Tracker Similarity

It allows searching for target sequences of interest within a set of longer sequences based on a reference sequence.

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

② Choose whether to translate the resulting sequence or not.

③ Select "Full Range" if you want to search throughout the length of the input sequences or "Select Range" to search within a specific region.

④ If you chose "Select Range," enter the positions that encompass the region where you want to search.

⑤ Define the minimum similarity percentage that the output sequences will have with respect to the reference sequence.

⑥ Enter the reference sequence without line breaks or spaces.

⑦ Select the output folder without naming the file. It will be automatically named as Tracked_Similarity_InputFileName.fasta.

⑧ Click Calculate.

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

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

IV. TRACKER IV.1 SIMILARITY