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Algorithm Engineering in Bioinformatics

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Message from the Guest Editors

The production of large-scale data and the complexity of analysis procedures in bioinformatics and computational biology, as well as the reproducibility of results, have posed numerous challenges to computer engineering in general and algorithm engineering in particular. The volume of data, their properties, and the inherent optimization problems have led to the extension and development of new, efficient algorithms and data structures for indexing, compressing, and succinctly representing sequences, trees, and graphs; aligning sequences and trees; the determination and inference of patterns; and information visualization. Furthermore, in real applications in the field of bioinformatics, where input data are often biased and where the hardware used may differ from that in theoretical models, the results are not always what is initially expected. In this context, algorithm-engineering-based approaches are fundamental to transfer ideas and theoretical results, to design and analyze, to experimentally evaluate, and to implement algorithms in libraries and applications in the scope of bioinformatics and computational biology.

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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.

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