Approximability of multiple sequence alignment

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Abstract

The multiple sequence alignment problem with the SP-cost measure (sum of all pairs) has known to be NP-complete. We will give an overview on the current state of knowledge how well this problem can be approximated - which Jiang, Kearney and Li have been presented as one of the open problems in computational molecular biology (ACM SIGACT News 30, 1999, 43-49). For metric cost functions the situation is still unresolved. However, Siebert has recently shown that a generalized version of this problem - weighted multiple sequence alignment - is MAX-SNP hard.