



# Quick Start

## I. Aligning Sequences

MEGA can align sequences, or you can open your own aligned sequences file.

To align sequences use the Alignment Explorer (see Fig.1):

1. Launch the Alignment Explorer by selecting *Alignment -> Alignment Explorer/CLUSTAL*, use *Create New Alignment*
2. Add unaligned sequences (eg. in fasta format) by *Retrieve Sequences* under *Data* OR use *Query Databanks* under *Alignment* to download sequences via NCBI
3. Run *Align by ClustalW* under *Alignment*, change alignment parameter if necessary.
4. Save the current session. Exit the *Alignment Explorer* and you will be prompted to save the data as a MEGA (\*.meg) file.

If you already have sequences aligned from another software, you can open it in a supported file (eg. \*.fasta, \*.nex, \*.msf, etc.) by *File-> Convert to MEGA Format...* and save it as a \*.meg file.

## II. Building Trees

1. Open the \*.meg file, if it's not active
2. Use *Phylogeny->Construct Phylogeny-> Neighbor-Joining* (or method of your choice), change parameters if needed - a green box appears if there are other options available for you to select.

Tree will be drawn in the TreeExplorer window. Branch lengths, based on the model selected, can be shown by checking *View->Show/Hide->Branch Length*

## III. Testing Tree Reliability (Boostrapping)

1. Activate the TreeExplorer window, if it's not already opened
2. Select *the Phylogeny->Bootstrap Test of Phylogeny->Neighbor-Joining Tree* (or method of your choice) - a green box appears if there are other options available for you to select. Click *Compute*.

Commands from drop-down menu in MEGA are *italicized*.

