Date:5/2/21

Phyloinformatics

Assignment 5

Answer the following questions and submit.

1. What are the advantages of Distance based tree building methods?

Answer:

Advantages of Distance based tree building methods:

- o It is less sensitive to variations in evolutionary rate than cluster analysis.
- o It is a fast method as in comparison.
- o Can handle many sequences at a time.
- o It produce a reasonable estimate of phylogeny.
- o It is fast and thus suited for large datasets and for bootstrap analysis.
- o Permits lineages with largely different branch lengths.
- Its suitability to handle large datasets has led to the fact that the method is widely used by molecular evolutionists.
- 2. Explain UPGMA method and construct a tree using the below distance matrix.

Answer:

UPGMA that is Unweighted Pair Group Method using Arithmetic averages. The simplest of the distance methods is the UPGMA. The PHYLIP programs DNADIST and PROTDIST calculate absolute pairwise distances between a group of sequences. Then the GCG program GROWTREE uses UPGMA to build a tree. Many multiple alignment programs such as PILEUP use a variant of UPGMA to create a dendrogram of DNA sequences which is then used to guide the multiple alignment algorithm. Unweighted – Pair – Group – Method –using Arithmetic averages Oldest Distance Method Proposed by Michener & Sokal in 1958 Produces rooted trees. Sometimes called as phenograms.It assumes that the trees are ultrametric, meaning that it assumes constant rate of substitutions in all branches of the tree.

Working of UPGMA:

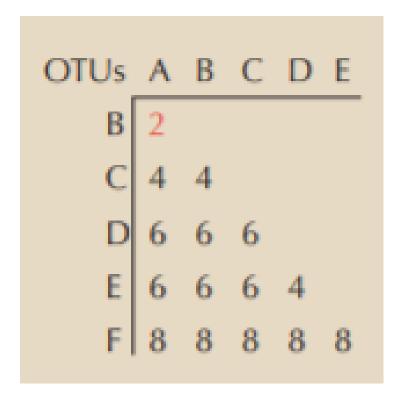
Employs a sequential clustering algorithm:

I.Identify the two OTU's from among all the OTUs, that are most similar to each other and then treat these as a new single OTU.

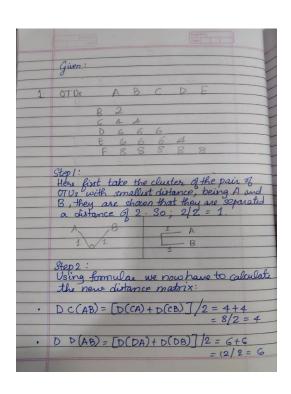
II. Subsequently from among the new group of OTUs, identify the pair with the highest similarity, and so on.

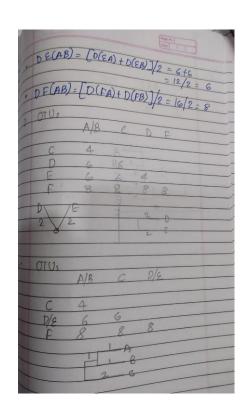
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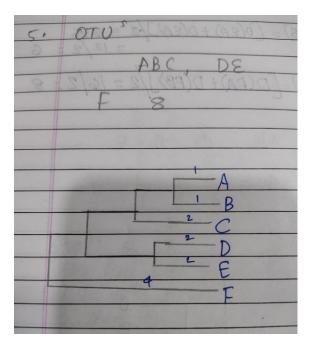
Answer:





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