

An Efficient Algorithm for Global Alignment of Protein-Protein Interaction Networks

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Abstract : Global aligning two protein-protein interaction networks is an essentially important task in bioinformatics/computational biology field of study. It is a challenging and widely studied research topic in recent years. Accurately aligned networks allow us to identify functional modules of proteins and/or orthologous proteins from which unknown functions of a protein can be inferred. We here introduce a novel efficient heuristic global network alignment algorithm called FASTAn, including two phases: the first to construct an initial alignment and the second to improve such alignment by exerting a local optimization repeated procedure. The experimental results demonstrated that FASTAn outperformed the state-of-the-art global network alignment algorithm namely SPINAL in terms of both commonly used objective scores and the run-time.

Keywords : FASTAn, Heuristic algorithm, biological network alignment, protein-protein interaction networks

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