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Mathematical Methods and Machine Learning in Biology

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Deadline for manuscript submissions:
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Message from the Guest Editors

Dear Colleagues,

In recent years, the combination of computing power and an increase in biological data sets has led to a breakthrough in the applications of machine learning (ML) techniques in mathematical modeling applied to biology and medicine. Mathematical models based on analytical concepts such as differential geometry, differential equations, persistent homology, and graph theory have been widely used to describe various biological processes and can be combined with advanced ML algorithms to help interpret biomedical data produced by high-throughput genomics and proteomics projects. Over a noticeably brief period, mathematics-based ML methods have made a remarkable impact on multiple fields of biology, including medical image analysis, predictions of disease outbreaks, protein structure predictions, protein–ligand binding affinity predictions, and drug design. This Special Issue provides a unique opportunity for researchers from academia and industry to present their new and unpublished work and to promote future studies in an emerging field such as applying mathematics-based ML models to highly diverse biological data.

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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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