

Creation and analysis of an agent-based computer model of the AIDS epidemic using an algorithm for explicit calculation of the HIV replicability

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Motivation and Aim: The epidemic of HIV spread is a serious problem for the whole world. A large number of models describe HIV at different levels of the biological organization, from population-epidemiological level to molecular-genetic one. However, we have not met models that combine genetic and population levels together. The aim of the study was to develop an agent-based computer model of the HIV epidemic, which would take into account both the genetic variability of the virus and its corresponding variability in replication, as well as socio-epidemic aspects.

Methods and Algorithms: We used the method of computer prediction of affinity of TBP/TATA complex [1], which made it possible to assess the replication and virulence of different genetic variants of HIV. Python programming language was used to process the data. The agent-based model was implemented in the C++ programming language.

Results: The analysis of the diversity of virulence and replicativeness of various genetic variants of HIV-1 was carried out using statistical methods for predicting the affinity of the TBP / TATA complex. Clustering of 2500 HIV strains into 3 visible groups was obtained. An agent-based model for the spread of HIV in the human population has been developed.

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References

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