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Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Introduction -- Method -- Software -- Experiments and Results -- Conclusion.
Sommario/riassunto	This work covers sequence-based protein homology detection, a fundamental and challenging bioinformatics problem with a variety of real-world applications. The text first surveys a few popular homology detection methods, such as Position-Specific Scoring Matrix (PSSM) and Hidden Markov Model (HMM) based methods, and then describes a novel Markov Random Fields (MRF) based method developed by the authors. MRF-based methods are much more sensitive than HMM- and PSSM-based methods for remote homolog detection and fold recognition, as MRFs can model long-range residue-residue interaction. The text also describes the installation, usage and result interpretation of programs implementing the MRF-based method.

