Modeling Dynamics of Malware with Incubation Period from the View of Individual

Pin-Yu Chen*, Han-Feng Lin†, Ko-Hsuan Hsu†, and Shin-Ming Cheng†
*Electrical Engineering and Computer Science Department,
University of Michigan, Ann Arbor, MI 48109. Email: pinyu@umich.edu
†Department of Computer Science and Information Engineering,
National Taiwan University of Science and Technology, Taipei 106, Taiwan.
Email: {m10215031, b9932006, smcheng}@mail.ntust.edu.tw

***Abstract*—In the last few years, the growing popularity of mobile devices with rich wireless communication capabilities has made them attractive to digital viruses and malicious contents. The user mobility and novel proximity-based communication technologies on one hand facilitate the information sharing and dissemination among people, on the other hand they increase the possibility of spreading malware. Understanding the propagation characteristics of malware could aid in planning protection strategies, but the most of the current models discuss it from the view of whole network. In this paper, we establish the model from the perspective of individuals by using Markov chain. Our model investigates the incubation period and remaining life time of a mobile smartphone when it is infected by malware. The numerical results provide comprehensive and intuitive explanations which are more realistic in real world.**

I. Introduction

In recent years, smartphone has become the human's necessary companion in everyday living due to its advanced networking capabilities, millions of applications, and high definition displays. Along with the popularity comes the increasing trend to infect applications on smartphones with malicious contents. The mobility of human and various kinds of communication technologies (such as SMS, MMS, Bluetooth, WiFi, 3G) on smartphones further increase the propagation speed and range [1]. How to model the behavior of malware propagation in current world with explosive growth in smartphones adoption is an interesting issue and receives lots of attentions [2].

Since the spread of epidemics among people is similar to the spread of malwares over smartphones, we typically adopt the idea from epidemiological models to build the models for malware propagation. The current propagation dynamics of malwares can be classified into three categories as follows, deterministic model, stochastic model, and spatial-temporal model [2]. Deterministic models use differential equations to describe the spread of infectious malwares from the view of network, including susceptible-infection (SI) models [1], [3], [4], susceptible-infection-susceptible (SIS) models [5]–[9] and susceptible-infection-recover (SIR) models [10]–[12]. Authors in [11] further considered the concept of incubation period from the perspective of whole network.

Faryad and Caterina proposed a paper using continuous-time Markov process to build the model [13], and Karyotis proposed the model for malware propagation using Markov random field (MRF) [14], which are both based on stochastic model. Szongott, Henne and Smith proposed a paper belong to spatial-temporal model [15]. All these works are done in the view of network, i.e., they regard nodes as the smartphones and the edges as the contact of smartphones in a graph and implicitly assume that all nodes should possess the same infection rate, which are different from our models which are in the view of individual. In real world, all smartphones should have different reactions when facing a spreading malware. Thus, the view of network is not suitable to solve this problem [16], because of the identity is actually lost when we consider this issue from the view of network.

In contrast to the top-to-down point of view, we provide a different approach that aims at modeling the dynamics of malware with incubation period of an individual with the aid of Markov chain model. We propose two models Impulse-Free Model (IFM) and Impulse-Reaction Model (IRM) of an individual and examine the incubation period, remaining life time (which means that the time before the infected smartphone will be broken), transition probability, accumulated infection probability, and steady state probability in both analytic and numerical results as well as provide comprehensive and intuitive explanations which are more realistic in real world. The proposed models are considered as a fundamental tools to better characterize the spread of malwares in network and show that the consequences of the network behavior are the aggregated interactions of distinct smartphones.

II. Impulse-Free Model (IFM)

We first consider the simple condition regardless of incubation period that the dynamics of malware for an individual due to contacts with infected individuals and the infection rate of the malware is a homogeneous Poisson process with exposure rate λ (contacts/unit time) and the recover dynamics for an individual due to firewall or anti-virus software is exponential distributed with mean $\frac{1}{\mu}$ unit time, thus we model the dynamics of malware with incubation period with the aid of Continuous-Time Markov Chain (CTMC) $\{X(t), t \geq 0\}$ with the states representing the malware level of such malware quantized by N degrees and hence we have $N+1$ states in total. The CTMC

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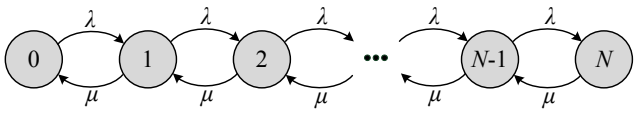

Fig. 1. Continuous-Time Markov Chain without incubation period.

