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Epidemic theory based H + 1 hop forwarding for intermittently connected mobile ad hoc networks

Xin Guan[1*], Min Chen[2,3] and Tomoaki Ohtsuki[1]

Abstract

In intermittently connected mobile ad hoc networks, how to guarantee the packet delivery ratio and reduce the transmission delay has become the new challenge for the researchers. Epidemic theory based routing had shown the better performance in the aspect of improving transmission successful rate and reducing the delay, which under the situation that there is no limitation of the node buffer and network bandwidth. In general, epidemic routing adopts the 2-hop or multi-hop forwarding mode to forward the relay packet. However, these two modes have the obvious disadvantage. In this article, we introduce a novel H + 1 hop forwarding mode that is based on the epidemic theory. First, we utilize the susceptible infected recovered model of epidemic theory to estimate the amount of relay node (epidemic equilibrium) and the delivery delay within the epidemic process. Second, we formulate the amount number of relay nodes into a single absorbing Markov chain model. Based on the Markov chain, we estimate the expected delay for the packet transmission. Simulation results show that compared with the basic epidemic and Spray and Wait protocols, the H + 1 hop forwarding mode has the better performance on the delivery delay and amount of copies.

Keywords: intermittently connected, mobile ad hoc and sensor networks, epidemic theory, forwarding, Markov chain

1 Introduction

Thanks to the increasing number of mobile devices with wireless capabilities [1-5], the possibility of communication without network infrastructure is becoming a reality. For example, pocket switched networks rely exclusively on users exchanging messages among themselves upon proximity encounters. Provided that a significant amount of traffic is composed of delay tolerant messages, this paradigm, known also as intermittently connected mobile ad hoc networks [6], could contribute to significantly reduce infrastructure costs and increase bandwidth by orders of magnitude [7].

In ad hoc and sensor networks, there are many factors can impact the performance of routing and forwarding protocol. Especially, the topology control algorithm can impact many aspects of performance. In the sparse mobile ad hoc networks, since the location of nodes are always changing and the network topology is also changing more frequently. This reason raise the issue of

topology control as an important research topic. First, towards ad hoc networks, topology control is a kind of important energy saving technique. Second, topology control algorithm can ensure the quality of coverage and connectivity. Third, topology control algorithm can reduce the communication interference, improve the efficiency of routing and forwarding protocols. In our future studies, we will consider combine the topology control algorithm into our epidemic forwarding protocol and make our protocol work in more real application scenarios.

In traditional wireless sensor or ad-hoc networks, general speaking, there always exists more than one permanent forwarding path between the source and destination to guarantee the successful transmission of packets [8]. However, in some special and practical application scenarios [9], that is difficult to guarantee there always exists the permanent path between the source and destination. It means the wireless network is intermittently connected [10]. In such network scenarios, the packet need to be forwarded in the store-carry-forwarding mode and it is the so called intermittently

* Correspondence: guanxin.hlju@gmail.com
[1]Department of Information and Computer Science, Keio University, Japan
Full list of author information is available at the end of the article

connected mobile ad hoc networks. In intermittently connected mobile ad hoc networks, how to ensure the packet transmission successful rate and reduce the transmission delay is the new challenge for the researchers.

Epidemic theory concerns about contagious diseases spreading in the human society. The key feature of epidemiology is the measurement of infection outcomes in relation to a population at risk. The population at risk basically comprises of the set of people who possess a susceptibility factor with respect to the infection. This factor is dependent on several parameters including exposure, spreading rate, previous frequency of occurrence etc., which define the potential of the disease causing the infection. Various models have been proposed and thoroughly investigated in epidemic theory that characterize the infection spreading process. Example models include susceptible infected susceptible (SIS) model, susceptible infected recovered (SIR) model, etc.

Since the seminal epidemic routing algorithm [11] was introduced, there has been a succession of algorithms aimed at maximizing throughput, the number of messages arriving to the destination while minimizing the traffic overhead caused by the number of forwards. In general, there are two categories of forwarding modes in epidemic routing, 2-hop and multi-hop [12]. Under the 2-hop forwarding scheme, when the source node with a packet encounters another nodes without a copy of the packet, the source node distributes the packet copy to them. The relay nodes which have the packet copy could not distribute the copy to another nodes even the nodes have not the packet copy unless the relay nodes encounter the destination. It means in 2-hop forwarding scheme, only the source node can distribute the packet copy to another nodes which are not the destination node. The 2-hop scheme can reduce the amount number of the relay copies and further, reduce the overhead of the networks. On the other hand, when the network is under the multi-hop scheme, the source node delivers the packet to any nodes which it encounters and further, the nodes which received the packet also can delivery to packet copy to any nodes which they encounter until to the destination node. In the aspects of delivery delay and transmission successful rate, the multi-hop scheme shows the better performance than the 2-hop scheme. By increasing the number of relay nodes, the multi copy mode improves the performance of throughput and the successful rate. Meanwhile, due to the flooding mechanism of packet distributed, the epidemic forwarding generates too much redundant duplicated packets and wastes too much network resource. Based on the above description, how to combine the advantages and avoid the disadvantages of the 2-hop and multi-hop forwarding is a quite interesting

issue for epidemic spreading based intermittently connected mobile ad hoc networks routing.

