

Circular Migrations and HIV Transmission Dynamics: A Comparison of Classical Ordinary Differential Equations and Modern Network Based Modeling

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1 Objectives

The objectives of the current work are to study the role of circular migrations (periodic movement of individuals between two or more locations [1]) in the transmission dynamics of HIV. While it has been established in the epidemiological literature that human population mobility is linked to infectious disease dispersal [2], the precise nature of this connection is not well understood. We use two different types of mathematical models to understand this connection. The first method will involve classic ordinary differential equations that build on the classic Susceptible-Infected-Removed (S-I-R) paradigm. We then compare the results obtained from these models with modern stochastic network-based models that allow us to more explicitly model the partnership structure and person to person transmission.

2 Background

According to the UNAIDS 2010 report, in 2009 there were 33 million people all over the world living with HIV. Of these, about 22.5 million are living in Sub-Saharan Africa [3]. In particular, South Africa alone has 5.6 million people living with HIV [3]. The prevalence of HIV in Africa increased from 0.76% in 1990 to 26.5% in 2002 [4].

Of the nine provinces in South Africa, Kwa-Zulu Natal has had the highest HIV prevalence (39.5% in 2009) [5]. In this province, migration has historically been an important part of the local economy [4]. The precise relationship between migration and sexually transmitted diseases is not well understood [6, 7]; however, there is evidence that human

migrations potentially play a prominent role in the transmission of sexually transmitted diseases [1, 8, 9, 10]. South Africa, in particular, has had a history of circular migrations, which involve the movement of individuals between two or more locations [1], often characterized by return to the same partners.

Besides South Africa, higher prevalence rates among migrants have been observed in other African countries, notably Uganda, Zimbabwe, Senegal [4, 7, 11], and Kenya [12]. However, other studies in Zimbabwe [13, 14] have found no link between migration/mobility and HIV and another study in Tanzania [15] found no significant differences in the sexual behavior of migrant and non-migrant men [6]. Migration is not a homogeneous process; when studying migration and its epidemiological implications, it is imperative to clearly define the pattern of mobility, and the populations at risk [6].

Mathematical modeling can play a useful role in understanding the connection between migrations and HIV transmission. Circular migrations are also unique on account of the underlying structure of temporal overlap in partnerships (called “concurrency”) because even if the migrant laborers have multiple partners, depending on their location, only the partnerships in that location will be active. Their partnerships in any other location, while still existent, will be inactive. It is not intuitively clear how this structure in partnerships impacts transmission dynamics, and mathematical models can play an important role in understanding this impact.

3 Methods

We consider a simple system where the population is divided equally between the urban and the rural locations. The total population consists of an equal proportion of women and men, and the male population is divided equally between migrants and non-migrant. As time evolves, the migrant men in the urban and rural areas change their locations; migrations by women are not considered. We assume only heterosexual contact, and

migrating men. These assumptions are made to be consistent with the framework of the underlying epidemiological literature [16, 17].

We consider four states of infection: susceptibility, acute, chronic and late-stage infection. The rural women can only exchange disease with the non-migrant men who live in that location, and the migrant men who are there. Similarly the men in any location can only exchange disease with the women in that location. Thus the members of our population are classified on migration-ability, sex, location, and disease-status.

We treat frequency of migration as our independent variable, and disease prevalence over time as our outcome. We obtain prevalence as a function of time at different migration frequencies, and analyze how migrations impact HIV transmission.

We first model this system using ordinary differential equations (ODE) that build on the classic Susceptible-Infected-Recovered (S-I-R) framework [18]. ODE models assume random mixing and therefore do not allow explicit modeling of person-to-person transmission. To explicitly model person-to-person transmission, and account for temporal overlap in partnerships, we use network based models.

Recent work in Exponential Random Graph Models (ERGMs) has allowed explicit modeling of the partnership structure in a population [19]. We now have the ability to model fully dynamic networks that account for vital demographic processes such as birth, death and aging [20]. These models are relevant to sexually transmitted infections in general, and HIV in particular because the mode of transmission is intimate, and very different from other common infectious diseases such as flu.

4 Significance

Through this study, we may develop a better understanding of the precise link between migrations and HIV. One of the major puzzles in HIV research is the reason Sub-Saharan Africa bears a disproportionate burden of the epidemic [8]. Migrations have been a major

component of the economic structure in Sub-Saharan Africa, and this project may help elucidate what role such movement has played in driving the HIV epidemic.

The comparison between classical and ordinary approaches helps clarify if modern network methods are necessary for understanding HIV transmission in complex systems.

Mathematical modeling has shown that concurrent partnerships can be a major driver of the HIV epidemic [21, 22, 23]. This argument has been criticized recently, as not providing a plausible explanation for HIV in Sub-Saharan Africa [24, 25]. Two of the prime arguments against Morris and Kretzschmar's work [21, 22, 23] are that they assume daily sex and a transmission probability that is much higher than the accepted level, even during the acute phase [25].

The proposed project provides an opportunity to address some of these concerns regarding concurrency as a driver of the HIV epidemic; the pattern of concurrency with regard to migrant men is unique because while they may have concurrent partners in the two locations (rural home area and urban working area), only those partnerships where they are present will be "active" at any given time. Hence, the assumption of daily sex with all concurrent partners does not hold true. Moreover, to parametrize the model, we use accepted infection probabilities from Wawer et al (2005) [26] and Hollingsworth et al (2008) [27] that provide infectivities during acute, chronic and late-stage HIV.

This work thus addresses both of the critiques mentioned above about some existing models of concurrency. It thus allows us to understand how the epidemic impact of circular migrations - which represent a structurally unique but important type of concurrency - relates to other forms of concurrency, and how the practice of circular migrations can drive HIV transmission in settings where it is practiced.

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