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Research Article

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Modelling the Transmission Dynamics of Tuberculosis in the Presence of Vaccination and Treatment on Graphs

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Abstract The objective of this study is to assess the effects of vaccination and treatment alongside the human contact interaction on the epidemiology of tuberculosis diseases. We constructed a graph that represents a population and their interconnectedness. The node-degree sequence obeys a Poisson distribution and the graph was generated by the mechanism of configuration model. The transmission dynamics of tuberculosis disease was simulated under different coverage of vaccination and treatment. The results show that effective combination of vaccination and treatment as a strategy is the best for the control of tuberculosis disease. Therefore, more concerted effort should be directed in this line to eradicate this menace.

Keywords Tuberculosis, infection, graph, network, configuration model

1. Introduction

Tuberculosis (TB) is a global health threat. It causes ill-health among millions of people each year and ranks alongside the human immunodeficiency virus (HIV) as a leading cause of death worldwide. In 2014, there were an estimated 9.6 million new TB cases: 5.4 million among men, 3.2 million among women and 1.0 million among children. There were also 1.5 million TB deaths (1.1 million among HIV-negative people and 0.4 million among HIV-positive people), of which approximately 890 000 were men, 480 000 were women and 140 000 were children [1]. As shown in Hattaf *et al* [2], about one third of the world human population constitutes a reservoir of TB infection.

Mycobacterium tuberculosis is the causative agent of TB. The tubercle bacilli live in the lungs of infected hosts. They spread in the air when infectious individuals sneeze, cough, speak or sing. A susceptible individual may become infected with TB if he or she inhales bacilli from the air. The particles containing Mycobacterium tuberculosis are so small that normal air currents keep them airborne and transport them throughout rooms or buildings. Hence, individuals who regularly share space with those with active TB (the infectious stage of the disease) have a much higher risk of becoming infected. These bacilli become established in the alveoli of the lungs from where they spread throughout the body if not suppressed by the immune system. The hosts' immune responses usually limit bacilli multiplication and, consequently, the spread that follows primary infections. The general symptoms of TB disease include feelings of sickness or weakness, weight loss, fever, and night sweats. The symptoms of TB disease of the lungs also include coughing, chest pain, and the coughing up of blood. Symptoms of TB disease in other parts of the body depend on the area affected [3-5]. About 10% of infected individuals eventually develop active TB. Most infected individuals remain as latently infected carriers for their entire lives. The average length of the latent period (noninfectious stage) ranges from months to decades. However, the risk of progression toward active TB increases markedly in the presence of co-infections that debilitate the immune system. Most forms of TB can be treated. Effective and widespread treatment for active and latently infected individuals has been available for about five decades. Streptomycin is still used today to treat TB but in combination with pyrazinamide [3,5].

In this research, human contact interaction network or graph, which is a conduit for disease transmission, is our focus. In this study a graph-based model for the transmission dynamics of tuberculosis in a population in the presence of vaccination and treatment alongside the human contact interaction is studied. The plan of this paper is as follows. Section 1 is devoted to introduction. Section 2 is devoted to graphs and modeling. Model description is given in section 3. Simulations and results are presented in section4. Discussion of results and concluding remark are passed in sections 5 and 6 respectively.

2. Graphs and Modeling

Mathematical models have been used for several decades to study the transmission dynamics of TB. As reported in Castillo-Chavez and Song [3], Waaler was the first that built a model for the transmission dynamics of TB in 1962. Since then manifold models have been ensuing. The list cannot be exhausted, and we do not try to be encyclopedic. For a survey of mathematical models of TB, see Castillo-Chavez and Song (2004). For some pioneer works in this area, see [6-13]. Models incorporating vaccination, treatment or both as control strategies for TB disease abound, see [2, 14-16].

These classical epidemiological models ignore the importance of the complex patterns and structures of social interactions on the spread of diseases. So, most of the earlier epidemiological models trivialize the social aspects of disease transmission. However, since the middle of the twentieth century, sociologists, mathematicians have been studying social networks and have come up with a large literature spanning many different aspects of social networks from empirical, conceptual and methodological points of view [17].

Graphs used in the literature can be classified on the properties of interest. From the dynamism point of view, graphs or networks can be classified as static or dynamic depending on whether their structures change with time. From the field of application perspective, we have social networks, information networks, technological networks, epidemic networks, to mention a few. Each of these types of networks can be narrowed to specific networks. Graph classifications based on degree distribution exist. For instance, scale-free graphs, Poisson graphs. Graphs such as unipartite, bipartite or multipartite are based on the node types. For a general knowledge of graphs and their theory, refer to [18-27].

