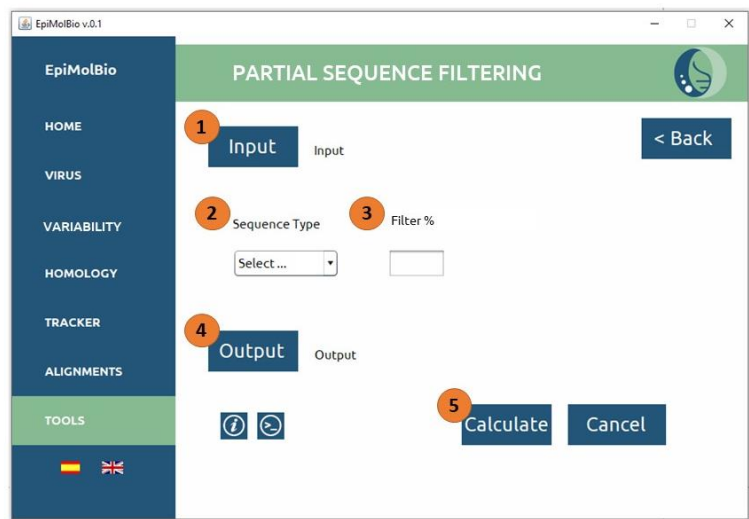


Tools Partial Sequence Filtering

It allows you to filter sequences from .fasta format files based on their quality, depending on the quantity of unknown residues they contain ('?' in AA sequences or 'N' in NT sequences).



- 1 Select the input folder. It should only contain the .fasta files you want to filter.
- 2 Select whether the input files are in NT or AA format.
- 3 Enter the filtering percentage with one decimal place (e.g., 95.0 to remove sequences with 5% or more of '?' or 100.0 to remove all sequences with unknown residues).
- 4 Select the output folder without entering the file name.
- 5 Click Calculate.

A .fasta file containing the sequences filtered by their quality will be generated, along with an .html file displaying the number of total sequences, recovered sequences, lost sequences, and the percentage of lost sequences.

Partial Sequence Filtering				
File	Total Sequences	Recovered Sequences	Lost Sequences	Loss Percentage
PR_procesado_traducido.fasta	124806	62516	62290	49.909%
Total	124806	62516	62290	49.909%

More information about this function can be found in the User Manual, section:
VI. TOOLS VI.2 FILTERS VI.2.C PARTIAL SEQUENCE FILTERING