Circular Migrations and HIV Transmission Dynamics

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Abstract

Circular Migrations and HIV Transmission Dynamics

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The objective of this work is to investigate the impact of circular migrations on the transmission dynamics of HIV. Circular migrations involve the repetitive movement of people between two or more locations. An example is South Africa, where labourers have been sent from their home villages to mining towns (with periodic returns), and these migrations have been a major component of the South African economy. It is known that HIV infectivity varies with time since infection. Since AIDS has a long latency period, the high infectivity of HIV before symptoms appear can have a major impact if infected individuals are changing locations and partners frequently, potentially without knowing their infection status. The interaction between timing since infection and variable infectivity is the major focus of the current work. I am investigating this interaction using compartmental ODE models that are an extension of the classic S-I-R structure, and a stochastic network-based framework based on Exponential Random Graph Models (ERGM). ODE models rely on homogeneous mixing and are easy to extend by adding vital dynamics. The ERGM framework allows us to model person to person transmission and consider relational timing, and

hence, concurrency. I will present results from the two modeling frameworks that allow us to study the relative properties of the two approaches.

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to my little sister, Deepti

to my uncle, Vijay

Chapter 1
INTRODUCTION

1.1 Background

Five young homosexual men were treated for *Pneumocystis* pneumonia between October 1980 and May 1981. This disease is known for suppressing the body's immune system. Around the same time, more cases of Kapsosi's sarcoma were reported in New York and California. By early 1982, researchers had gathered evidence that established a connection between the two cases that pointed to a sexual route of transmission of the disease. These were the early beginnings of what came to be termed as "Acquired Immune Deficiency Syndrome," commonly called AIDS [3].

The search for a transmissible agent narrowed down to a virus. The isolation and cultivation of a virus was first accomplished by a research group at the Pasteur Institute in France, which was termed lymphadenopathy-associated virus (LAV). Shortly after, another team at the National Institutes of Health in the United States identified a virus in AIDS patients which they called the human T-cell lymphotrophic virus type III (HLTV-Type III). It was found that the two strains of the virus were the same and the International Committee for the Taxonomy of Viruses called it the human immunodeficiency virus (HIV) [3].

By 1984, most developed and many developing countries reported major epidemics of the disease. As early as 1987, approximately 39,000 cases in the United States alone had been reported to the Centers for Disease Control (CDC) [44]. According to the

UNAIDS 2008 report, in 2007 there were 33 million people all over the world living with HIV. Of these, about 22 million are supposed to be living in Sub-Saharan Africa. In particular, South Africa alone is supposed to have 5.7 million people living with AIDS [58]. The prevalence of HIV in Africa increased from 0.76% in 1990 to 26.5% in 2002 [33].

Of the nine provinces in South Africa, Kwa-Zulu Natal has had the highest HIV prevalence (36.5% in 2002). In this province, migration has historically been an important part of the local economy [33]. The precise relationship between migration and sexually transmitted diseases is not well understood [29]; however, there is evidence that human migrations potentially play a prominent role in the transmission of sexually transmitted diseases [21, 51, 66]. South Africa, in particular, has had a history of circular migrations, which involve the movement of individuals between two or more locations [51], often characterized by return to the same partners.

There are many possible reasons behind the high prevalence of HIV in South Africa, and the movement of individuals is potentially an important one. This thesis broadly aims to study the nature of repetitive movement between locations on HIV transmission.

We will begin by studying the history of the migration and outline the subtleties behind the question.

1.2 Definition and Brief History

Quinn [51] defines migration as

> the movement of people in space, often involving a change in the usual place of residence. Migration is further defined on the basis of movement in time. The principal distinction is between circulation - i.e. involving repetitive, nonpermanent moves such as daily commuting and other short

> term mobility - and definitive migration. Periodic movements are mostly short term, whereas seasonal movements have a regular annual rhythm. Definitive migration by contrast implies a permanent movement away from one residence with little indication of return.

Migration has been an important component of the South-African economic and political structure for the past century [21, 29]. The mining and agricultural industries employed black workers by controlling the movement of labour "so as to ensure a continuing supply of cheap black workers...while ensuring the relative privilege of white workers" [29]. This organization ultimately lead to apartheid. The system of migrant labour was formalized by the Glenn Grey Act in early part of the twentieth century, and the 1913 Native Land Act which "restricted black people's access to land" [29]. The victory of the National Party in 1948 led to the institutionalization of apartheid, and forced black people to settle in rural areas, with only temporary access to white urban areas. Thus a system of migrant labour was firmly established.

Remittances sent home by migrant labour constituted a bulk of the rural economy. By 1970, local economic activities like agriculture generated only about 10% of the rural economy, and the rest mostly consisted of contributions made by migrant labourers. Similarly at the same time, the gold mines of Africa employed about 800,000 men, where nearly 80% of the work-force came from outside South Africa. These workers resided mostly in single-sex hostels, without access to family or partners [29].

After apartheid was lifted in 1994, some patterns of migration changed. Currently most labour migration is for a longer period of time, and workers are generally allowed to visit home at shorter intervals. Approximately 90% of black labourers in the mines are migrants, with restricted opportunities to visit family, and a low likelihood of visits by their partners [29].

Thus migrant labour continues to constitute an essential component of the South African economic structure.

1.3 Migration and HIV Progression

As we have discussed earlier, the linkage between human population mobility as a cause of infectious disease dispersal is well established in epidemiological literature [65]; however, the mechanism underlying this connection is not completely understood. The general consensus seems to be that migrants are more likely to engage in high risk behaviour due to relaxed social norms [51, 66] in the following ways [65]:

1. Migrants may change partners more frequently.

2. Migrants may have form partnerships with individuals who are at a high risk of infection, such as commercial sex workers.

3. Migrants may have a higher number of relationships that overlap in time (called concurrent relationships).

Moreover, several studies have found migrants to have a higher rate of HIV prevalence than non-migrants [11, 29, 30, 33, 67]. Higher prevalence rates among migrants have been observed in other African countries, notably Uganda, Zimbabwe, Senegal [29, 30, 33], and Kenya [5].

An important study of the differences in HIV prevalence among migrants and non-migrants in South Africa was conducted in the Kwa-Zulu Natal province of South Africa [31, 32]. This study is important for several reasons, especially since migrant labour is a prominent component of the local economy. In the Hlabisa district of the province, 62% of adult men migrate for employment, mostly to the towns of Carletonville and Richards Bay. The two places represent different patterns of migration, with the former being farther away from the rural area of Hlabisa, and allowing

the migrants relatively fewer trips home. Richards Bay, on the other hand, is much closer, allowing migrants to return home more often [11, 30, 31, 67]. It was found that migrant men in Carletonville were 3.2 times as likely to be infected as their rural partners. In Richards Bay migrant labourers were as likely to be infected as their rural partners, but migrant couples were twice as likely to be infected as non-migrant couples, and in one-third of cases, the woman was the infected partner [11].

Migration is thus potentially an important factor behind the high HIV prevalence in KwaZulu Natal, and possibly in South Africa as a whole.

1.4 The Question

One of the main puzzles surrounding the AIDS pandemic is the disproportionate number of AIDS cases in Africa, compared to the United States, where people have reported comparable numbers of lifetime sexual partners. Morris and Kretzschmar [26, 42, 43] did much work in showing the impact of concurrent partnerships, i.e. relationships that overlap in time, on the spread of HIV. However, in the case of circular migrations, when an individual is in one location, their relationships in the other are not sexually active for the period of their absence. Hence, the structure of concurrency is unique, and it is not clear how this structure affects transmission of the disease.

Moreover, recent work by Wawer et al. [64] has shown that the infectivity of an individual after getting infected by HIV is not constant. It is highest for a period of about two and a half months after infection is first transmitted. Since AIDS has a long latency period, this period of high infectivity in the beginning can potentially have a high impact on HIV transmission because people might migrate between two locations without knowledge of their infection status, and hence have no incentive to modify their sexual behaviour to reduce the risk of transmission.

As we have seen earlier, patterns of migration have changed over the past century. Today, the distance of the mining town from a labourer's village is an important determinant of the frequency of the migrant labourer's trips home. Ordinarily we might think of migration as a bridge between high and low risk areas, which it is. But migration may also impact disease transmission by altering the impact of the underlying concurrency in the population, depending upon how frequently returns occur.

Therefore the primary objective of this work is to conduct an exploratory study of the interaction between variable infectivity of HIV, and rates of circular migrations, on the transmission dynamics of the disease.

1.5 Methods

Mathematical models play an important role in studying the dynamics of HIV, since this is an area where experimental testing is "neither feasible, nor ethical" [9]. So the computer becomes a de-facto laboratory [9]. In this paper, we will use two different approaches to study the question. Classical approaches in epidemiology have relied on deterministic, compartmental models. We will develop a version of this model in Chapter 2. Chapter 3 considers a stochastic agent-based approach. Using these approaches we will study the impact of migration frequency, on the circular migrations, given that infectivity of an individual infected by HIV transmission is not constant.

To study this question, we create a hypothetical population and create models based on the two paradigms. The set-up consists of two regions, one urban, and the other rural, with each region containing 50% of the population. Males and females are present in a 1:1 ratio. The urban and rural areas both consist of migrant men, non-migrant men and non-migrant women. The number of migrant men and non-migrant men are equal, and the women do not migrate.

The structure of human behaviour in these populations is based on certain trends that we know from epidemiological studies. Firstly, since migrant men are restricted to less stringent social norms, especially when they are away from their home location, they generally have a greater number of sexual partners per unit time [29, 33]. These characteristics are present in both the deterministic differential equation model and the stochastic agent based model.

The deterministic model is based on homogeneous mixing, and can be easily extended by addition of vital dynamics which are an important consideration over the long term. The stochastic model further incorporates some other information on the structure of partnerships in the population and allows us to account for relational timing and hence, concurrency. These added assumptions potentially give us a more realistic picture of the partnership structure in the population. We are also able to consider the formation and dissolution of sexual partnerships, and use that information to think about this partnership strcuture in the population over a length of time. Finally we simulate disease through the population based on the variable infectivity of HIV.

A sub-question we will study in this work is the difference in the properties and predictions of the two modeling frameworks.

Chapter 2

DETERMINISTIC COMPARTMENTAL MODELS

2.1 Introduction

Classical models in infectious diseases are compartment-based and use ordinary differential equations to model the spread of HIV. There is a rich literature that shows how compartmental models can be used effectively for epidemiological research [9, 15, 20, 44]. In terms of the broader goals with regards to this research, this exercise serves the following purposes:

1. Creates a simple epidemic model whose dynamics and structural properties can be compared to the stochastic network based model in Chapter 3.

2. Extends this basic simple epidemic compartmental model developed here to an endemic model, which incorporates a recruitment-death process.

2.2 The Model

2.2.1 The System

The goal here is to create a model with the same structural properties that we will have in the stochastic network based study in Chapter 3. The population consists of 500 males and 500 females, divided equally between the urban and the rural locations. At the start of the simulation the urban population consists of 125 migrant males, 125 nonmigrant males, and 250 non-migrant females. The rural area is structurally

identical with 125 migrant males, 125 non-migrant males, and 250 non-migrant females. Thus the population consists of six sub-populations (also called classes). As time evolves, the migrant men in the urban and rural areas change their locations; migrations by females are not considered. We assume only heterosexual contact, and migrating men. These assumptions were made to be consistent with the framework of the underlying epidemiological literature [31, 32].

2.2.2 The Notation

Let us start by defining the state variables. We classify individuals in the population (also called actors) based upon their infection status, migration ability, sex, and location. There are three states of infection: susceptiblity, acute infection, and chronic infection. Let us denote these three states by S, A and C respectively. Thus we describe an individual by the notation S_{XYZ}, A_{XYZ} or C_{XYZ}. For the subscript, X denotes the migration status of the individual (migrant M or non-migrant N); Y denotes the sex (male M or female F); and Z denotes the location (urban U or rural R). So S_{MMU} represents a susceptible migrant male in the urban area, and C_{NFR} represents a chronically infected female in the rural area. Since in the model females do not migrate, the first subscript N for females is redundant, but we will include it for symmetry.

Since we have three infectious states and six different classifications based on migration status, sex and location, there are a total of 18 different state variables. Members of each of the susceptible classes of individuals can only contract the disease upon contact with an acutely or chronically infected partner. The probability that a susceptible individual gets infected at any time point depends upon [25, 36]

1. average number of contacts[1] per unit time (t_{XYZ}) for class XYZ, where the

[1]Here "contact" refers to a sexual act. More on the interpretations of contacts in the discussion

subscript X, Y, Z is defined as explained above;

2. the proportion of acutely infected

$$\frac{A_{XYZ}}{N_{XYZ}}$$

or chronically infected contacts

$$\frac{C_{XYZ}}{N_{XYZ}}$$

where N_{XYZ} is the total number of individuals of group XYZ.

3. the probability of acquiring the infection from an infected partner, (β_A if the infected partner is in the acute stage of infection, β_C otherwise).

Figure 2.1 shows the schematic for the system.

2.2.3 The Equations

Consider the urban region. A susceptible male can be infected either by an acutely or chronically infected female in the urban area. Moreover, at every time step, a certain number of migrant males (in all three infection states) change locations at some rate. So we can describe the rate of change in the population of susceptible males as

$$\frac{dS_{MMU}}{dt} = -S_{MMU}t_{MMU}\frac{A_{NFU}}{N_{NFU}}\beta_A - S_{MMU}t_{MMU}\frac{C_{NFU}}{N_{NFU}}\beta_c - \delta S_{MMU} + \delta S_{MMR} \quad (2.1)$$

where δ is the rate of migration between the urban and rural area.

The change in population of acutely infected males is

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section.

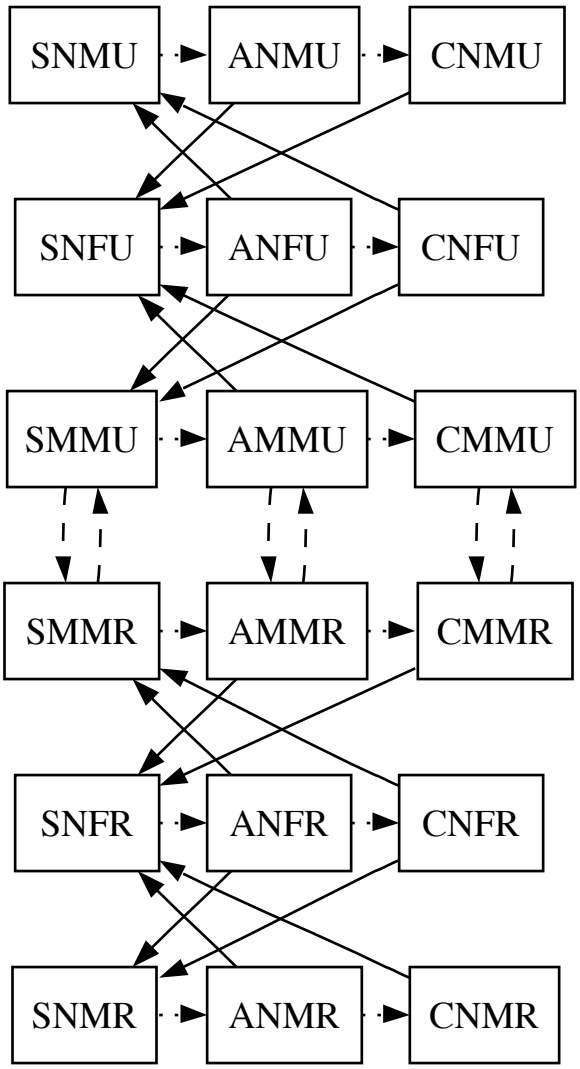

Figure 2.1: Transfer diagram for the system. Solid arrows represent flows due to infection, dashed arrows represent flows due to migration, and dotted arrows show pathways for potential transmission of infection. The compartments are labeled in the following order: Infection Status, Migration Status, Sex, and Location. This convention is the same as described in Section 2.2.2.

$$\frac{dA_{MMU}}{dt} = S_{MMU}t_{MMU}\frac{A_{NFU}}{N_{NFU}}\beta_A + S_{MMU}t_{MMU}\frac{C_{NFU}}{N_{NFU}}\beta_c - \delta A_{MMU} + \delta A_{MMR} - \gamma A_{MMU}, \tag{2.2}$$

where γ is the rate at which an acutely infected individual becomes chronically infected.

The change in population of chronically infected males is

$$\frac{dC_{MMU}}{dt} = \gamma A_{MMU} - \delta C_{MMU} + \delta C_{MMR}. \tag{2.3}$$

Now let us consider the females in the urban area. An urban female can become infected either by an acutely or chronically infected male, who is either a migrant or a non-migrant. Therefore we have

$$\frac{dS_{NFU}}{dt} = -S_{NFU}t_{NFU}\frac{A_{MMU}}{N_{MMU}}\beta_A - S_{NFU}t_{NFU}\frac{C_{MMU}}{N_{MMU}}\beta_C - S_{NFU}t_{NFU}\frac{A_{NMU}}{N_{MMU}}\beta_A - S_{NFU}t_{NFU}\frac{C_{NMU}}{N_{NMU}}\beta_C, \tag{2.4}$$

$$\frac{dA_{NFU}}{dt} = S_{NFU}t_{NFU}\frac{A_{MMU}}{N_{MMU}}\beta_A + S_{NFU}t_{NFU}\frac{C_{MMU}}{N_{MMU}}\beta_C + S_{NFU}t_{NFU}\frac{A_{NMU}}{N_{MMU}}\beta_A + S_{NFU}t_{NFU}\frac{C_{NMU}}{N_{NMU}}\beta_C - \gamma A_{NFU}, \tag{2.5}$$

and

$$\frac{dC_{NFU}}{dt} = \gamma A_{NFU}, \tag{2.6}$$

to describe the various interactions of females in the urban area.

