Special Issue

Research on Mathematical and Computational Modelling of Systems Biology

Message from the Guest Editor

Recent breakthroughs in computational systems biology have revolutionized our comprehension of complex biological systems. Central to these advances are improved algorithms that facilitate the modelling of intricate biological networks, enabling accurate simulations of cellular processes. The integration of machine learning techniques has become pivotal in analyzing large-scale genomic and proteomic datasets, thus improving the identification of critical biomarkers and therapeutic targets. The fusion of multi-omics data—encompassing genomics, transcriptomics, proteomics, and metabolomics—offers a comprehensive perspective on cellular functions and interactions, providing unprecedented insights into biological processes. High-performance computing has been instrumental in processing extensive datasets, enhancing the development of robust predictive models. Artificial intelligence is increasingly being used in drug discovery, thus expediting the identification of promising drug candidates. This Special Issue explores these cutting-edge developments and their profound implications for the future of biomedical research.

Guest Editor

Dr. Mainul Haque
School of Mathematical Sciences, University of Nottingham Ningbo China, Ningbo 315100, China

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Mathematics
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
mathematics@mdpi.com

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Message from the Editor-in-Chief

The journal *Mathematics* publishes high-quality, refereed papers that treat both pure and applied mathematics. The journal highlights articles devoted to the mathematical treatment of questions arising in physics, chemistry, biology, statistics, finance, computer science, engineering and sociology, particularly those that stress analytical/algebraic aspects and novel problems and their solutions. One of the missions of the journal is to serve mathematicians and scientists through the prompt publication of significant advances in any branch of science and technology, and to provide a forum for the discussion of new scientific developments.

Editor-in-Chief

Prof. Dr. Francisco Chiclana
School of Computer Science and Informatics, De Montfort University, The Gateway, Leicester LE1 9BH, UK

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