3. Model Description

We construct a graph or network model, wherein each individual is represented by a node and the edges are the links between the individuals. A Poisson distribution is used to generate degree sequence; and the graph is constructed using the mechanism of configuration model.

We simulate epidemics on our graph based on the following procedure.

1. Specify the total population $T = N$.
2. Specify the degree distribution as a Poisson distribution with the parameter value λ.
3. Generate the graph by the mechanism of configuration model.
4. At each time step, apply the infection operator ξ_1. A susceptible node may be exposed and latently infected by neighbouring active TB infected nodes with probability p_1, which is determined by the number of infected nodes $i, i = 1, \dots, k$.
5. At each time step, susceptible individual are vaccinated at the rate v.
6. At each time step, apply local progression operator ξ_2. An individual with latent infection progresses to an active infectious state at the rate p_2.
7. At each time step, latently infected individuals are diagnosed and treated at the rate σ_1.
8. At each time step, individuals with active TB are diagnosed and treated at the rate σ_2.
9. At each time step, an active infectious individual without treatment recovers at the rate p_3.
10. At each time step, an active infectious individual on treatment recovers with probability p_4.
11. At each time step, the graph may evolve, depending on the length of time.

Repeat these steps until statistical significance is obtained.

4. Simulation and Results

Table 1: Variables and Parameters of the model

$S(t)$ =the number of susceptible individuals at time t
$L(t)$ =the number of latently infected individuals at time t
$I(t)$ =the number of infectious individuals at time t
$T(t)$ =the number of recovered/treated individuals at time t
$V(t) = the\ number\ of\ individuals\ vaccinated\ at\ time\ t$
p_1 =the probability that a susceptible individual becomes infected by one infectious individual per contact per unit
$v = rate\ at\ which$ susceptible individual are vaccinated.
$p_2 = the\ rate\ that\ an\ individual\ with\ latent\ infection\ progresses\ to\ an\ active\ infectious\ state.$
$\sigma_1 =$ the rate at which latently infected individuals are diagnosed and treated.
$\sigma_2 = the\ rate\ at\ which$ individuals with active TB are diagnosed and treated.
$p_3 = the\ rate\ that$ an active infectious individual without treatment recovers.
$p_4 = the\ rate\ that$ an active infectious individual on treatment recovers.
$c = the\ number\ of\ respiratory\ contacts\ per\ year$

Simulations are performed using the parameter values in Table 2.

Table 2

$Variable/parameter$	$Value$	Source
$S(0)$	5000	assumed
$L(0)$	0	assumed
$I(0)$	1	assumed
$T(0)$	0	assumed
$V(0)$	$variable$	
v	$variable$	
σ_1	$0-1$	
σ_2	$0-1$	
p_1	0.1	Tuite *et al*. (2017)
p_2	$0.05-1.5$	Tuite *et al*. (2017)
p_3	0.1	Tuite *et al*. (2017)
p_4	0.2	Tuite *et al*. (2017)
c	$40-1000$	Tuite *et al*. (2017)

The results of simulations for varying vaccination and treatment rates are shown in Figures 1 through 8. All other parameter values are fixed as in Table 2.