Finally the interactions of the non-migrant males are similar to those of the migrant males defined in equations (2.1) to (2.3), without the migration related term. So

$$\frac{dS_{NMU}}{dt} = -S_{NMU}t_{NMU}\frac{A_{NFU}}{N_{NFU}}\beta_A - S_{NMU}t_{NMU}\frac{C_{NFU}}{N_{NFU}}\beta_C, \tag{2.7}$$

$$\frac{dA_{NMU}}{dt} = S_{NMU}t_{NMU}\frac{A_{NFU}}{N_{NFU}}\beta_A + S_{NMU}t_{NMU}\frac{C_{NFU}}{N_{NFU}}\beta_C - \gamma A_{NMU}, \tag{2.8}$$

and

$$\frac{dC_{NMU}}{dt} = \gamma A_{NMU} \tag{2.9}$$

describe the changes in population for the three infection states of urban non-migrant males.

In this model the structure of interactions is assumed to be identical in the rural and urban areas. Therefore the basic structure of equations (2.1) to (2.9) is the same for the rural area and we can write the equations for the migrant males in the rural location as

$$\frac{dS_{MMR}}{dt} = -S_{MMR}t_{MMR}\frac{A_{NFR}}{N_{NFR}}\beta_A - S_{MMR}t_{MMR}\frac{C_{NFR}}{N_{NFR}}\beta_C - \delta S_{MMR} + \delta S_{MMU}, \tag{2.10}$$

$$\frac{dA_{MMR}}{dt} = S_{MMR}t_{MMR}\frac{A_{NFR}}{N_{NFR}}\beta_A + S_{MMR}t_{MMR}\frac{C_{NFR}}{N_{NFR}}\beta_C - \delta A_{MMR} + \delta A_{MMU} - \gamma A_{MMR}, \tag{2.11}$$

$$\frac{dC_{MMR}}{dt} = \gamma A_{MMR} - \delta C_{MMR} + \delta C_{MMU}. \tag{2.12}$$

The various equations for females in the rural area are

$$\frac{dS_{NFR}}{dt} = -S_{NFR}t_{NFR}\frac{A_{MMR}}{N_{MMR}}\beta_A - S_{NFR}t_{NFR}\frac{C_{MMR}}{N_{MMR}}\beta_C - S_{NFR}t_{NFR}\frac{A_{NMR}}{N_{MMR}}\beta_A - S_{NFR}t_{NFR}\frac{C_{NMR}}{N_{NMR}}\beta_C, \tag{2.13}$$

$$\frac{dA_{NFR}}{dt} = S_{NFR}t_{NFR}\frac{A_{MMR}}{N_{MMR}}\beta_A + S_{NFR}t_{NFR}\frac{C_{MMR}}{N_{MMR}}\beta_C + S_{NFR}t_{NFR}\frac{A_{NMR}}{N_{MMR}}\beta_A + S_{NFR}t_{NFR}\frac{C_{NMR}}{N_{NMR}}\beta_C, - \gamma A_{NFR} \tag{2.14}$$

and

$$\frac{dC_{NFR}}{dt} = \gamma A_{NFR}. \tag{2.15}$$

The equations for the nonmigrant males in the rural area are

$$\frac{dS_{NMR}}{dt} = -S_{NMR}t_{NMR}\frac{A_{NFR}}{N_{NFR}}\beta_A - S_{NMR}t_{NMR}\frac{C_{NFR}}{N_{NFR}}\beta_C, \tag{2.16}$$

$$\frac{dA_{NMR}}{dt} = S_{MMR}t_{MMR}\frac{A_{NFR}}{N_{NFR}}\beta_A + S_{NMR}t_{NMR}\frac{C_{NFR}}{N_{NFR}}\beta_C - \gamma A_{NMR}, \tag{2.17}$$

and

$$\frac{dC_{NMR}}{dt} = \gamma A_{NMR}. \tag{2.18}$$

2.2.4 The Simulation

The system of equations above is simulated over 6000 time steps at intervals of 0.1 time units with the parameter values[2] in Table 2.1 and initial values in Table 2.2.

[2]These are hypothetical parameter values, chosen to be consistent with the parameter values in the stochastic simulation.

Each time step represents one week. The various t_{XYZ} are chosen to give a mean number of 3 sexual acts per week. All simulations are run in the R-programming language [47, 48, 49]. The algorithm used by the solver relies on [46]:

> a scheme for automatically determining whether a problem can be solved more efficiently using a class of methods suited for nonstiff problems or a class of methods designed for stiff problems. The technique uses information that is available at the end of each step in the integration for making the decision between the two types of methods. If a problem changes character in the interval of integration, the solver automatically switches to the class of methods which is likely to be most efficient for that part of the problem.

Table 2.1: Parameter Values for Simulation

Parameter	Value
t_{MMU}	450/125 (per week)
t_{MMR}	450/125 (per week)
t_{NMU}	300/125 (per week)
t_{NMR}	300/125 (per week)
t_{NFU}	750/250 (per week)
t_{NFR}	750/250 (per week)
β_A	0.0082 (per coital act)
β_C	0.0007 (per coital act)
γ	0.10
δ	varies

The parameter values in Table 2.1 were chosen to reflect some basic known characteristics of human sexual behaviour. The average number of contacts per week for migrant men is greater than that for non-migrant men. It is generally assumed that migrant men are exposed to less stringent social norms, and generally have more sexual partners [29, 33], hence they have a higher average contact rate per unit time. Also with the given parameter values we have

$$\begin{aligned} t_{MMU}N_{MMU} + t_{NMU}N_{NMU} &= t_{NFU}N_{NFU} \\ t_{MMR}N_{MMR} + t_{NMR}N_{NMR} &= t_{NFR}N_{NFR} \end{aligned} \tag{2.19}$$

implying conservation of sexual contacts i.e. the total contacts of urban males must equal the contacts of urban females and the total contacts of rural males must equal the conctacts of rural females.

Table 2.2: Initial values for State Variables. The urban area was disease-free.

State Variable	Value
Susceptible Migrant Males	125
Acutely Infected Migrant Males	0
Chronically Infected Migrant Males	0
Susceptible Females	249
Acutely Infected Females	1
Chronically Infected Females	0
Susceptible NonMigrant Males	124
Acutely Infected Non-Migrant Males	1
Chronically Infected Non-Migrant Males	0

The probabilities of infection per coital act, β_A and β_C are taken from the literature [64]. The same values for β_A and β_C in the stochastic network are chosen to be consistent with these values, though the definition of "contact" is different there; more on that in Chapter 3. The parameter γ is chosen to be 0.10, so the mean time spent by an individual in the acute phase of infection is 10 weeks, also in accordance with Wawer et al. [64]. Due to the structure of this ODE model, therefore, the time spent by an individual in the acute phase has a negative exponential distribution with a mean of 10 weeks. The parameter δ is varied to investigate the impact of varying migration rates on the dynamics of disease transmission.

Table 2.2 shows that disease was introduced in the rural area, by considering one female and one non-migrant male as being acutely infected. The urban area was disease-free. Hence the initial values for S_{NMU}, S_{NFU} and S_{MMU} are 125, 250 and 125 respectively. The other state variables for the urban area are therefore initially 0.

From Table 2.3 we see that on average, the 500 urban individuals in this population have 1500 sexual contacts (acts) per week, implying an average of 3 acts per week (ditto for the 500 rural individuals). Notice that the mean number of contacts between N_{NMU} and N_{NFR} is 0. This structual zero occurs because non-migrant males in the urban area can never make contact with females in the rural area. Likewise, the entry corresponding to N_{NMU} and N_{NFU} is a structural zero. Since migrant males in the urban and rural areas periodically switch locations, depending upon their location, the average number of contacts with females in the opposite location at any given instant is 0.

Table 2.3: Mixing Matrix. The mean number of contacts per person are per week. A contact is defined as a coital act.

	N_{NFU}	N_{NFR}	Mean Number of Contacts
N_{NMU}	300	0	300/125
N_{MMU}	450	0	450/125
N_{MMR}	0	450	450/125
N_{NMU}	0	300	300/125
Mean Number of Contacts	750/250	750/250	1500/500

Due to the nature of compartmental models, the assumption of random mixing implies that an entire class of males is making sexual contact with an entire class of females; hence this paradigm neither distinguishes between sexual partnerships, nor does it account for formation of new partnerships or dissolution of existing ones.

Figure 2.2 considers transmission of the disease through each of the six subpopulations in the base case where no migrations occur. No disease is seen in the urban

area through the 6000 time-steps, as is to be expected. Moreover, all susceptible individuals in the rural area are infected; we will revisit this point in Section 2.3. The important question here is how migration rates impact the rate of disease transmission through the populations; this question is explored in Figures 2.3 to 2.5.

Figure 2.3 shows the time to 10% and 30% prevalence in all six sub-populations. These times do not vary with migration in any of the six-subpopulations, except in the case where migrations occur at a mean of 600 weeks, where these times are slightly higher. Figure 2.4 shows a similar pattern for the time to 10% and 30% prevalence in all males, all females, and the entire population.

In Figure 2.5 we see the prevalence as a function of time for the entire population. For the base case with no migrations, the prevalence equilibrates at the 50% level. The rise in prevalence occurs most slowly for migration steps of 600 weeks (blue curve), and is almost identical for the remaining cases where migrations occur between mean times of 5 and 200 weeks (green curve). The prevalence plots for graphs for all males and all females showed similar patterns.

In conclusion, in this model without vital dynamics, migrations show no impact on the rate of transmission, an average migration occurs at really long intervals ($\approx$ 12 years). The no migration case is special here, because the model was seeded by only introducing disease in the rural area. But again the simple pattern in prevalence rise was similar to the cases where migrations were considered. It is worth noting that migrations every 600 weeks are probably unrealistic, especially in the example of KwaZulu-Natal that motivated this study. Migrations ranging from an average of a few weeks to a few months are much more typical.

2.2.5 Analytic Equilibria

It is straightforward to check that there are two equilibria for the system. The disease-free equilibrium occurs when all people are susceptible, so that $S_{XYZ} = N_{XYZ}, \quad \forall \quad X, Y, Z$, and $A_{XYZ} = C_{XYZ} = 0 \quad \forall \quad X, Y, Z$. The chronic equilibrium occurs when all people are chronically infected, so that $C_{XYZ} = N_{XYZ} \quad \forall \quad X, Y, Z$ and $S_{XYZ} = A_{XYZ} = 0 \quad \forall \quad X, Y, Z$.

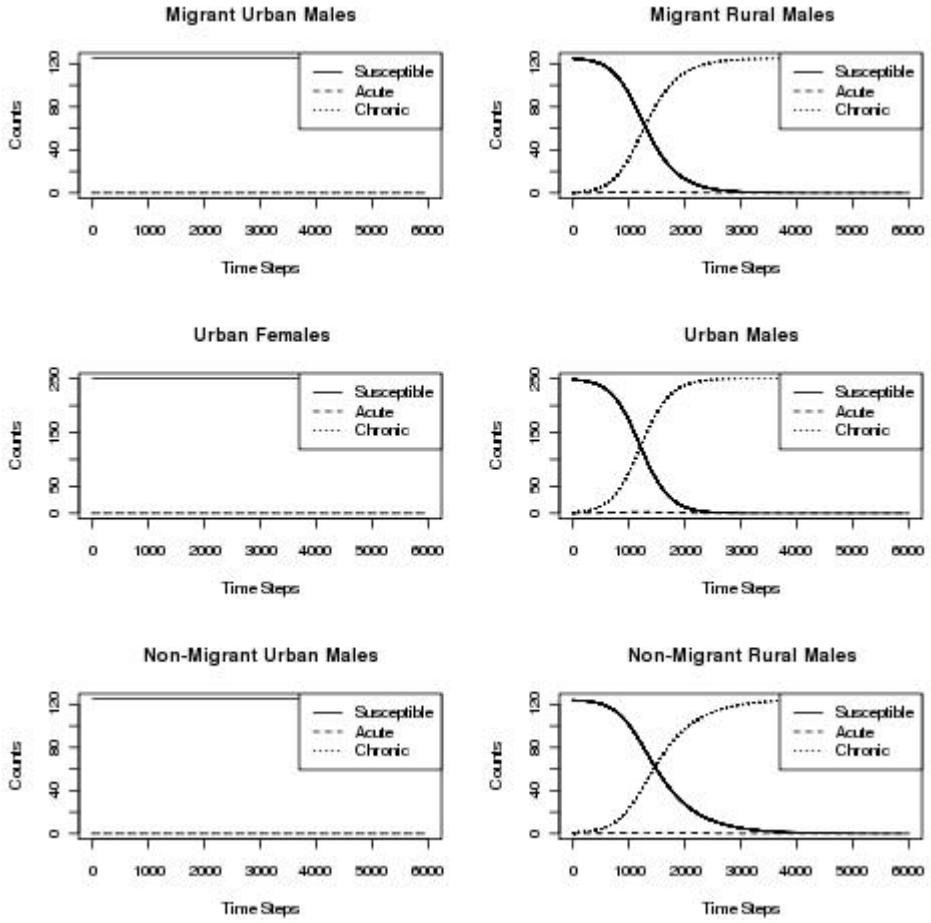

Figure 2.2: Disease transmission for case with no vital dynamics, $\delta = 0$, i.e. no migration. The left column shows simulations for the urban population and the right column shows plots for the rural population. Within each column, the top plot shows the migrant males, the middle figure shows the females, and the bottom plot shows the non-migrant males. The solid plot is for susceptibles, the dashed plot is for acutely infected, and the dotted plot is for chronically infected.

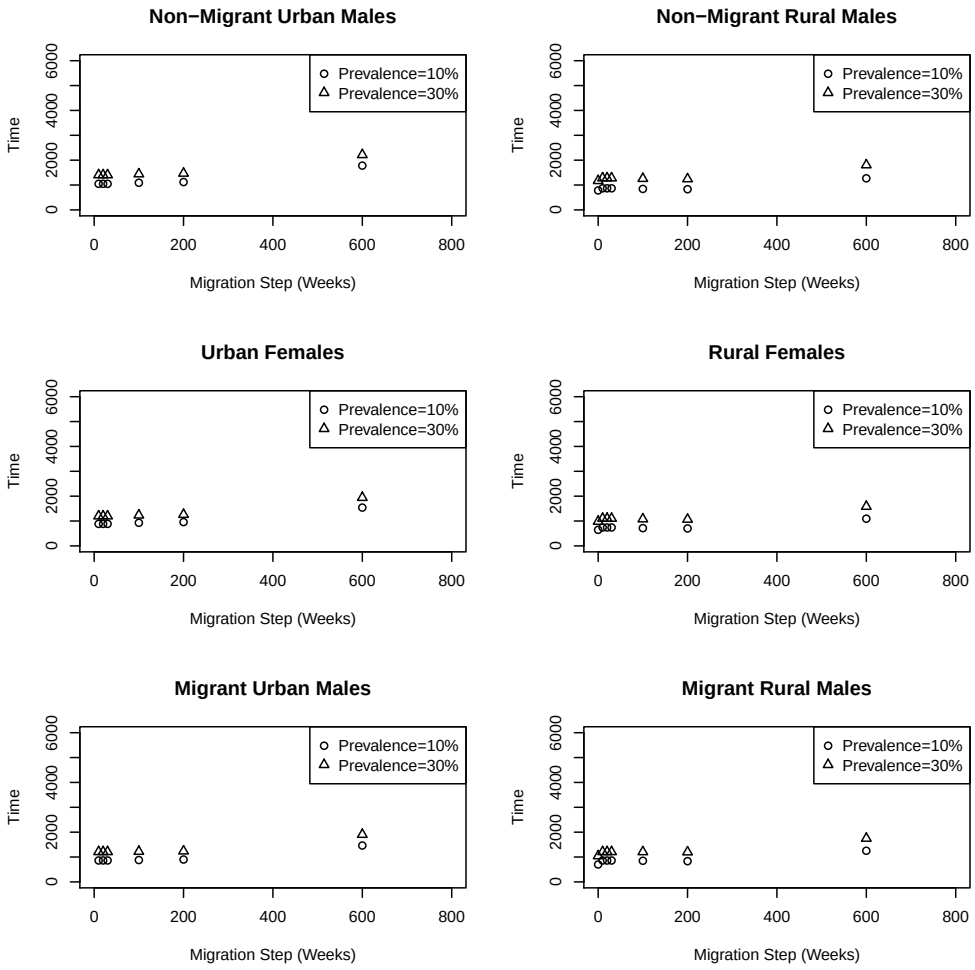

Figure 2.3: Time to 10% and 30% prevalence in all six-subpopulations. No vital dynamics are included in the model.