In the epidemic routing, when one node with the message comes into the communication range of another node which does not have the message, it forwards the message to this node. If this node is destination, the communication ends. Otherwise, the epidemic forwarding continues. By this way, this routing strategy floods the message over the whole network, and attempts to send each message over all possible paths in the network. Therefore, it is an extreme flooding-based routing strategy. Since it tries every possible path, the epidemic routing delivers messages with the minimum delivery delay and with the maximized delivery ratio. Consequently, epidemic routing is particularly useful for DTNs.

In this article, we consider the advantage of 2-hop and multi-hop forwarding scheme in the aspect of epidemic theory. Toward the 2-hop forwarding, the scheme generates the less duplicate copy and reduce the network overhead, however, the 2-hop forwarding has the higher delivery delay and lower successful delivery rate. The multi-hop is on the opposite of 2-hop forwarding. In order to solve the above issues, we divide the whole forwarding process into two sub-processes and it is the so called H + 1 hop forwarding scheme for intermittently connected mobile ad hoc networks.

In the first sub-process, the source generates packet and distributes it to any nodes which they are within the same transmission range. Also for the relay nodes, they distribute the duplicate copies to the nodes which do not carry the packet copy yet by using the SIR model of epidemic spreading. As we know, at the beginning of the SIR spreading, the amount of infective nodes would become larger rapidly, it also means that when the nodes which have not carried the duplicate copy is much less than the nodes which have carried the copy, the distribution increasing speed is rapid enough. With the time pass by, the copy distribution speed become slower, it is because of that the probability of encounter the nodes which have not the copy is lower than the initial process. Therefore, we introduce the equilibrium point of SIR model to separate the forwarding process. When the network get to the epidemic spreading gets the equilibrium point, it transfers into the second sub-process. We calculate that there are n nodes carry the duplicate copy at the beginning of the second sub-process. In the second sub-process, the nodes which carry the packet do not distribute the copy to another one besides the destination node. It means they only send the packet to the destination.

Delivery delay and the number of duplicate copies of the packet are the two most important performance measurements for intermittently connected mobile ad

hoc networks forwarding scheme. In this article, we formulate the infective nodes of SIR model as the transition states of single absorbing Markov chain to estimate the expected delivery delay and the number of the copies. The detail explanation appears in the main part of this article. To the best of authors' knowledge, this is the first article of introducing the SIR model of epidemic spreading to control the forwarding process and analyze the performance in intermittently connected mobile ad hoc networks.

The rest of this article is organized as follows: Section 2 describes the related studies for some typically intermittently connected mobile ad hoc networks routing algorithm and summarizes the epidemic routing. In Section 3, we introduce the SIR model to calculate when the network would get to the epidemic spreading equilibrium point. In Section 4, the single absorbing Markov chain is applied to estimate the delivery delay of H + 1 hop forwarding scheme. In Section 5, the performance evaluation shows that compare with 2-hop and multi-hop forwarding scheme, our H + 1 hop forwarding scheme shows the better performance. Finally, in Section 6, we make the conclusion for our epidemic theory based forwarding scheme.

2 Related studies

There are various classifications of routing algorithms for intermittently connected mobile ad hoc networks [13,14]. Here, we divide them into two classes: replication-based algorithms and coding-based algorithms. In replication-based algorithms, multiple or a single copy of the message is generated and distributed to other nodes (often referred to as relays) in the network. Then, all of these nodes, independently of others, try to deliver the message copy to the destination. In coding-based algorithms [15,16], a message is converted into a large set of code blocks such that any sufficiently large subset of these blocks can be used to reconstruct the original message. Consequently, a constant overhead is maintained, and the network is made more robust against the packet drops when the congestion arises. However, these algorithms introduce an overhead of extra work needed for coding, forwarding, and reconstructing code blocks.

Epidemic routing is an approach used by the replication-based routing algorithms. Basically, during each contact between any two nodes, the nodes exchange their data so that they both have the same copies. As the result, the fastest spread of copies is achieved yielding the shortest delivery time.

The performance analysis of epidemic routing is well studied in many articles, including [17,18]. The main problem with this approach is the overhead incurred in bandwidth, buffer space, and energy consumption by the greedy copying and storing of messages. Hence, this approach is inappropriate for resource-constrained networks. To address this weakness of epidemic routing, the algorithms with controlled replication or spraying have been proposed [19-22]. In these algorithms, only a small number of copies are distributed to other nodes, and each copy is delivered to the destination independently of others. Of course, such an approach limits the aforementioned overhead and provides an efficient utilization of network resources.

