BHARATHIDASAN UNIVERSITY

Tiruchirappalli- 620024,
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Programme : M.Sc., Biomedical Science

Course Title : Bioinformatics
Course Code : BM35S1BI

Unit - III

TOPIC: Method for Construction and Representation of Phylogenetic tree using MEGA Software.

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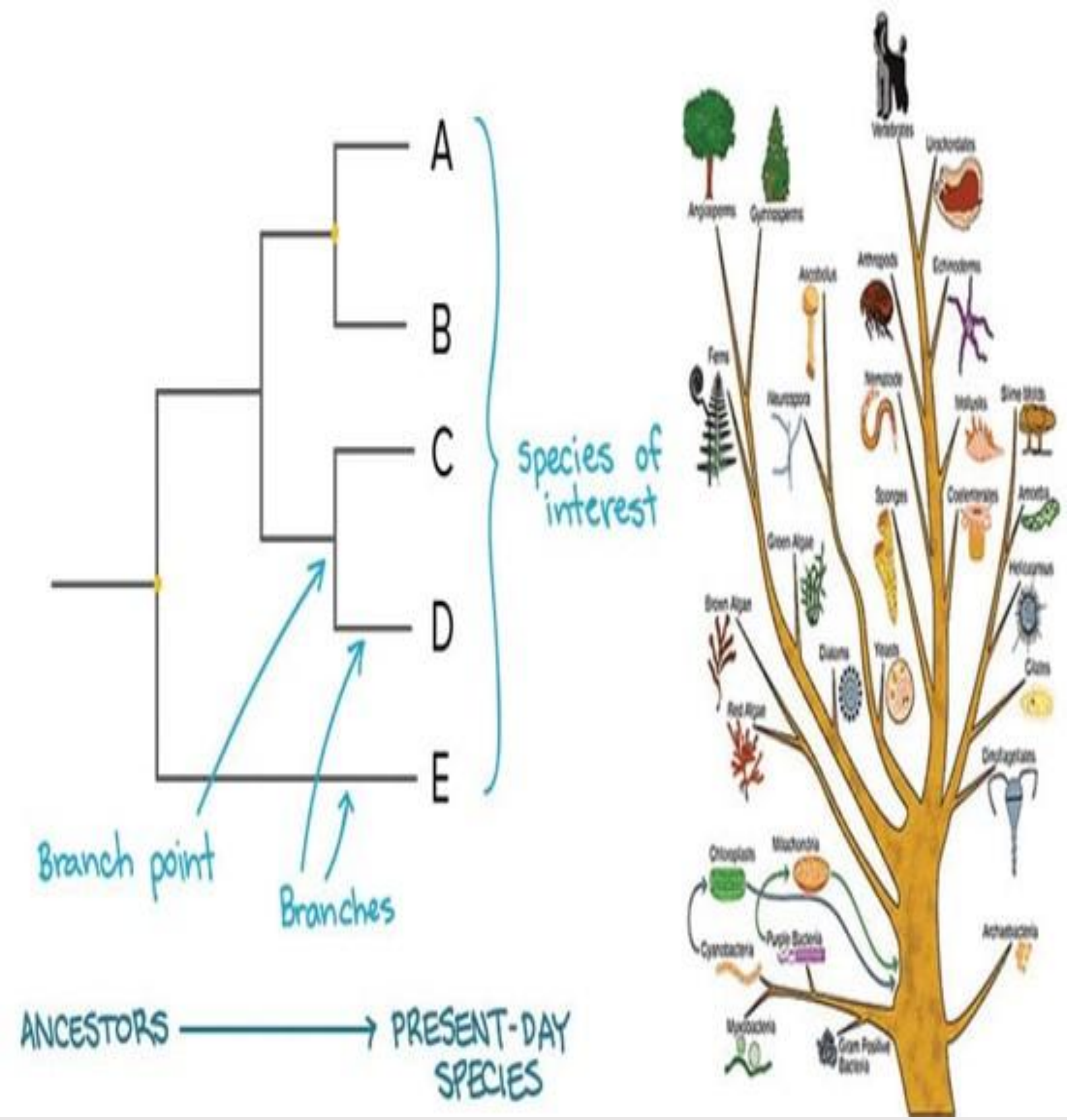
Method for construction and representation of phylogenetic tree using MEGA software

