多種デバイス間の多種ウイルス拡散モデルにおける エンデミック閾値と定常状態の解析

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あらまし USB ケーブルなどを用いてスマートフォンを PC へ接続し充電する際，スマートフォンから PC へ，コンピュータウイルスが伝搬することが知られている．そのため，異なるデバイス間でのウイルス感染における拡散過程について，新たな解析が必要となる．本研究では，多種デバイス間での多種ウイルス拡散について，感染 SIR モデルを用いてエンデミックとなる閾値を表す基本再生産数および，定常状態におけるウイルス感染期待台数と分散を導出する．さらに，数値計算により，ウイルス拡散の特性を解析する．

An analysis of endemic threshold and steady state for multi-virus propagation model for multi devices

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Abstract When users charge their smart phone battery from a PC by using USB cables, the most recent smart phone virus can transfer to a laptop PC. Thus, the increase in the number of mobile devices has led to the growing importance of analyzing the propagation process of these computer viruses. In this paper, we derive the basic reproduction number by using a modified SIR model, and the infection statistics are derived by using a Markov model where there are multiple virus and multiple devices, such as smartphones, tablets and PCs. Moreover, we use our model to show the numerical results.

1 Introduction

In recent years, smart phones such as iPhones and Android devices have rapidly become popular. Many users of smart phones install various applications which may include unauthorized applications to their own smart phone. However, the

smart phone users have little consciousness of computer viruses compared with that of personal computer (PC) users. When a user uses a smart phone, there is a risk the computer virus is transmitted to the other's smart phone by using other's personal information, because a smart phone has many personal information such as e-mail address or phone number. The risk of computer virus infection of smart phones is increasing steadily.

The number of mobile devices is increasing and has led to the growing importance of analyzing the propagation process of these computer viruses. Several *traffic parameters*, such as infection rate and recovered rate, affect whether a specific computer virus will cause an *epidemic* which would lead to an outbreak of the computer virus in a large area. To analyze the propagation of a computer virus quantitatively, we refer *endemic threshold (the basic reproduction number)* as a condition of the parameters that an epidemic occurs [1][2]. The endemic threshold plays a key role in analyzing the propagation of a computer virus. Many studies to clarify the endemic threshold of a computer virus have been proposed for the PC environment [3]. Almost all conventional models of computer virus assumed that a single type of virus infects a single type of device such as PCs [3]–[5]. A few conventional models assumed that multiple types of viruses infect a single type of device [6][7].

Meanwhile, the battery run time of a smart phone is short and the battery requires daily charging. Thus, users need to charge the smart phone battery from a PC by using USB cables. However, according to a recent report [8], the latest smart phone virus can be transferred to a laptop PC during this kind of charging. Therefore, new computer viruses can propagate between different types of devices, such as smart phones and PCs. These new types of computer virus which can infect both smart phones and PCs are different from a conventional type of computer virus which affects a single type of device. In this situation, we need to consider *second infection* which means infections from smart phones to PCs, and need to consider various types of computer virus that infect multiple types of devices.

As we mentioned before, studies on conventional computer viruses assumed the existence of single devices. On the other hand, in the influenza virus model [9], the susceptible population is split up into two groups (adults and children). Thus, this model appears to be applicable to multiple types of device model which are considered in our paper. However, this model assumed that only a single type of virus of influenza virus exists. Therefore, we cannot apply these conventional computer virus models to our model with multiple types of virus and multiple types of devices.

Moreover, the conventional model of virus propagation cannot derive an expectation and a variance of the number of infections. If the expectations of the number of infections are same between different traffic situations, the variances of the number of infections may differ from those of the traffic situations. Thus, it is important to analyze *infection statistics* which means the expectations and variance of the number of infections.

In this paper, we analyze the endemic threshold by using a modified SIR model and the infection statistics by using a Markov model under the multiple types of virus and multiple types of device.

