ClustalO

Clustal is a widely used multiple sequence alignment program. It is used for both nucleotide and protein sequences.Clustal Omega is the latest addition to the Clustal family. It offers a significant increase in scalability over previous versions, allowing hundreds of thousands of sequences to be aligned in only a few hours. It will also make use of multiple processors, where present.

Clustal home page: http://www.clustal.org

If you are using Windows OS, there are no additional configuration steps required, as *ClustalO* executable file is included to the UGENE distribution package. Otherwise:

- Install the *Clustal* program on your system.
- Set the path to the *ClustalW* executable on the *External tools* tab of UGENE *Application Settings* dialog.

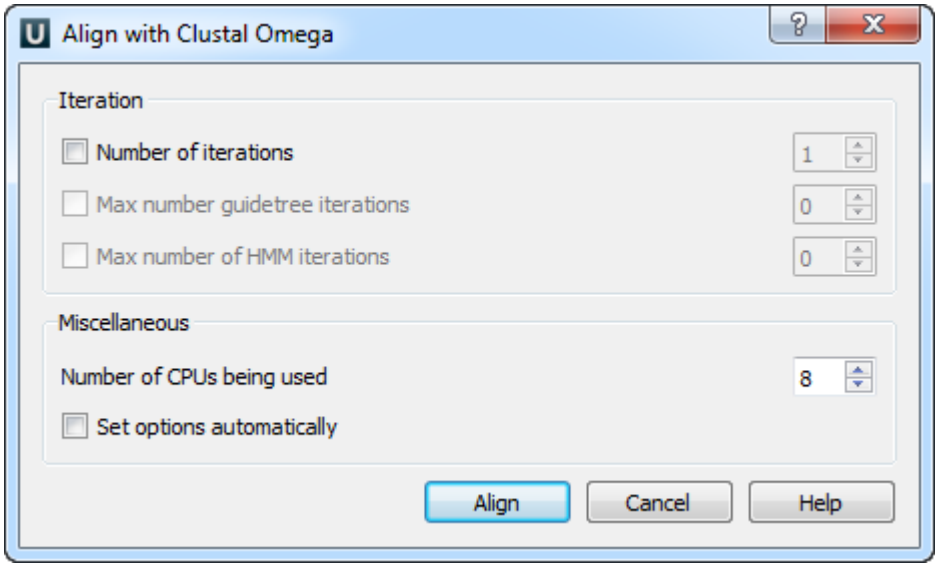
Now you are able to use *ClustaOl* from UGENE.

Open a multiple sequence alignment file and select the *Align with ClustalO* item in the context menu or in the *Actions* main menu. The *Align with ClustalO* d ialog will appear (see below), where you can adjust the following parameters:

Number of iterations — number of (combined guide tree/HMM) iterations.

Max number guidetree iterations — maximum guide tree iterations.

Max number of HMM iterations —maximum number of HMM iterations.

Number of CPUs being used - number of processors to use.

Set options automatically - set options automatically (might overwrite some of your options).