MEGA (Molecular Evolutionary Genetics Analysis)

- It is a computer software for conducting statistical analysis of molecular evolution and for constructing phylogenetic tree.
- MEGA 5 is an integrated program that carries out all four steps in a single environment, with a single user interface eliminating the need for interconverting the formats.
- MEGA 5 is sufficiently flexible to permit using other programs for particular steps.

- In MEGA software phylogenetic tree can be constructed using four steps they are :
    1 .Acquiring the sequences
    2 .Aligning the sequences
    3 .Estimate the tree
    4 .Present the tree



1. Acquiring the sequences :

- If the investigator is interested in a particular gene or protein that has been the subject of investigation and wishes to determine the relationship of that gene or protein to its homologs.
- If the sequences are not actually descended from a common ancestor , then it will be meaningless and may be quite misleading.
- MEGA 5 opens its own browser window to show a nucleotide BLAST page from National Center for Biotechnology Information (NCBI).
- There is a set of five tabs near the top of that page (blastn, blastp, blastx, tblastn and tblastx).
- If your sequence is that of a protein click the blastp tab to show the standard protein **BLAST** page.

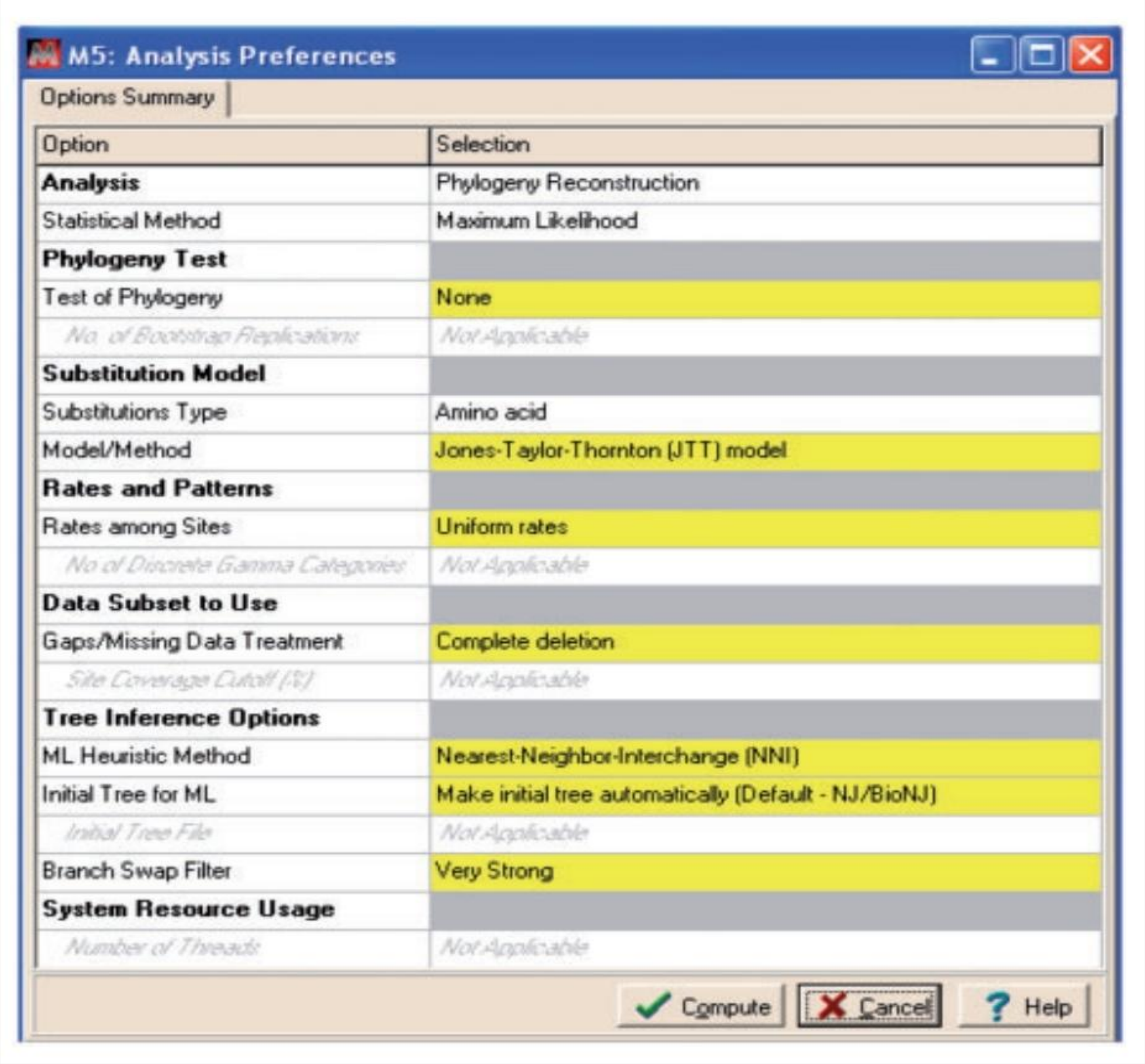
2. Aligning the sequences :

