Special Issue

Algorithms and Models for Bioinformatics and Biomedical Applications

Message from the Guest Editors

Omics data analysis has fulfilled its promise of shedding light on many complex mechanisms that regulate life, including the onset and progression of diseases. In addition to being intrinsically difficult to tackle, distilling knowledge from these data is complicated, requiring a joint effort between the life science and computer science communities. Efficiency in dealing with the enormous size of genomic data is not sufficient for algorithms to derive meaningful information unless the underlying computational model is coherent with biology. On the other hand, the complexity of the relationships among the elements that determine cell phenotypes cannot be captured if not computationally. Mathematical models are ubiquitous in bioinformatic and biomedical applications and have contributed to the solution of practical problems. Notable examples include the distribution of expression levels to infer dysregulated genes, the assessment of biomarkers, and the identification of families of cooperating proteins. The aim of this Special Issue is to collect contributions related to new algorithms and models that can solve practical problems in bioinformatics and biomedicine.

Guest Editors

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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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