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 of 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 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 have 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 constant development of new or upgradation 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 of 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 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 have 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 constant development of new or upgradation of existing programs [3].

2. Computerized Simulation Models for HIV/AIDS

Through integrative review of the literature by databases (CIELO, LILACS, BDENF), three descriptive variables HIV, treatment care, humanization of assistance were checked. Articles published between 2013 and 2018 were studied. Out of 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 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 anti-retroviral 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 was 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 condition [5, 6].

A simulation model was developed by using data from multiple medical centers during 1984 to 1985 to study the change in number of CD4 T-cells in HIV patients. Rates of decrease in cell count and initiation of AIDS were analyzed. Model measured variable cell count within same person as well as between different patients by three techniques that contributed in 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 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. Models predictions were more accurate as compared to previous trials. Multi-pattern micro-simulation models are latest means of economical evidence-based therapeutic plans [8] as shown in fig.1.
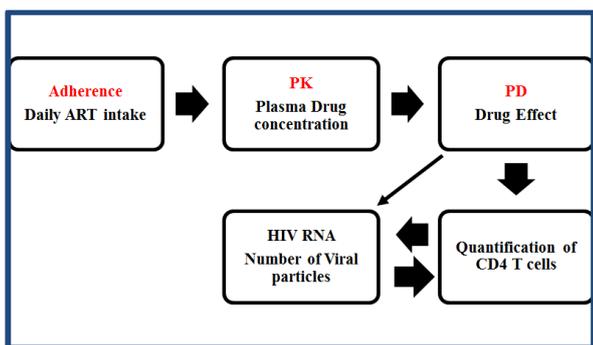

Fig. 1 Model for HIV progression

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

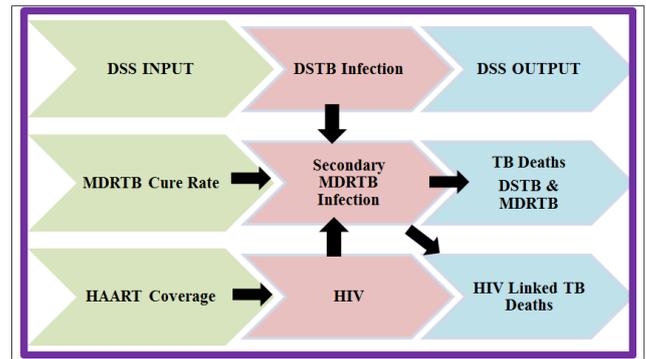policy makers to eradicate wide-spread HIV infection rates and associated deaths [9].

Fig.2 Computational model to predict the outcomes of HIV and associated tuberculosis

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 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, effect of vaccine in terms of death prevention in adults and infants were studied by simulation model with 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 most vulnerable population that is women and children in South Africa. Similarly, through computational program, number and clinical features of HIV-positive populations were evaluated. During 3 years period, 62% population had greater viral load [13].
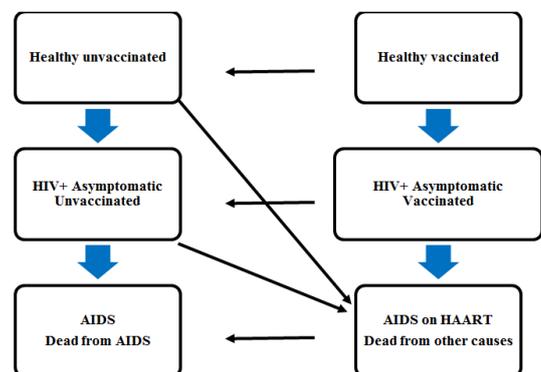

Fig.3 Simulation model to predict vaccination outcomes

As the virus involved in HIV infection has 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 modelling 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 into an artificial neural network. Such approach was beneficial to design HIV bnAbs and to develop therapeutic strategies by simulation programs [14]. ML (machine learning) and MDS (multi-dimensional scaling) methods can predict 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 computational study. Notable changes in immune response were observed. Highest working efficiency of DNN with better medicine results was evident [15].

GPSM (general purpose simulation model) was used in modeling HIV transmission through injection needle. Same model was used to study 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. System is combined with data sets and it gives efficient results by using numerous algorithms [17].

Human immunodeficiency virus causes AIDS. Scientist are constantly working to discover 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 pharmaceutical sector. As drugs act on at one particular step in virus cycle, 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 infected population [18].

Conclusions

It can be learnt 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, 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 constant development of new or upgradation of existing programs.

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