This paper is organized as follows. Section II describes related studies on virus propagation models. Section III describes our model for endemic threshold. Section IV develops the infection statistics by using the Markov process. Section V shows the numerical results and concludes the paper.

2 Related works

This section shows the related works on analyzing the virus diffusion with a mathematical model. Those models for the growth process of computer virus are similar to the propagation model in immunology and ecology. The conventional model for propagation is the SIR model [3]. This model

treats states of individual terminals as S(*susceptible*), I(*infected*) and R(*recovered*). A lot of SIR models have been proposed as shown in [3]. Moreover, SIR model considering computer virus has been proposed [4][5]. The computer virus propagation model proposed in [5] has taken in user awareness into consideration. However, these computer propagation models only assume the existence of a single type of computer virus.

On the other hand, recent work has looked at a two-virus SIR model [6][7]. Prakash et al. in [6] extended the SIR model to two types of virus. Moreover, A. Beutel in [7] analyzed the interaction model between those two types of viruses. However, these models assume that only two viruses infect single devices. Thus, we cannot apply these models to the problem with multiple types of virus and multiple types of devices such as for example, PCs and mobile devices that are considered here.

Moreover, with influenza as a virus model, a single susceptible population was split up into two groups (adult and children) [9]. However, this model assumed only a single virus. Our first contribution in this paper is to analyze the propagation of multiple types of viruses for two types of devices by using SIR model.

However, the SIR model cannot derive an expectation and a variance of the number of infections. Okamura et al. in [10] has proposed a computer propagation virus model that uses the Markov model. This model can derive an expected number of infections. However, the model cannot apply to the multiple-viruses model and two groups of susceptible devices. Our second contribution in this paper is to analyze the probability of the number of the devices by using the Markov model.

3 SIR model

3.1 SIR model without birth rate and death rate

We assume that two types of devices (for example, PCs and smart phones) exist and that each device can interact with each virus. Here, β_{ij} means the transition of infection from state j to state i. A parameter γ_i represents the transition of recovery of state i. As shown in Fig. 1, devices are not newly added or discarded.

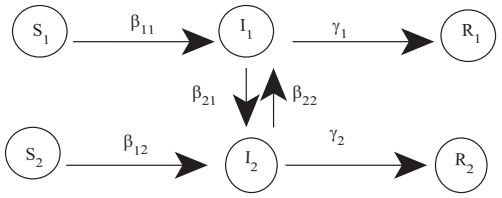

図 1: Our proposed SIR model

$$
\begin{aligned}
\frac{dS_1(t)}{dt} &= -(\beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) \\
\frac{dI_1(t)}{dt} &= (\beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) \\
&\quad -\gamma_1 I_1(t) \qquad (1) \\
\frac{dR_1(t)}{dt} &= \gamma_1 I_1(t) \\
\frac{dS_2(t)}{dt} &= -(\beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) \\
\frac{dI_2(t)}{dt} &= (\beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) \\
&\quad -\gamma_2 I_2(t) \\
\frac{dR_2(t)}{dt} &= \gamma_2 I_2(t) \qquad (2)
\end{aligned}
$$

In Eqs. (1)(2), $N_1(t)$ and $N_2(t)$ mean the total number of PCs and smart phone devices respectively. When $N_i(t) = S_i(t) + I_i(t) + R_i(0)$, $\frac{dN_i(t)}{dt} = 0$. Thus, the total number of the PCs and mobile devices is maintained. Here, let $N0_1$ be the total number of the PCs, and $N0_2$ be the total number of mobile devices. Let $S0_1$ and $R0_1$ be a constant satisfying $S0_1 + R0_1 = N0_1$, and let $S0_2$ and $R0_2$ be constant satisfying $S0_2 + R0_2 = N0_2$. Under this assumption, the system has one disease-free steady state $(S0_1, 0, R0_1)$ and $(S0_2, 0, R0_2)$, which is stable.