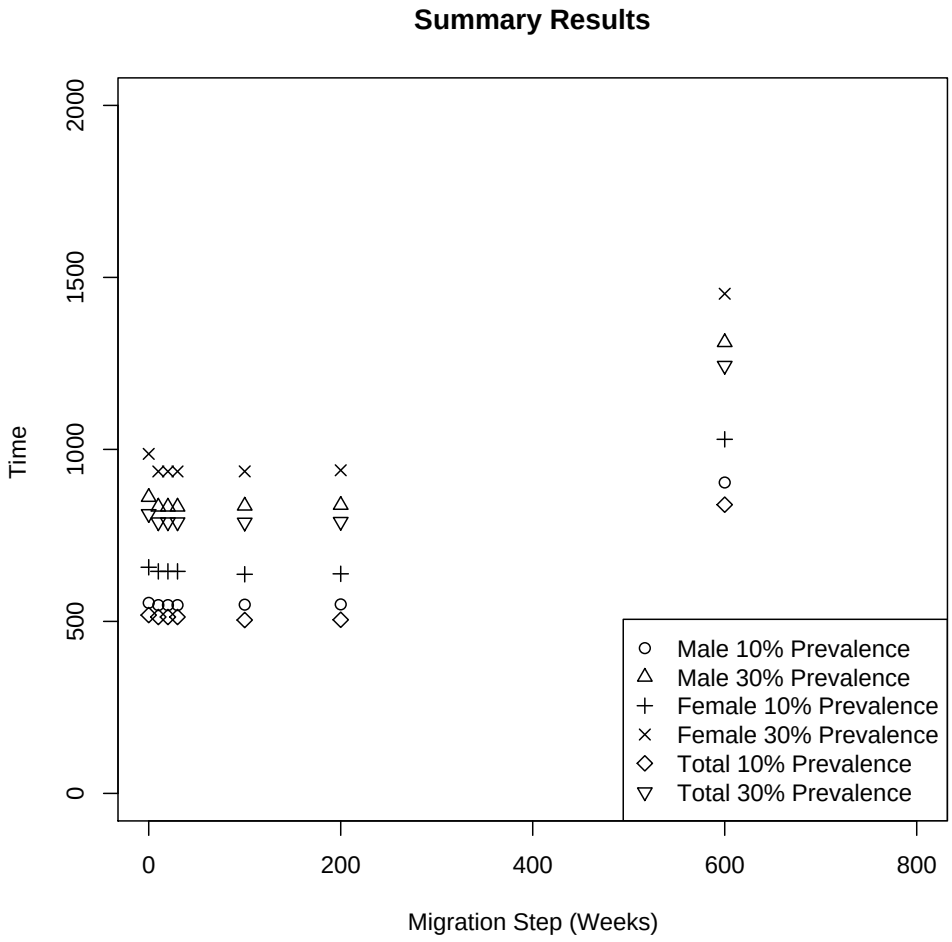

Figure 2.4: Minimum time to 10% and 30% prevalence in all males, females and the entire population. No vital dynamics are included in the model.

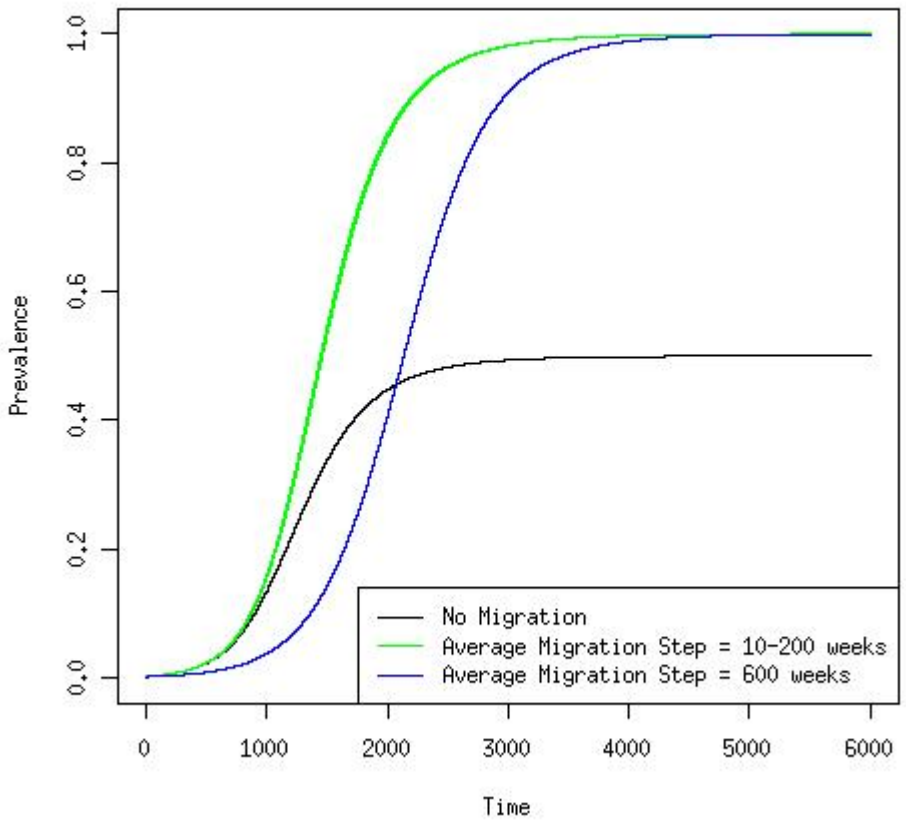

Figure 2.5: HIV prevalence in all males, all females, and the entire population as a function of time. No vital dynamics are included in the model.

2.3 Adding Vital Dynamics

The model presented above includes neither (natural or disease-related) mortality, nor addition of new individuals to the sexually active population. This model without vital dynamics is useful for comparison to the stochastic model in Chapter 3. Adding vital dynamics is a useful extension because it lends us a more realistic picture of the system over long time periods such as the ones we considered in Section 2.2. We now consider an endemic model with inflow and natural and disease-related deaths.

2.3.1 The Equations

Given that we broadly have three infectious states: susceptible, acute and chronic infection, it is reasonable to consider that populations in the first two will experience natural mortality at a constant rate μ and those in the chronically infected state will also experience mortality due to the disease with constant rate μ_d, in addition to the natural mortality μ. New individuals become sexually active at the rate ν. To incorporate inflow of new susceptibles, equations (2.1) to (2.3) are rewritten as

$$\frac{dS_{MMU}}{dt} = \nu - S_{MMU}t_{MMU}\frac{A_{NFU}}{N_{NFU}}\beta_A - S_{MMU}t_{MMU}\frac{C_{NFU}}{N_{NFU}}\beta_c - \delta S_{MMU} + \delta S_{MMR} - \mu S_{MMU}, \tag{2.20}$$

$$\begin{aligned}\frac{dA_{MMU}}{dt} = {} & S_{MMU}t_{MMU}\frac{A_{NFU}}{N_{NFU}}\beta_A + S_{MMU}t_{MMU}\frac{C_{NFU}}{N_{NFU}}\beta_c \\ & - \delta A_{MMU} + \delta A_{MMR} - \gamma A_{MMU} - \mu A_{MMU},\end{aligned} \tag{2.21}$$

and

$$\frac{dC_{MMU}}{dt} = \gamma A_{MMU} - (\mu + \mu_d)C_{MMU}. \tag{2.22}$$

Equations (2.4) to (2.18) are modified in a similar fashion by adding parameters ν, μ and μ_d with one small difference, the rate of recruitment of susceptibles into the two female sub-populations in (2.4) and (2.13) is defined as 2ν, since they are twice as large as the male subpopulations. The values for these additional parameters are in Table 2.4. The initial conditions are the same as shown in Table 2.2.

Table 2.4: Additional Parameters for Simulation with Vital Dynamics

Parameter	Value
μ	$1/(45 \times 52)$
μ_d	$1/(10 \times 52)$
ν	$125/(45 \times 52)$

Since the parameter μ represents the rate of natural mortality (which for our purposes is the rate of removal from the sexually active population), $1/\mu$ is the average sexual lifespan of an uninfected individual. We assume that an unifected individual will remain sexually active from the age of 15 years to the age of 60 years; thus setting $\mu = 1/(45 \times 52)$ sets the sexual lifespan of an individual to (45×52) weeks, or 45 years. Similarly, the average lifespan of an infected individual, $1/\mu_d$, is 10 years.

For ν, we set equation (2.20) equal to 0 in the disease free state. Then

$$\frac{dS_{MMU}}{dt} = \nu - \mu S_{MMU} = 0$$

implying

$$\nu = S_{MMU}\mu = \frac{125}{45 \times 52}. \tag{2.23}$$

Similarly, the females in the urban area will have

$$\frac{dS_{NFU}}{dt} = 2\nu - \mu S_{NFU} = 0,$$

which also yields

$$\nu = \frac{125}{45 \times 52}$$

as in (2.23). Thus by using 2ν as the rate at which new susceptible females flow in to the population; we have a fixed value for ν in the model.

Without vital dynamics, conservation of sexual contacts was guaranteed as we saw in (2.19). Since the population size is not constant anymore, we need to redefine the parameters for average contact rate for urban and rural females (t_{NFU} and t_{NFR}) respectively. Hence, we write these parameters as

$$t_{NF.} = \frac{t_{MM.}N_{MM.} + t_{NM.}N_{NM.}}{N_{NF.}}, \tag{2.24}$$

where the dot can either represent urban (U) or rural individuals ($R.$)

2.3.2 The Simulation

With the additional parameters specified in Table 2.4, and the modification in (2.24), the simulations were run again. Simulation results for each of the six subpopulations with no migrations are in Figure 2.6. As in the model without dynamics illustrated in Figure 2.2, disease was initially introduced only in the rural area, hence the urban area shows no infectives. Notice that in the disease-free state the population of susceptibles stays constant in all six sub-populations because the parameters corresponding to rates of fertility and natural mortality were chosen so the net change in population in the disease-free state is zero. However, the key difference between the model without vital dynamics and this model is that in the former case not all rural individuals eventually become chronically infected. When vital dynamics are added, Figure 2.6 shows that at equilibrium, the number of susceptible individuals is greater than those who are chronically infected. Clearly adding fertility and mortality to the model considerably alters its dynamics.

Figure 2.7 is different from its corresponding non-vital dynamics version (Figure 2.3). Now the time to 10% and 30% prevalences with migrations at a mean of 100 weeks are higher than the times for migrations that happen at a mean of 10, 20 or 30 weeks (and no migrations). In the case without vital dynamics, this change was not observed this early. This difference might be because with vital dynamics, while no infection spreads to the urban area before the first round of migrations, the population keeps increasing with the addition of new susceptibles. 100 weeks is a long enough time-frame that the impact of growth in the number of susceptibles can be seen in terms of how long it takes to achieve a certain prevalence.

In Figure 2.7, non-migrant men in the rural area do not reach 30% prevalence with migrations every 100, 200 and 600 steps through the length of the simulation of over 20000 time steps. In the two former cases, the prevalence maximizes at about 25%, while in the latter case at about 29% over the 20000 steps. Similarly for non-migrant men in the urban area, migrations every 100 and 200 time-steps produce a maximum of 22% prevalence.

The picture in Figure 2.8 agrees with our observations so far in Figure 2.7. The times to 10% and 30% prevalence with mean migration times of 10, 20 and 30 weeks are identical for males, females and the entire population. The times required to achieve the same prevalence in the range when migrations occur between an average of 100 and 600 weeks are higher than the 10 to 30 week range, but equal to each other.

Figure 2.9 shows that for the entire population, the prevalence as a function of time (and the rise in prevalence as a function of time) is highest for migrations every 10, 20, and 30. Even at equilibrium, the prevalence is highest in these cases. Note that migrations at an average interval between 10 and 30 weeks is the most realistic from what is known about migrations in KwaZulu Natal.

For the new model with vital dynamics as given in (2.20) and analogus differential equations, there are two equilibrium points. The disease-free equilibrium has only susceptible indindividuals, so that every subpopulation is entirely susceptible.

The endemic equilibrium is found by setting the right hand sides of all equations equal to zero, but it is not possible to solve these 18 equations analytically. Figure 2.9 gives us an idea of where these equilibria lie numerically.

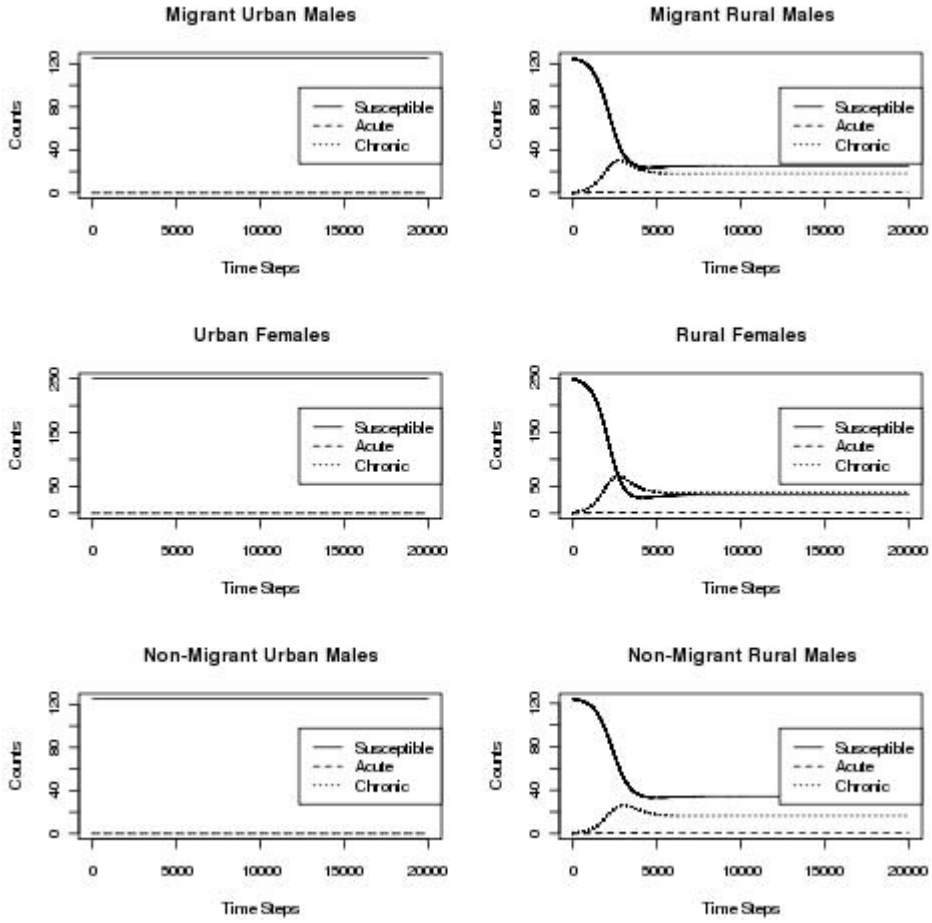

Figure 2.6: Disease transmission for case with vital dynamics, and no migration $\delta = 0.0$.. The left column shows simulations for the urban population and the right column shows plots for the rural population. Within each column, the top plot shows the migrant males, the middle figure shows the females, and the bottom plot shows the non-migrant males. The solid plot is for susceptibles, the dashed plot is for acutely infected, and the dotted plot is for chronically infected.

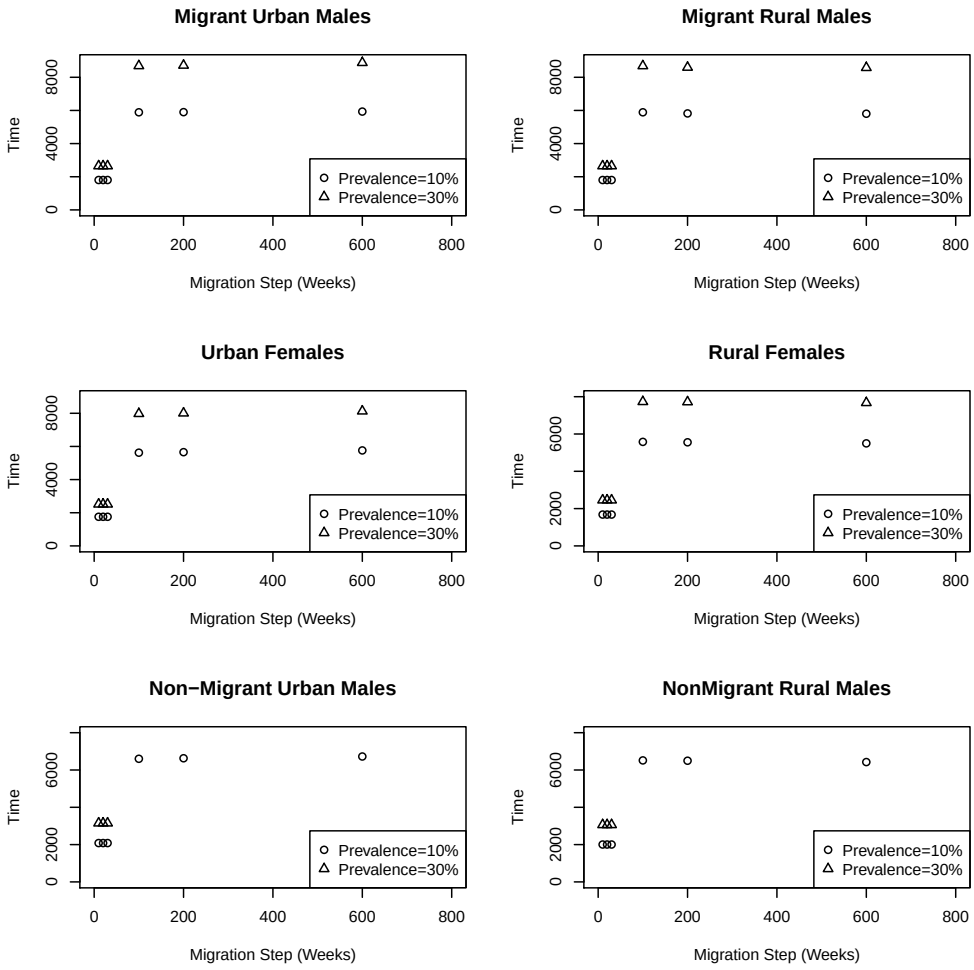

Figure 2.7: Time to 10% and 30% prevalence in all six-subpopulations with vital dynamics.