The replication-based schemes with controlled replication differ from each other in terms of their assumptions about the network. Some of them assume that the trajectories of the mobile devices are known, while some others assume that only the times and durations of contacts between nodes are known. Moreover, in some of them [23], it is assumed that even the node movements can be controlled. Other than these studies that assume some additional features, there are also some studies that assume zero knowledge about the network. The algorithms that fall in this last category seem to be the most relevant to the applications because most often neither the contact times nor the trajectories are known for certain in the applications of intermittently connected mobile ad hoc networks in real life. An example could be a wildlife tracking application [13], where the nodes are attached to animals that move unpredictably.

In the aspect of mathematical epidemiology, there exists a vast of number of research results about the mathematical model on the spreading of infectious diseases, such as stochastic and deterministic models and so on. These mathematical models have been applied in the field of controlling the urgent infectious diseases, e. g., controlling the influenza A (H1N1) virus spreading in the world in 2009. For the application, the epidemic theory has been applied in various computer and communication networks problems that exhibits a stronger analogy to epidemic spreading of disease. For example, [24] model the computer virus spreading in computer and communication networks. Furthermore, lots of network protocols have adopted epidemic-style spreading communication for data dissemination and resource discovering, these cases prove that the epidemic theory is a better way to study the performance. In intermittently connected mobile ad hoc networks, the epidemic theory based routing differs from the above mentioned broadcast protocols in that it supports uni-cast application, using epidemic flooding to decrease the delivery delay.

3 SIR Model based H + 1 hop forwarding scheme
3.1 Network model and assumption
In our network scenario, there are N nodes distribute and move in a 2D square according to a random mobility model. The transmission range of each node is t.

Furthermore, we assume the buffer size in a node is limited. As for the intermittently connected mobile ad hoc networks, since the node distribution is sparse enough, we could ignore the impact of the channel collision. Therefore, we also assume that the communication pair of nodes is perfectly separable, it means that for any communication pair of nodes, they would not interfere with any other simultaneous communication. As for the channel collision avoidance, In [11], host A comes into contact with host B and initiates an anti-entropy session. Anti-entropy session have three steps, in the first step, A transmit it summary vector to B. If B has no idol channel, it will neglect the summary vector. As a result, A cannot receive the request from B. So the anti-entropy session stopped. In such case, the channel collision could be avoided.

3.2 Two stages forwarding

In intermittently connected mobile ad hoc networks, there exists multiple source-destination pair nodes. Meanwhile, multiple packets are transmitted via multi-hop transmission mode at the same time. In order to explain the transmission process more clearly, we pick one pair of source-destination nodes to describe the model. We consider a set of N nodes and each one with a finite transmission range. The nodes move in a closed area. We define that two nodes meet when they come within transmission range of each other, at which point they can exchange their packets. According to the classical SIR model of epidemic theory, at any time point t, in general, there are three categories of nodes in the networks. The first category is the set of susceptible node, it means that these nodes do not receive the packet yet and if they meet the nodes which have already carry the packet, they would be the relay nodes. We define the ratio of these nodes as $S(t)$. The second category is the set of infective node, it means that these nodes have already store, and carry the packet which needed to be relay to the other node or the destination. We define the ratio of these nodes as $I(t)$. The third category is the set of recovered node, it means that the node which carry the packet has forwarded the packet to the destination. When the node meets the destination, they would remove the packet from their buffer and never receive the same packet. We define the ratio of these nodes as $R(t)$. In this article, the number of wireless nodes is a constant N. We have the following Equation (1) to show the relation of $S(t)$, $I(t)$, and $R(t)$. In Equation (1), since the number of nodes is an constant N, the summation of $S(t)$, $I(t)$, and $R(t)$ is 1.

$$S(t) + I(t) + R(t) = 1 \tag{1}$$

Towards the variable rate of the node state, we have the differential equations to denote the foundational SIR model. We assume the initial ratio of $S(0) = S_0$ and $I(0) = I_0$.

$$\begin{cases} \dfrac{dI}{dt} = \lambda S(t)I(t) - \mu I(t) \\ \dfrac{dS}{dt} = -\lambda S(t)I(t) \end{cases} \tag{2}$$

In the above differential equations, dI/dt is the variable rate of relay nodes which have carried the duplicated packets. dS/dt is the variable rate of nodes which do not received the packet yet. I_0 and S_0 are the initial values of received packet nodes and no packet nodes separately. λ is the meeting probability between any two nodes in the given field, μ is the meeting probability between a certain node which has carried the duplicated packet and the destination. Refer to [17], λ is shown by the following equation. $\lambda S(t)I(t)$ is the transferring amount from state S to state I. $\mu I(t)$ is the reducing amount in time I. Therefore, $\lambda S(t)I(t)$ is the changing amount of I in the time of dt.

