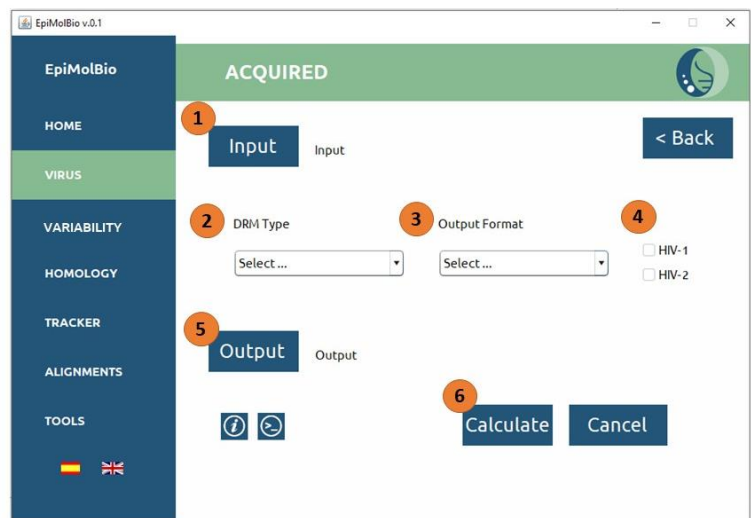# HIV Aquired Drug Resistance Mutations

It allows obtaining the percentage of acquired resistance mutations, with respect to a reference sequence, from amino acid sequences of HIV Pol protein.

① Select the input folder. It should only contain the .fasta files of the Pol protein to be analyzed, translated into amino acids 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), INSTIs (Integrase Strand Transfer Inhibitors), and CAI (Capsid Inhibitors).

The MDRs are summarized in https://cms.hivdb.org/prod/downloads/resistance-mutation-handout/resistance-mutation-handout.pdf (last updated on 25-10-2022) from the Stanford HIV Drug Resistance Database v9.5.

③ Choose the desired output format by selecting from **List, Table and Summary Table**:

List

It displays the positions with mutations along with the corresponding residues and their percentage, marking DRMs with an asterisk (*) and indicating their classification in the title. The total number of valid sequences for each position appears at the end of each line.

Table

Shows in the first row: the type of DRM according to its classification. In the first column: the names of the input files. In the rest of the columns, it displays the detected DRM with the cell colored according to the percentage of occurrence in each input file.

Summary Table

It displays in the first column: the names of the input files used for generating the analysis. In the next column: the type of DRM according to its classification. Below this it shows the corresponding found residues for the DRMs, colored based on their percentage following the color-code..

④ Choose the type of HIV you wish to analyze, selecting between HIV-1 and HIV-2. The program automatically establishes the reference sequence.

⑤ Select the output folder and input the filename as follows: /NAME.html.

⑥ Click Calculate.

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

I. VIRUS I.1 HIV I.1.A) RESISTANCE MUTATIONS (Individual Acquired Mutations)