Phylip: Sptlc1.I

Aligned sequences in ClustalX and output alignment (sptl1alignout.phy)

Input file into PROTDIST

* Default settings
* Output=protdistout

Input file into NEIGHBOR

* NJ tree
* No outgroup…all default settings
* Nieghborout and neighbortree

Input neighbortree into DRAWGRAM

* Move font file (font1) into directory
* Default settings
* Select “Plot”

Sptlc1.II

Input aligned sequences into SEQBOOT

* Default settings
* Outfile = seqout

Input seqout into PROTDIST

* Analyze multiple datasest (“M”); multiple data sets, D; 100 data sets
* Outfile = distout

Input distout into NEIGHBOR

* Analyze multiple datasets, M (100)
* Outfiles are neighborout and neighbortree

Input neighbortree into CONSENSE

* Default settings
* Outputs are consensout and consenstree

Input consenstree into DRAWGRAM

* Final plotting device, P, to M (macintosh PICT file for drawing programs)