

## Assignment 3

Phylogeny construction by MEGA-software <http://www.megasoftware.net/>.

The program has been installed in the computers in class C128. You can also install it in your own computer. However, only the Windows-version is readily usable.

During the course session 15. Sept the Example dataset (in course webpage) is used as an example for performing neighbor-joining, UPGMA and parsimony phylogenies.

You home-work (to be submitted in week 40, details given later):

- Collect a dataset of sequences from <http://www.ncbi.nlm.nih.gov/>. Start, for example, by a query of an animal, bacteria, a gene, whatever sounds interesting. Pick up one sequence item and by BLASTing collect a reasonable dataset, 20-30 sequences.
- Construct a FASTA-file
- Align the sequences by Clustal <http://www.ebi.ac.uk/Tools/clustalw2/index.html>, or some other facility (aligning is also possible by the MEGA-software)
- Construct a MEGA-file and perform neighbor-joining, UPGMA and parsimony phylogenies.
- Use Jukes-Cantor model and Kimura 2-parameter models. Explain the differences.
- Perform the analyses with and without bootstrapping. Explain the differences.
- Learn (by inspecting the MEGA “help”), how are the distances between the sequences computed.
- Consult [sirkka-liisa.varvio@helsinki.fi](mailto:sirkka-liisa.varvio@helsinki.fi) if you have problems.

You can work alone or as a group of two students.