Here, we assume that $R0_1 = 0$ and $R0_2 = 0$. The total number of PCs and mobile phone devices have only the state of $S0_i$ and this system has a condition of equilibrium. When $t = 0$ and $S0_i =$

$S_i(0) > 0$, we assume that a few infective PCs and smart phones occur. The effective decrease in the number of susceptible PCs and mobile phone devices are small. Thus, the dynamic state of the population of infection can be described by the following linear equation:

$$\begin{aligned}\frac{dv_1(t)}{dt} &= (\beta_{11}I_1(t) + \beta_{12}I_2(t))S0_1 \\ &\quad - \gamma_1 v_1(t) \\ \frac{dv_2(t)}{dt} &= (\beta_{21}I_1(t) + \beta_{22}I_2(t))S0_2 \\ &\quad - \gamma_2 v_2(t)\end{aligned}$$

where v_i means perturbation from the original point of I_i. We need to drive *endemic threshold (basic reproduction number)* R_{th} which the condition of the parameters in which an outbreak of the computer virus occurs in a large area [11]. Here, our model has two-states (for example PC and smart phone). Moreover, we assume that the characteristic of system with time does not depend on the infection. This means that even a long incubation period will not vary the progression of an infection. When some PCs or smart phones acquire a computer virus, the incubation period of the virus will generally be short. Under this assumption, R_{th} in the multistate model can represent the spectral bound $r(-\mathcal{M}\mathcal{Q}^{-1})$ of *represent coefficient matrix* $\mathcal{Q}$ and $\mathcal{M}$ [12]:

$$R_{th} = r(-\mathcal{M}\mathcal{Q}^{-1}). \tag{3}$$

These linearized equations can be derived as the following equation:

$$\mathcal{M} = \begin{pmatrix} \beta_{11}S0_1 & \beta_{12}S0_2 \\ \beta_{21}S0_1 & \beta_{22}S0_2 \end{pmatrix},$$

$$\mathcal{Q} = \begin{pmatrix} -\gamma_1 & 0 \\ 0 & -\gamma_2 \end{pmatrix}. \tag{4}$$

Thus, when t means the incubation period from the infection, the transition process between each state can represent $\mathcal{Q}$ and the reproduction number of secondary cases can also represent $\mathcal{M}$.

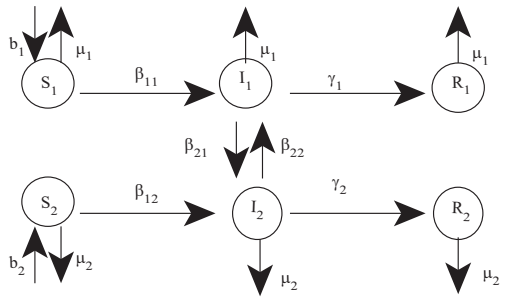

図 2: proposed SIR model

Thus, we can derive R_{th} as Eq. (5). This model can describe the virus diffusion. Moreover, we showed that this system has the epidemic steady state when $R_{th} > 1$. However, this model does not take the addition of devices (birth rate) and waste of devices (death rate) into consideration. In the next section, we describe the SIR model by using the birth and the death rate.

3.2 SIR model with birth rate and death rate

In this subsection, we propose a modification of SIR model. Fig. 2 described the model. We assume that two types of devices, e.g., PCs and smart phones, and each type of device can interact with each virus. Moreover, we assume that both devices have the birth rate, b_i, and death rate, d_i. As described in Section 3.1, β_{ij} means the transition of infection from state j to state i, and γ_i represents the transition of recovery of state i.

