Mathematical Models and Computer Science Applied to Biology

Guest Editor:

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Message from the Guest Editor

High-throughput data techniques bring a large amount of biological data, such as gene expression, chromatin accessibility profiles, etc. Various mathematical methods and computer science techniques can be used to interpret and analyze these biological data, which can provide a more reliable and holistic depiction of biological mechanisms. Though related research has been done, due to the explosive growth of biomedical data at different scales, the research in related fields is still insufficient.

This Special Issue aims to provide a forum for exchanging ideas and tools among scientists, mathematicians, statisticians, biologists, computer scientists, and other domain experts. We invite original and review papers dedicated to network medicine, multi-layered network analysis, multiscale analysis, and other methods to contribute to analyzing the correlation between multi-scale data and provide a better explanation for complex diseases or biological processes. We would like to invite original research articles that provide new results on this subject.

Special Issue

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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.

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