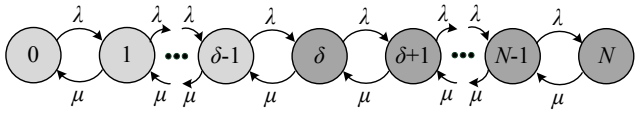

Fig. 2. Continuous-Time Markov Chain with incubation period.

is ergodic with finite states and the state transition rate diagram is shown in Fig. 1.

However, the CTMC described in Fig. 1 is not suitable to describe a malware that possesses the property of incubation period. To make our model more realistic, we term the incubation period T as the time spent from state 0 to some threshold δ for an individual, and the probability $P_{0\delta}(t)$ that an individual is initially safe and eventually be infected at time t. The interpretation is more practical since the spread of malware depends both on the exposure rate and the self-immune ability, which is due to firewall or anti-virus software, of an individual, and the threshold has its meaning not only from the view point of the mobile network but also from the view point of an individual.

We are interested in the states of the expected level of the malware $E[X(t)]$, the incubation period T, the remaining life time R, the probability $P_{ij}(t)$ that the state of an individual transfers from safe to infected at time t and the steady state probability P_n to evaluate the characteristics of the malware. As a consequence, we remodel the CTMC as in Fig. 2.

A. Expected malware level $E[X(t)]$

We assume that N is relatively large or in the sense that the highest accumulated level (fatal level) is very difficult to achieve (the malware is fatal if it reaches state N) so that we may view this CTMC as an unbounded CTMC. For a small interval h, given $X(t)$ and $X(0) = i$, we have

$$X[t+h|X(t)] = \begin{cases} X(t)+1, & \lambda h + o(h), \\ X(t)-1, \text{ with prob. } & \mu h + o(h), \\ X(t), & 1-(\lambda+\mu)h + o(h). \end{cases}$$

Thus we have

$$\begin{aligned} E[E[X(t+h)|X(t)]] &= E[(X(t)+1)(\lambda h + o(h)) \\ &\quad +(X(t)-1)(\mu h + o(h)) \\ &\quad +X(t)(1-(\lambda+\mu)h + o(h))] \\ &= E[X(t) + (\lambda-\mu)hX(t) + o(h)] \\ &= E[X(t)] + (\lambda-\mu)hE[X(t)] + o(h) \\ &= E[X(t+h)] \end{aligned}$$

Denote $M(t) = E[X(t)]$, then

$$M'(t) = \lim_{h\to 0} \frac{M(t+h) - M(t)}{h} = (\lambda - \mu)M(t)$$

and

$$M(t) = E[X(t)] = \begin{cases} (\lambda-\mu)t + i, & \text{if } \lambda \neq \mu, \\ i, & \text{if } \lambda = \mu. \end{cases}$$

B. Incubation period T and remaining life time R

We define the incubation period T the time spent from state 0 to threshold δ for an individual. For a birth and death process with constant parameters λ and μ, the time spent to leave state x for state $x+1$ is denoted as Z_x and hence the expected time and variance for Z_x is

$$E[Z_x] = \begin{cases} \frac{1-\left(\frac{\mu}{\lambda}\right)^{x+1}}{\lambda-\mu}, & \text{if } \lambda \neq \mu, \\ \frac{x+1}{\lambda}, & \text{if } \lambda = \mu, \end{cases}$$

and

$$Var(Z_x) = \frac{1}{\lambda(\lambda+\mu)} + \frac{\mu}{\lambda} Var(Z_{x-1}) + \frac{\mu}{\lambda+\mu}(E[Z_{x-1}] + E[Z_x])^2$$

where $E[Z_0] = \frac{1}{\lambda}$ and $Var(Z_0) = \frac{1}{\lambda^2}$.

