Modeling the dynamics of HIV/AIDs with computer simulations

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Abstract

Computer simulations can predict underlying pathophysiological mechanisms, progression, and results of treatment for chronic diseases. These provide information on human immunodeficiency virus (HIV) multiplication, pathological outcomes, management, and therapeutic consequences. Such techniques give access to internal mechanisms and strategic antiviral interventions. Epidemiologic computational programs not only recognize the effect of HIV on populations but frequently process medical records to estimate the latest secondary infections in humans suffering from HIV. AIDS is a chronic disease triggered by the HIV retrovirus, causing unending and progressive immune dysfunction due to the decreased CD4 lymphocyte levels. A range of models based on machine learning algorithms has been evolved to understand the dynamics of the acquired immunodeficiency syndrome (AIDS) epidemic. Models have played a chief role in raising our knowledge of the variable disease patterns. These work under specific rules and their applications may be limited. Machine learning and multi-dimensional scaling simulation methods such as hybrid (2 phases) system equipped with IT2FL (interval type-2 fuzzy logic) and DNN (deep neural network), GPSM (general-purpose simulation model) can predict progression, transmission, management of HIV/AIDS during highly active antiretroviral therapy (HAART). The intentions of healthcare researchers to gain maximum knowledge from computer programs are leading to the constant development of new or up-gradation of existing programs.

Keywords: HIV/AIDS, highly active anti-retroviral therapy, computer simulation, machine learning

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1. Introduction

Computer simulations can predict underlying pathophysiological mechanisms, progression, and results of treatment for chronic diseases. For human immunodeficiency virus (HIV) disease, computational models evaluate the progression and impact of HIV treatment techniques [1]. These provide information on HIV virus multiplication, pathological outcomes, management, and therapeutic consequences. Such techniques give access to internal mechanisms and strategic antiviral interventions. Epidemiologic computational programs not only recognize the effect of HIV on populations, but models frequently use medical records to estimate the latest secondary infections in humans suffering from HIV [2]. AIDS is a chronic disease caused by the HIV retrovirus, causing unending and progressive immune dysfunction due to the decreased CD4 lymphocyte levels. A range of models based on machine learning algorithms has been evolved to understand the dynamics of the acquired immunodeficiency syndrome (AIDS) epidemic. Models have played a chief role in raising our knowledge of the variable disease patterns. These works under specific rules and their

applications may be limited. The intentions of healthcare researchers to gain maximum knowledge from computer programs are leading to the constant development of new or up-gradation of existing programs [3].

2. Computerized simulation models for HIV/AIDS

Through an integrative review of the literature by databases [SciELO (Scientific Electronic Library Online), LILACS (Latin American & Caribbean Health Sciences Literature), BDENF, (Base de dados em Enfermagem – Nursing Database)], three descriptive variables HIV, treatment care, humanization of assistance were checked. Articles published between 2013 and 2018 were studied. Out of a total 200 articles; 12 articles were selected for discussion. Respect for patient's singularity and the sympathy to the problems faced by HIV/AIDS people may lead to humanized nursing care, which can lead to the acceptance of the disease, promoting patient's privacy and subsequent therapeutic adherence [4].

Simulation modeling has taken care of a huge collection of healthcare issues. HAART (highly active antiretroviral therapy) prolongs temporary endurance in

patients. By computational programs within lesser time, patient's records can give future disease progression. These survival estimates can also help patients and clinicians to decide future plans. Observational data were used to design a computer simulation for the prediction of survival rate in HIV/AIDS patients undergoing HAART. It was found that survival was dependent on treatment outcome, CD4 cell number and age-related mortality. It also recommended that continuous HAART can lead to healthier conditions [5, 6].

A simulation model was developed by using data from multiple medical centers from 1984 to 1985 to study the change in the number of CD4 T-cells in HIV patients. Rates of decrease in cell count and initiation of AIDS were analyzed. The model measured variable cell count within the same person as well as between different patients by three techniques that contributed to designing and clarification of clinical data [7].

Epidemiological cost-effective model for HIV (EPICE-HIV) is a multi-pattern program that is used to assess HIV progression. Similarly, SCN (sexual contact network) determines HIV transmission. Both models determined disease mechanisms, CD4 T cells levels, genetic changes, mutations, and treatment adherence. Primary treatment was the everyday use of antiretroviral therapy (ART). Plasma levels of drug and its outcome are determined by PK (pharmacokinetics) and PD (pharmacodynamics). In secondary treatment, HIV RNA values were measured and CD4 T cells were counted. Treatment compliance and interventions directly affected HIV outcomes. Model's predictions were more accurate as compared to previous trials. Multi-pattern micro-simulation models are the latest means of economical evidence-based therapeutic plans [8] as shown in figure 1.
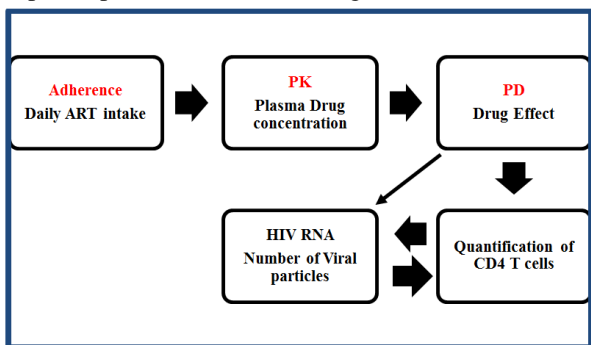