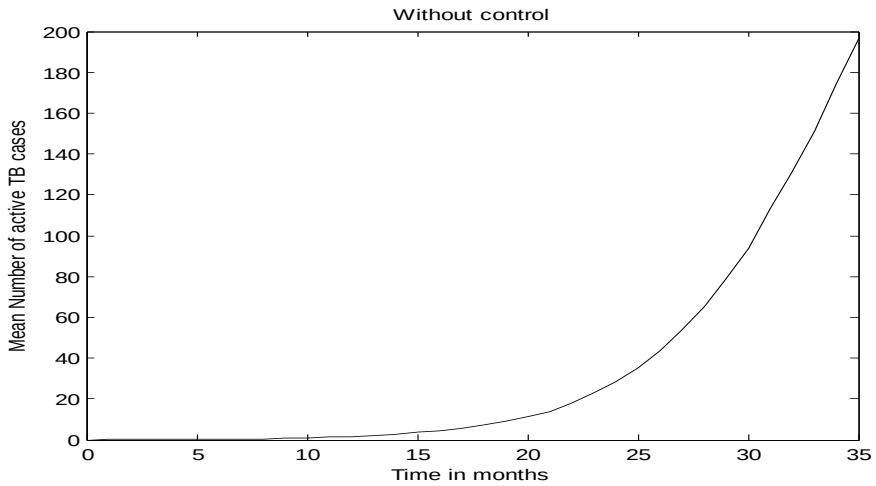

Figure 1: Graph showing the mean number of active TB cases without control

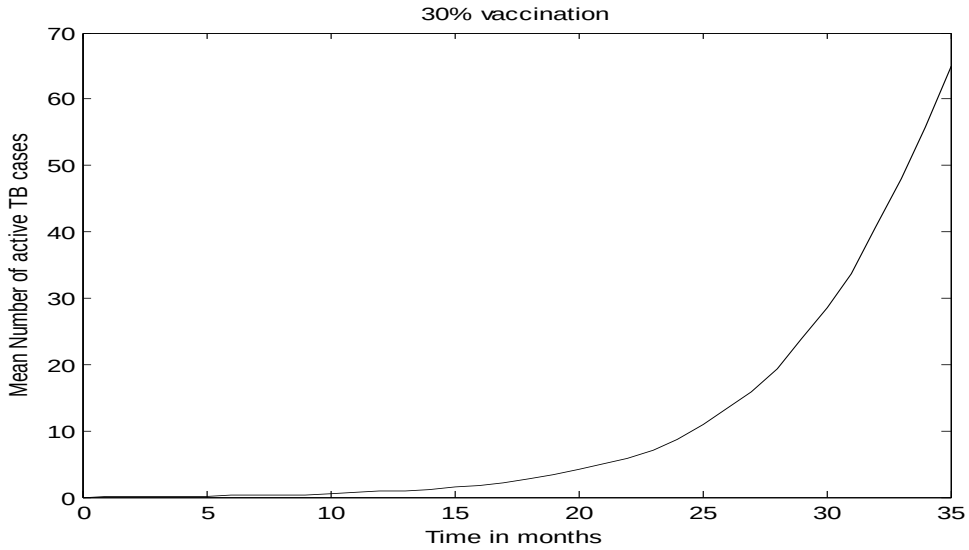

Figure 2: Graph showing the mean number of active TB cases with 30% vaccination

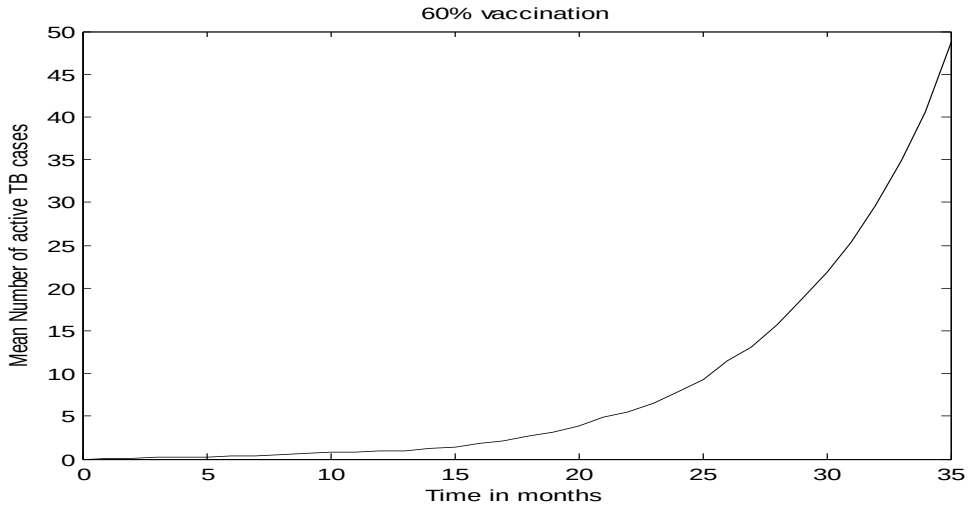

Figure 3: Graph showing the mean number of active TB cases with 60% vaccination

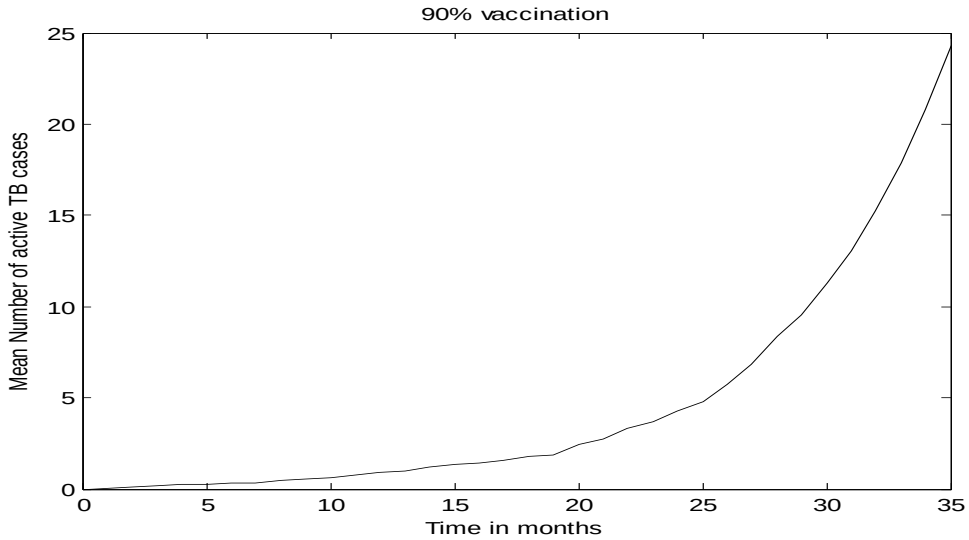

Figure 4: Graph showing the mean number of active TB cases with 90% vaccination

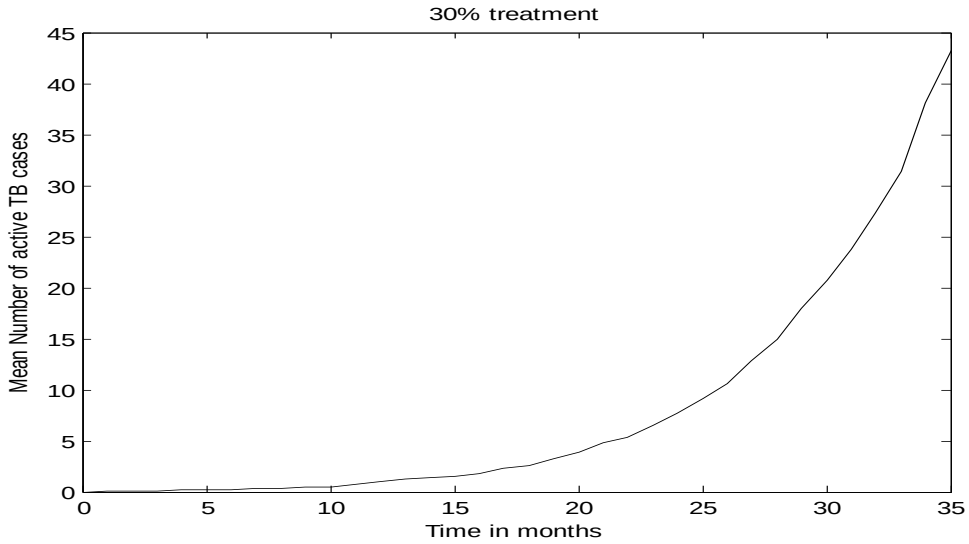

Figure 5: Graph showing the mean number of active TB cases with 30% treatment

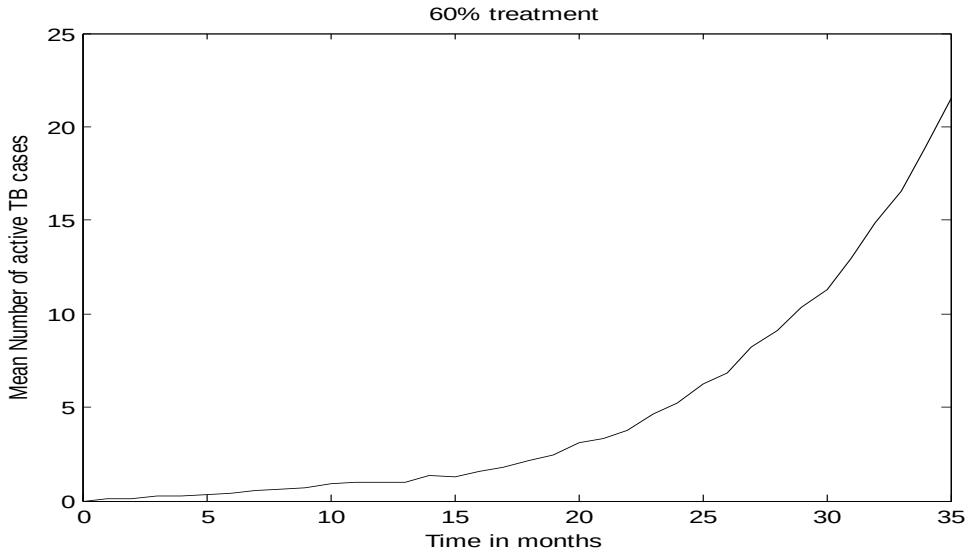

Figure 6: Graph showing the mean number of active TB cases with 60% treatment

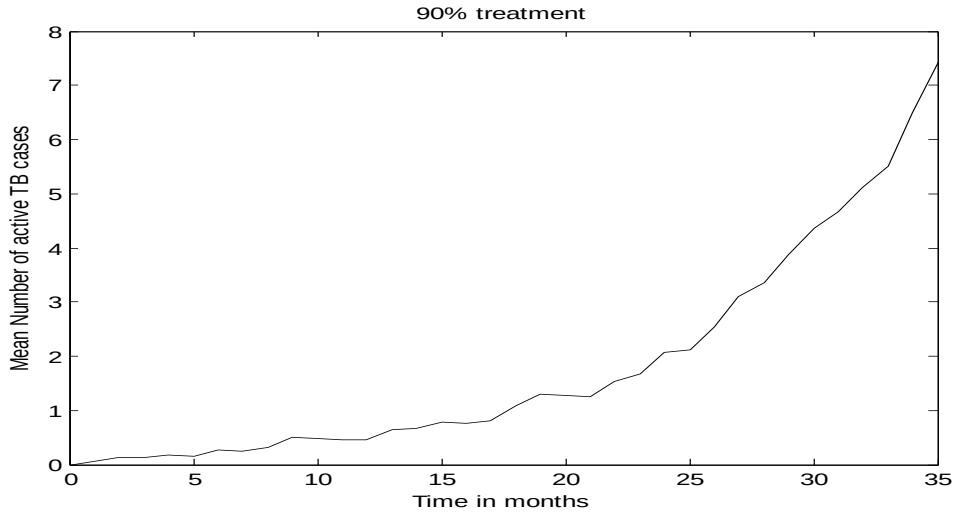

Figure 7: Graph showing the mean number of active TB cases with 90% treatment

