Abstract

Phylogenetic tree is a branched structure which represents the evolutionary relationships among genes and organisms. Multiple sequence alignment is an initial step in constructing a phylogenetic tree. The most widely used tools for phylogenetic analysis i.e. PHYLIP (Phylogeny Inference Package) and PAUP (Phylogenetic analysis using parsimony) have so far been used for inferring phylogenies. However, the above referred packages in turn had to rely on other tools for input. In this context, many open source MSA tools are available for generating both multiple sequence alignment and phylogenetic tree. The purpose of the present paper is to highlight various open source MSA tools for constructing phylogenetic trees.
using distance based methods after generating the alignment. A comparative study of five MSA tools Geneious, ClustalX, DNAMAN, STRAP and MUSCLE is presented here with a motive of creating awareness among bioinformaticians about MSA tools that helps in constructing phylogenetic trees.

References


Index Terms

Computer Science
Soft Computing
Keywords
Multiple Sequence Alignment  Neighbor-joining  Upgma  Distance Matrix