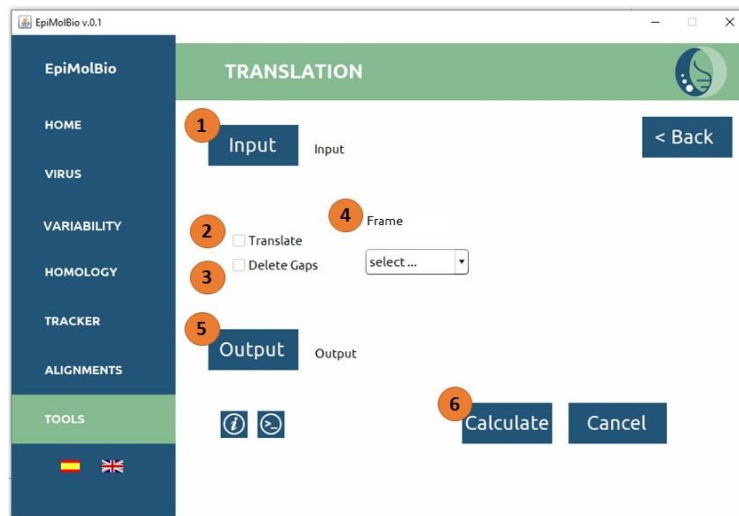


## Tools Translation

**It allows you to translate .fasta sequences from nucleotides to amino acids.**



- ① Select the input folder. It should only contain the .fasta files in NT format that you want to translate.
- ② Check the "Translate" box to perform the translation.
- ③ Optionally, check the "Delete Gaps" box.
- ④ Select the reading frame to set the NT of the first codon. Typically, this is Frame 1 (provided they are in-frame).
- ⑤ Select the output folder without entering the file name. It will be automatically named as 'Translated\_InputFileName.fasta' or 'Translated\_No\_Gaps\_InputFileName.fasta'.
- ⑥ Click Calculate.

You will obtain a .fasta file with the same sequences as the input file, but translated into amino acids.

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

VI. TOOLS VI.3 TRANSLATION