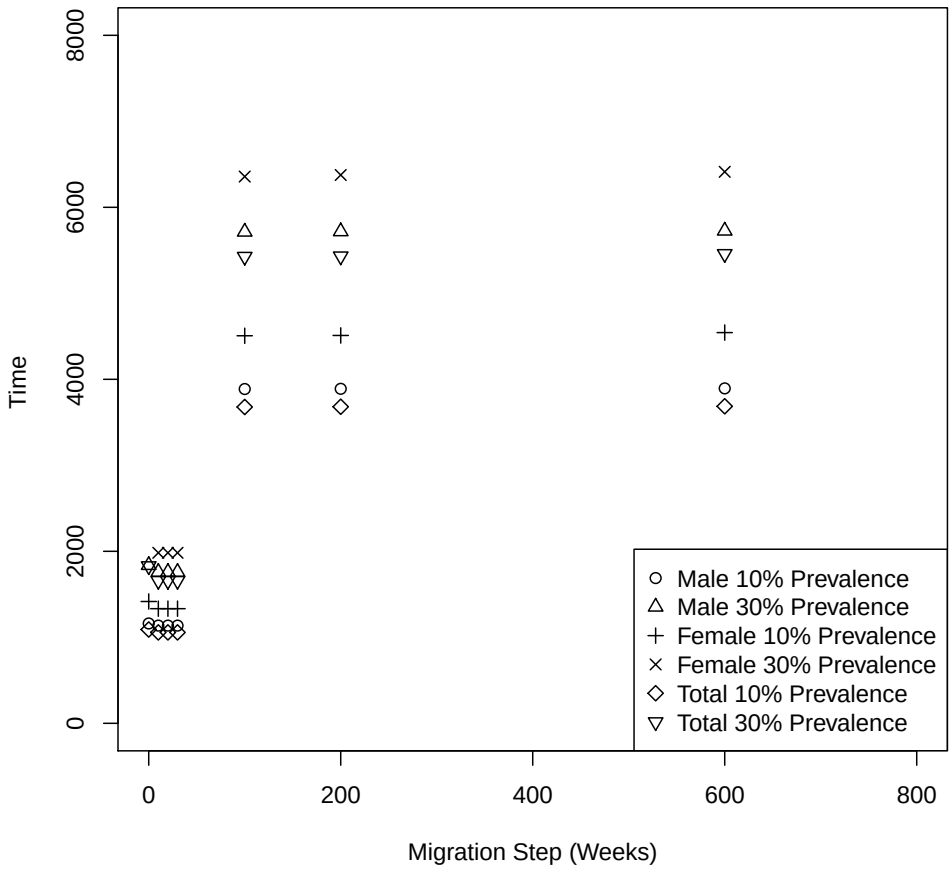

Figure 2.8: Time to 10% and 30% prevalence in all males, all females, and the entire population with vital dynamics.

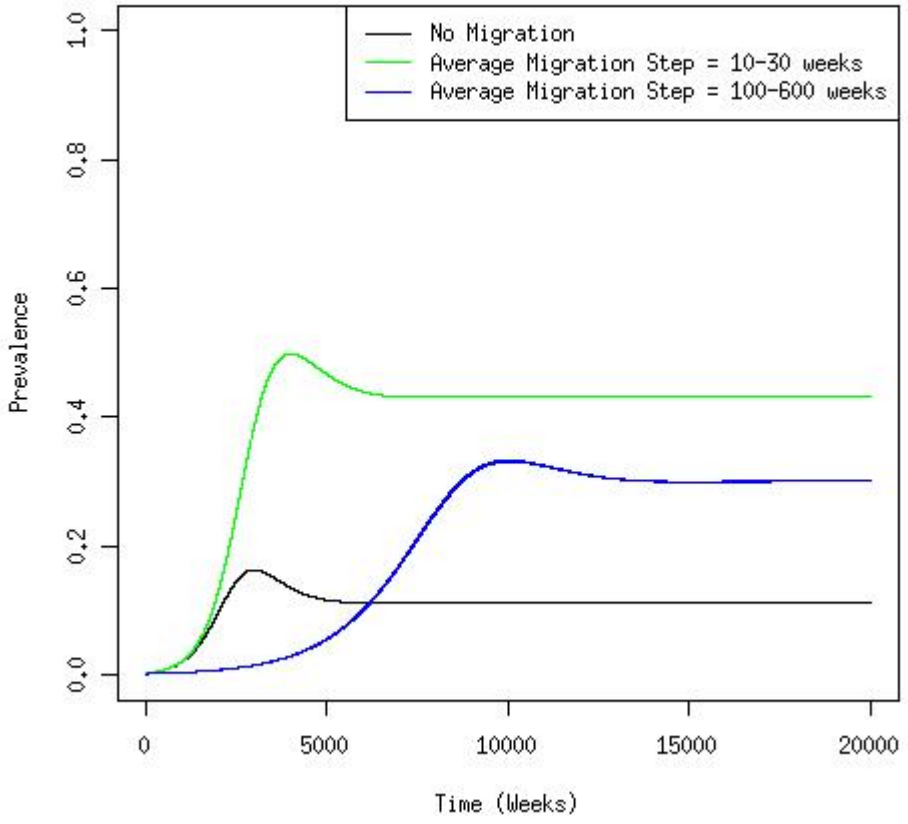

Figure 2.9: HIV prevalence as a function of time in the entire population. Fertility and mortality are considered.

2.4 Discussion

The dynamics of the model with and without vital dynamics are quite different. When vital dynamics are not included, the impact of migration is not seen unless the migrations occur very slowly. This impact is seen at shorter average migration intervals when vital dynamics are included. However, from a "real -world" perspective, migrations every 10, 20 and 30 weeks are more plausible than migrations every 100, 200 and 600 weeks. A model with vital dynamics is much more realistic than one without it, especially at the long time periods over which these simulations were run. In the latter case, the most rapid rise in prevalence was seen at migrations that occur at mean of a 100 weeks or less. The vital dynamics model seems to indicate that all else being equal, frequent migrations at short intervals ($\leq$ 30 weeks) result in the fastest rise in high disease prevalence.

These models have 18 different compartments, and all the individuals within each compartment are assumed to be homogeneous in terms of their interactions with the other classes. That is one of the key differences between this model and the stochastic network based model in that the latter can easily incorporate heterogenity within each compartment. This assumption of homogenity above is key in terms of thinking about the average number of "contacts" (t_{XYZ}) between any of the susceptible groups and the corresponding infectious groups. As we saw in equations (2.1) to (2.18) this term can be used to calculate the expected number of infections for each group. This definition of contacts implies that each coital act occurs with a different individual, which is clearly unrealistic for our system in which a significant number of sexual partnerships would be expected to be long term.

The other difference is the definition of sexual contacts, which are defined as sexual acts in the current framework. Another possible interpretation of contacts is as sexual partnerships (which is our working definition for the stochastic models in Chapter 3),

rather than sexual acts. In this case, consider a relationship between a sero-discordant couple. Let us say that during the course of this relationship n sexual acts occur, and the probability of infection being transmitted between this couple during any one sexual act is β. Then the probability that the infection will be transmitted over the course of a "contact" or relationship is $(1-(1-\beta)^n)$. Thus the expected number of infections under this paradigm is

$$St\frac{I}{N}\left(1-(1-\beta)^n\right)$$

where S, I and N are the number of susceptibles, infectives, and total population size, respectively. With this definition of contacts, we evaluate discordant relationships at the start, and simulate disease transmission through them. We neglect the fact that during the course of a partnership, say between two susceptible individuals, one might seroconvert and thus put their partner at risk as well [25].

Between the two interpretations of contacts, there is no middle ground, and both assumptions are unrealistic in their own ways. A stochastic network-based model will allow us to avoid both the potential pitfalls mentioned above, because we evaluate sero-discordance *at* every time step, rather than just the beginning of the simulation. Moreover, we can also more easily model long term and casual partnerships in the population.

One advantage of the compartmental model is that it allows easy addition of vital dynamics to its structure, which gives a reasonable idea of the long-term behaviour of the system. Dynamically, the predictions of the model in terms of the disease spread, with a peak, and an endemic state at equilibrium also correspond more closely with what is known from biology.

Chapter 3

STOCHASTIC AGENT BASED MODELS

3.1 Introduction

The deterministic model without vital dynamics in Chapter 2.2 is a null model for the system we are trying to study. In this chapter we use a different paradigm to approach the same problem, and compare the results obtained from both approaches.

As we have seen, the focus of this project is to study the impact of variable infectivity of HIV in the context of circular migrations. In the deterministic model, we approached this problem by characterizing the infected individuals as acutely infected, or chronically infected. Due to this set-up, the time spent by individuals in the acute state has a negative exponential distribution. We retain the concept of two infectious stages, with the transition from the acute to the chronic stage occuring after a fixed number of time steps, rather than being drawn from an exponential distribution, which might be a more consistent assumption with biology. We then compare the predictions from the stochastic network based model to the deterministic model. These two frameworks have some inherent structural differences, but aside from those structural differences, they have been set-up to be as identical as possible. Hence we can also compare the relative properties of the two approaches. These similarities and differences are discussed in greater detail later in this chapter.

3.2 The Problem

The objective is to study the impact of variable infectivity of HIV in conjunction with the rate of circular migration of individuals between two locations. It is now

well-accepted that the infectivity of an individual varies with time since infection. If an infected male is making sexual contact with individuals in two separate locations during his period of high infectivity then the rate of disease transmission can accelerate. Or, a susceptible migrant male that is frequently migrating can make contact with his partners during their periods of high infectivity. Thus the variable infectivity of HIV along with the rate of migration can play a significant role in determining how a disease transmits through a population.

The basic structure of the population remains identical to the one we used in Chapter 2: the population is divided between two regions, one urban, and the other, rural. Each location consists of males and females; half of the males are migrants, and the females stay fixed in their respective locations. Thus at any given time, both the urban and the rural regions consist of migrant and non-migrant males, with the former changing locations at a certain rate, and the non-migrant males remaining fixed where they are. Due to the nature of the available data, homosexual contact and migration by women are not considered.

Conceptualize the set of all men and women in the population at any given point in time along with all their sexual partnerships as nodes and ties respectively in a graph theoretic sense. This undirected graph, at any given time, is what we will call a "cross-sectional network," or simply, a "network," for brevity. (The term "partnership" from now on refers to a sexual partnership between two individuals). Given some data about the sexual behaviour of the individuals in the model, the partnership structure in a population can be modeled. (Details on the structure of this data and the modeling process are given in Section 3.3.)

The cross-sectional network is then evolved over time to model the process of formation of new partnerships and dissolution of existing ones. This process yields a series of networks over discrete time steps (henceforth called "network-series"). Once

we have this information on which actors are partnered with each other, we can model disease transmission through the population.

An important point to note here is that if individuals A and B are in a partnership, they do not necessarily have to be in the same location. For example, A might be a migrant man, married, or in a long-term relationship with B. While B is fixed in one of the two locations throughout the simulation, A is changing his location every few time steps. To model disease transmission, however, we need to evaluate if A and B are in the same location, in which case, their partnership is labeled "active;" otherwise, it is inactive.

Disease is then simulated over the "network-series" to derive certain quantities of epidemiological interest, for example, where people are infected, who infected whom, and when each infected individual got infected. This information is then used to study how different migration rates impact the patterns of disease transmission through the population. This analysis can hopefully aid in interventions with the objective of controlling the disease.

3.3 The Model

3.3.1 Key Concepts

In order to develop a network model, we need to first clarify some key concepts that will be used in the process of network generation. The population consists of a certain number of males and females, divided equally between the urban and rural areas. The males in each location consist of migrants and non-migrants, with the migrants changing location periodically.

Some of the important quantities with regards to sexual behaviour that can be measured in the population are:

1. the total number of partnerships (called "ties" in graph-theory/network-science

lingo); this quantity has to be the same for both males and females to maintain conservation of partnerships as we saw with the deterministic models in Chapter 2,

2. the degree distribution for males,

3. the degree distribution for females,

4. and, the structure of partnerships in the population, i.e. the degree to which a sub-population of males and females can "mix," for example, the number of partnerships between migrant males and females in the rural area. This information is represented in a mixing matrix.

The four points mentioned here help model the connection between sexual behaviour and HIV transmission; let us discuss how each of these quantities help establish that connection.

1. The total number of ties in the population is a direct measure of how many "pathways" there are for HIV to propagate.

2. The momentary degree distributions for men and women are counts of the number of partners that males and females in a given population have at a moment in time and hence capture the inherent "concurrency" in the population. Concurrency can simply be thought of as a measure for "relationships that overlap in time;" populations that have a higher number of individuals with more than one going partnership at any given time have a greater level of concurrency. The level of concurrency in the population has a direct impact on the rate at which sexually transmitted infections can propagate through the population [26, 42, 43].

3. The mixing matrix provides a way to represent the degree to which sub-populations can partner with each other. The degree of mixing here is measured by the number of ties between the two sub-populations. If such mixing is not possible, then the entry corresponding to those sub-categories is a structural zero. The mixing matrix allows us to define the differences in the sexual behaviour of migrant and nonmigrant men.

Given these data, we can then generate a network model for the population at a given time step. This network then evolves over time, as existing partnerships dissolve and new partnerships form. Separating from an existing partner, or forming a new relationship can both occur for several reasons. Migration is one of the possible underlying factors behind this change in the partnership structure. Therefore, it is necessary to evolve the cross-sectional network as time passes.

A heuristic explanation for how this network evolves is as follows: if the average duration of partnerships is set to m time steps (we assume that partnership dissolution probabilities are independent and identically distributed for all ties), the probability that any tie dissolves at the next step is $1/m$. Therefore the probability that a tie persists is $1-1/m$. Given the state of the network at time step t, new ties are generated in the empty dyads conditional upon the state of the network at time t, and ties in non-empty dyads are dissolved conditional upon the state of the network at time t. Results from the these two intermediate steps of formation and dissolution are then combined to obtain the network at time step $t+1$. This process is then repeated for time steps $t+2, \ldots, t+n$ and the mean value of the specified statistics over the n simulations is very close to the specified values. Theoretical details are in Section 3.3.3.

The above process generates network data that give the information on all partnerships in the population, along with their start and end dates. The information

obtained can be conceived in the form: given the list of ties at a particular time, actors A and B are in a partnership from time-step i to time-step j. Not all of the actors, however, stay fixed in their locations. We then evaluate if the partnership is "active" or not at the particular instant, since we know whether a particular actor is in the urban or rural location at any given instant.

All active partnerships that are sero-discordant have a non-zero probability of infection passing from the infected to the uninfected partner. Since a major aspect of this project is to evaluate the impact of the variability of HIV in the context of circular migrations, the probability of transmission depends upon how much time has elapsed since the infected partner became infected. The probability of tranmission for a certain period of time is assumed to be at a particular level, and once that time passes, it drops to a lower value. The probabilities for male to female and female to male transmission are assumed to be equal. We thus model transmission through all active, sero-discordant partnerships in the population over the n time steps. From this simulation, we can see who infected whom, when the infection was passed, the location of transmission, and the actor that served as the primary source or "seed" for transmission between a particular pair of partners. This investigation is then repeated for different migration rates and average partnership durations (called m above) to investigate how the variation in migration rates and partnership durations impacts the dynamics of disease transmission.

3.3.2 Theory for Estimating the Cross-Sectional Network

As motivated above, a natural way to think about the process here is in terms of a graph, or network. Random graphs also provide an easily adaptable terminology, and are a powerful tool for creating stochastic models by evolving the partnership structure in the population, and simulating the process of disease transmission. The network

here consists of all actors in the two locations, urban and rural, along with all the ties that exist between them and is generated by some underlying stochastic process. The stochastic framework takes into account the complexity of social behaviour, consisting of both deterministic and variable random components [52].

