Alignments Delete Insertions

It allows automatically removing insertions from a sequence with respect to a reference with gaps after performing the alignment.

① Select the input folder. It should only contain .fasta files of aligned NT or AA sequences to be analyzed.

② Enter the reference sequence with gaps and without line breaks or spaces.

③ Select the output folder without entering the file name. It will be automatically named as 'Insertions_Deleted_InputFileName.fasta'.

④ Click Calculate.

A .fasta file will be generated with the sequences having insertions removed.

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

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