$$\begin{aligned}\frac{dS_1(t)}{dt} &= \\ b_1 &- (d_1 + \beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) \\ \frac{dI_1(t)}{dt} &= (\beta_{11}I_1(t) + \beta_{12}I_2(t))S_1(t) \\ &\quad - (d_1 + \gamma_1)I_1(t) \\ \frac{dR_1(t)}{dt} &= -d_1R_1(t) + \gamma_1 I_1(t)\end{aligned} \tag{6}$$

$$R_{th} = \frac{\frac{\beta_{11}S0_1}{\gamma_1} + \frac{\beta_{12}S0_2}{\gamma_2} + \left((\frac{\beta_{11}S0_1}{\gamma_1} + \frac{\beta_{12}S0_2}{\gamma_2})^2 + 4\left(\frac{\beta_{11}S0_1}{\gamma_1}\frac{\beta_{12}S0_2}{\gamma_2} + \frac{\beta_{21}S0_1}{\gamma_1}\frac{\beta_{22}S0_2}{\gamma_2}\right)\right)^{\frac{1}{2}}}{2}. \quad (5)$$

$$\begin{aligned}
\frac{dS_2(t)}{dt} &= \\
b_2 &- (d_1 + \beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) \\
\frac{dI_2(t)}{dt} &= (\beta_{21}I_1(t) + \beta_{22}I_2(t))S_2(t) \\
&\quad - (d_2 + \gamma_2)I_2(t) \\
\frac{dR_2(t)}{dt} &= -d_2R_2(t) + \gamma_2I_2(t) \quad (7)
\end{aligned}$$

This system has a steady state, $(S_i, I_i, R_i) = (\frac{b_i}{d_i}, 0, 0)$. When few infections occur, the dynamics of the number of devices represent the following linear equation:

$$\begin{aligned}
\frac{dv_1(t)}{dt} &= (\beta_{11}I_1(t) + \beta_{12}I_2(t))\frac{b_1}{d_1} \\
&\quad - (d_1 + \gamma_1)v_1(t) \\
\frac{dv_2(t)}{dt} &= (\beta_{21}I_1(t) + \beta_{22}I_2(t))\frac{b_2}{d_2} \\
&\quad - (d_2 + \gamma_2)v_2(t)
\end{aligned}$$

where v_i means perturbation from the original point of I_i. By using these equations, we need to drive R_{th} whether the infections become the endemic virus. The matrix $\mathcal{Q}$ and $\mathcal{M}$ can be derived as the following equation:

$$\mathcal{M} = \begin{pmatrix} \beta_{11}\frac{d_1}{b_1} & \beta_{12}\frac{d_2}{b_2} \\ \beta_{21}\frac{d_1}{b_1} & \beta_{22}\frac{d_2}{b_2} \end{pmatrix},$$

$$\mathcal{Q} = \begin{pmatrix} -(d_1 - \gamma_1) & 0 \\ 0 & -(d_2 - \gamma_2) \end{pmatrix}.$$

Thus, we can derive R_{th} as Eq. (8). This model can describe the virus diffusion. Moreover, we showed that this system has the endemic steady state when $R_{th} > 1$. However, this model cannot derive the probability of infection of each number of devices or variance. Analyzing the infection statistic of each number of devices and variance will be important. In the next section, we use the Markov model to show the infection statistics for the expectation and variance of the number of infective devices in a steady state.

4 Markov model

4.1 Our proposed model

We propose the infection model in a steady state with two types of devices (PCs and smart phones). Each type of devices has a different virus. Moreover, we assume that smart phones also have a virus that infects PCs. When sufficient time has elapsed, we derive the expectation value and variance value of the number of infective terminals. Therefore, we assume a steady state after a sufficient amount of time has passed.

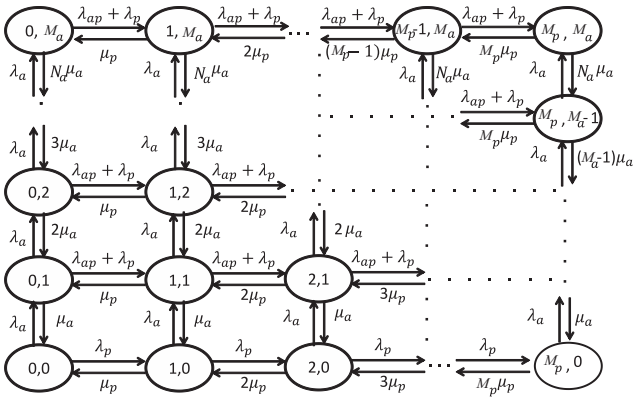

図 3: Virus infection model for PC and smart phone

Fig. 3 shows the state transition diagram of our proposed model. The horizontal axis is the number of infections in PCs and the vertical axis is the number of infections in Android terminals. The

