

---

## Guest Editorial

---

### Swetha Sunkar

Department of Bioinformatics,  
Sathyabama Institute of Science and Technology,  
Jeppiaar Nagar, Rajiv Gandhi Salai,  
Chennai – 600119, Tamilnadu, India  
Email: swethauk78@gmail.com

**Biographical notes:** Swetha Sunkar is working as an Associate Professor and is currently heading the Department of Bioinformatics, Sathyabama Institute of Science and Technology, Chennai India. She has pursued her graduation in Life Sciences and Post-graduation in Bioinformatics. She finished her PhD in Bioengineering. Her research began by exploring endophytes from various medicinal plants for various bioactivities. With her bioinformatics and cheminformatics background, she ventured into studying genetic polymorphisms involved in the genes in oral cancer and Vitamin D metabolism. She has 44 papers to her credit in impact journals and is also a reviewer for Elsevier and Springer journals.

---

Science is mysterious. The data generated from scientific endeavours ranges from amoeba to human beings, common cold to cancers. The advancements in technology facilitated fast and efficient experimental methods which has produced huge data. Analysing this data is a major challenge, which in the present times is effectively tackled by bioinformatics and computational biology. In the last decade, bioinformatics has become indispensable in deciphering the information generated by experiments. Emergence of powerful technologies in studying whole DNA, protein, and RNA content has further made bioinformatics essential in understanding the secrets of science. With the advent of the so-called ‘omic’ era, that includes genomics, proteomics, transcriptomics, regulomics, metabolomics, and interactomics, an enormous amount of information has been piling up which needs to be analysed by developing new and powerful algorithms. In order to create a platform for various people from the research fraternity to exchange their research ideas, efforts and discoveries, we organised this “National Conference in Computational Biology and Medical Biotechnology in health care (CBMH)” at Sathyabama Institute of Science and Technology, Chennai, India.

The conference was able to gather a variety of participants from different fields of research – biology to computer science. There were papers related to system pharmacology, gene expressions, drug designing, small molecule analysis, mutational studies, image processing, neural networks, algorithm development, etc. This special issue titled **CMBH 18: Special Issue on: ‘Advances in bioinformatics and biotechnology towards medicine and health’** would therefore include papers related to diverse bioinformatics approaches in biological data analysis which would aid further research.

It is my honour to be the to be the Guest Editor for this special issue as this provided me a chance to associate with research community for which I would like to thank the 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 bioinformatics research and applications” with the papers received in our conference. I would like to express my thanks to the authors who were eager to give 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 spared their valuable time to critically review the papers. Almost a year was dedicated 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 I thanks to the journal team, reviewers and authors for making this special issue noteworthy.