

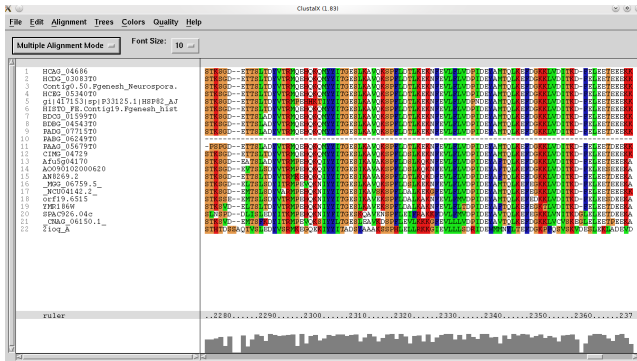
Practical Bioinformatics

Mark Voorhies

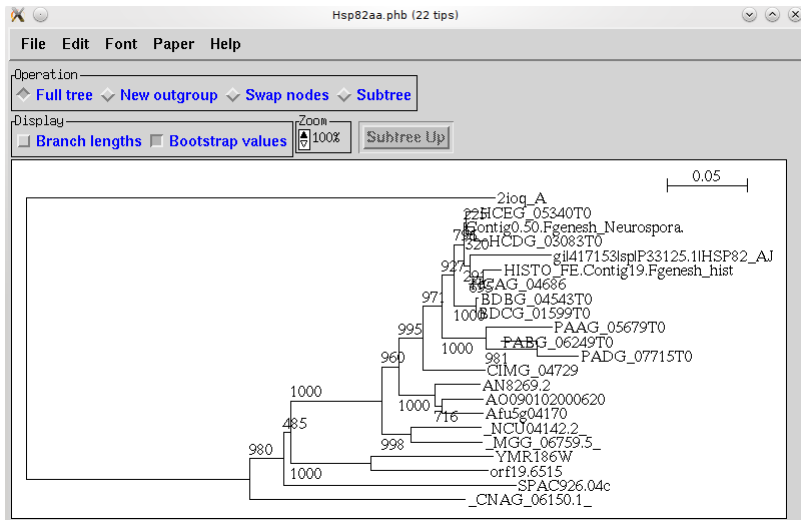
6/24/2010

- 1 Calculate distance matrix from pairwise sequence alignments
- 2 Generate UPGMA guide tree (*very similar to average linkage clustering*)
- 3 Progressive multiple alignment following guide tree
- 4 Re-calculate distances from multiple alignment
- 5 Generate neighbor-joining tree from new distance matrix (*differs from the clustering methods we've seen in that branch lengths can be asymmetric*)
- 6 Re-build distance matrices and trees from subsets of aligned positions to generate bootstrap values

CLUSTALX



- NJPLOT
- JALVIEW
 - Overview window
 - Adding annotations from GFF files
- Java TreeView



jalview 2.3

File Tools Help Window

Overview home/mvoorhiedata/SinemAntibodies_2_11_2010Hsp82aa.aln

home/mvoorhiedata/SinemAntibodies_2_11_2010Hsp82aa.aln

File Edit Select View Format Colour Calculate Web Service

Seq A: 210Q Be View Colours Help

1820 1840 1860 1880 1900

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```

Conservation Colour Increment. (Background)

Enter value to increase conservation visibility.

55 Apply to all Groups

Conservation

Quality

Consensus

Sequence S: 0: @G17153spP33129_1HSP82_A1

1820 1840 1860 1880 1900

...AAH-...-EYFEDARISLLELIINTVYSHKTEFLRELISGSGALDIEYEAALSDPSKLSLNDKLAIDITFDKSNKTE

jmol