And the expected time to go from state k to state j is

$$\begin{aligned} E\left[\sum_{x=k}^{j-1} Z_x\right] &= \sum_{x=k}^{j-1} E[Z_x] = \sum_{x=k}^{j-1} \frac{1-\left(\frac{\mu}{\lambda}\right)^{x+1}}{\lambda-\mu} \\ &= \begin{cases} \frac{1}{\lambda-\mu}\left[j-k-\frac{\left(\frac{\mu}{\lambda}\right)^{k+1}-\left(\frac{\mu}{\lambda}\right)^{j+1}}{1-\frac{\mu}{\lambda}}\right], & \text{if } \lambda \neq \mu, \\ \frac{j(j+1)-k(k+1)}{2\lambda}, & \text{if } \lambda = \mu. \end{cases} \end{aligned}$$

Hence

$$T = E\left[\sum_{x=0}^{\delta-1} Z_x\right] = \begin{cases} \frac{1}{\lambda-\mu}\left[\delta - \frac{\left(\frac{\mu}{\lambda}\right)-\left(\frac{\mu}{\lambda}\right)^{\delta+1}}{1-\frac{\mu}{\lambda}}\right], & \text{if } \lambda \neq \mu, \\ \frac{\delta(\delta+1)}{2\lambda}, & \text{if } \lambda = \mu, \end{cases} \quad (1)$$

and $Var(T) = \sum_{x=0}^{\delta-1} Var(Z_x)$.

If we assume that a malware reach fatal level N is the cause of system-broken for an individual, then the remaining life time is defined as the time staring from the emergence of the malware to state N. Hence

$$\begin{aligned} R &= E\left[\sum_{x=\delta}^{N-1} Z_x\right] \quad (2) \\ &= \begin{cases} \frac{1}{\lambda-\mu}\left[N-\delta-\frac{\left(\frac{\mu}{\lambda}\right)^{\delta+1}-\left(\frac{\mu}{\lambda}\right)^{N+1}}{1-\frac{\mu}{\lambda}}\right], & \text{if } \lambda \neq \mu, \\ \frac{N(N+1)-\delta(\delta+1)}{2\lambda}, & \text{if } \lambda = \mu, \end{cases} \end{aligned}$$

and $Var(R) = \sum_{x=\delta}^{N-1} Var(Z_x)$.

C. Transition probability $P_{ij}(t)$

The transition probability $P_{ij}(t)$ is defined as $P_{ij}(t) = \{X(t) = j | X(0) = i\}$ since we care about the probability $P\{X(t) = j, j \geq \delta | X(0) = i, i < \delta\}$ that an individual is initially in safe status and eventually be infected at time t, where we set the observation time 0 to mean the time an individual have inspection or diagnosis for a certain malware by firewall or anit-virus software. We can rewrite Kolmogorov forward equation as $P'(t) = P(t)\mathbf{R}$, where $P(t)$ is the transition probability matrix with elements $P_{ij}(t)$ and $\mathbf{R}$ is

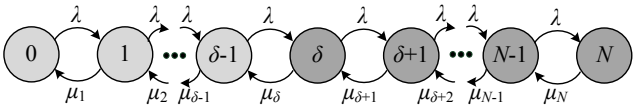

Fig. 3. A general Continuous-Time Markov Chain model.

the rate transition matrix with elements

$$r_{ij} = \begin{cases} q_{ij}, & \text{if } i \neq j, \\ -v_i, & \text{if } i = j. \end{cases}$$

So we can write the rate transition matrix $\mathbf{R}$ for the CTMC model in Fig. 2 as

$$\mathbf{R} = \begin{pmatrix} -\lambda & \lambda & 0 & 0 & 0 \\ \mu & -\lambda-\mu & \lambda & 0 & 0 \\ 0 & \mu & -\lambda-\mu & \lambda & 0 \\ 0 & 0 & \mu & -\lambda-\mu & \lambda \end{pmatrix}. \tag{3}$$

