

Integrating HIV and HPV: A Novel Approach with Hybrid Agent-Based and Compartmental Simulation Methods

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BACKGROUND

Traditional single-disease simulation models fall short in addressing the interconnectedness of diseases like human papillomavirus (HPV) and human immunodeficiency virus (HIV), which share transmission routes and interact biologically [1–3]. Drivers of sexual and care risk behaviors include common social burden (e.g., mental health and substance use disorder), and social and economic vulnerability (housing instability, incarceration, poverty, abuse). A multi-disease simulation model is crucial for capturing disease syndemics, quantifying the contribution of biological and behavioral risks to overall disease burden, and facilitating targeted intervention analysis. This approach can inform care and treatment interventions for biological risk interventions and behavioral and social support programs for behavioral risk interventions, while also enabling more accurate cost-effectiveness analyses of preventive measures like housing and employment assistance in bolstering overall disease prevention.

CURRENT LITERATURE

Existing models either rely on statistical methods that can't fully grasp disease dynamics [4–15] or use simulation models that don't adequately simulate dynamic transmission networks, missing out on the complex interactions between diseases [16–20]. The unavailability of agent-based network models for joint modeling related diseases can be associated to computational challenges. For instance, women comprise 25% of the 0.4% HIV prevalence [21], and women with HIV are ~2-7 times more likely to develop cervical cancer (caused by HPV) than those without [22–24], making it crucial to model HPV and cervical cancer among HIV. However, while HPV is more prevalent (40%) [25], the prevalence of cervical cancer is only 0.3% [22], meaning a simulated population of 100,000 would include about 100 women with HIV and 40 women with HPV but scarcely any cervical cancer cases. Computational challenges increase exponentially with simulation population size and are moreover unnecessary since a large fraction of the population is never exposed to these disease cases.

METHODS

We applied a new simulation framework mixed agent-based and compartment model (MAC) for joint disease modeling. This innovative approach overcomes the above computational challenges by simulating individuals with less common diseases (here HIV, and thus HPV and cervical cancer in persons with HIV) in a network, while modeling all others (including those with only HPV) in a compartmental model [27,28]. At the core of this framework is an evolving network algorithm that employs deep learning and Markov processes for dynamic network growth and configuration, moving persons from compartmental to network as they become exposed to HIV over time. We validated the epidemiological and network features of the HIV model against data from National HIV Surveillance System (NHSS) while the HPV model was calibrated against to well-established targets in the literature. Cervical cancer incidence and mortality, as predicted by the model under natural history and screening, align closely with surveillance estimate from Connecticut Tumor Registry and Surveillance, Epidemiology, End Results (SEER), respectively.

CONCLUSIONS

Results from the study underscore the importance of care and treatment for biological risk intervention and behavioral and social support programs for behavioral risk interventions, showcasing MAC's ability across various related diseases for more realistic cost-effectiveness analyses of interventions such as housing and food assistance on overall disease prevention [29–

31]. Additionally, the network features of the model can help identify vulnerable populations, enabling a more targeted approach to intervention and prevention strategies [27,32].

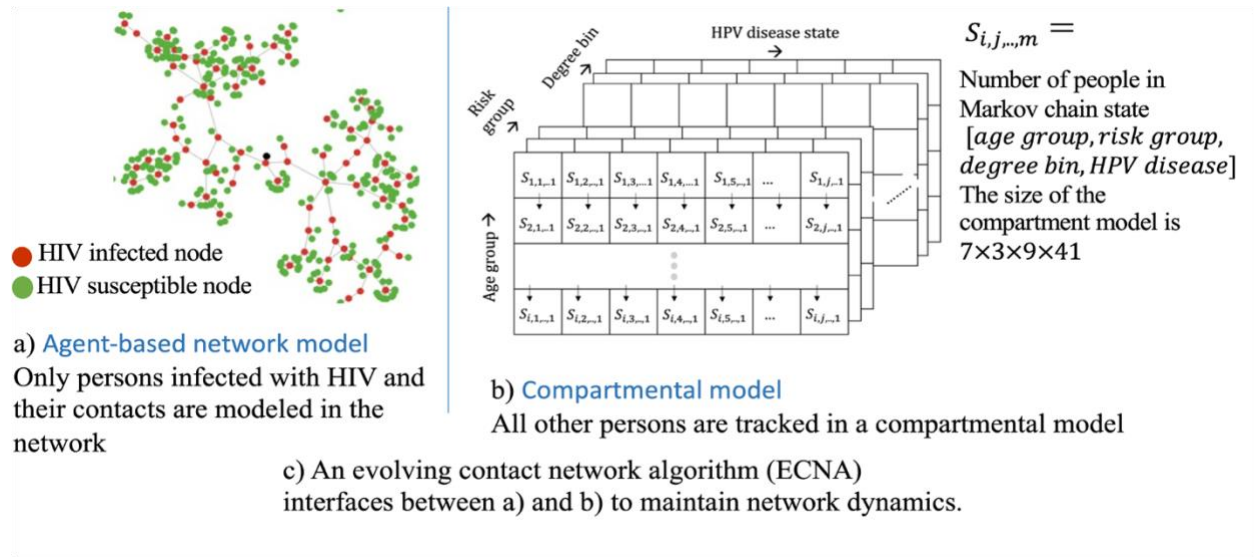


Figure 1. Computational structure of MAC simulation framework for multi-disease modeling: a) HIV, HPV, and b) associated cancer.

SUMMARY

The traditional single-disease model might lead to inaccurate estimations of an intervention's effectiveness, as it fails to consider the syndemic nature of diseases. This oversight is particularly evident in sexually transmitted diseases (STDs) like human papillomavirus (HPV) and human immunodeficiency virus (HIV), where co-infection can compromise the immune response to either virus, or shared behavioral factors influence their transmission. Often, it is the underlying social conditions, such as mental health challenges, poverty, and housing instability, that drive these risky behaviors. Recognizing these complexities and existing computational challenges, a new mixed agent-based network and compartmental (MAC) simulation framework has been developed. This model simulates individuals with less common diseases (here HIV, and thus HPV and cervical cancer in persons with HIV) in a network illustrated on the left side of the graph, while modeling all others (including those with only HPV) are represented within a compartment model shown on the right side. After calibrating and validating the model with U.S. disease burden data, we quantified the fraction of biological and behavioral risks contributing to the HPV disease burden among HIV-positive women. The findings highlight the necessity for comprehensive interventions: biomedical measures like vaccination, screening, and treatment are crucial for mitigating biological risks, while addressing behavioral risks calls for structural changes through enhanced social support, educational programs, and access to affordable housing.

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