Practical 10

12 April 2024

Questions

1. Obtain the consensus phylogenetic tree for the following two sets of sequences:

Set 1: tim.dat
Set 2: tim-hemo.dat

Hint:
(i)   Multiple sequence alignment using MAFFT
(ii)   Save in Phylip format
(iii)   Install Phylip (windows) / Phylip (Mac OS)
(iv)   Bootstrapping (Seqboot program)
(v)   Maximum likelihood method (proml program)
(vi)   Consensus tree (Consens program)
(vii)   Use TreeView / MEGA-X to view the tree
(viii) NJ and UPGMA methods (protdist and neighbor programs)

Refer to practical 10.ppt for detailed steps.

2. Obtain the weight matrix for the following sequences

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MVLSPADKTNVKGKVGAHAGEYGAAAW
MKRLPADPPCVKGKVKAKAGDYGATTW
MALSAADKTNVKSKVGGHAGEYGAATS
MVLSAADKTNVKSKAGGNAGEWWAAAW
MVLSAADKTNVKSKVLANAGEFGAAAW
ALLPIRTTYHKKCASGHIPEEKDLNNV
DEASSLKGHHIKKLEADALLIPLSASS
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Deadline: 19 April 2024