The transition probability matrix $P(t)$ has solution $P(t) = e^{\mathbf{R}t}$ and we can apply an approximation method in $[X]$ to obtain the result by $P(t) = \lim_{n\to\infty}(\mathbf{I} + \mathbf{R}\frac{t}{n})^n$ where $\mathbf{I}$ is the identity matrix and $e^{\mathbf{R}t}$ is defined as $e^{\mathbf{R}t} = \sum_{n=0}^{\infty} \mathbf{R}^n \frac{t^n}{n!}$. Thus we may obtain the transition probability $P_{ij}(t)$ and have more information about the probability $P\{X(t) = j, j \geq \delta | X(0) = i, i < \delta\}$ that an individual is initially in safe state and eventually be infected at time t.

D. Steady state probability P_n

The steady state probability P_n of a birth and death process with constant parameters λ , μ and finite states is a truncated M/M/1/N queue with

$$P_n = \begin{cases} \frac{(1-\rho)\rho^n}{\sum_{x=0}^{N}(1-\rho)\rho^x}, \text{ if } \lambda \neq \mu, \\ \frac{1}{N+1}, \qquad \text{if } \lambda = \mu, \end{cases} \quad 0 \leq n \leq N,\ \rho = \frac{\lambda}{\mu}. \tag{4}$$

III. Impulse-Reaction Model (IRM)

The CTMC model listed in Fig. 2 assumes that the exposure rate and the mean self-immunity period at state n are the same for all states and implicitly indicates that the exposure rate never decreases. With the modeling experiences above we propose a general CTMC model that aims at capturing the dynamics in a much more general way in Fig. 3.

To examine the convenience of the general model for the dynamics of malware with incubation period, we consider a practical case that an individual will look for help upon the emergence of the malware with the aid such as computer engineer and take more method which brings to the reduction of malware mobility. Moreover, the impulse reaction of the self-immune such as firewall and anti-virus software contribute to the enhancements of recover rate as well. Hence one practical assumption is

$$\lambda_n = \begin{cases} \lambda, & 0 \leq n \leq \delta - 1, \\ \alpha\lambda, & \delta \leq n \leq N-1, \end{cases} \tag{5}$$

and

$$\mu_n = \begin{cases} \mu, & 1 \leq n \leq \delta - 1, \\ \beta\mu, & \delta \leq n \leq N, \end{cases} \tag{6}$$

where $0 \leq \alpha < 1$ and $\beta > 1$. From (5) and (6), if we denote $\lambda' = \alpha\lambda$, $\mu' = \beta\mu$, then we can rewrite the incubation period T, remaining life time R, transition probability $P_{ij}(t)$, and steady state probability P_n.

A. Incubation period T and remaining life time R

From (1) the incubation period T is unchanged,

$$T = E\left[\sum_{x=0}^{\delta-1} Z_x\right] = \begin{cases} \frac{1}{\lambda-\mu}\left[\delta - \frac{(\frac{\mu}{\lambda})-(\frac{\mu}{\lambda})^{\delta+1}}{1-(\frac{\mu}{\lambda})}\right], & \text{if } \lambda \neq \mu, \\ \frac{\delta(\delta+1)}{2\lambda}, & \text{if } \lambda = \mu, \end{cases}$$

and $Var(T) = \sum_{x=0}^{\delta-1} Var(Z_x)$.

The remaining life time R from (2) is

$$R = E\left[\sum_{x=\delta}^{N-1} Z_x\right] = \begin{cases} \frac{1}{\lambda'-\mu'}\left[N - \delta - \frac{(\frac{\mu'}{\lambda'})^{\delta+1}-(\frac{\mu'}{\lambda'})^{N+1}}{1-(\frac{\mu'}{\lambda'})}\right], & \text{if } \lambda' \neq \mu', \\ \frac{N(N+1)-\delta(\delta+1)}{2\lambda'}, & \text{if } \lambda' = \mu', \end{cases}$$

and $Var(R) = \sum_{x=\delta}^{N-1} Var(Z_x)$,

where

$$E[Z_x] = \begin{cases} \frac{1-(\frac{\mu}{\lambda})^{x+1}}{\lambda-\mu}, \text{ if } \lambda \neq \mu \\ \frac{x+1}{\lambda}, \qquad \text{if } \lambda = \mu \end{cases} \text{ for } 0 \leq x \leq \delta - 1,$$