- The alignment explorer shows a name for each sequence at the left, followed by the sequence with coloured residues.
- If the name is very long, that name would eventually appear on the tree, and long names are generally undesirable. But we could edit the names only at this stage . Simply double click each name and change it to something more suitable.
- If your sequence is DNA you will see two tabs: **DNA Sequences** and **Translated protein sequences**.
- The DNA tab is chosen by default. Click the translated protein sequences tab to see the corresponding protein sequence.

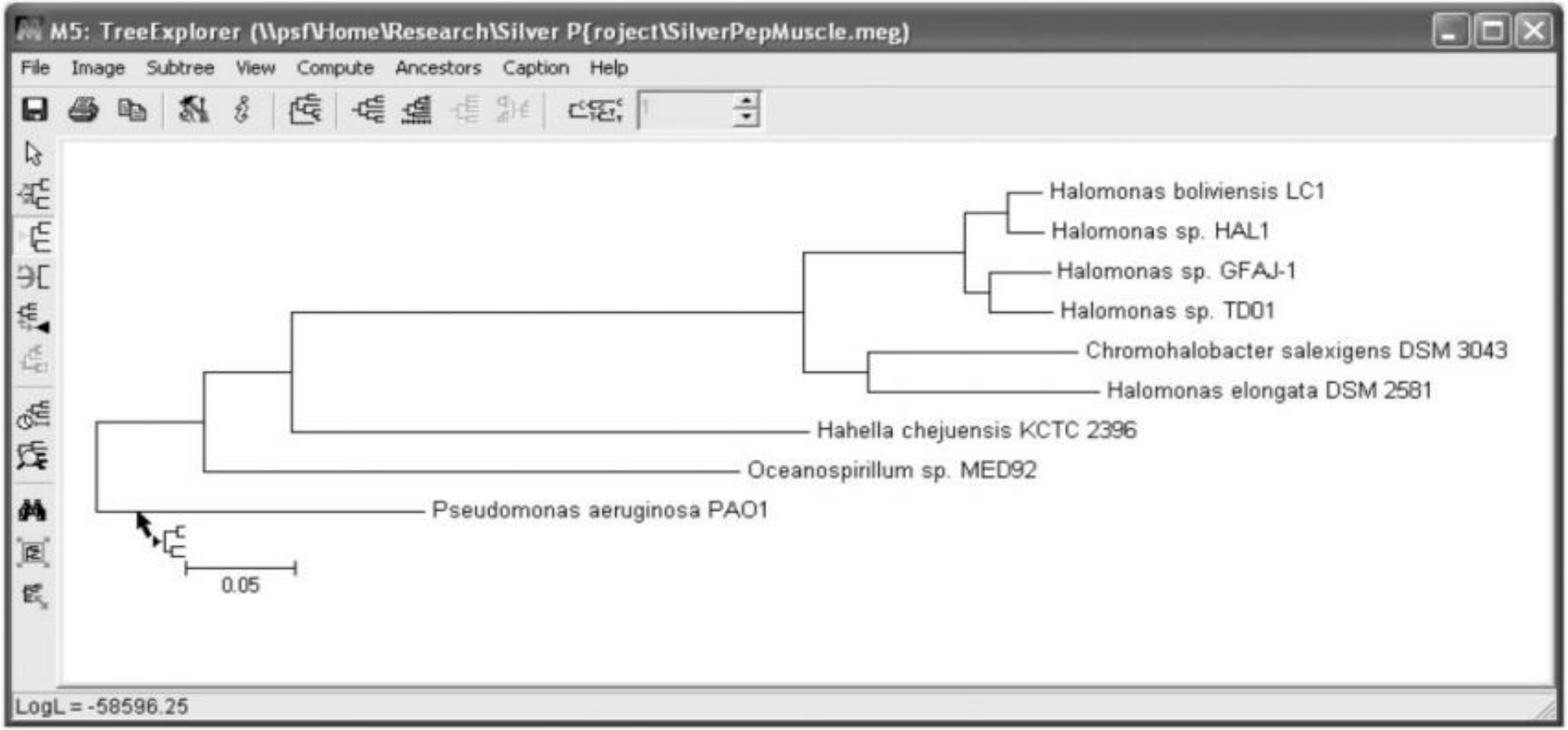
3. Estimate the tree :