Exponential Random Graph Models (ERGMs, also called p^* in the literature) can be used to model these networks. In this framework, $\mathbf{Y}$ represents the adjacency (or socio-) matrix (defined below) of a network, and let $\mathcal{Y}$ represent the support of $\mathbf{Y}$. So $\mathbf{y}$ is a particular realization of the random variable $\mathbf{Y}$, where $\mathbf{y}$ is an $n \times n$ matrix where each (i, j) entry is either 1 or 0, depending upon whether a tie exists between i and j or not [23].

The distribution of $\mathbf{Y}$ can then be written as

$$\mathrm{P}_{\boldsymbol{\theta},\mathcal{Y}}(\mathbf{Y} = \mathbf{y}) = \frac{\exp\{\boldsymbol{\theta}^T \boldsymbol{g}(\boldsymbol{y})\}}{\kappa(\boldsymbol{\theta}, \mathcal{Y})} \tag{3.1}$$

where "$\boldsymbol{\theta} \in \Omega \subset \mathbb{R}^q$ is the vector of model coefficients and $\mathbf{g}(\mathbf{y})$ is a q-vector of statistics based on the adjacency matrix $\mathbf{y}$" [23, 61].

The denominator in (3.1)

$$\kappa(\boldsymbol{\theta}, \mathcal{Y}) = \sum_{\mathbf{z} \in \mathcal{Y}} \exp\{\boldsymbol{\theta}^T \boldsymbol{g}(\boldsymbol{z})\} \tag{3.2}$$

is a normalizing constant that sums over all possible realizations of $\mathbf{Y}$ to ensure that (3.1) is a probability distribution [23].

The vector of statistics $\mathbf{g}(\mathbf{y})$ can be generalized to $\mathbf{g}(\mathbf{y}, \mathbf{X})$ to allow "attribute" information about the nodes to be included in the model. (Attribute information refers to inherent characteristics about the nodes, for example, sex, race, or occupation.) The elements of $\mathcal{Y}$ depend on the particular characteristics of the network being modeled; more on this in Section 3.3.4.

Model (3.1) can be transformed to allow easier interpretation of the $\boldsymbol{\theta}$ coefficients [23]. Let $\mathbf{Y}^c_{ij}$ represent the full conditional distribution of $\mathbf{Y_{ij}}$ i.e. the distribution of

$\mathbf{Y}$ when $\mathbf{Y}_{ij}$ is excluded. The terms Y_{ij}^{+} and Y_{ij}^{-} represent $\mathbf{Y_{ij}}^{c}$ taken with $Y_{ij} = 1$ and $Y_{ij} = 0$ respectively. Then following the methods of [56], model (3.1) can be transformed to

$$\text{logit}\left(P_{\theta}(Y_{ij} = 1|\mathbf{Y_{ij}}^{c} = \mathbf{y_{ij}}^{c})\right) = \theta^{\mathbf{T}}\delta_{\mathbf{g}}[\mathbf{g}(\mathbf{y})]_{ij} \tag{3.3}$$

where $\delta[\mathbf{g}(\mathbf{y})]_{\mathbf{ij}} = \mathbf{g}(\mathbf{y_{ij}}^{+}) - \mathbf{g}(\mathbf{y}_{ij}^{-})$ is the change in network statistics when Y_{ij} changes from 0 to 1 [23].

From (3.3) we can make three important conclusions [23]:

1. The log-odds of a tie, depend upon the rest of the network ($\mathbf{y_{ij}}^{c}$) only through the change statistics $\boldsymbol{\delta_g(\mathbf{y}, \boldsymbol{X})}_{ij}$). Because the space of networks is usually large, computing $\boldsymbol{\delta_g(\mathbf{y})}_{ij}$ is much more computationally efficient than computing either $\mathbf{g}(\mathbf{y}_{ij}^{+})$ or $\mathbf{g}(\mathbf{y}_{ij}^{-})$.

2. Secondly, components of "the $\boldsymbol{\theta}$ vector may be interpreted as the increase in the conditonal log-odds of the network, per unit increase in the corresponding component of $\mathbf{g}(\mathbf{y})$, resulting from switching a particular Y_{ij} from 0 to 1 while leaving the rest of the network fixed at $\mathbf{Y}_{ij}^{c}$" [23]. If the only statistic in $\mathbf{g}(\mathbf{y})$ is the number of edges in the network, then $\boldsymbol{\delta_g(\mathbf{y}, \boldsymbol{X})}$ is always 1.

3. Equation (3.3) is the pseudolikelihood equation for (3.1). The pseudolikelihood is exactly the same as the likelihood equation if we assume that all $\mathbf{Y_{ij}}$ are mutually independent (not a realistic assumption in most cases). This assumption of mutual indepependence among all Y_{ij} leads to

$$\mathrm{P}_{\boldsymbol{\theta},\mathcal{Y}}\left(\mathbf{Y}_{ij} = 1|\mathbf{Y}_{ij}^{c}\right) = \mathrm{P}_{\boldsymbol{\theta},\mathcal{Y}}\left(\mathbf{Y_{ij}} = 1\right). \tag{3.4}$$

Given a vector of statistics $\mathbf{g}(\mathbf{y})$, the $\boldsymbol{\theta}$ vector in (3.1) needs to be estimated. This estimation can be carried out by maximizing the pseudolikelihood equation in

(3.3). The resulting maximum pseudolikelihood estimate (MPLE) is not optimal [23]. However, it is the best possible estimate for $\boldsymbol{\theta}$ at this stage; we call this estimate $\boldsymbol{\theta_0}$.

Once the inititial vector of coefficients $\boldsymbol{\theta_0}$ is estimated, a full conditional MCMC method is implemented to estimate $\boldsymbol{\theta}$. In order to generate the Markov Chain, a tie (Y_{ij}) is then picked. As we have discussed Y_{ij} is either equal to 1 or 0. This process of switching Y_{ij} from 0 to 1 or vice-versa is called "toggling" a tie. Let us call the current state of the network $\mathbf{y}_{\text{current}}$ and the proposed state of the network after the toggle $\mathbf{y}_{\text{proposed}}$. We can then compute the relative probabilities of the two networks by

$$\frac{\mathrm{P}_{\boldsymbol{\theta}_0,\mathcal{Y}}\left(\mathbf{Y}=\mathbf{y}_{\text{proposed}}\right)}{\mathrm{P}_{\boldsymbol{\theta}_0,\mathcal{Y}}\left(\mathbf{Y}=\mathbf{y}_{\text{current}}\right)}=\exp\left(\boldsymbol{\theta}_0[\boldsymbol{g}(\mathbf{y}_{\text{proposed}})-\boldsymbol{g}(\mathbf{y}_{\text{current}})]\right) \tag{3.5}$$

where $\boldsymbol{g}(\mathbf{y}_{\text{proposed}})-\boldsymbol{g}(\mathbf{y}_{\text{current}})=\boldsymbol{\delta}_{\boldsymbol{g}}(\mathbf{y}_{ij})$ as defined in (3.3).

We can then generate a chain of networks by moving from the current state $\mathbf{y}_{\text{current}}$ to $\mathbf{y}_{\text{proposed}}$ using either the Gibbs sampling technique, which toggles ties by the probability in 3.5, or the Metropolis alogorithm, which uses the probability

$$\min\left\{1,\frac{\mathrm{P}_{\boldsymbol{\theta}_0,\mathcal{Y}}\left(\mathbf{Y}=\mathbf{y}_{\text{proposed}}\right)}{\mathrm{P}_{\boldsymbol{\theta}_0,\mathcal{Y}}\left(\mathbf{Y}=\mathbf{y}_{\text{current}}\right)}\right\} \tag{3.6}$$

to move from the current to the proposed state, or the even more general Metropolis-Hastings algorithms [23, 55]. Using ratios of the probabilities of the two networks given in (3.5) gets rid of the normalizing constant (3.2) which typically is impossible to compute.

However, sexual networks tend to be sparse, which means that relatively few of all the possible ties are actually realized. Hence, the probability of selecting a non-tie, and then staying stuck in that state is high. In order to ensure the chain mixes well, i.e. to increase the probability of a higher number of transitions from the current to a

proposed state we use the Tie-No-Tie (TNT) sampling technique. This modification selets a tie ($Y_{ij} = 0$), with the same probability that it selects a non-tie ($Y_{ij} = 1$). Thus, the chain mixes at a faster rate [41].

Once the entire Markov Chain is generated, we sample intervals at a specified interval (1000 for our purposes) and the result is the simulation of a cross-sectional network. We can then plot the summary statistics of our simulated networks and see how they compared to the empirical data. If the fit is not good, we have to restimate $\boldsymbol{\theta}_0$ and repeat the process.

3.3.3 Dynamic Evolution of the Network

Since the process we are studying involves relatively long time scales, it is quite likely that the partnership structure in the population will evolve, i.e. new partnerships will be formed, and existing partnerships will dissolve. Let us see how we estimate an Exponential Random Graph Model that incorporates formation and dissolution of ties (called a dynamic ERGM).

In a typical social process, the forces that govern formation of ties are typically separate from those that influence their disolution. Hence in estimating an ERGM these two steps are considered separately. Thus given the network $\mathbf{Y}^t$ at time t, we want to infer the network $\mathbf{Y}^{t+1}$. The formation process is considered separately from the dissolution process. For the process of tie-formation [27],

$$\mathrm{P}_{\boldsymbol{\theta}^+,\mathcal{Y}}(\mathbf{Y}^+ = \mathbf{y}^+ | \mathbf{Y}^t, \boldsymbol{\theta}^+) = \frac{\exp\{(\boldsymbol{\theta}^+)^T \boldsymbol{g}^+(\boldsymbol{y}^+)\} 1_{\mathbf{y}^+ \supseteq \mathbf{y}^t})}{\kappa^+(\boldsymbol{\theta}^+, \mathbf{y}^t} \tag{3.7}$$

where $\mathbf{y}^+$ has at least all the ties of $\mathbf{y}^t$ and $\boldsymbol{\theta}^+$ is the vector of coefficients for the network $\mathbf{y}^+$.

Similarly, the dissolution process is represented as

$$\mathrm{P}_{\boldsymbol{\theta}^-,\mathcal{Y}}(\mathbf{Y}^- = \mathbf{y}^- | \mathbf{Y}^t, \boldsymbol{\theta}^-) = \frac{\exp\{(\boldsymbol{\theta}^-)^T \boldsymbol{g}^-(\boldsymbol{y}^-)\} 1_{y^- \subseteq y^t})}{\kappa^-(\boldsymbol{\theta}^-, \mathbf{y}^t} \tag{3.8}$$

where $\mathbf{y}^t$ contains at least all the ties of $\mathbf{y}^-$ and $\boldsymbol{\theta}^-$ is the corresponding vector of coefficients [27].

The formation of $\mathbf{Y}^+$ and $\mathbf{Y}^-$ can be considered to be intermediate steps in the transition from $\mathbf{Y}^t \rightarrow \mathbf{Y}^{t+1}$. The generation of $\mathbf{Y}^+$ and $\mathbf{Y}^-$ are independent steps. Therefore

$$\begin{aligned} \mathrm{P}(\mathbf{Y}^{t+1} = \mathbf{y}^{t+1} | \mathbf{Y}^t = \mathbf{y}^t, \theta^+, \theta^-) \quad &= \mathrm{P}(\mathbf{Y}^+ = \mathbf{y}^t \cup \mathbf{y}^{t+1} | \mathbf{Y}^t = \mathbf{y}^t, \theta^+) \times \\ &\quad \mathrm{P}(\mathbf{Y}^- = \mathbf{y}^t \cap \mathbf{y}^{t+1} | \mathbf{Y}^t = \mathbf{y}^t, \theta^-) \end{aligned} \tag{3.9}$$

enables generation of $\mathbf{Y}^{t+1}$ conditional upon the network $\mathbf{Y}^t$ [27].

3.3.4 Fitting a Dynamic ERGM model

As mentioned above, the statistics $g(\mathbf{y})$ in Equation 3.1 required to estimate the model are

1. the number of edges in the network; 600 for the current purposes,

2. the degree counts for males in Table 3.1,

Table 3.1: Degree Distribution for Males

Degree	0	1	2	3
Number of Males	130	215	100	42

3. the degree counts for females in Table 3.2,

4. the mixing matrix in Table 3.3, and,

5. the average partnership duration for existing ties in the network; we consider two separate instances, with average partnership durations of 500 weeks and 10

Table 3.2: Degree Distribution for Females

Degree	0	1	2
Number of Females	85	305	55

Table 3.3: Mixing Matrix For Simulation

		Females	
		Rural (250)	Urban (250)
Males	Rural (125)	100	0
	Migrant(250)	200	200
	Urban(125)	0	100

weeks respectively. All ties are assumed to be homogeneous and have the same average duration, hence have the same proability of dissolution per time step (0.002 and 0.10 respectively).

These data are hypothetical; the numbers were chosen to reflect some general trends in sexual behaviour, for example, the degree distribution for men tends to have a higher variance and a longer tail. The given values represent the mean values of the specified statistics, and for the purpose of estimating the model these statistics are sufficient. The first four statistics mentioned above are sufficient to estimate a cross-sectional ERGM, and in combination with the fifth, they are sufficient to estimate a dynamic network.

It is intuitively reasonable to assume that the total number of ties for men should equal the total number of ties for women (we call this "structural balance"). From Tables 3.1 and 3.2 there are a total of 541 ties defined for 487 men and 415 ties for 445 women. Hence, for the remaining 13 men we have 59 ties with a mean degree of

4.5, and 185 ties for the remaining 55 women with a mean degree of 3.4. The right tail is unspecified to ensure our estimated network is structurally balanced, i.e. the total number of ties for males and females are equal.

We are restricting attention to heterosexual behaviour, therefore, for our network $\mathbf{Y}$, $Y_{ij} = 0$ if i, j both match on the attribute of sex. Additionally, if i and j happen to be of the opposite sex, but are in different regions at a particular time-step, and the male is a nonmigrant, then once again $Y_{ij} = 0$. These are the structural zeros mentioned in Table 3.3. Thus the space $\mathcal{Y}$ of networks is restricted due to the presence of these structural zeros. Ties are also only possible between males and females; male to male ties and female to female ties are not possible because we are only considering heterosexual contact. Since contact is only possible between nodes of different attribute (sex in this case), we have a bipartite graph. This restriction on the nature of ties further reduces $\mathcal{Y}$, the space of all graphs.

In order to generate this network, we estimate an ERGM with the above specified parameters, with the following modifications: of the six elements of the mixing matrix specified in Table 3.3, only 5 were specified to avoid over-specifying the model; the parameter corresponding to mixing between urban males and urban females was not specified (We will revisit this point in Appendix A.2). And, the male and female degree distributions in Tables 3.1 and 3.2 were only specified until degree counts 3 and 2 respectively to maintain structural balance as explained above.

Each partnership was defined to persist for 500 time steps on average. Here, a time step is defined as being equal to one week. From section 3.3.1, the probability that any partnership breaks from one step to the next is 0.002. Since all ties are structurally equivalent, the process of tie dissolution is homogeneous.The log-odds of partnership perpetuation are then $\log\left(\frac{0.002}{1-0.002}\right) = -6.212$.

In going from one time step to the next, thus ties are dissolved with a given probability. Therefore, the number of ties at a time step can be no greater than the ties at the previous time step. However, the mean number of edges at any given time-step has to be 600. Hence new ties are formed, within sub-populations that may mix with each other, (i.e. their corresponding entry in Table 3.3 is not a structural zero).

From this estimation process, we can then simulate a series of dynamically evolving networks over a given number of time-steps (13000 in this case with a mean partnership duration of 500 weeks). The mean values for the thirteen[1] specified statistics in the network series were very close to the parameter values specified above (600 edges, the degree distributions for males and females in Tables 3.1 and 3.2 and the the mixing matrix in Table 3.3.)

ERGMs were then used to simulate 10 network-series with the above the appropriate mean statistics specified in Tables 3.1, 3.2 and 3.3 for each of the respective parameters (the statistic for the parameter corresponding to mixing between urban males and urban females was not specified to avoid collinearity). The mean value for each of the parameters over 10 simulations $\mathbf{g}(\mathbf{y})$ was within statistical variation of the specified mean statistics.

3.3.5 Simulating Disease Transmission

In every network series, we have information on where every actor in the network is located. The location of actors is the key criteria with regard to a partnership being active or not, in the sense defined in Section 3.3.1. The distribution of active partnerships is the important quantity with regards to studying disease transmission.

[1]The thirtteen statistics consisted of one statistic for edges, for for the male degree distribution, three for the female degree distribution, and five for the mixing matrix. One entry in the mixing matrix was left out to avoid over specifying the model. The dissolution parameter is not estimated.

The migrant urban and rural men switch positions at a specified interval. The active partnerships are then evaluated to check if the partners are sero-discordant; if so, there is a postive probability of disease transmission between those partners. This probability depends upon how much time has passed since the infected partner got infected. For the first 10 weeks, this probability is 0.0082 per coital act, after which it falls to 0.0007. These numbers were chosen in accordance with Wawer et. al. [64]. In their study, Wawer found that the transmission probability rises up to 0.0028 six to twenty-five months before death; however, in this work we are not considering vital dynamics. Hence this late stage rise in transmission probability is ignored. They also found the mean number of coital acts to vary between 8.3 and 9.7 per month, depending upon whether the infected partner was male or female. This observation translates to a range of 2.1 to 2.5 sexual acts per week.

