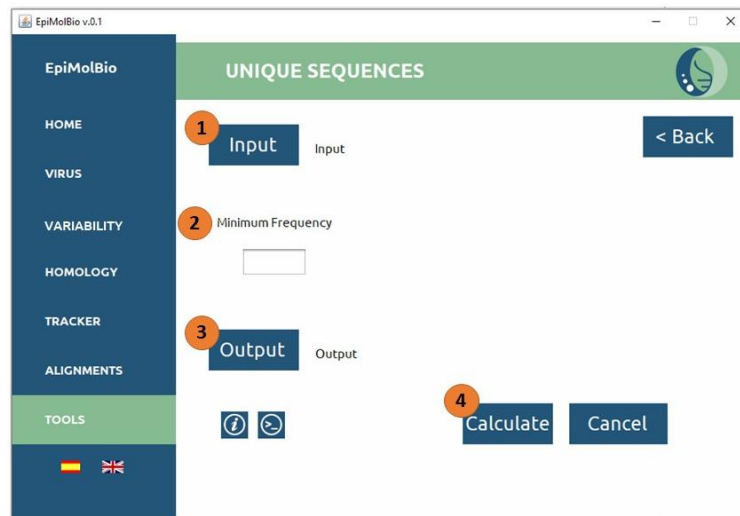


Tools Unique Sequences

It allows you to remove duplicated sequences from one or multiple input .fasta files.



- ① Select the input folder. It should only contain the .fasta files you want to filter.
- ② Enter the filtering frequency as a number with one decimal place (e.g., 0.0 to keep all unique sequences).
- ③ Choose the output folder without entering the file name. It will be automatically named as 'Unique_InputFileName.fasta'.
- ④ Click Calculate.

A single .fasta file with the filtered sequences will be generated.

More information about this function can be found in the User Manual, section:
VI. TOOLS VI.1 FILE EDITING VI.1.B) UNIQUE SEQUENCES