- There are several methods for estimating phylogenetic trees (Neighbor joining, Maximum parsimony, Maximum Likelihood), but this is about Maximum Likelihood (ML).
- ML uses a variety of substitution models to correct for multiple at the same site during the evolutionary history of the sequences.
- When a complete window appears that lists the models in order of preference. Note the preferred model, then estimate the tree using that model.

- The yellow areas are parameters that we can modify:
  1. **Model/ Method**
  2. **Rates among sites**
  3. **Gap / missing data treatment.**



Option	Selection
Analysis	Phylogeny Reconstruction
Statistical Method	Maximum Likelihood
Phylogeny Test	
Test of Phylogeny	None
No. of Bootstrap Replications	*Not Applicable*
Substitution Model	
Substitutions Type	Amino acid
Model/Method	Jones-Taylor-Thornton (JTT) model
Rates and Patterns	
Rates among Sites	Uniform rates
No of Discrete Gamma Categories	*Not Applicable*
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Tree Inference Options	
ML Heuristic Method	Nearest-Neighbor-Interchange (NNI)
Initial Tree for ML	Make initial tree automatically (Default - NJ/BioNJ)
Initial Tree File	*Not Applicable*
Branch Swap Filter	Very Strong
System Resource Usage	
Number of Threads	*Not Applicable*



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LogL = -58596.25
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When the preferences are set, click the compute button to compute the tree. Eventually , a tree explorer window will open that displays the tree.