From Table 3.3 the mean momentary degree distribution is 1.2. If we assume 2.5 sexual acts per partnership per week on average for the entire population, then the mean number of coital acts per week is 3. Consider migrant men, who constitute one-fourth of the total population, only 50% of all partnerships are active on average at a given time. For the other non-migrant men (one-fourth of the population), all 100% of partnerships are active. For the females, all partnerships except those with the migrant men in the opposite location are active. Therefore, we can compute a weighted average based on 3 coital acts per week:

$$(1.5 \times 1/4) + (3 \times 1/4) + (2.25 \times 1/2) \approx 2.4$$

which is in the range observed by Wawer et al.

With these disease transmission probabilities, we can now simulate disease through the population and make comparisons. For the sake of uniformity with the deterministic models, disease was introduced in the population in every case by infecting one non-migrant rural male, and one rural female. This structure also provided a natural

check on the simulation, for example, in the case of no migration, no disease appeared in the urban area. More on this in Appendix A.2.

This procedure of disease transmission is then applied to all 10 network series. In any given network series, we then record how many people in a sub-population belong to a particular infection status (susceptible, acute or chronic infection) at every time step. These numbers are then averaged over the 10 network series to get the mean number of people in every infection status at each time step. These computations then allow us to evaluate how the disease progresses through every subpopulation over time.

We then change the migration rate of 10 time-steps and the average partnership duration of 500 time-steps to see how the rate of migration affects disease transmission. All simulations were run using the "statnet" package in the R-programming language [19]. Some modifications to the disease simulation algorithm were made in C.

3.4 Analysis

A major theme of this work is to investigate the interaction between variable infectivity and frequency of migrant return. Hence, we construct different scenarios, where the migration rate is varied to see how that variation impacts the transmission of infection through the population. To investigate this question, we ran simulations with average partnership durations of 10 weeks (1 week is 1 time step in the simulation), followed by simulations with average partnership duration 500 weeks. Figures 3.1 and 3.2 show the time average time to 10% and 30% prevalences and the prevalence in all males, all females and the entire population with respect to time when average partnership duration is 10 weeks. Figures 3.3 and 3.4 show the corresponding pictures for average duration of 500 weeks. Figure 3.5 shows the time to 10% and 30% prevalence in each of the six subpopulations for both average partnership durations considered.

From Figure 3.1 we see the impact of migration on time to 10% or 30% prevalence is more pronounced when migration steps are shorter ($\leq$ 50 weeks) than when they are larger ($\geq$ 100 weeks). The structure of this impact, however, is unclear. From migrations every 5 weeks to migrations every 15 weeks, we see a slight increase in how long it takes to achieve a certain prevalence. However, this required time then drops between 20 and 50 steps. The time to 10% and 30% prevalence is roughly the same when migrations occur every 100, 200 or 600 weeks, though this time in the case of 600 weeks is clearly lesser than for 100 and 200 weeks. That might be because in every case, the disease is first introduced only in the rural area, and it takes a much longer time to reach the urban area when migrations happen so slowly.

From Figure 3.2, however, it seems that at higher prevalences ($\geq$ 40%), the disease disperses fastest with a migration interval of 600 steps and slowest with migration rates of 200 steps. This may be because, with migrations every 600 steps, the disease infects a sizeable mass of the rural region. After the first round of migrations, for the next six hundred steps the disease spreads efficiently through both regions since some infectives are now in the urban area. However, for higher prevalences, from 5 to 200 steps the rate of disease transmission seems to get slower. This result makes intuitive sense as well, at smaller migration rates, people migrate faster between the two locations. Hence, the faster infectives will travel between the two locations and the disease will spread. It is also intuitive that in the case of no migration, 50% of the population is infected at equilibrium; because no disease spreads to the urban area, and everyone in the rural area gets infected.

Now consider the cases where the average partnership duration is 500 weeks. Note that this case is more realistic; we know that a "steady" long-term partnership is closer to 10 years than 10 weeks. Comparing both cases, however, allows us study the impact of average partnership duration on HIV transmission. It is quite noticeable that the

times in Figure 3.3 are greater than the times seen in Figure 3.1 indicating that longer average partnership durations lead to slower disease transmissions. For both 10% and 30% prevalence, the time required seems to be the highest when the migrations happen every 5 steps, and then seems to be the shortest when the migrations happen every 10, 20 and 30 steps. For 50 steps, there is a slight increase, nothing changes with 100 steps, and then 200 and 600 are successively shorter.

Consider prevalence as a fuction in time, for both long and short average partnerships, shown in Figures 3.2 and 3.4. In both cases, the base case of no migration shows the lowest prevalence as a function of time. However, notice that the variation for other migration rates (ignoring the base case) is much greater when average partnership durations are 10 weeks. The fastest and slowest migrations seem to occur at intervals of 600 weeks and 300 weeks respectively (opposite of what we observed in the deterministic model without vital dynamics in Figure 2.5.

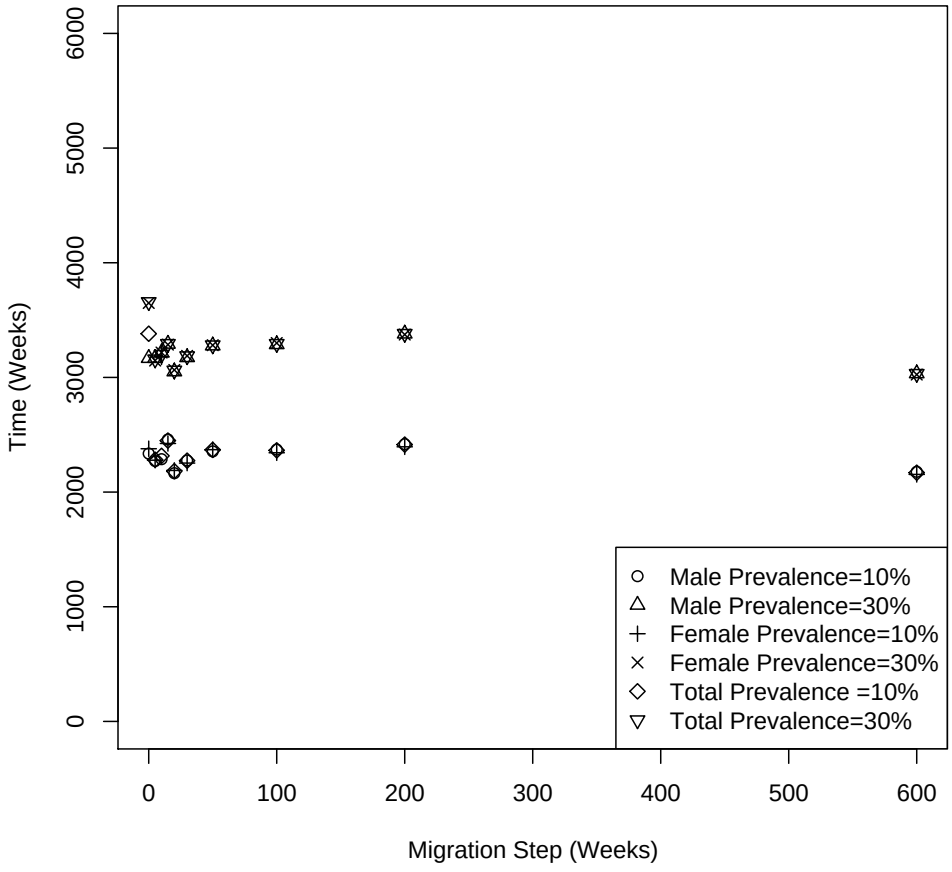

Figure 3.1: Time to 10% and 30% prevalence with average partnership duration of 10 weeks

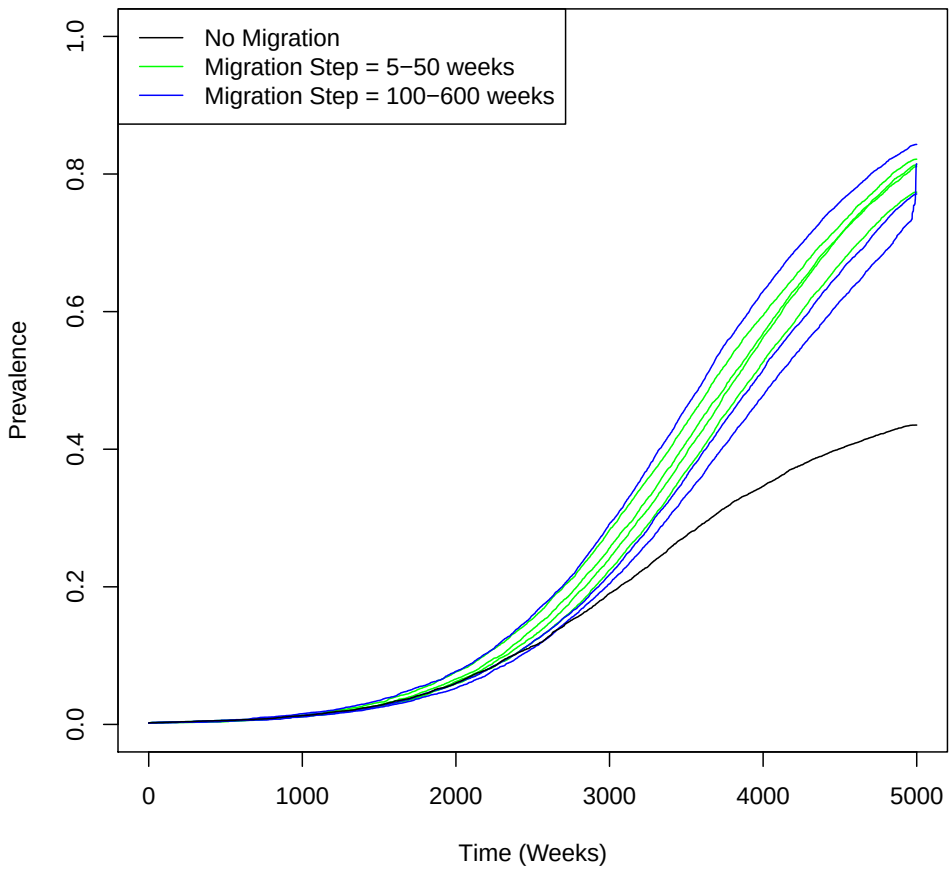

Figure 3.2: Prevalence in entire population with average partnership duration 10 weeks

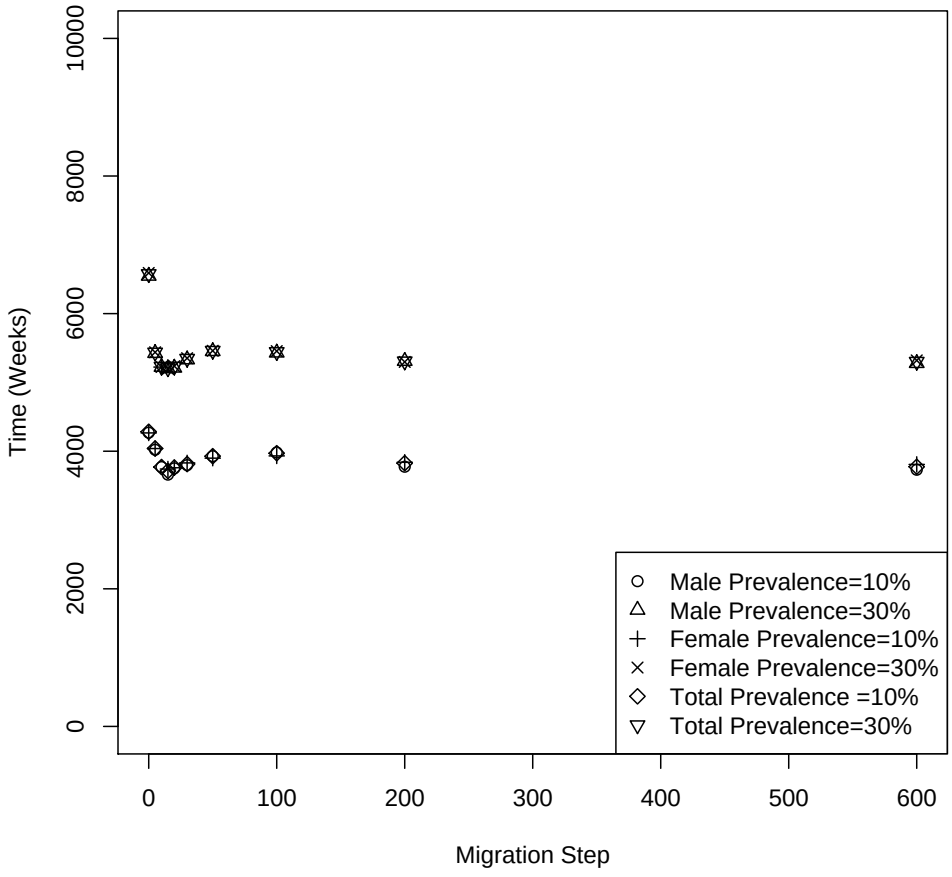

Figure 3.3: Time to 10% and 30% prevalence with average partnership duration 500 weeks

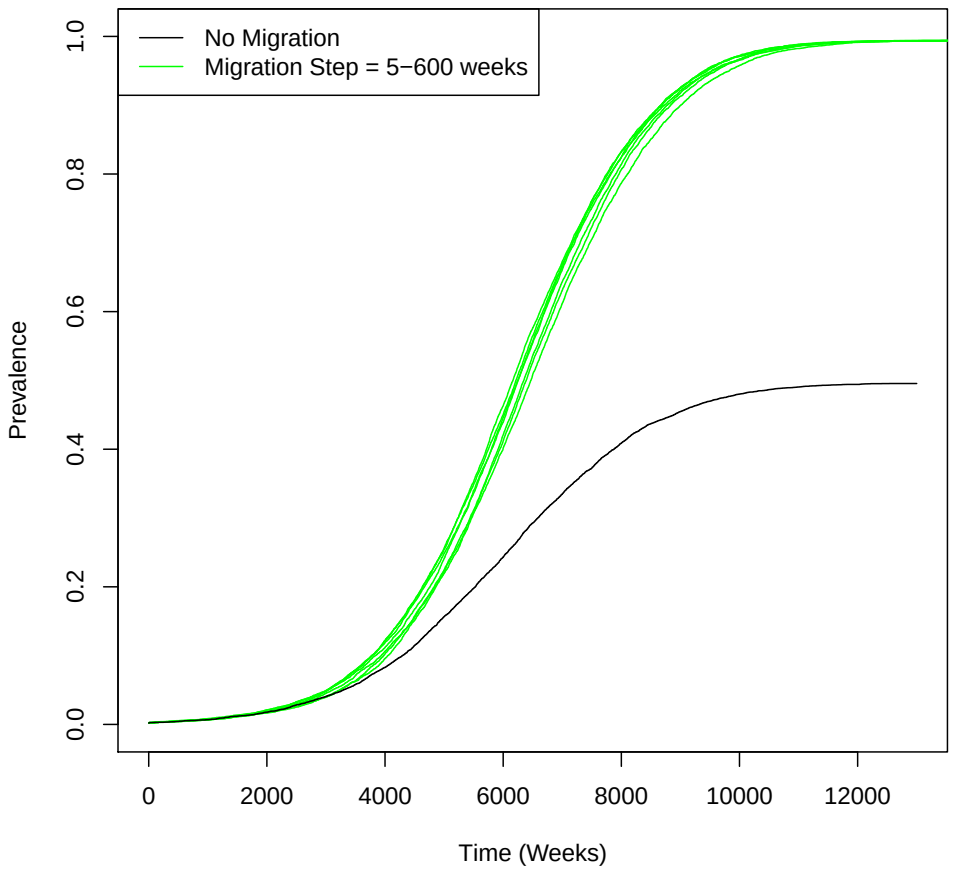

Figure 3.4: Prevalence in the entire population with average partnership duration 500 weeks

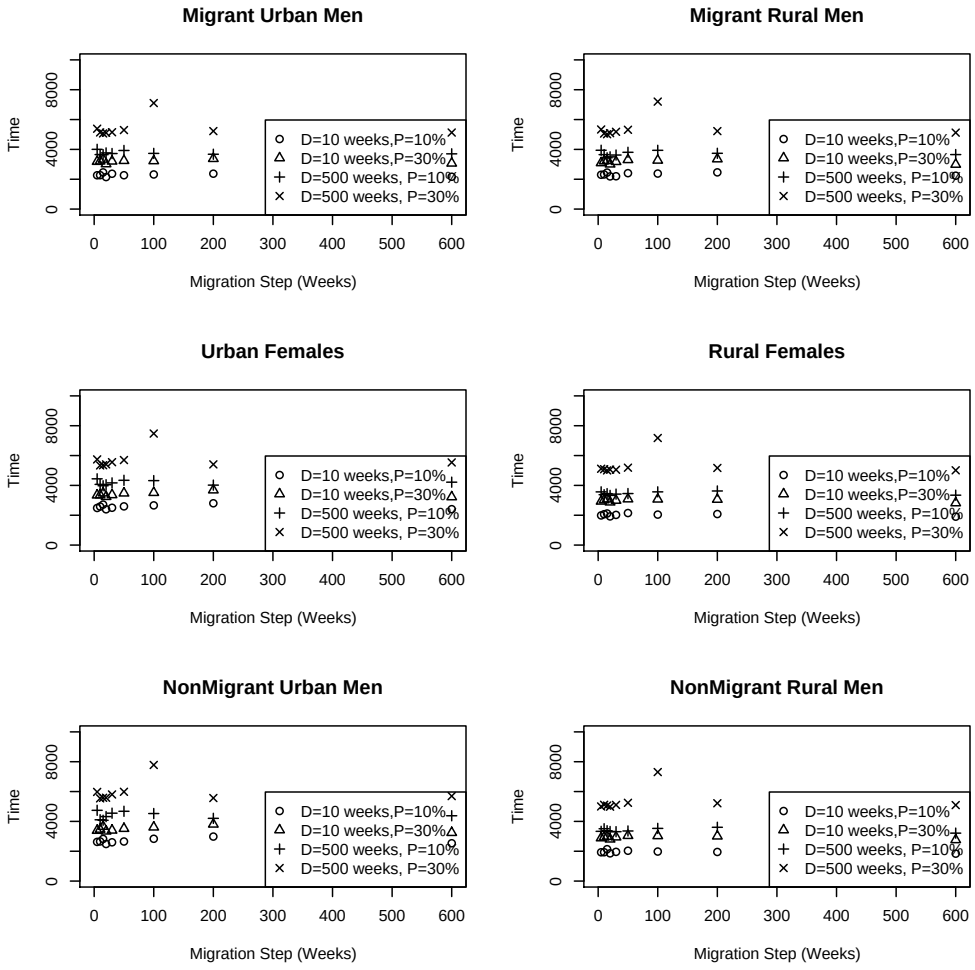

Figure 3.5: D is average duration of partnerships, P is prevalence.