and

$$E[Z_x] = \begin{cases} \frac{1-(\frac{\mu'}{\lambda'})^{x+1}}{\lambda'-\mu'}, \text{ if } \lambda' \neq \mu' \\ \frac{x+1}{\lambda'}, \qquad \text{if } \lambda' = \mu' \end{cases} \text{ for } \delta \leq x \leq N-1,$$

$$Var[Z_x] = \begin{cases} \frac{1}{\lambda(\lambda+\mu)} + \frac{\mu}{\lambda} Var(Z_{x-1}) \\ \quad + \frac{\mu}{\lambda+\mu}(E[Z_{x-1}] + E[Z_x])^2, & 0 \leq x \leq \delta - 1, \\ \frac{1}{\lambda'(\lambda'+\mu')} + \frac{\mu'}{\lambda'} Var(Z_{x-1}) \\ \quad + \frac{\mu'}{\lambda'+\mu'}(E[Z_{x-1}] + E[Z_x])^2, & \delta \leq x \leq N-1. \end{cases}$$

B. Transition probability $P_{ij}(t)$

The transition rate matrix $\mathbf{R}$ from (3) is shown in (7). And transition probability matrix can be obtained by the same procedure described in Sec. II-C.

C. Steady state probability P_n

The steady state probability P_n for the general birth and death model in Fig. 3 is

$$P_n = \left[1 + \sum_{n=1}^{N} \frac{\prod_{x=0}^{n-1}\lambda_x}{\prod_{x=1}^{n}\mu_x}\right]^{-1} \frac{\prod_{x=0}^{n-1}\lambda_x}{\prod_{x=1}^{n}\mu_x}.$$

For the case with parameters in (4) with $\rho = \frac{\lambda}{\mu}$, if $\rho \neq 1$, we have

$$P_n = \begin{cases} C(1-\rho)\rho^n, & \text{if } 0 \leq n \leq \delta - 1, \\ C(1-\rho)\rho^n \frac{\alpha^{n-\delta}}{\beta^{n-\delta+1}}, & \text{if } \delta \leq n \leq N, \end{cases}$$

$$\mathbf{R} = \begin{array}{c} \\ 0 \\ 1 \\ 2 \\ \vdots \\ \delta \\ \vdots \\ N-1 \\ N \end{array} \begin{array}{c} \begin{array}{ccccccccccc} 0 & 1 & 2 & \dots & \dots & \delta & \dots & \dots & N-1 & N \end{array} \\ \begin{pmatrix} -\lambda & \lambda & 0 & \dots & & & & & & \\ \mu & -\lambda-\mu & \lambda & 0 & \dots & & & & & \\ 0 & \mu & -\lambda-\mu & \lambda & 0 & \dots & & & & \\ 0 & 0 & \vdots & \vdots & \vdots & & & & & \\ 0 & \dots & & & \beta\mu & -\alpha\lambda-\beta\mu & \alpha\lambda & 0 & \dots & \\ 0 & & \dots & & 0 & \beta\mu & -\alpha\lambda-\beta\mu & \alpha\lambda & 0 & \dots \\ 0 & & \dots & & & & 0 & \mu & -\alpha\lambda-\beta\mu & \lambda \\ 0 & & \dots & & & & & 0 & \beta\mu & -\beta\mu \end{pmatrix} \end{array} \tag{7}$$

where C defines as $[\sum_{x=0}^{\delta-1}(1-\rho)\rho^x + \sum_{y=\delta}^{N}(1-\rho)\rho^y \frac{\alpha^{y-\delta}}{\beta^{y-\delta+1}}]^{-1}$. In the case of $\rho = 1$, we have

$$P_n = \begin{cases} \left[\delta + \sum_{y=\delta}^{N} \frac{\alpha^{y-\delta}}{\beta^{y-\delta+1}}\right]^{-1}, & \text{if } 0 \le n \le \delta - 1, \\ \left[\delta + \sum_{y=\delta}^{N} \frac{\alpha^{y-\delta}}{\beta^{y-\delta+1}}\right]^{-1} \frac{\alpha^{n-\delta}}{\beta^{n-\delta+1}}, & \text{if } \delta \le n \le N. \end{cases}$$

