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Finding the Longest Common Subsequence in Normal DNA and Disease Affected Human DNA Using Self Organizing Map

Authors : G. Tamilpavai, C. Vishnuppriya

Abstract : Bioinformatics is an active research area which combines biological matter as well as computer science research. The longest common subsequence (LCSS) is one of the major challenges in various bioinformatics applications. The computation of the LCSS plays a vital role in biomedicine and also it is an essential task in DNA sequence analysis in genetics. It includes wide range of disease diagnosing steps. The objective of this proposed system is to find the longest common subsequence which presents in a normal and various disease affected human DNA sequence using Self Organizing Map (SOM) and LCSS. The human DNA sequence is collected from National Center for Biotechnology Information (NCBI) database. Initially, the human DNA sequence is separated as k-mer using k-mer separation rule. Mean and median values are calculated from each separated k-mer. These calculated values are fed as input to the Self Organizing Map for the purpose of clustering. Then obtained clusters are given to the Longest Common Sub Sequence (LCSS) algorithm for finding common subsequence which presents in every clusters. It returns nx(n-1)/2 subsequence for each cluster where n is number of k-mer in a specific cluster. Experimental outcomes of this proposed system produce the possible number of longest common subsequence of normal and disease affected DNA data. Thus the proposed system will be a good initiative aid for finding disease causing sequence. Finally, performance analysis is carried out for different DNA sequences. The obtained values show that the retrieval of LCSS is done in a shorter time than the existing system.

Keywords : clustering, k-mers, longest common subsequence, SOM
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