$$R_{th} = \frac{\frac{\beta_{11}b_1}{d_1(d_1+\gamma_1)} + \frac{\beta_{12}b_2}{d_2(d_2+\gamma_2)}}{2} + \frac{\left(\left(\frac{\beta_{11}b_1}{d_1(d_1+\gamma_1)} + \frac{\beta_{12}b_2}{d_2(d_2+\gamma_2)}\right)^2 + 4\left(\frac{\beta_{11}b_1}{d_1(d_1+\gamma_1)}\frac{\beta_{12}b_2}{d_2(d_2+\gamma_2)} + \frac{\beta_{21}b_1}{d_1(d_1+\gamma_1)}\frac{\beta_{22}b_2}{d_2(d_2+\gamma_2)}\right)\right)^{\frac{1}{2}}}{2}. \quad (8)$$

number of total PCs is M_p, and the number of total smart phones is M_a.

Let λ_p be the virus infection rate of PCs, λ_a be virus infection rate of smart phones and λ_{ap} be virus infection rate from a smart phone to a PC respectively. These devices are independent and these infection rates are a Poisson distribution respectively. Let μ_p be the disinfect rate of PCs, μ_a be the disinfect rate of smart phones. The disinfect rates of each terminal are an exponential distribution.

The state probability when the number of PCs is i ($0 \leq i \leq M_p$) and the number of smart phones is j ($0 \leq j \leq M_a$) is p_{ij}. Note that because $i \geq 0$ and $j \geq 0$ are required, when $i < 0$ or $j < 0$, let $\mathrm{p}_{(i,j)} = 0$.

4.2 State Transition Equations

As shown in Fig. 3, the infection rate differs between $j = 0$ and $j \geq 1$. Thus, we divide the state transition equations whether $j = 0$ or not. Our proposed state transition equations are as follows:

When $j = 0$,

$$\begin{aligned}&(\lambda_p + \lambda_a + i\mu_p)p_{(i,0)} \\ =\ & i\mu_a p_{(i,1)} \\ &+ \lambda_p p_{(i-1,0)} + i\mu_p p_{(i+1,0)}. \end{aligned} \quad (9)$$

When $j \geq 1$

$$\begin{aligned}&(\lambda_p + \lambda_a + \lambda_{ap} + i\mu_p + j\mu_a)p_{(i,j)} \\ &= \lambda_a p_{(i,j-1)} + i\mu_a p_{(i,j+1)} \\ &\quad + \lambda_p p_{(i-1,j)} + i\mu_p p_{(i+1,j)}. \end{aligned} \quad (10)$$

The summation of all state probabilities is equal to 1. This summation is given by the following equation:

$$\sum_{\forall(i,j)} \mathrm{p}(i,j) = 1. \quad (11)$$

These above equations, which relate to all states, are simultaneous linear equations with variable $\mathrm{p}_{(i,j)}$.

By using $\mathrm{p}_{(i,j)}$, which is derived from these state transition equations, the expectation E and variance V of the number of infective devices can respectively be given by the follow equations:

$$E[i+j] = \sum_{\forall(i,j)} (i+j)\mathrm{p}(i,j).$$

$$V[i+j] = E[(i+j)^2] - E[(i+j)]^2. \quad (12)$$

In the next section, we show a numerical example by using our SIR model and our Markov model.

5 Numerical example

This section shows numerical examples obtained by using our models. First, we show the characteristics of the numbers of each state (susceptible devices, infected devices and recovered devices) in Figs. 4–7. The horizontal axis shows elapsed time. The vertical axis in the figures shows the normalized total devices when $t = 0$. We assumed for our model that each type of device infects some computer viruses among the same kind of device. When a smart phone is connected to a PC to charge the battery, PCs are infected from these devices. Thus, $\beta_{21} = 0$.

