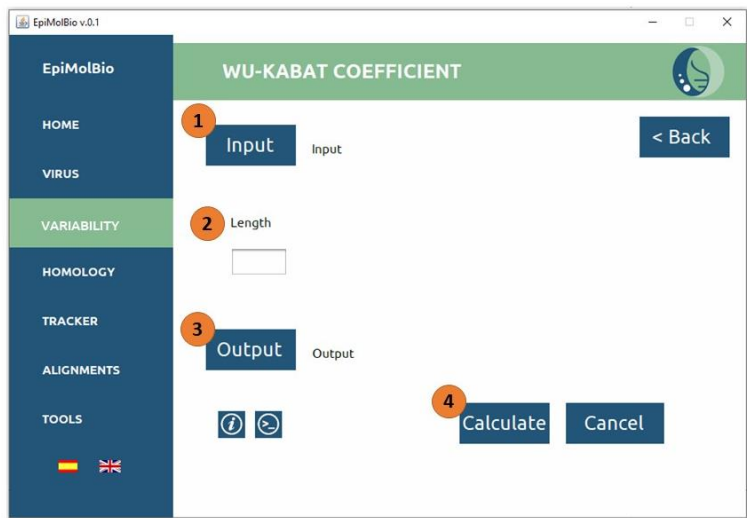


Variability Wu-Kabat Coefficient

It allows obtaining the Wu-Kabat variability coefficient of protein sequences to study the susceptibility of an amino acid position to evolutionary replacements.



- ① Select the input folder. It should only contain .fasta files of aligned amino acid sequences to be analyzed (one or multiple files).
- ② Enter the length of the protein to be analyzed in AA.
- ③ Enter the reference sequence in AA without line breaks.
- ④ Select the output folder and enter the file name in the following format: /NAME.csv.
- ⑤ Click Calculate.

	A	B	C	D	E	F
1	File	Position	Wu-Kabat	Number of Sequences	Number of Amino Acids	Frequency
2	PR_01_AE.fa	1	7.007	26838	7	26810
3	PR_01_AE.fa	2	11.024	26649	11	26591
4	PR_01_AE.fa	3	5.007	26831	5	26793
5	PR_01_AE.fa	4	9.013	26816	9	26778
6	PR_01_AE.fa	5	7.008	26780	7	26750
7	PR_01_AE.fa	6	5.004	26836	5	26817
8	PR_01_AE.fa	7	10.025	26536	10	26470
9	PR_01_AE.fa	8	5.004	26792	5	26771
10	PR_01_AE.fa	9	6.003	26613	6	26601
11	PR_01_AE.fa	10	14.866	25952	13	22694
12	PR_01_AE.fa	11	9.044	26416	9	26287
13	PR_01_AE.fa	12	12.628	26469	12	25153
14	PR_01_AE.fa	13	17.825	26150	10	14670
15	PR_01_AE.fa	14	13.657	26270	13	25006

The .csv file is a table containing the following information for each analyzed file: file name, residue position, Wu-Kabat coefficient, number of valid sequences for each position, number of different amino acids at each position, and the absolute frequency of the most common amino acid for that position.

More information about this function can be found in the User Manual, section:
II. VARIABILITY II.4 WU-KABAT COEFFICIENT