An information model for the classification of HIV-1 virus inhibitors

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Motivation

Classification algorithms are proposed based on information entropy. It is studied the feasibility of mixing a given human immunodeficiency virus type 1 (HIV-1) inhibitor with dissimilar ones, in a complex drug. The 31 inhibitors are classified by structural chemical properties. Many classification algorithms are based on information entropy. An excessive number of results appear compatible with the data, suffering combinatorial explosion.

Methods

However, after the equipartition conjecture one has a selection criterion. According to this conjecture, the best configuration of a flowsheet is that in which entropy production is most uniformly distributed. The analysis includes inhibitors fitting the general scheme: (base derivative)-(furan ring). The base portion is often a guanine or cytosine derivative; the furan normally contains one O heteroatom.

Results

The structural elements of an inhibitor can be ranked according to their inhibitory activity, in the order: base > furan. In didanosine (ddI) the base is a guanine derivative, and the furan contains only one O heteroatom (N4O3S0P0X0, X = F, Cl, Br); its associated vector is <11111>. The ddI is selected as a reference. In some inhibitors the base is a guanine (ddI, novel proposed ligand), in some others, a cytosine derivative [zalcitabine (ddC), stavudine (d4T), lamivudine (3TC)]. In most inhibitors the furan contains only one O heteroatom (ddI, ddC, d4T, novel proposed ligand, N3-4O3S0P0X0), while in 3TC the furan includes one O and one S heteroatoms (N3O3S1P0X0). The analysis is in agreement with principal component analysis and other classification taken as good. The good comparison of our classification results, with other taken as good, confirm the adequacy of the property vector selected for the molecular structures of the HIV-1 inhibitors. Information entropy and principal component analyses permit classifying the inhibitors and agree. The inhibitors are grouped and the classical classes are recognized: non-nucleoside reverse transcriptase, nucleoside reverse transcriptase, nucleotide reverse transcriptase and protease inhibitors. The final classification is shown more precise. A periodic classification is proposed. The periodic law has not the rank of the laws of physics: (1) the properties of the human immunodeficiency virus type 1 inhibitors are not repeated; perhaps their chemical character; (2) the order relationships are repeated with exceptions. The analysis forces the statement: The relationships that any inhibitor p has with its neighbour p + 1 are approximately repeated for each period. Periodicity is not general; however, if a natural order of the inhibitors is accepted the law must be phenomenological.

Availability: http://www.uv.es/~uiqt/index.htm

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