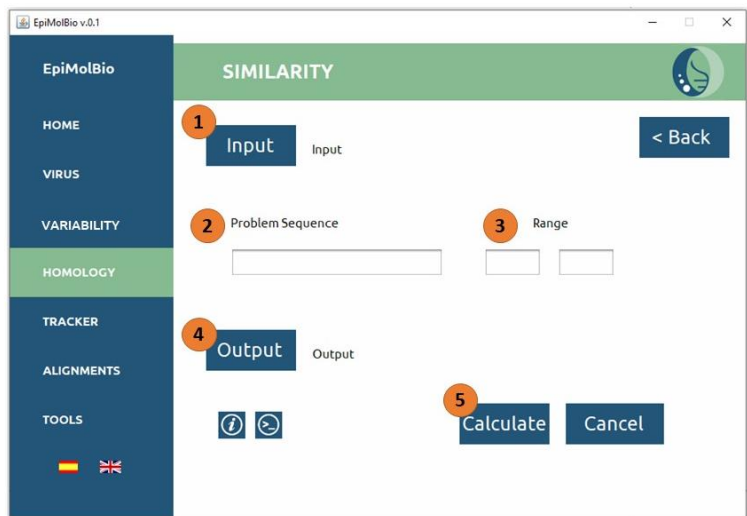# Homology Similarity

It allows searching for a user-introduced target sequence among the sequences in the input file, obtaining the proportion of sequences per file that contain the target sequence.

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

② Enter the target sequence (e.g., KLKPGMDGPKVK).

③ Enter the positions of the input protein that encompass the region where you want to search.

④ Select the output folder and enter the file name in the following format: /NAME.html.

⑤ Click Calculate.

The .html file is a table containing the target sequence, the names of the input files, the frequency of occurrence of the target sequence in each file, colored according to the color code, and the total number of sequences in the analyzed file.

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

III. HOMOLOGY III.1 SIMILARITY