
Approximate the Distance Matrix Based Structure Alignment

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Proteins of similar structures are likely to share similar functions. Comparing the structures of proteins allows us to study protein functions, which are important to the biological and medical sciences. Here, we focus on the Squared Euclidean Distance. People thought this problem is hard due to its similarity to the underlying problems with the subgraph isomorphism problem. However, by a careful analysis, we discover that this problem is easier than the subgraph isomorphism problem, and there are polynomial time schemes to solve the distance matrix based structure alignment problems. The techniques developed in this work can be extended to other problems.