

# MAFFT

Originally, MAFFT is a multiple sequence alignment program for UNIX-like operating systems. However, currently, it is available for macOS, Linux, and Windows. It is used for both nucleotide and protein sequences.

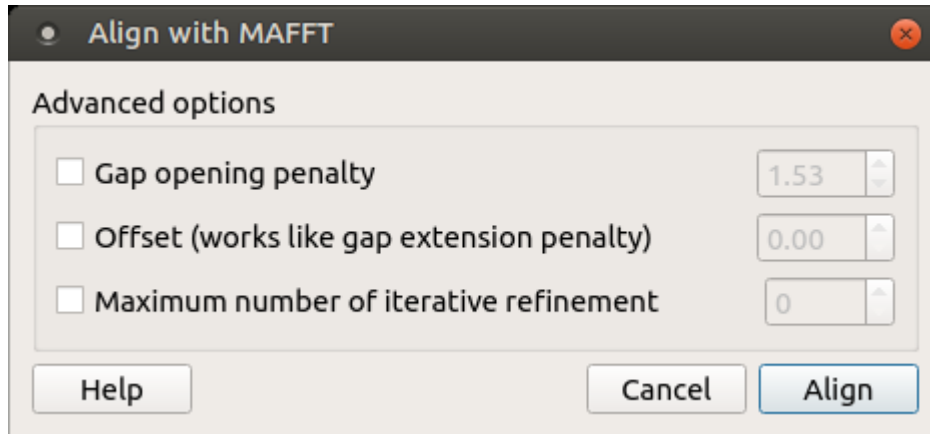
**MAFFT homepage:** <http://mafft.cbrc.jp/alignment/software>

To make *MAFFT* available from UGENE:

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

For example, on Windows, you need to specify the path to the *mafft.bat* file.

To use *MAFFT* open a multiple sequence alignment file and select the *Align with MAFFT* item in the context menu or in the *Actions* main menu. The following dialog appears:



The following parameters are available:

*Gap opening penalty* — Gap opening penalty at group-to-group alignment.

*Offset (works like gap extension penalty)* — offset value, which works like the gap extension penalty, for group-to-group alignment.

*Maximum number of iterative refine* — specifies the number of cycles of iterative refinement to perform.