3.5 Conclusions and Discussion

The model we have analyzed here is an extension of the $S - I$ model, with two stages of infection. In addition we incorporated some characteristics of human sexual behaviour in the model. In a closed population, for an S-I model with no recovery the number of susceptibles approaches zero and the population gets entirely infected; our observations agree with this hypothesis.

The obvious result to come out of this study is the impact of average partnership duration on the rate at which HIV transmits through a population. At the higher partnership duration, it took much longer for the disease to infect the population.

In the case with average partnership duration of 500 weeks, the results at shorter migration intervals ($\leq$ 30 weeks) seem comparable to the deterministic models; in that, the time to 10% and 30% prevalence is similar when migrations occur at intevals between 10 and 30 weeks (albeit with some steady decline, though it is unclear how significant that decline is). In the deterministic model with vital dynamics, when average migrations occured at intervals of 100 weeks or more, there was an obvious rise in the time to achieve certain prevalence. However, this early increase in time was not seen this early in the case when no vital dynamics are included in the deterministic model. The stochastic model is also based on a closed population, and the trends seen here of idential results between 10 and 30 weeks and not much variation thereafter is similar to what we saw in the deterministic case applied to a closed population.

The case of average partnership duration of 10 weeks shows similar trends with regards to the both points concerning times to reach a certain prevalence between 10 and 30 weeks, and longer migration intervals; but the patterns seem unclear especially in the range where migrations happen at intervals of between 10 and 30 weeks.

Recall "real" circular migrations typically happen at intervals ranging from a weeks to a few months; migrations at intervals greater than a 100 weeks are unrealistic but

possibly useful in discerning patterns and understanding the dynamics of the models. Slower migrations seemed to have much less of an impact on the rapidity of disease transmission with both short and long average partnerships. The disease transmission seemed to be quickest between 10 and 30 week migrations in the more realistic case of an average partnership duration of 500 weeks. If the deterministic case is any indication, then the impact of longer intervals might be much more pronounced if vital dynamics are included in the model.

A useful extension to this stochastic model would be incorporating vital dynamics in networks estimated using the Exponential Random Graph Models. This is one of the projects members of the UW Net-Modeling group are currently working on. Using real data to estimate other parameters besides the transmission probabilities would also be a natural next step.

Another key difference observed between the stochastic model and its deterministic cousin (closed population model) is that the population of susceptibles fell to zero much more quickly in the latter case, and correspondingly the population of chronically infected grew much faster. The differential equation model is based on random mixing, hence, the infection can transmit much more efficiently relative to the stochastic model which is based on person to person transmission.

The structure of the compartmental models in Chapter 2 resulted in the pool of migrant labourers being drawn from an exponential distribution, while the in the stochastic case all migrant and non-migrant labourers simply switched locations. Two make the models more comparable, the underlying migration structures should be made identical in the two cases.

It would also be helpful to investigate more realistic migration patterns; for example, exploring seasonality in movement. It is quite likely that at a certain time of the year labourers from a particular village leave and migrate for some peiod of time,

but there is no corresponding influx of men in to the rural area. Also, since migrant labourers are subject to relaxed social norms when they are *away* from the village, when there is no migration it might be worth investigating if the sexual behaviour of migrating and non-migrating men is closer in terms of contact-rate. The potential impact of this modification on disease transmission dynamics might be worth investigating.

Finally, exploring homosexual transmission and migrations by females might be an important addition [66].

The one clear result to emerge from the stochastic model is the effect of average partnership duration on disease transmission. The predictions by the deterministic and compartmental model are generally quite different (except for showing quick transmission of the disease when migrations occur between 10 and 30 weeks). Using real data will also potentially help potentially illuminate predictions made by which modeling paradigm are closer to reality.

Appendix A

APPENDIX TO STOCHASTIC MODEL

A.1 Motivation

The code is in written in several different stages, using the "statnet" package in the R-programming language [19]. It is imperative to test it at the various stages to make sure it does what we expect it to do. This testing procedure can be divided into four categories:

1. Check the parameter values for the dynamic ERGM, i.e. the mean values of the sample are reasonably close to the specified values.

2. Check if the average duration of partnerships is equal to the specified length.

3. Check if the statistics for the cross-sectional networks that comprise the dynamic network are close to the specified values.

4. The distribution of active partnerships is the critical factor with regards to transmission of disease. Make sure spread of infection is consistent with the specified migration structure. For example, if the rate of migration is 200 time steps, and the infection is initially only introduced in the rural area, then no infection should spread to the urban area before 200 time steps. This is because before the 200th time step, all the partnerships of the migrant men in the rural area with their urban partners are inactive, and likewise for migrant men in the rural area with their urban partners. Hence, infection introduced initially in the rural area cannot be transmitted to the urban area.

Let us discuss each of these check-points.

A.2 Tests

A.2.1 Dynamic ERGM fit

Figures A.1 to A.4 show that the dynamic exponential random graph model was a well-fitting one. We see the fit for 11 of the specified statistics; the statistics corresponding to the two structural zeros are not estimated, and as we saw in Section 3.3.4 the statistic corresponding to non-migrant urban males and urban females was not specified to avoid overspecifying the model.

A.2.2 Partnership Duration

To test if the average partnership duration was close to 500 time steps, we looked at all 10 dynamic network-series. Each of these network seties consisted of cross-sectional networks over 13000 time steps. However a number of partnerships are censored, because they are unbroken at the final time-step, so we do not know their true duration. Hence a straightforward computation of mean partnership duration over these 10 network-series (where each series consists of 13000 time-steps) is not possible. If we ignore the censored partnerships, the mean duration of the remaining partnerships over the ten dynamic network simulations was 482.3. If censored partnerships are given an end-time of 13001 and included in the computation, the mean partnership duration is 483.8.

A.2.3 Network Structure at every time step

The next phase of the testing process involves ensuring that the cross-sectional networks that constitute the dynamic network series are structurally similar to the specified network structure. Checking this process over all 13000 time steps of the 10 dynamic network simulations causes memory allocation problems. Hence, 1000 cross-sectionaly networks were randomly selected from the first dynamic network series.

There are 4 specified statistics for the network model: the number of edges, the degree distributions for males and females, and the mixing matrix. Please see Figures A.5 and A.6. Notice in Figure A.6 the structural zeros are never violated.

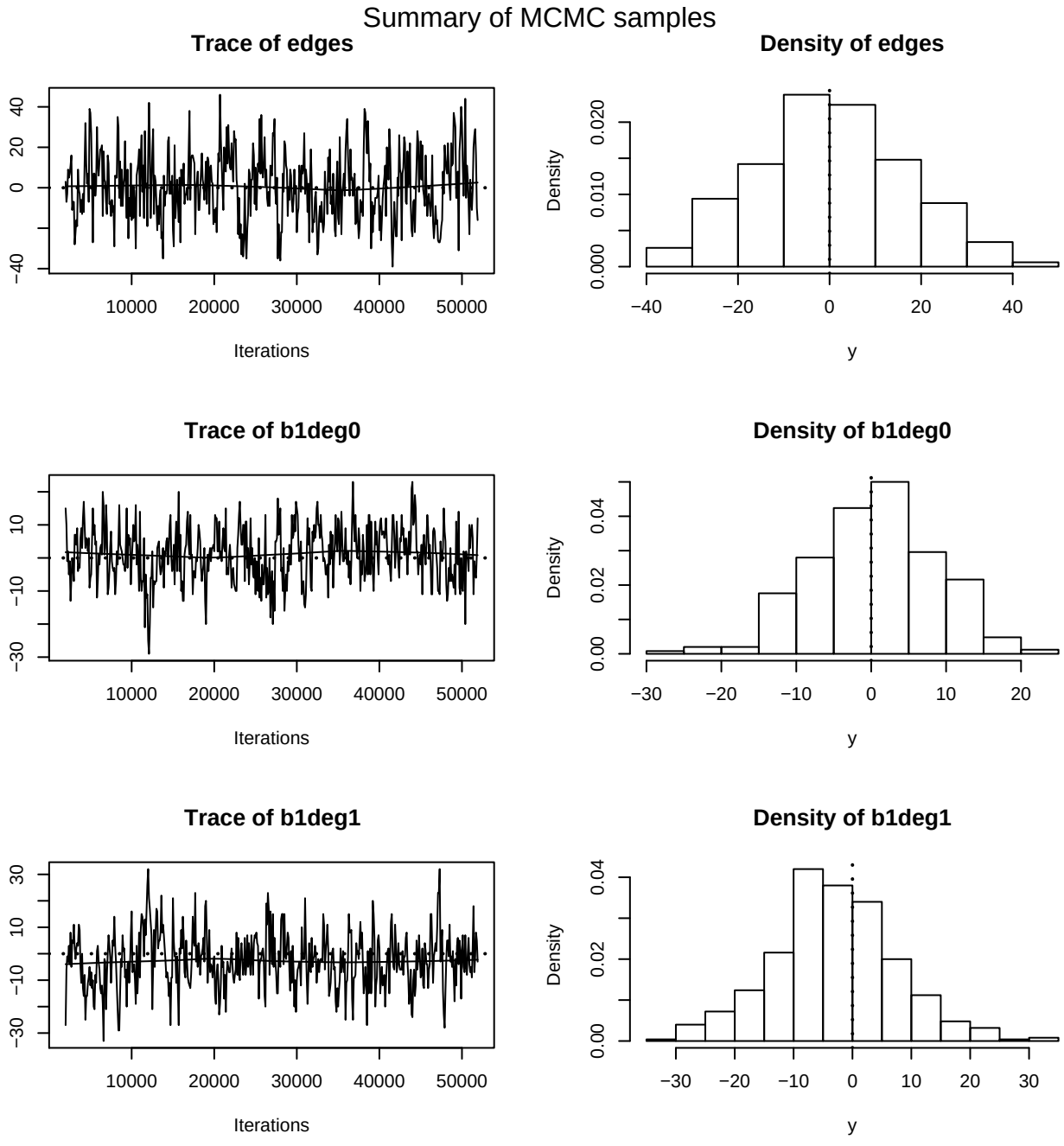

Figure A.1: Testing Dynamic ERGM Fit for statistics corresponding to Edges and Male Degree Distributions. "b1degX" refers to males of degree X.

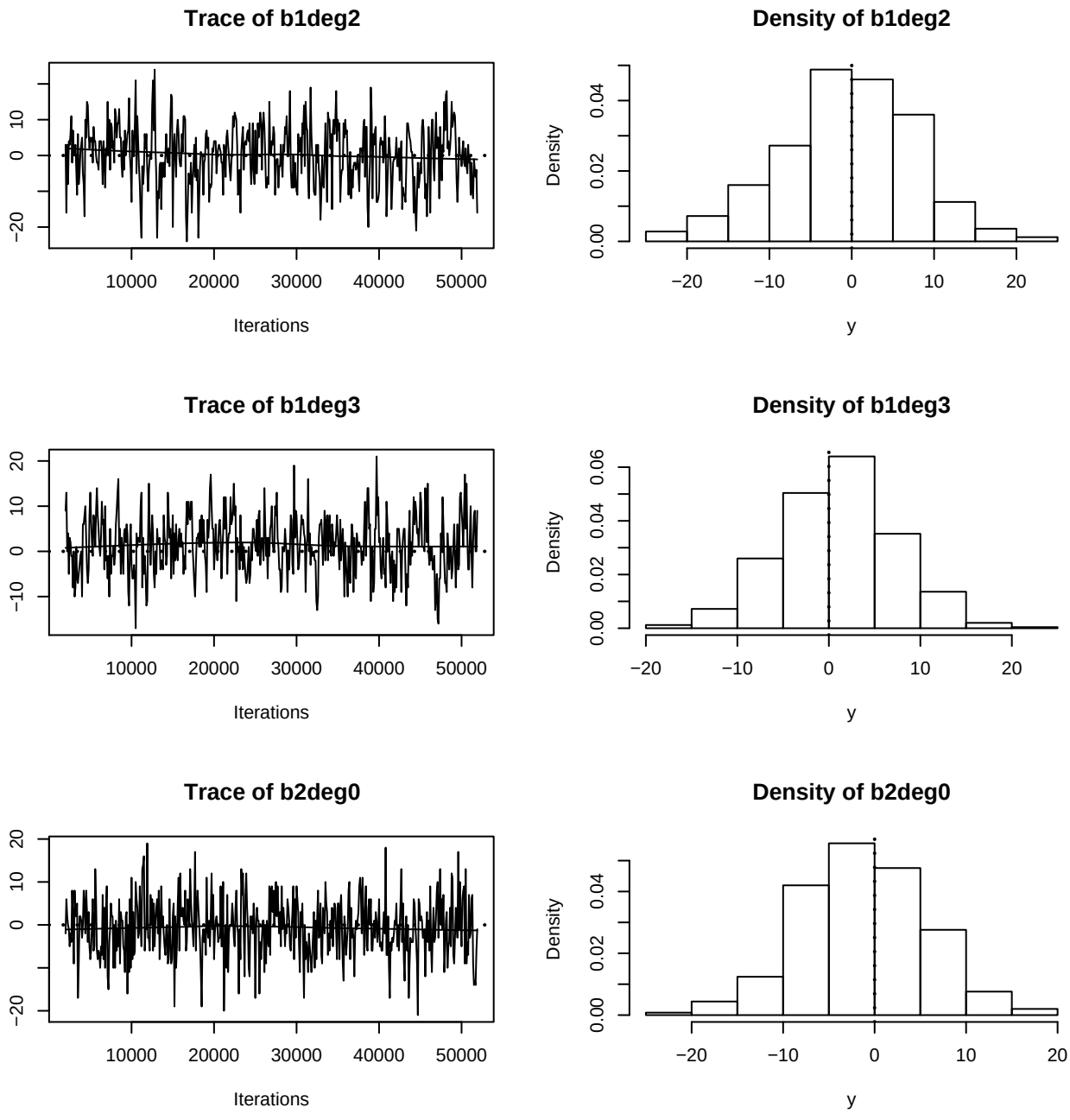

Figure A.2: Testing Dynamic ERGM Fit for statistics corresponding to Degree Distributions of Males and Females. "b2degX" refers to females of degree "X."