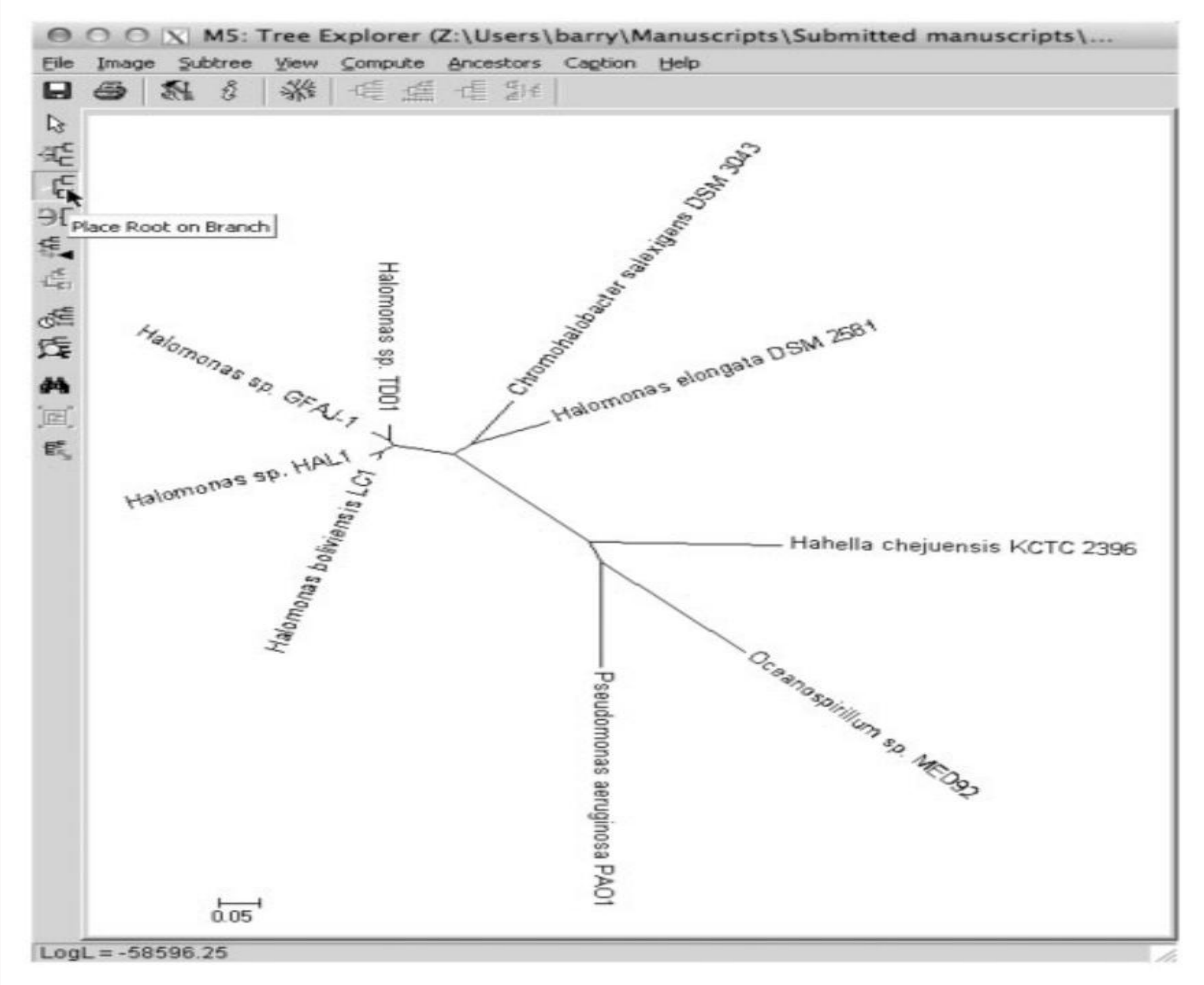
4. Present the tree :

- A phylogenetic tree consists of external nodes that represent the actual sequences that exist today.
- Internal nodes that represent hypothetical ancestors, and branches that connects nodes to each other.
- The length of the branches represent the amount of change that is estimated to have occurred between a pair of nodes.
- The trees can be presented in two forms , they are:

1. Unrooted tree
2. Rooted tree

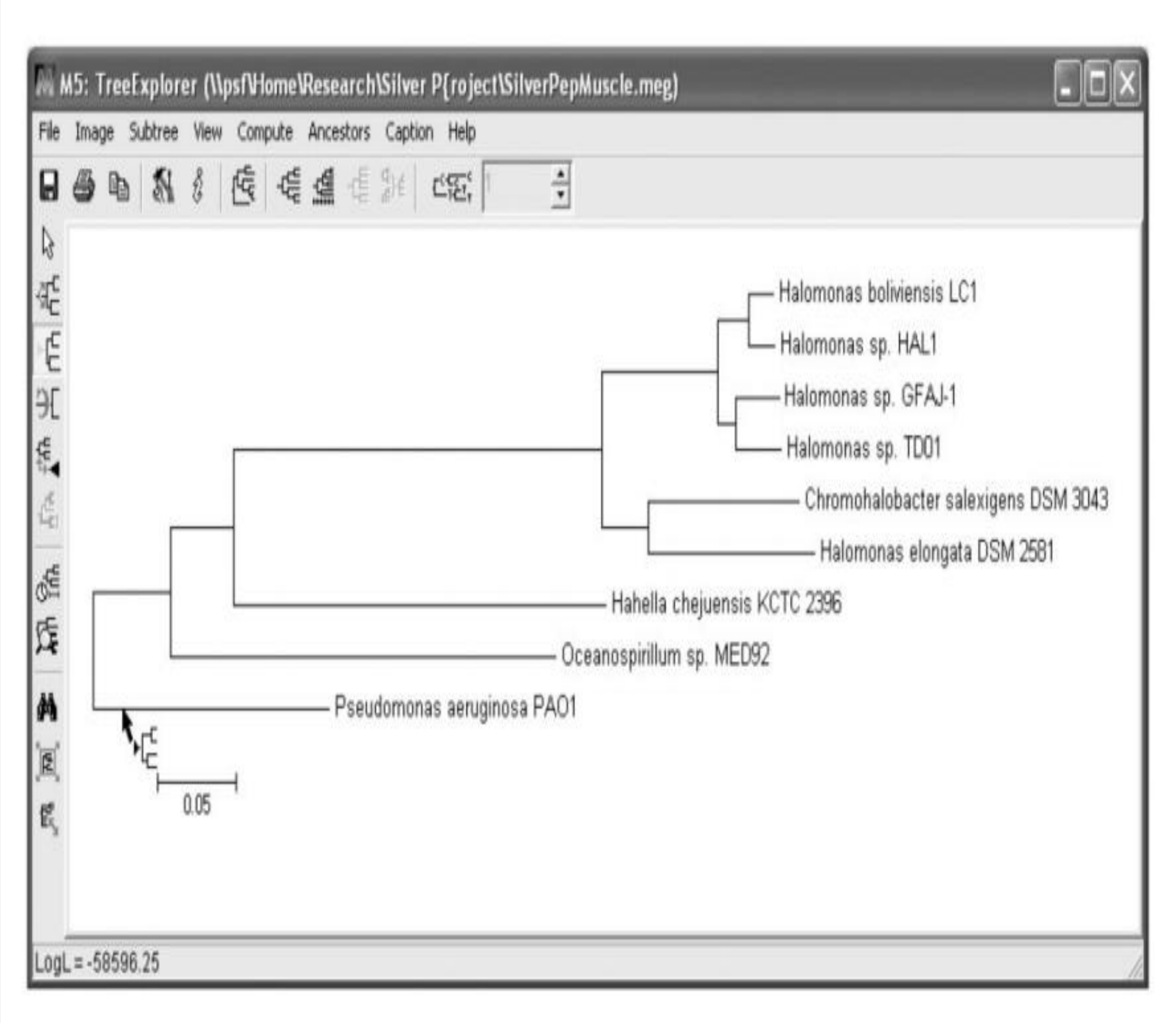
UNROOTED TREE

- The radiation or unrooted is a better way to draw because it does not allow the viewer to assume a root that is known.
- To avoid the unjustified implication of directionality , it is important to specify in the figure that the tree is unrooted.



Rooted Tree

- A rooted tree provides direction to the evolutionary process, with the order of descent from the root towards the tip.



LogL = -58596.25

Reference

Hall, B.G., 2013. Building phylogenetic trees from molecular data with MEGA. *Molecular biology and evolution*, *30*(5), pp.1229-1235.

THANK YOU