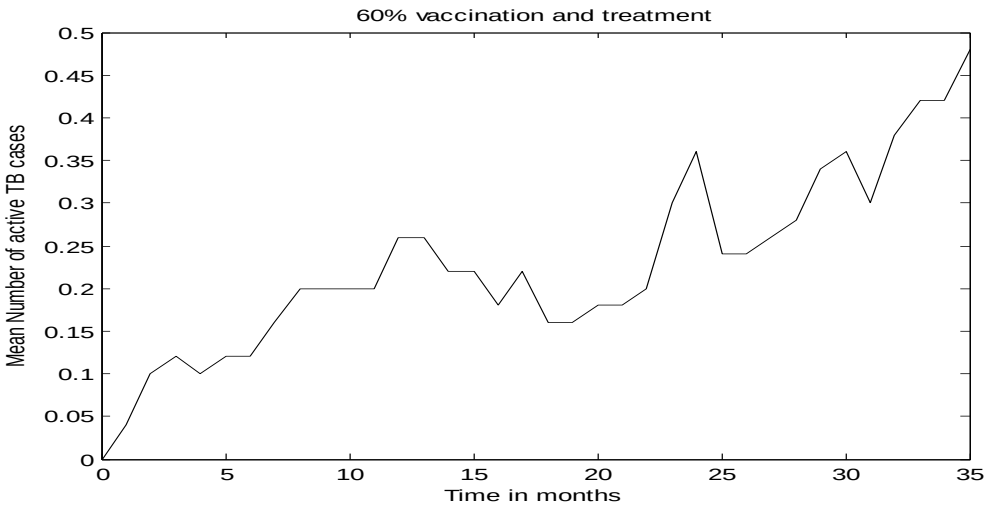

Figure 8: Graph showing the mean number of active TB cases with 60% vaccination and treatment

5. Discussion

In this article, we developed a graph-based model to investigate the effects of vaccination and treatment on the transmission dynamics of tuberculosis. The simulation results for varying levels of vaccination and treatment are shown in Figures 1 through 8. Figure 1 shows an exponential increase in the number of active TB cases. Figures 2 through 4 show that the number of cases decreases with increasing level of vaccination coverage. The results further show that vaccination alone cannot eliminate TB disease from a population, but can slow the rate of transmission. This is because the efficacy level of TB vaccine is not very high. In the same vein, Figures 5 through 7 demonstrate that treatment alone cannot eliminate TB disease. Individuals that have active TB and are on treatment may transmit the disease. However, high vaccination and treatment coverage can eliminate TB from a population. See Figure 8. The findings in this research suggest that high vaccination and treatment coverage as a strategy is crucial for the control of TB disease.

6. Conclusion

We have developed a graph-based model to study the effects of vaccination and treatment on the control of TB. Simulation experiments were performed for varying rates of vaccination and treatment. The results are shown in Figures 1 through 8. The findings in this study highlight the importance of a strategy of a combination of high rates of vaccination and treatment for the control of TB.

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