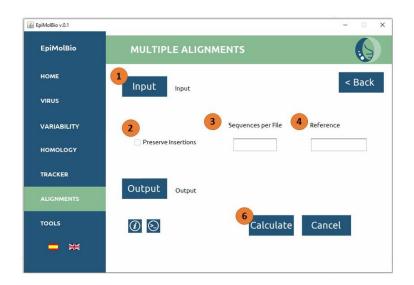# Multiple Alignments

It allows aligning amino acid and nucleotide sequences using the MUSCLE v3.8.31 program.

① Select the input folder. It should only contain .fasta files NT or AA sequences that you want to align.

② Choose whether to retain insertions (alignment will be done without a reference sequence).

③ Enter 1 to align incomplete sequences or for lightweight alignments. For sequences with many mutations (including deletions and insertions), enter the total number of sequences in the input file for lightweight alignments, or a value between 100-500 for heavy alignments.

④ Enter the reference sequence in NT or AA according to the input files, without line breaks or spaces.

⑤ Select the output folder without naming the file. It will be automatically named as 'Aligned_InputFileName.fasta'.

⑥ Click Calculate.

The output is a .fasta file with the aligned sequences.

More information about this function can be found in the User Manual, section:

V. ALIGNMENTS V.1 MULTIPLE ALIGNMENTS