

Practical 10

28 March 2022

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](#)
- (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 practical 10.ppt for detailed steps.

2. Obtain the weight matrix for the following sequences

```
MVLSPADKTNVKGKVGAGHAGEYGAAAW  
MKRLPADPPCVKGKVKAKAGDYGATTW  
MALSAADKTNVKS KVGGHAGEYGAATS  
MVLSAADKTNVKS KAGGNAGEWWAAAW  
MVLSAADKTNVKS KVLNAGEFGAAAW  
ALLPIRTTYHKKCASGHIPEEKDLNNV  
DEASSLKGGHHIKKLEADALLIPLSASS
```

Deadline: 3rd April 2022