Special Issue

Advanced Research on Machine Learning Algorithms in Bioinformatics

Message from the Guest Editors

Epigenetic variation and, more generally, somatic mutations represent molecular components of biodiversity that directly link the genome to the environment. Recently, epigenetics emerged as a promising aspect for the diagnosis of several disorders. It could become an opportunity to uncover new mechanisms as well as therapeutic targets for cancer and analyze their links with metabolic dysregulation. The application of machine learning and automated reasoning techniques to mutational studies composed of huge amounts of multi-omics data could significantly boost discovery and therapy development. For these reasons, we invite you to submit your latest research related to the development and application of artificial intelligence methods to this kind of problem to this Special Issue. It will focus on algorithms in the following areas:

- Epigenomic and multi-omics data clustering;
- Computational approaches to modeling and optimizing cancer treatment;
- Patient-specific integrated network modeling;
- Single-cell analysis in cancer genomics and epigenomics;
- Modeling the evolutionary dynamics of cancer: from epigenetic regulation to cell population dynamics.

Guest Editors

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About the Journal

Message from the Editor-in-Chief

Algorithms are the very core of Computer Science. The whole area has been considered from quite different perspectives, having led to the development of many sub-communities: Complexity theory (limitations), approximation or parameterized algorithms (types of problems), geometric algorithms (subject area), metaheuristics, algorithm engineering, medical imaging (applications), indicates the range of perspectives. Our journal welcomes submissions written from any of these perspectives, so that it may become a forum for exchange of ideas between the corresponding scientific subcommunities.

Editor-in-Chief

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