Special Issue

Machine Learning Techniques in Molecular Function and Structure Analysis

Message from the Guest Editor

The rapid increase in data dimension is a challenge for traditional analysis methods in bioinformatics and computational biology. Accordingly, there is an urgent need to develop computational methods to exploit these masses of molecular data more effectively, characterize the molecular structures from such large data, and reveal their functional roles in biological processes. For this purpose, machine learning naturally appears as one of the main drivers of progress. Machine learning and pattern recognition techniques are able to extract useful patterns hidden in the large-scale data and make effective use of these patterns to perform accurate predictions regarding future data. In recent years, bioinformatics has already induced significant new developments of general interest in machine learning, for example in the context of learning with structured data, graph inference, semi-supervised learning, and novel combinations of optimization and learning algorithms. Please kindly note that all submitted papers should be within the scope of the journal.

Guest Editor

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Deadline for manuscript submissions

closed (31 December 2022)

About the Journal

Message from the Editor-in-Chief

As the world of science becomes ever more specialized, researchers may lose themselves in the deep forest of the ever increasing number of subfields being created. This open access journal Applied Sciences has been started to link these subfields, so researchers can cut through the forest and see the surrounding, or quite distant fields and subfields to help develop his/her own research even further with the aid of this multi-dimensional network.

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