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New Approaches to the Identification of Organism Evolution

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Message from the Guest Editor

The aim of this Special Issue is to collect research articles among other topics, new methods on. and implementations of new algorithms for the identification of organism evolution. The known methods are based on "brutal calculation power" performed by ever-faster computers. The algorithms implemented in these methods allow for the generation of phylogenetic trees, the number of which depends strongly on the number of organisms. For a larger number of organisms, the number of generated trees is so huge that the calculations have to be prematurely interrupted. In this case, the conclusions are drawn on the basis of often a small fraction of all possible trees. Moreover, regardless of the method used, the interpretation of the results always plays a key role. For these reasons, the reconstruction of real evolution remains a mystery, and new methods are sought that will allow for more reliable discovery of the truth about evolution. New approaches are especially important for understanding transformed cell development, which can be considered as a special kind of evolution.



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Specialsue





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Message from the Editor-in-Chief

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