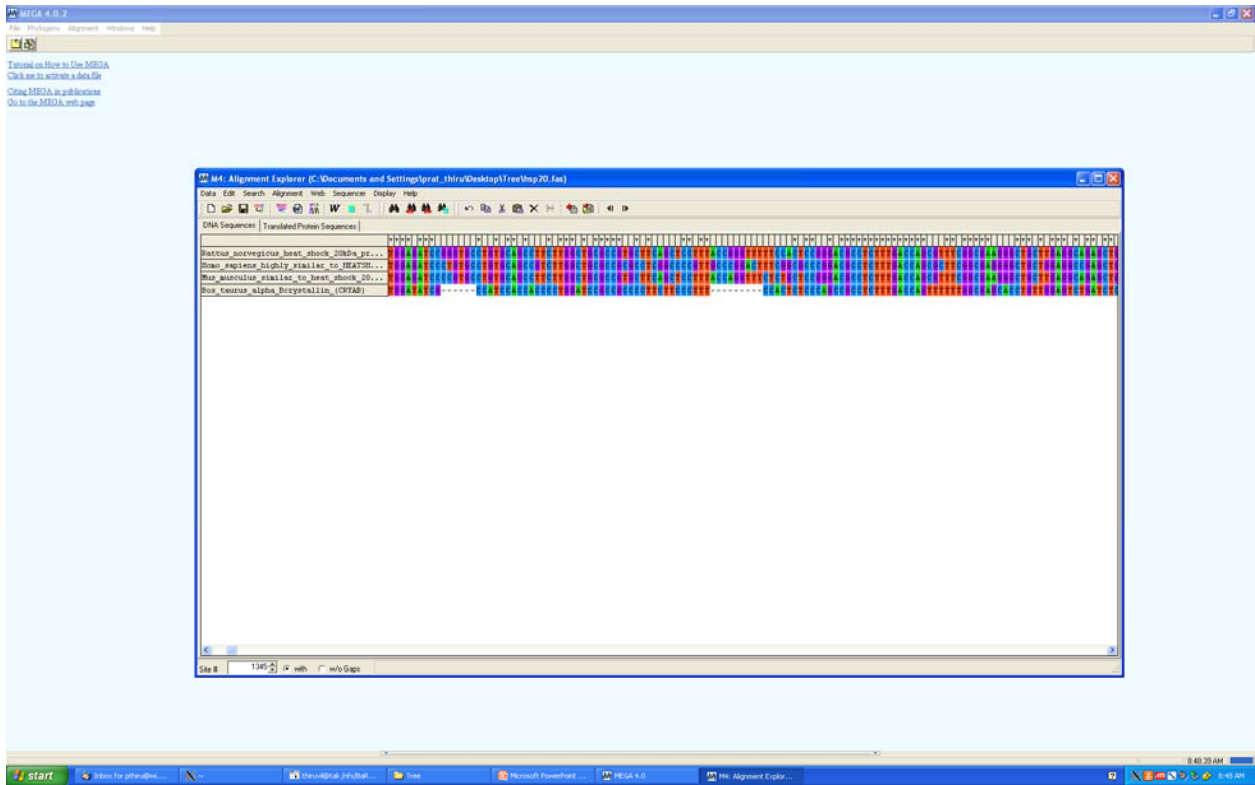


Figure 1: Alignment Explorer in MEGA

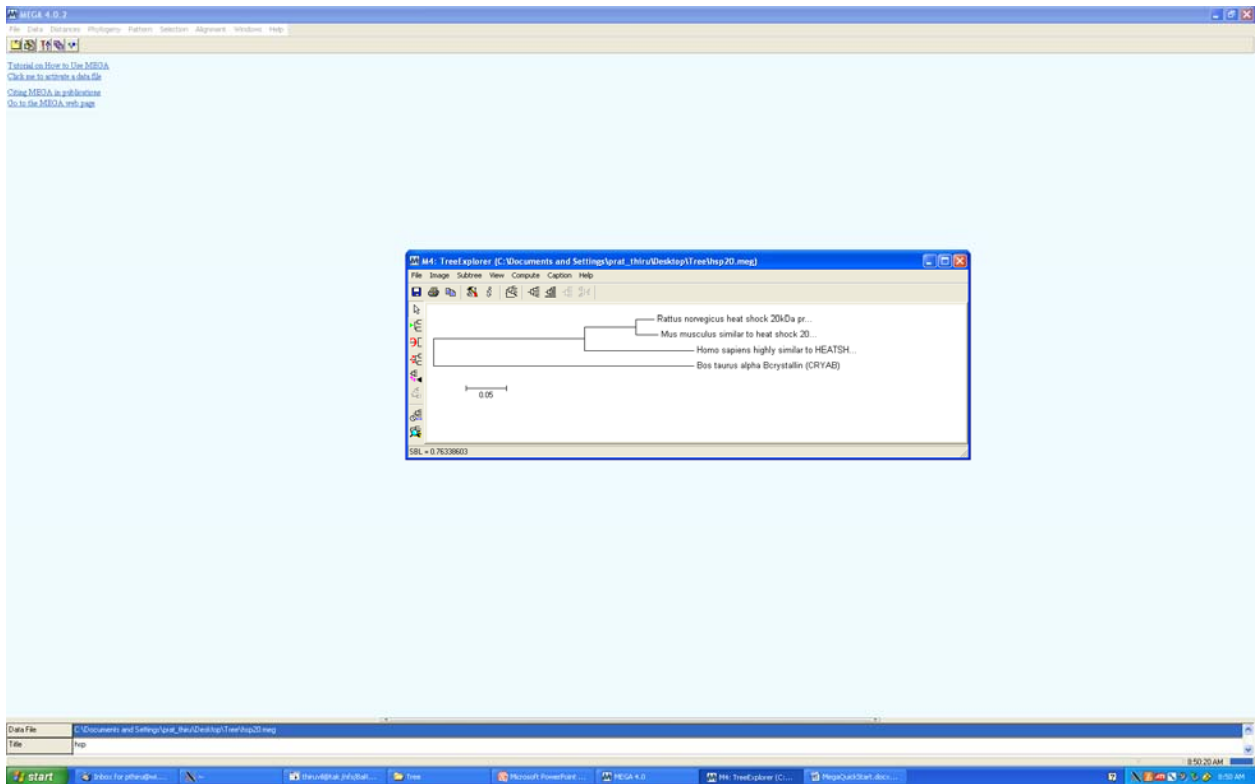


Figure 2: Tree Explorer in MEGA