Simulation of HIV Infection Propagation Networks: A Review of the State of the Art in Agent-Based Approaches

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ABSTRACT

Simulating the transmission of HIV requires a model framework that can account for the complex nature of HIV transmission. In this paper the authors present the current state of the art for simulating HIV with agent-based models and highlight some of the significant contributions of current research. The authors then propose opportunities for future work including their plan that involves identifying and monitoring high-risk drug users that can potentially initiate high-risk infection propagation networks.

Keywords: Agent-Based Models, Human Immunodeficiency Virus (HIV), Propagation Networks, Simulation, Virus Growth

1. INTRODUCTION

It is currently estimated that around 38 million people live with Human Immunodeficiency Virus (HIV) worldwide (UNAIDS, 2006). It is well established that important gateways to prevention and care for HIV populations are knowledge of HIV status and adherence to therapy (Rennie & Behets, 2006). On one hand, the highest levels of viraemia are seen during acute infection and advanced HIV disease, and high plasma viraemia has been found to increase the risk of transmission by as much as an order of magnitude (Wawer et al., 2005). Innovative approaches to the management of sexually transmitted infections in settings with generalized epidemics has the potential to affect current epidemic trajectories: the influence of high-risk individuals who are key to transmission has shown to exert a major effect on propagation networks, and can result in major changes in infection rates (Gregson et al., 2006). This means that finding innovative methods for the monitoring and prediction, early identification, monitoring and treatment of high-risk infected people that could eventually create large propagation networks could provide a significant tool to reduce the creation of such networks in the first place. In
this paper we explore simulation approaches to the propagation of infection networks, specifically the state of the art in agent-based models, a type of approach that has consistently proved to be a significant tool to simulate the spread of infection disease. Some of the more cited agent-based approaches found in the literature are presented, along with a discussion of future work in the context of our efforts on monitoring the pandemic within high-risk, drug abusing HIV+ populations.

2. BACKGROUND

According to the World Health Organization, in 2011 there are 34.2 million people living with AIDS, 1.7 million AIDS deaths, and 2.5 million people newly infected with HIV in 2011. Since the 1980s, scientists have used simulation models to learn more about HIV and to aid in predicting the spread of the HIV epidemic. HIV is unique, as it does not fit traditional epidemiological models for disease. In other words, it is not transmitted by air or casual contact. Instead, the transmission of HIV is mainly a result of human behavior, with the exception of mother-to-child infection and other lower risk routes such as blood transfusions. Infection typically occurs through human behaviors such as unprotected sexual intercourse or sharing intravenous drug needles. The ability to simulate human behavior makes agent-based models an effective model for HIV transmission. Agent-based simulations consist of individual autonomous agents that can be designed to have human characteristics and exhibit multi-faceted behaviors of human beings. Agents can interact with other agents and agents and therefore transmit disease and influence behavior. This interaction simulates the complex social and sexual networks of individuals. Agents attributes that impact behavior can also be calibrated by environmental or population parameters. Agent-based models are typically defined by a common structure that consist of some or all of the following components for simulation:

- Agents that with demographic, behavioral, and other parameters;
- HIV transmission algorithms or equations that execute the transmission of HIV between agents;
- A unit of time that is used to simulate the passing of time in the model;
- A network structure that represent relationships between agents;
- A function for updating dynamic network structures as agents enter and leave the population;
- A notion of HIV disease progression. Some stages besides not infected and infected are sometimes represented in order to represent details that impact transmission;
- Population input parameters to incorporate specific characteristics of the population.

In addition to understanding the typical components of agent-based models, it is also important to note the significant necessity for empirical data in the design of the model, input parameters simulations, and for validating results. Current research supports that agent-based models are generally considered to be the optimal models for simulating HIV transmission. Alam, Meyer, and Norling (2008) concluded that commonly used Monte Carlo based models are not able to simulate interactions within complex social networks. Simon and Koopman (2005) suggest the use of agent-based models for capturing the important details of HIV transmission. After surveying existing HIV transmission models, Rhee (2006) reported the relevance of agent-based modeling due to ability to more easily model the risk factors and behaviors (including preferential attachment) of individuals, idea diffusion, and the affect of policy interventions. Richardson and Grund (2012) highlight the conclusions of previous research in favor of agent-based modeling systems: agent-based models are more effective at representing individual behavior and network structures (Rhamandad & Sterman, 2008), more effective at modeling complex social networks.
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