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Digital signal processing-based translation of genomic information into phenotypic characteristics: HIV-1 drug resistance as a case study

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Background: Sequence information of protein targets or proteins encoding bio-active substances (genomic information) engaged in clinical investigations (phenotypic assessments) is usually deposited in Uniprot, etc. Their possible translation into phenotypic features has become a concern.

Aim: Here, we demonstrate how genomic information could be translated back into phenotypic properties.

Materials and method: As preliminarily determined, the consensus and 292 mutated sequences of HIV-1 protease enzyme (genomic information) were first translated into numerical sequences (signals) representing their physio-chemical and structural (phenotypic) characteristics using the 22 amino acid scales (AASs) involved. These signals are further processed using informational spectrum method (ISM) and aggregated to obtain the entire phenotypic characteristics. There are about 575 scales.

Result: Table 1 is the ISM-based results from 19 mutants found at position 50, and one hydrophobicity-based scale, BROC820102.

Discussion: Bio-molecules first bind using Electron-ion Interaction Potential scale. Thereafter, their molecular contents mingle at different degrees (Figure 1) using physio-chemical and structural scales.

Conclusion: Computerizing this process will help revolutionize bio-assessments. The procedure has helped develop several biomedical devices.

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