Controlling the Spread of Nipah Virus in Bangladesh

Exploring the effect vaccination would have had on the outbreak size of Nipah virus in Faridpur, Bangladesh 2004

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1. Introduction

Nipah virus is a tropical disease with annual outbreaks occurring in Asia, mostly in Bangladesh. The virus is carried by bats and then transmitted to humans as the bats contaminate raw date palm sap which is then drunk as a delicacy. There is also evidence of human to human transmission after the initial spillover event from the bat population.

No vaccine currently exists but there is ongoing research into creating one. We aim to discover the required efficacy of such a vaccine, thus informing researchers of its viability.

2. The Model

We begin by constructing a compartmental model for the spread of the disease, this splits the population into several distinct categories with each category representing a state an individual could be in.

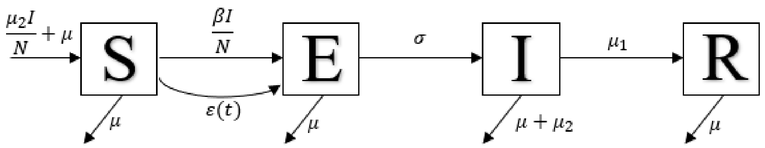

Figure 1 – A schematic of the compartmental model used to describe spread of Nipah virus

In figure 1, we split the population up into four categories (S, E, I and R; standing for susceptible, exposed, infectious and recovered respectively) and we allow people to transfer between those categories at certain rates:

- N – Total population (S+E+I+R, assumed to be 1500)
- β – Human to human transmission rate of Nipah virus
- ε(t) – Bat to human transmission rate of Nipah virus equal to zero during the period where no date palm sap is collected
- σ – Latency period of the virus
- μ – The natural death rate, assumed to be $\frac{1}{67}$ years^{-1}
- μ_1 – The disease recovery rate, assumed to be $\frac{1}{56}$ days^{-1}
- μ_2 – The disease fatality rate, assumed to be $\frac{1}{16}$ days^{-1}

3. Parameter Fitting

Once the model has been constructed we need to choose the parameters so that the total cumulative number of infections match that which is seen during the Faridpur 2004 outbreak. This is done using an 'adaptive approximate Bayesian computation algorithm'. This procedure generates a distribution that each of the parameters lie in.

The parameters we are fitting are β, ε and σ; we also fit the start date and end date of the date palm sap collection season and the initial number of exposed individuals as this is impossible to know at the start of an outbreak.

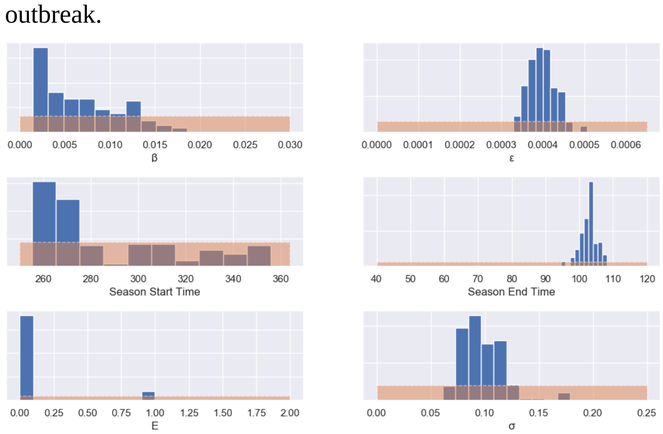

Figure 2– The final distribution of each free parameter after 15 iterations of the ABC algorithm (coloured in blue) and the initial distributions (coloured in orange)

4. Vaccination Model

We now explore the effect of vaccination on outbreak size using another compartmental model (figure 3) and investigate how changing the efficacy of the vaccine and vaccination rate effects the size of the average resulting outbreak.

- V_S – Individuals who are successfully immunised against Nipah
- V_F – Individuals who have received an unsuccessful vaccination
- N – Total population (S+E+I+R+V_S+V_F, assumed to be 1500)
- γ – Number of vaccinations that are administered each day.
- p – Probability that a vaccination is successful

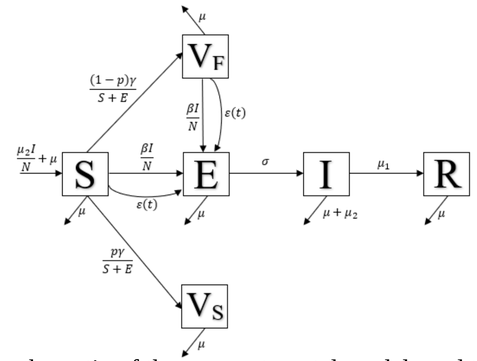

Figure 3 – A schematic of the compartmental model used to describe spread of Nipah virus when individuals are vaccinated

5. Results

By analysing the data shown in figure 4, it appears that a vaccine efficacy of 0.6-1.0 can reduce the expected outbreak size by 42.7-87.2% if more than 40 people are vaccinated each day. To reduce the expected outbreak size by more than 80% we need to vaccinate at least 80 people each day with a vaccine efficacy of 0.96, or at least 64 people a day with a vaccine efficacy of 1.

In conclusion, a significant reduction in the expected outbreak size can be achieved even with a poor vaccine efficacy provided that enough individuals are vaccinated each day. However to reduce the expected infection size significantly, a very effective vaccine is required.

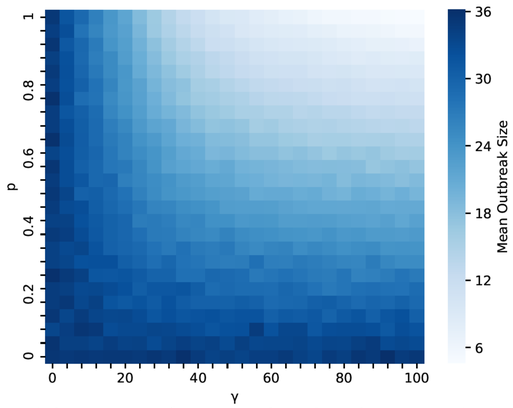

Figure 4 – A heat map of expected outbreak size against vaccine efficacy and vaccine rate