

## PROTEIN HOMOLOGY DETECTION THROUGH ALIGNMENT OF MARKOV RANDOM FIELDS%0A

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Ma J, Wang S, Wang Z, Xu J (2014) MRFalign: Protein Homology Detection through Alignment of Markov Random Fields. In: Research in Computational Molecular Biology, Springer, pp 173-174. In: Research in Computational Molecular Biology, Springer, pp 173-174. MRFalign: Protein Homology Detection through Alignment of ...

Sequence-based protein homology detection has been extensively studied and so far the most sensitive method is based upon comparison of protein sequence profiles, which are derived from multiple sequence alignment (MSA) of sequence homologs in a protein family. MRFalign: Protein Homology Detection through Alignment of ...

Sequence-based protein alignment and homology detection has been extensively studied and widely applied to many biological problems such as homology modeling [1-4], phylogeny inference [5-7] and protein function prediction [8-10].

Protein Homology Detection Through Alignment of Markov ...

Detection Through Alignment of Markov Random Fields, which won the best paper award at a premier computational biology conference RECOMB2014 and also appeared at PLoS Computational Biology.

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Abstract. Sequence-based protein homology detection has been extensively studied, but it still remains very challenging for remote homologs with divergent sequences.

MRFalign: Protein Homology Detection through Alignment of ...

MRFalign: Protein Homology Detection through Alignment of Markov Random Fields Jianzhu Ma, Sheng Wang, Zhiyong Wang, Junbo Xu\* Toyota Technological Institute at Chicago, Chicago, Illinois, United States of America

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Abstract. Sequence-based protein homology detection has been extensively studied and so far the most sensitive method is based upon comparison of protein sequence profiles, which are derived from multiple sequence alignment (MSA) of sequence homologs in a protein family.

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This article is from PLoS Computational Biology, volume 10. Abstract Sequence-based protein homology detection has been extensively studied and so far the most sensitive method is based upon comparison of protein sequence profiles, which are derived from multiple sequence alignment (MSA) of sequence homologs in a protein family.

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This work covers sequence-based protein homology detection, a fundamental and challenging bioinformatics problem with a variety of real-world applications.