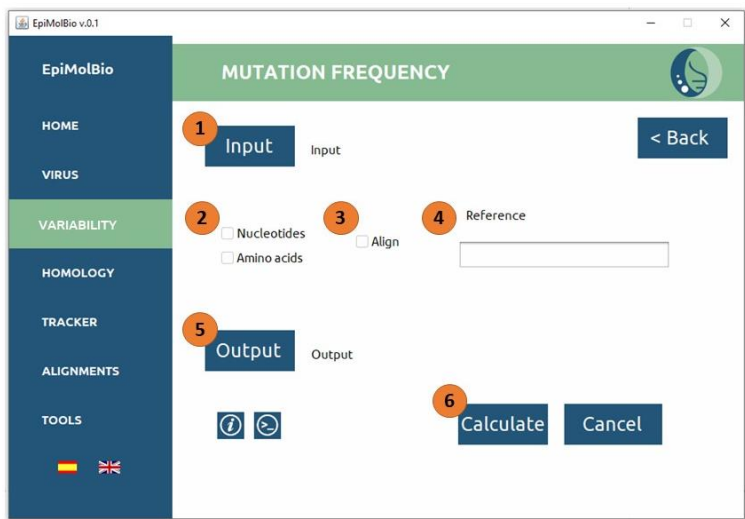


Variability Mutation Frequency

It generates a set of parameters related to the frequency of mutations in a group of sequences, such as mutation frequency, conservation percentage, and average mutations per sequence.



- 1 Select the input folder. It should only contain .fasta files of sequences to be analyzed in either nucleotide (NT) or amino acid (AA) format.
- 2 Mark NT/AA according to the format of the input sequences.
- 3 Mark Align if the input sequences are unaligned.
- 4 Enter the reference sequence without line breaks.
- 5 Select the output folder and enter the file name in the following format: /NAME.csv.
- 6 Click Calculate.

	A	B	C	D	E	F
1	File	Mut. Frequency	Mut. Frequency %	Conservation %	Average Mut. Sec.	Total Sec.
2	1-2022-AS.fasta	0.10456	10.46%	89.54%	10.138	94
3	1-2022_CL.fasta	0.01139	1.14%	98.86%	0.84	287

The .csv file displays the following information for each input file: file name, number of mutated residues / total valid positions (Mutation Frequency), mutation frequency times 100 (Mutation Frequency %), 100 minus mutation frequency percentage (Conservation %), number of mutated residues / total sequences in the input file (Average Mutations per Sequence), and the total number of sequences per file (Total Sequences).

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

II. VARIABILITY II.5 MUTATION FREQUENCY