Abstract

A RNA or DNA sequence motif is a short sequence found within a particular nucleic acid sequence families. Most amino acid and nucleic acid sequences have some level of functional or structural similarities. These similarities are mostly represented by short, contiguous sequences called motif. Motif discovery is an important aspect of molecular biology. This is because the knowledge of these sequences helps determine their structural properties, signal sites and/or ligand-binding sites. In most cases, depending on the function of the motif, these contiguous regions can be highly conserved with an homology of nearly 100%. Several algorithms have been proposed for the discovery of motifs. In this paper, the codon-based scoring method is employed to detect motifs and with their invariants. The result obtained shows the reliability and robustness of the method as motifs are discovered irrespective of their length and position in a sequence.

References

- B. B. Baridam. A scoring method for the clustering of nucleic acid sequences.
Application of the Codon-based Scoring Method in Motif Detection


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**Keywords**

Codon  motif  homology  similarity measure  sequences