

Software for viewing and analysing sequences

- Lots of programs – should be free, but not always...
- Visualization
- Multiple sequence alignment algorithms (Mafft, Muscle, T-Coffee, Clustal...)
- Phylogenetic reconstruction (Maximum Likelihood, distance, Bayes...)
- Other (population size, mutation rates, substitution patterns, selection tests...)

Mesquite (<http://mesquiteproject.wikispaces.com/>)

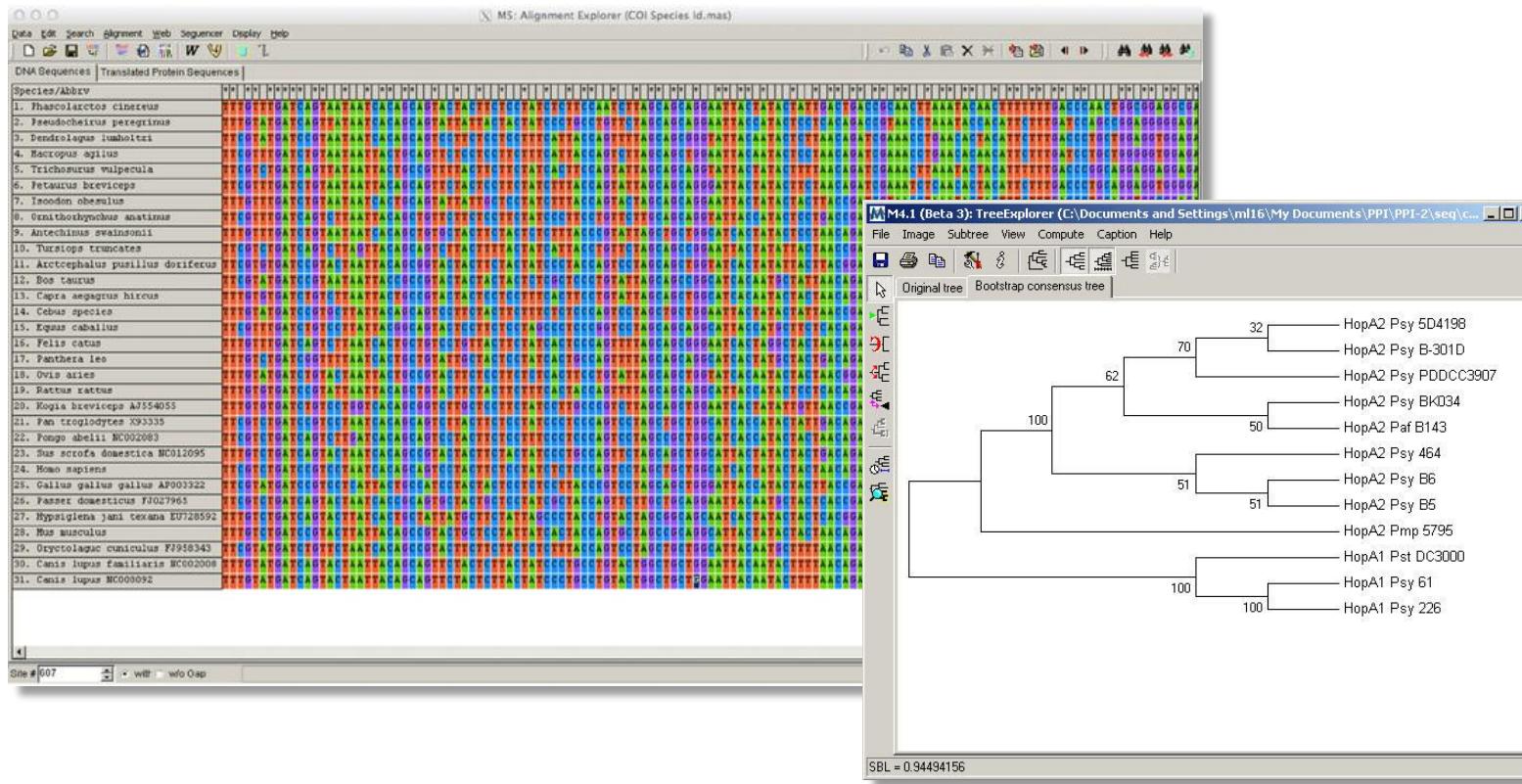
The image displays three windows of the Mesquite software interface:

- BembidionWithTrees**: A matrix editor window showing a 20x22 grid of characters and taxa. The columns represent characters (1-20) and rows represent taxa. Many cells contain numerical values like 1, 2, or 3, with some being bolded.
- 006r.285BembRelaxed.nex**: A phylogenetic tree window showing a tree rooted at the bottom. The tree has several clades, with some nodes labeled with taxon names. The tree is colored by character state.
- CADBembML.nex**: A matrix editor window showing a large grid of characters (285 rDNA) and taxa. The grid uses color coding to represent character states. A specific row for "taxon "Geocharidius" is highlighted in yellow.

Below the main windows, there are chromatogram plots showing DNA sequence data for various samples, with labels like "F09_BP23585.DNA4002_1S1_r1052268_069.ab1".

At the bottom, a status bar indicates: "[t:1 c:515 s:A] Character 515; Sequence site 492 [in taxon 'Diplochaetus planatus'] Color of cell: Colored to show state of character".

MEGA (<http://www.megasoftware.net/>)



Geneious (<https://www.geneious.com/>)

The screenshot displays the Geneious software interface, version 10.0.2, running on a Mac OS X system. The window is divided into several panels:

- Top Left Panel:** A tree viewer showing a phylogenetic tree for "Dicer_Drosophila_alignments". The tree includes nodes for various species and accessions, such as Dm_Dl_NP_524453, Hs_Dl_NP_085121, and Nv_Dl_AB210559.
- Top Right Panel:** A "bpcomp.com.tr(Tree) - Dicer_Drosophila_alignments" viewer showing a detailed tree structure with node labels and expansion controls.
- Middle Left Panel:** A sequence alignment viewer titled "Dicer_Drosophila_alignments (24)". It shows a table of alignments between 14 species and 24 Dicer genes. One entry for *Dm* has a score of 583.314 and an E-value of 0. The table includes columns for Bit-Score, E Value, Grade, Hit start, Hit end, Name, Description, and a list of sequences.
- Middle Right Panel:** A sequence viewer titled "Annotations & Tracks". It shows a chromatogram of sequence data across a genomic region from Dec 5 to Dec 9. Annotations include "Deletion (12)" and "Peg_drosha_Gene_14628".
- Bottom Left Panel:** A search bar and a list of recent searches and databases.
- Bottom Right Panel:** A status bar showing memory usage ("Using 275 / 7996 MB memory") and the date ("Fri 11 Nov 10:54 Jon Bråte").

JalView (<http://www.jalview.org/>)

The screenshot displays three windows of the JalView 2.8 interface:

- Main Window:** Shows a MAFFT Multiple Sequence Alignment of Retrieved from Uniprot. The alignment covers residues 60 to 120 across various FER protein sequences. A secondary structure diagram at the bottom indicates regions 1 through 5, Fe binding sites, and Iron Sulphur Contacts.
- Average distance tree window:** Displays a phylogenetic tree based on average distances, showing the evolutionary relationships between the FER proteins.
- FER1_SPIOL:A70 window:** A 3D Jmol viewer showing the crystal structure of the FER1_SPIOL protein domain A70. It highlights specific residues, including THR 89, in green and yellow.

Sample file