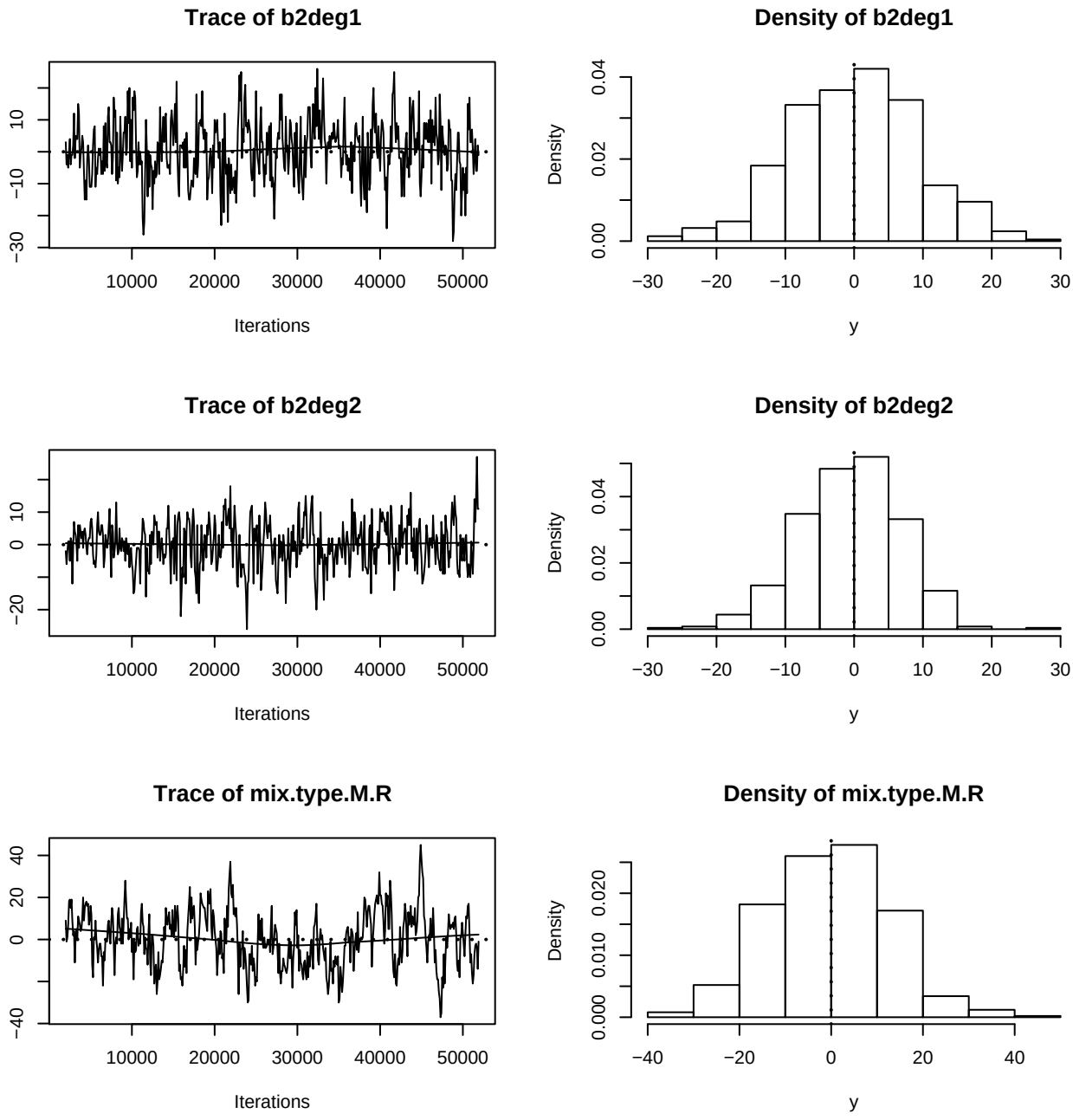

Figure A.3: Testing Dynamic ERGM Fit for statistics corresponding to Female Degree Distributions and Mixing: "M.R." refers to mixing between migrant males and rural females.

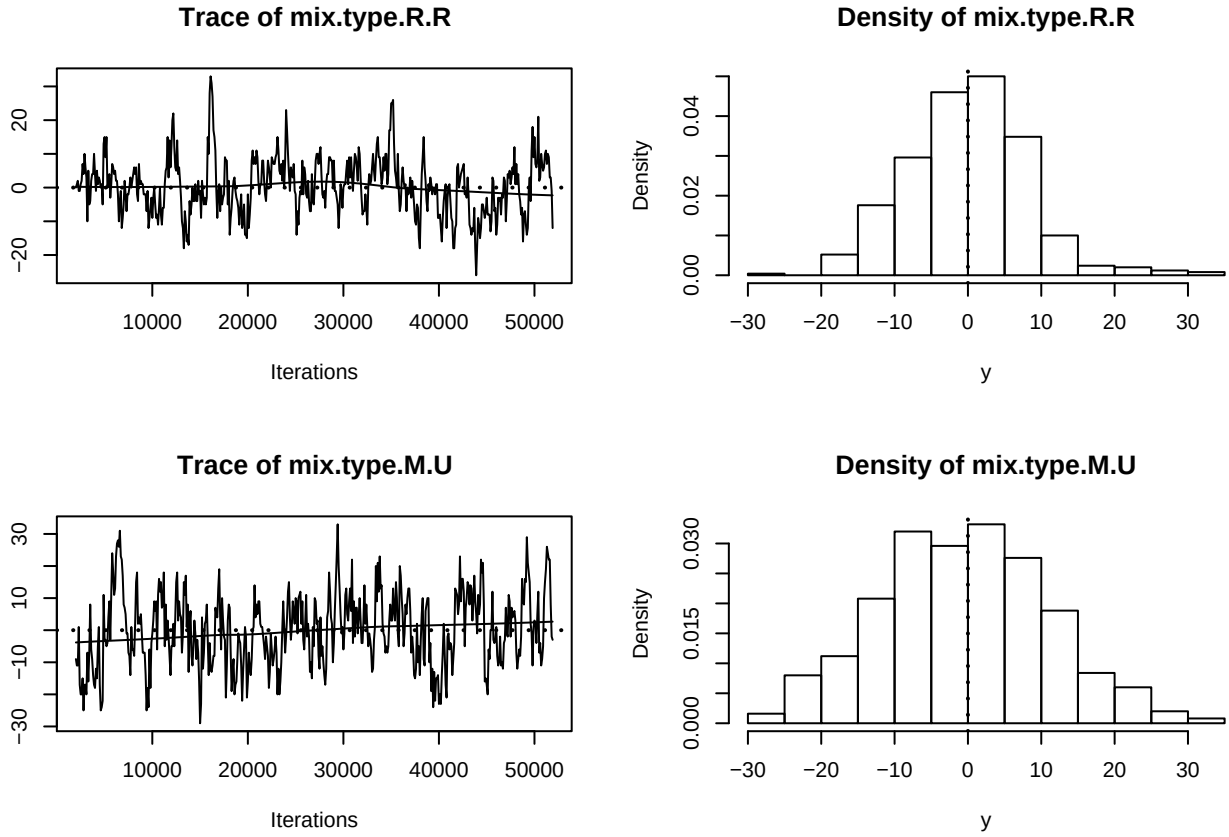

Figure A.4: Testing Dynamic ERGM Fit for statistics corresponding to Mixing: "R.R" refers to mixing between non-migrant rural men and non-migrant rural women; "M.U" referes to mixing between migrant males and urban females.

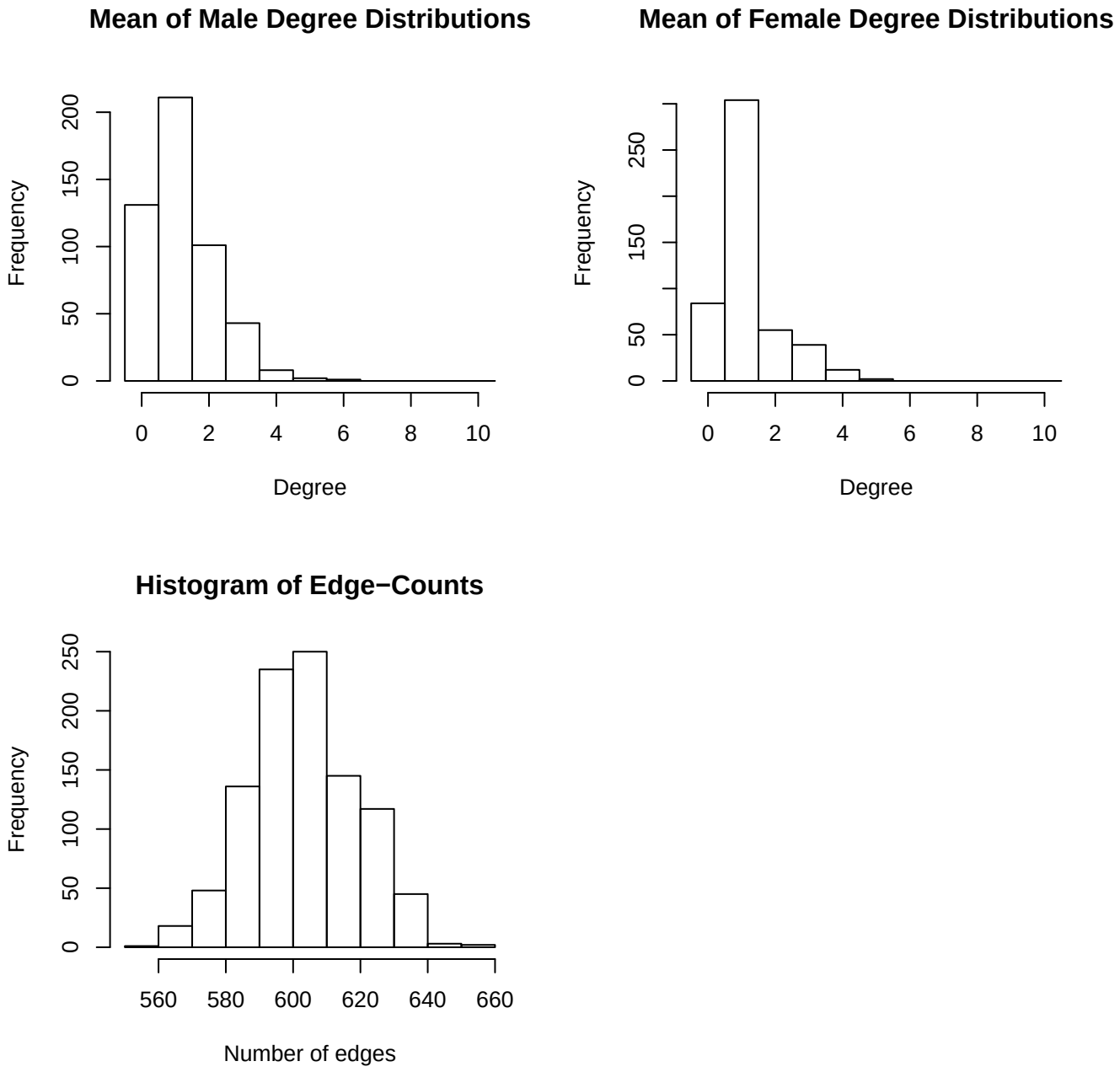

Figure A.5: (Top Left) Mean of Male Degree Distributions over the 1000 sampled networks. (Top Right) Mean of the Female Degree Distributions over the 1000 sampled networks.(Bottom Left) Edge counts for the 1000 sampled networks, mean=602.

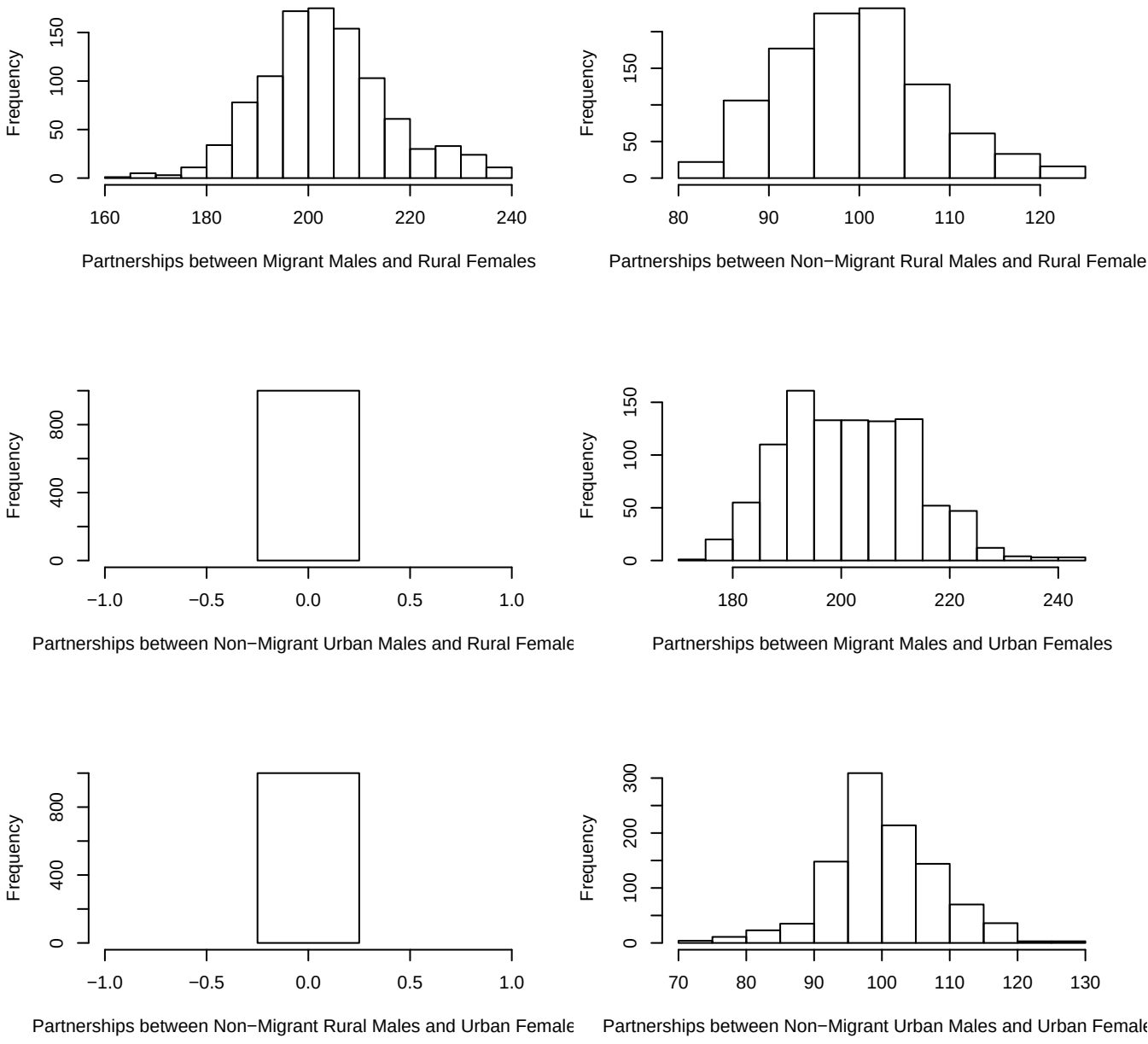

Figure A.6: Distribution of the degree of mixing over the 1000 randomly sampled networks

As we have seen in Section 3.3.4, the specified degree distribution for men for degrees 0 to 3 is (0,215,100,42) and the degree distribution for females with degrees 0 to 2 is (85, 305, 55). From Figure A.5, we see that the mean values for the male and female degree distributions over 1000 randomly chosen networks correspond well with the specified values.

We also specified 600 edges for the network. The mean over these 1000 sampled networks is 602 (Figure **??**. The mean statistics for the mixing matrix in Figure A.6 also correspond well with the specified values over these 1000 sampled networks. Notice the structural zeros are never violated/

Hence, we see that the network structure at every for these sampled networks with respect to the specified statistics is close enough to the specified values for those statistics.

A.2.4 Active Partnerships

The logic for testing if disease was spreading only through "active" partnerships is for disease to transmit through a population it not only has to exist but also the two partners have to be in the same location. An easy way to test this is to see who gets infected in a population before the first round of migrations. Tables A.1, A.2 and A.3 present results for who is infected before time-step 10, 200 and 600 respectively. We check to see which individuals get infected for these imgration rates before the first round of migrations.

Table A.4 shows where individual actors were located.

In each of the instances presented in Tables A.1, A.2 and A.3 the disease was initially introduced in the rural area by infecting one male and one female (actors 1 and 501). It is clear from the data in these tables that the disease did not spread to the urban area before the first round of migrations.

Table A.1: Actors infected before time-step 10 for migrations every 10 steps.

Simulation	Individuals Infected before migration
1	1, 501
2	1, 501
3	1 501
4	1, 501
5	1, 42, 501
6	1, 501
7	1, 501
8	1, 501
9	1, 501
10	1, 501

Table A.2: Actors infected before time-step 200 for migrations every 200 steps.

Simulation	Individuals Infected before migration
1	1, 42, 501, 506
2	1, 501
3	1, 501, 571
4	1, 501
5	1, 501
6	1, 42, 106, 501, 536, 571, 711, 748
7	1, 42, 501, 748
8	1, 42, 501, 711, 748
9	1, 501, 571
10	1 , 501 , 571

Table A.3: Actors infected before time-step 600 for migrations every 600 steps.

Simulation	Individuals Infected before migration
1	1, 42, 501, 506, 536, 561, 711, 748
2	1, 501
3	1, 32, 42, 501, 536, 571, 696
4	1, 173, 501
5	1, 42, 106, 501, 536, 587, 622, 671, 711
6	1, 20, 42, 201, 210, 501, 536, 571, 683, 696
7	1, 42, 501, 536
8	1, 203, 501, 571, 672
9	1, 501
10	1, 21, 47, 501, 571

Table A.4: Actors and their location, gender and migration status at time step from $t = 0$ to first round of migration

Actors	Sex	Location	Migrant Status
1 to 125	Male	Rural	Non-migrant
126 to 250	Male	Rural	Migrant(at time 0)
251 to 375	Male	Urban	Migrant(at time 0)
376 to 500	Male	Urban	Non-Migrant
501 to 750	Female	Rural	Non-Migrant
751 to 1000	Female	Urban	Non-Migrant

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