IV. Numerical Results and Discussion

We denote the model described in Fig. 2 as IFM and the model described in Fig. 3, (5) and (6) as IRM. Without loss of generality, we further assume that the recover rate before the threshold, μ, equals one. We will show the incubation period T, the remaining life time R, the transition probability $P_{ij}(t)$ and the Steady state probability P_n for both models and provide intuitive explanations for the results. The parameters of numerical result are set as $N = 100$, $\delta = 20$, $\alpha = 0.6$ and $\beta = 1.5$.

We perform the numerical results of incubation period T and remaining life time R in feasible regions for both IFM and IRM in Fig. 4, the results show that the incubation period is unchanged since the both models have the same CTMC parameters before the threshold. However, due to the impulse reaction, the reduced infection ratio directly give rise to higher remaining lifetime, which is quite plausible since an individual may recover from illness by self immunity or the aid of engineer.

We are also interested in the transition probability that an individual is originally safe (initial state is 0) and eventually comes to the threshold δ that evolves with time, i.e., $P_{0\delta}(t)$. Moreover, we are also interested in the accumulated probability that an individual is originally safe (initial state is 0) and eventually be infected (reach states that above δ) that also evolves with time, i.e., $F(t) = \sum_{k \ge \delta} P_{0k}(t)$.

We perform the two dynamics in Fig. 5 and Fig. 6 respectively. In Fig. 5 the peak of transition probability $P_{0\delta}(t)$ emerges earlier if the infection ratio ρ is larger, which is plausible since we have larger exposure rate for larger. To emphasize on the effect of impulse reaction, we set $\alpha = 0.6$ and $\beta = 8$ in Fig. 6. Intuitively, the infection transition probability $F(t)$ is greatly reduced if we take IRM model into consideration.

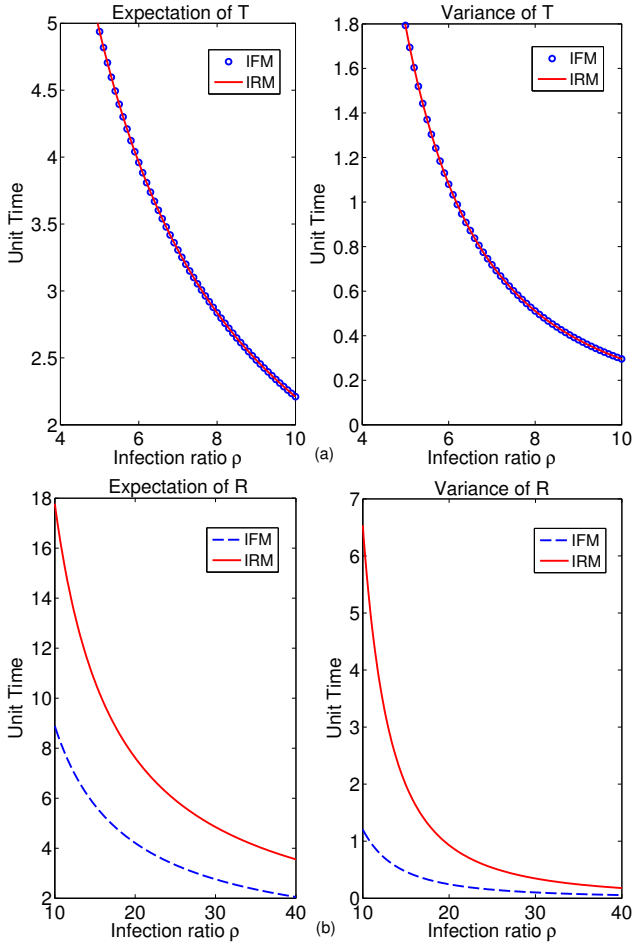

Fig. 4. Numerical results of incubation period T and remaining life time R in feasible regions. (a) Expection and Variance of T (b) Expection and Variance of R.

