Biotechnology and Bioinformatics as my background, I am working on genetic variations and their effect on functionality. Therefore accessing the latest papers helped me to understand the nuances related to my area of research. As the guest Editor for this journal, I would like to take this opportunity to thank the Journal Editor and the corresponding team for accepting my proposal to publish a special issue for "*International journal of Computational Biology and Drug Design*" with the papers received in our conference. I would like to express my thanks to the authors who were keen to put forth their findings in this special issue. The papers received went through a rigorous process of peer review by at least three reviewers to maintain the standards of the paper and the journal. I would like to specially thank all the reviewers who bailed out their valuable time to review the papers and give their critical comments for enhancing the quality of the paper. Almost a year was devoted for the entire process after which the special issue is now ready with quality research.

I hope our association would continue in future to bring the best of research in the forefront which the journal aspires to. Once again a note of thanks to the journal team, reviewers and authors for making this special issue noteworthy.