Figs. 4–5 show the characteristics when the birth rate b_i and the death rate d_i are set to zero. In this traffic situation, the number of each type of infecting device converges to zero because the devices

are not newly added. Thus, the number of infection I_i converges to zero.

In Fig. 4, each infection rate is $\beta_{11} = \beta_{12} = \beta_{22} = 0.20$. We set to $\frac{S0_1}{N0_1} = 0.25$, $\frac{S0_2}{N0_2} = 0.99$, $\gamma_1 = \gamma_2 = 0.25$. In Fig. 5, each infection rate $\beta_{11} = \beta_{12} = \beta_{22} = 0.20$. We set to $\frac{S0_1}{N0_1} = 0.50$, $\frac{S0_2}{N0_2} = 0.99$, $\gamma_1 = \gamma_2 = 0.25$. The endemic threshold R_{th} is set to 4.00. As shown in these figures, these viruses do not cause endemic when $R_{th} < 1$. On the other hand, when $R_{th} > 1$, endemic occur. We also clarified that the endemic in PCs occurs before that in smart phones. This is because the second infection is a one-way virus transfer from PCs to smart phones.

In Fig. 6, each infection rate is $\beta_{11} = 0.85, \beta_{12} = 0.20, \beta_{22} = 0.40$. We set to $b_1 = b_2 = \mu_1 = \mu_2 = 0.20$, $\gamma_1 = \gamma_2 = 0.50$. The endemic threshold R_{th} is set to 0.93. In Fig. 7, each infection rate $\beta_{11} = 0.50, \beta_{12} = 0.25, \beta_{22} = 0.60$. We set $b_1 = b_2 = 0.30$, $\mu_1 = \mu_2 = 0.20$, $\gamma_1 = \gamma_2 = 0.50$. The endemic threshold R_{th} is set to 3.00. As shown in these figure, endemic do not occur when $R_{th} < 1$. On the other hand, when $R_{th} > 1$, endemics occur. Moreover, we confirmed that the PCs and smart phones are infected by computer viruses at a steady rate.

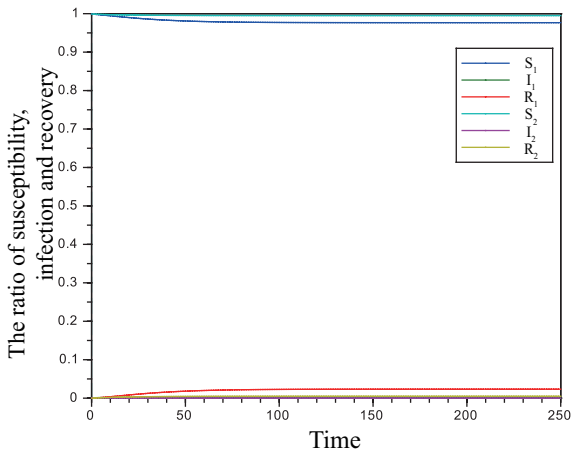

図 4: The virus propagation result with $R_{th} < 1$ (without birth rate and death rate).

Finally, we confirmed that the infection statistics which the value of expectation and variance

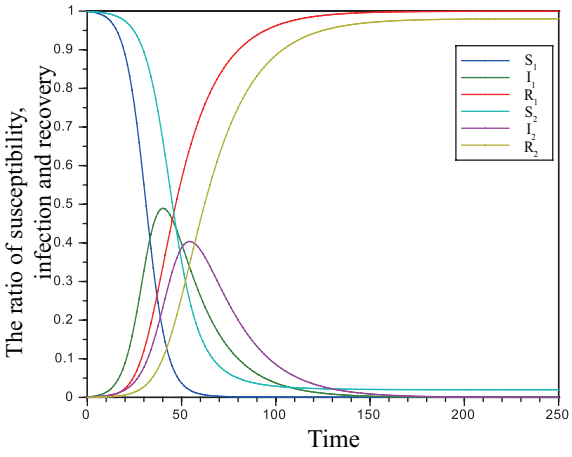

図 5: The virus propagation result with $R_{th} > 1$ (without birth rate and death rate).

