

Clustering of Amino Acid Sequences Based on K-Medoids Method

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【Abstract】 We describe a new approach to clustering of amino acid sequences using K-Medoids Method. This method combines K-Medoids method, Dynamic Programming and other new theories in Biology. Experiments have proved that our method can get satisfying results. We believe that the method we proposed in this paper is a powerful and flexible tool for clustering of amino acid sequences.

【Keywords】 Clustering of amino acid sequences, Data Mining, K-Medoids Method, Dynamic Programming, Bioinformatics

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