A Clique-Based Method for Improving Motif Scanning Accuracy

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Abstract

Motif scanning - searching for all protein motifs sufficiently similar to a given query - is a common task in bioinformatics. I will present a simple method that improves accuracy of motif scanning procedures. The method works by analysing pair-wise similarity within a hypothetical set of positive hits, and computing the maximal clique with respect to a certain threshold. This turns out to be extremely efficient in distinguishing between true and false positives.