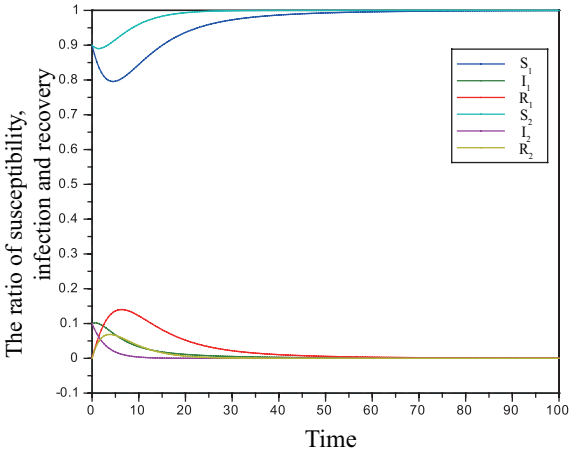

図 6: The virus propagation result with $R_{th} < 1$ (with birth rate and death rate).

when some PCs and smart phones are steadily being infected. We compared two traffic parameters, A and B. In traffic parameter A, we assume that $\lambda_a p = \frac{1}{80}$, $\lambda_a = \lambda_p = \frac{1}{100}$, $\mu_a = \frac{1}{200}$, $\mu_p = \frac{1}{400}, N = M = 30$. For traffic parameter B, we assume that $\lambda_a p = \frac{1}{58}$, $\lambda_a = \lambda_p = \frac{1}{100}$, $\mu_a = \frac{1}{100}$, $\mu_p = \frac{1}{447}, N = M = 30$.

As shown in Table 1, the value of variance is different even if the values of expectation are the same. For example, the second infection of traffic parameter B is smaller than that of traffic parameter A. However, the recovered rate μ_a of traffic

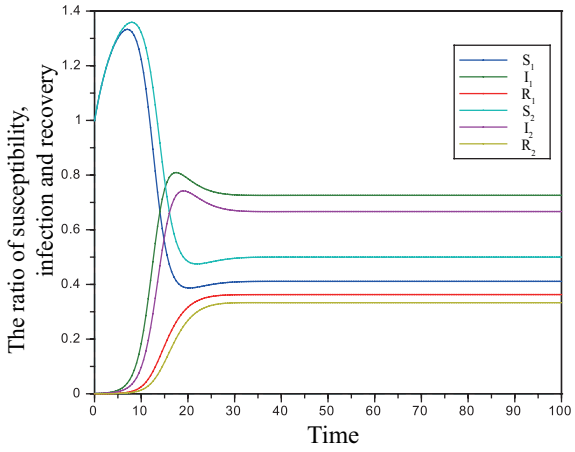

図 7: The virus propagation result with $R_{th} > 1$ (with birth rate and death rate).

parameter B is also smaller than that of traffic parameter A. In this situation, the value of variance of traffic pattern B is larger than that of parameter A. Thus, we need to supervise the virus propagation because the value of variance of traffic parameter B is large.

表 1: Results of expectation and variance.

	Expectation E	Variance V
The traffic A	10.3	11.8
The traffic B	10.3	13.4

6 Conclusion

In this paper, we analyzed the propagation of multiple types of viruses for two types of devices. We theoretically derived the endemic threshold by using a modified SIR model. Moreover, we derived the infection statistics by using a Markov model. Our model can be used to analyze the propagation of computer viruses.

In the future, we will estimate the parameters of our model for computer virus propagation from real data, and analyze the virus propagation by using real data. Using this analysis will enable us to propose a system for preventing virus propagation.

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