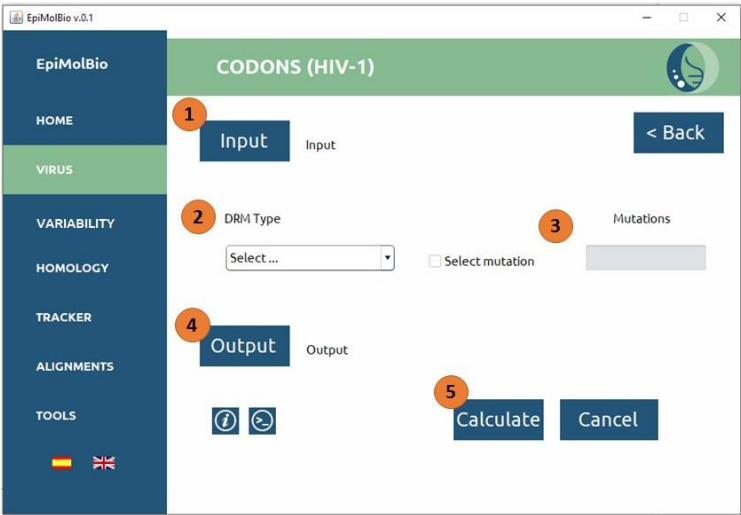# HIV Resistance Mutations - Codons

It allows obtaining the percentage of codons that, when translated, generate resistance mutations (DRM) relative to a reference sequence, from nucleotide sequences of the Pol protein of HIV-1.

① Select the input folder. It should only contain the .fasta files of the Pol protein to be analyzed, in NT (nucleotide) format and aligned (1 file or multiple files).

② Choose the type of DRM analysis you want to perform, selecting from mutations against PIs (Protease Inhibitors), NRTIs (Nucleoside Reverse Transcriptase Inhibitors), NNRTIs (Non-Nucleoside Reverse Transcriptase Inhibitors), and INSTIs (Integrase Strand Transfer Inhibitors).

③ Optionally, instead of analyzing the entire sequence, you can search for specific mutations in one or multiple codons. To do this, check the "Select Mutation" box and write one or more DRMs in AA format in the "Mutations" box. If there are multiple mutations, separate them by "," without spaces.

④ Output: If "Select Mutation" has not been checked, select the output folder and enter the filename in the following format: /NAME.html. Otherwise, select the output folder without naming the file; it will be automatically named with the DRM entered in the "Mutations" box, generating a file for each introduced DRM.

⑤ Click Calculate.

The output file is a table that displays the positions with DRM. All the found residues for each position appear alongside the codon that encodes them, and the percentage of occurrence of that codon is colored according to the color code. DRMs are indicated with an asterisk (*). Non-coding codons will be indicated with a question mark (?). At the end of each line, the total number of valid sequences for that position present in the analyzed file is shown.

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

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