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Applications of Systems Biology Approaches in Biomedicine

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Message from the Guest Editors

Human diseases such as cancer can be viewed as a system failure, and studying the complexity of a disease requires us to understand its system structure, function, and dynamics. Disease complexity rises from enormous amounts of information on the components (such as genes, RNAs, and proteins) and interactions that comprise a biological system. Advanced mathematical and computational models have played a significant role in improving our understanding of biological systems. Furthermore, translational modeling approaches to a full understanding of the underlying molecular mechanisms of human diseases and their clinical relevance are currently ongoing. However, the systematic integration of multi-omics datasets (such as genomics, transcriptomics, proteomics, and metabolomics) into computational modeling brings about numerous challenges in the field.

Therefore, we call for contributions from researchers with diverse backgrounds (e.g., biomathematics and bioinformatics) and practices in computational biology that aim to address some of the mentioned challenges and difficulties in this field, as well as tools, techniques, and application studies.

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Prof. Dr. Le Zhang

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