Figure 1: Model for HIV progression

Computerized simulation programs are frequently used as DSS (Decision Support System) to deal with serious health concerns like HIV and associated tuberculosis (TB). Pandemic infections of HIV and related multidrug-resistant TB (MDRTB) or DSTB (drug-resistance TB) are on the rise in Russia. Using simulation models, it was concluded that higher cure rates are due to highly active antiretroviral treatment (HAART) (Fig.2). Such models are helpful for policymakers to eradicate wide-spread HIV infection rates and associated deaths [9].
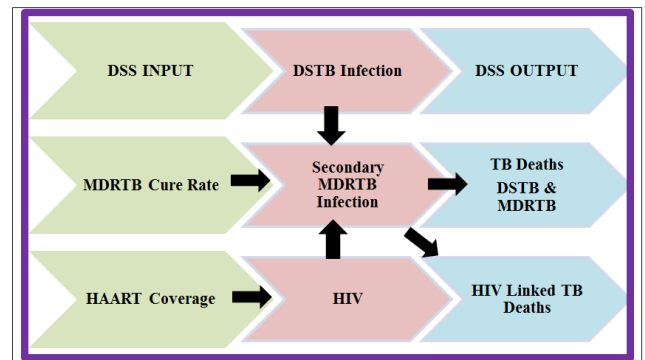

Figure 2: Computational model to predict the outcomes of HIV and associated tuberculosis

The health belief model was used to measure barriers to HIV/AIDS. Condom use, education and disease knowledge were perceived barriers [10]. Variable cognitive disabilities (CD) in HIV/AIDS patients are reported in the literature. Machine learning analyses were applied to determine CD prevalence and types. Classification algorithms identified HIV-linked CD separately from normal cognitive behaviors. Machine learning models identified those variables that were not known through statistical models [11]. HIV infection rate, the effect of the vaccine in terms of death prevention in adults and infants were studied by the simulation model with the bayesian computation method as shown in Fig.3. Vaccination reduced HIV incidence by 28.7-9% [12]. Figure 3 models the effect of HIV vaccine on HIV infections and mortality rate among the most vulnerable population that is women and children in South Africa. Similarly, through the computational program, the number and clinical features of HIV-positive populations were evaluated. During the 3 years period, 62 % population had greater viral load [13].
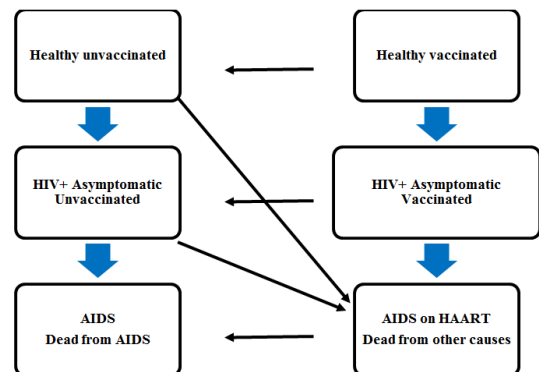

Figure 3: Simulation model to predict vaccination outcomes

As the virus involved in HIV infection has a high mutation rate, all efforts to develop a potent vaccine have failed. However, sometimes, HIV patients have broadly neutralizing antibodies (bnAbs). As these bnAbs may neutralize (half- maximum inhibitory concentration; IC50) many viral variants, therefore, a generalized vaccine is needed. An efficient computer model made from atomistic and machine leaning modeling was used to measure IC50. Firstly, amino acid sequences were used to build a structure

for each antibody and viral complex. Secondly, descriptive values were added to an artificial neural network. Such an approach was beneficial to design HIV bnAbs and to develop therapeutic strategies by simulation programs [14]. ML (machine learning) and MDS (multidimensional scaling) methods can predict the outcome of HIV/AIDS treatment. HIV/AIDS patient's data was collected from different sources to create a database. Hybrid (2 phases) system equipped with IT2FL (interval type-2 fuzzy logic) and DNN (deep neural network) optimized results of the computational study. Notable changes in immune response were observed. The highest working efficiency of DNN with better medicine results was evident [15].

GPSM (general-purpose simulation model) was used in modeling HIV transmission through an injection needle. The same model was used to study the rate of injection use and cleaning of needle attitudes [16]. DSS (decision support systems) are derived as a part of information systems for HIV interventions. DSS was based on the fact that it will lead to consistent up-gradation of models and software. The system is combined with data sets and it gives efficient results by using numerous algorithms [17].

Human immunodeficiency virus causes AIDS. Scientists are constantly working to discover an efficacious therapeutic solution despite drug resistance. Computer programs have huge potential to guide in drug synthesis and to solve resistance issues. Sophisticated software programs with rapid calculation abilities have completely changed the paradigm of the pharmaceutical sector. As drugs act on at one particular step in the virus cycle, a combination of drugs targeting multiple steps of virus replication and growth stages is more potent. This procedure known as highly active antiretroviral therapy (HAART) reduced mortality in the infected population [18].

Conclusions

It can be learned from the literature review that designing and application of computer-based simulation programs are essential to curb the pandemic growth of HIV/AIDS worldwide. By applying machine learning algorithms, the processing of big data sets can predict underlying pathophysiological mechanisms, progression and results of treatment for these chronic diseases. The intentions of healthcare researchers to gain maximum knowledge from computer programs are leading to the constant development of new or up-gradation of existing programs.

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