Tools Header Filtering

It allows you to filter one or multiple ".fasta" format files using parameters from their headers.

① Select the input folder. It should only contain the .fasta files you want to filter.

② Choose the item for which the filtering will be performed.

③ Enter the character that serves as a separator in the header of the sequences.

④ You can select "Remove Gaps" to eliminate all gaps without using a reference sequence, and "Translate" to translate from NT to AA.

⑤ Select the output folder without entering the file name. It will be automatically named as 'Header_Filter_InputFileName.fasta'.

⑥ Click Calculate.

A .fasta file will be generated for each filtered item, containing the ".fasta" sequences that share the same characters for that item.

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

VI. TOOLS VI.2 FILTERS VI.2.A) HEADER FILTERING