Computational Biology Approaches to Genome and Protein Analyzes

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Message from the Guest Editor

The aim of this Special Issue is to collect research articles on, among other topics, methods, algorithms and their implementations in the field of computational biology.

New approaches are especially important during the analysis of genomes and proteins, and striving to establish a complex sequence–function relationship. These approaches can rely on the "computing power" needed, for example, when generating phylogenetic trees by ever faster computers. New approaches can also use artificial intelligence methods, especially artificial neural networks, fuzzy logic, and expert systems. Using artificial neural networks, for example, makes it possible to replace computation with recognition. Moreover, regardless of the method used, the interpretation of the results always plays a key role, and in this area, computer methods can also play an important role by effectively supporting scientists. New approaches are particularly important when analyzing genome changes during the evolution of normal organisms and the development of transformed cells, as these areas are relatively poorly understood.

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Message from the Editor-in-Chief

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