At last, we present the steady states in Fig. 7. For IRM we fix $\alpha = 0.6$ and observe the distribution of steady state probabilities with different β compared with that of IFM. The tendency of steady state probabilities shows that higher β may better refine the distribution of steady state probability around the threshold or at least reduce the steady state probability at extreme high levels. This result well describes the effect of impulse reaction.

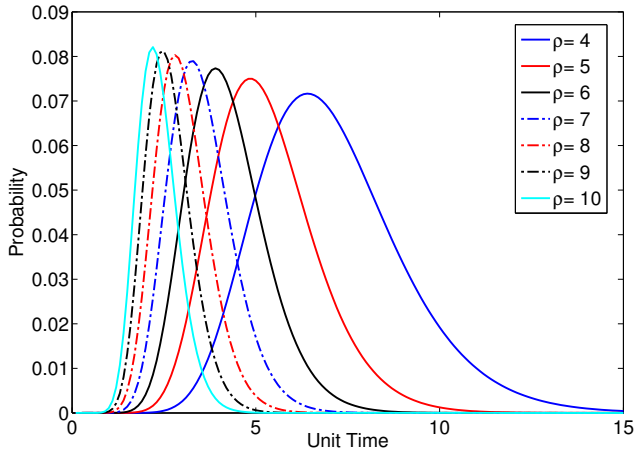

Fig. 5. Transition probabilities $P_{0\delta}(t)$

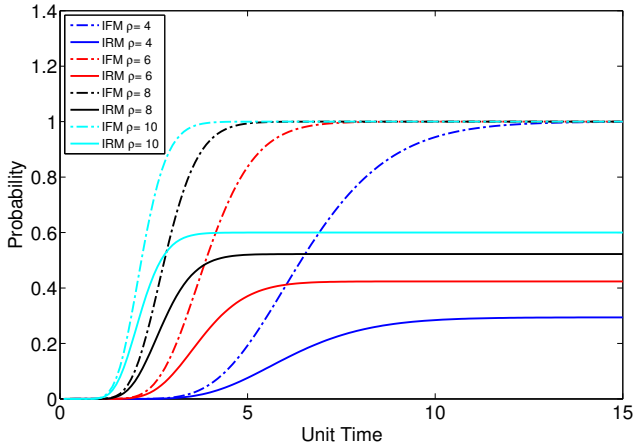

Fig. 6. Infection transition probability $F(t)$

V. Conclusion

In our work, we model the dynamics of malware with incubation period by CTMC concerning the exposure and recover rates of an individual, the generalized birth and death process along with the effect that an individual is infected once the malware level overpasses some certain threshold provides better insights for the dynamics of malware. We proposed two models Impulse-Free Model (IFM) and Impulse-Reaction Model (IRM) and derive the analytic solutions for the malware level, incubation period, remaining life time, transition probability, steady state probability. Furthermore, we provide numerical results to show that while the expected incubation period are the same in both cases, IRM has higher remaining life time and tend to reduce both accumulated infection probability and steady state probability at fatal levels and refine the malware level around the threshold in the feasible regions of infection ratio.

Acknowledgments

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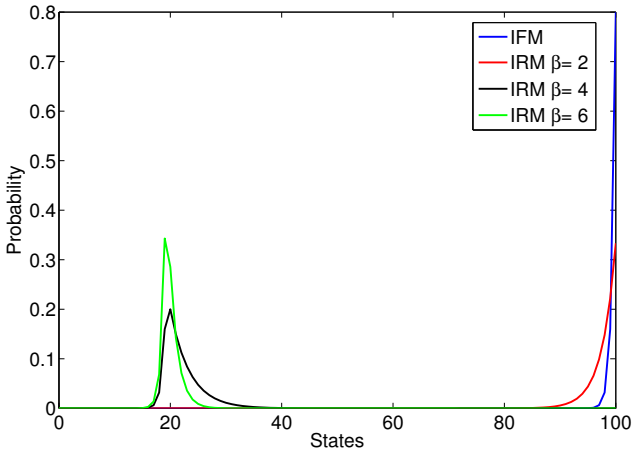

Fig. 7. Steady state probabilities corresponds to β

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