$$\lambda = \frac{2tE[V^*]}{L^2} \tag{3}$$

In Equation (3), t means the transmission range for each node, $E[V^*]$ means the relative velocity expectation of mobile nodes. L^2 means the area of given sensing field. According to the SIR model of epidemic theory, the relation between λ and μ is shown by the following equation. Ω is the effective linear meeting rate. The value of μ is refer to [11].

$$\Omega = \lambda/\mu \tag{4}$$

For Equation (2), we cancel the dt, having the following equation.

$$\begin{cases} \dfrac{dI}{dS} = \dfrac{1}{\Omega S} - 1 \\ I|_{s=s_0} = I_0 \end{cases} \tag{5}$$

The integral expression of Equation (5) is shown by Equation (6).

$$dI = \left(\frac{1}{\Omega S} - 1 \right) dS \Rightarrow \int_{I(0)}^{I} dI = \int_{S(0)}^{S} \left(\frac{1}{\Omega S} - 1 \right) dS \tag{6}$$

By using the property of integral, we could have the solution of Equation (5). It is shown by Equation (7). By using this equation, we represent the I for the latter calculation.

$$I = (S_0 + I_0) - S + \frac{1}{\Omega} \ln \frac{S}{S_0} \qquad (7)$$

According to the *SIR* model of epidemic theory, we conclude ratio of the un-infective node during the packet forward process and denote the ratio as S_ω, it is shown in the following Equation (8).

$$S_0 + I_0 - S_\omega + \frac{1}{\Omega} \ln \frac{S_\omega}{S_0} = 0 \qquad (8)$$

In the process of epidemic spreading, the packet is forwarded by several relay nodes. Based on the above description, it is easy to conclude that the ratio of infective node is shown in the following Equation (9) and we denote it as X. Since S_0 is the initial un-infection ratio, S_w is the un-infection ratio for the whole transferring process. Therefore, X is the infection ratio for whole process.

$$X = S_0 - S_\omega \qquad (9)$$

From the Equation (8), at the beginning of spreading process, we think about that the initial I_0 is small enough and we can omit it. Therefore, we have the following Equation (10).

$$X + \frac{1}{\Omega} \ln \left(1 - \frac{X}{S_0} \right) \approx 0 \qquad (10)$$

By using the Taylor expansion for above equation, we have the Equation (11). Through Equation (11), we can evaluate the number of infection nodes and the number of un-infection nodes when the packet copies reached the equilibrium point. Furthermore, based on the number of infection to evaluate the time of equilibrium point. The timer of nodes would notify that do not forward the copies anymore and switch to the many to one scheme.

$$X \left(1 - \frac{1}{S_0 \Omega} - \frac{X}{2 S_0^2 \Omega} \right) \approx 0 \qquad (11)$$

From the above description, we can evaluate the amount number of the un-infected node when the network gets epidemic spreading equilibrium point. When the SIR model is at the equilibrium point, the spreading speed of the packet would not be faster than the scheme of many-to one scheme. Therefore, the forwarding mode transfer to the many-to-one mode which means the nodes which carry the packet only send the packet to the destination instead of conventional epidemic theory. In the above description, we can conclude the amount number of the infective nodes. It is means that we can know which node carry the packet. Meanwhile, we need to know when the infective nodes should change their forwarding mode to many-to-one. In the following

section, we will estimate the expected time from the original packet is generated to the time of the network get the epidemic equilibrium point.

In the process of epidemic forwarding, the source node generates packet which is needed to be relayed to the destination. Along with the random moving in the sense field, the source would send the packet to any node that it will meet. Furthermore, when the relay nodes received the original packet, the packet will be copied and stored in the buffer of the relay nodes. Then the relay nodes would send the copy to any node they will meet. This process is based on the epidemic theory. In our forwarding scheme, we introduce the two subprocess forwarding. Therefore, we need to know when the first sub-process should transfer to the second sub process. In this section, we introduce the single absorbing Markov chain to estimate the time of equilibrium point. Nodes stop the epidemic process is based on a timer. Nodes would predict the time when the forwarding scheme would transfer to many to one scheme, when the forwarding scheme transfer to many to one, then the forwarding activity switch to the second stage. For stage transition, the equilibrium point is not the optimal point. The equilibrium point is the infection ratio which is calculated by the encounter probability of nodes. When the packet copies reached this equilibrium point, the spreading of packet would not be faster than the scheme of many to one scheme. We also calculate the time when reached this equilibrium point by using Markov chain. Nodes stop the epidemic process is based on a timer. Nodes would predict the time when the forwarding scheme would transfer to many to one scheme, this special is the timer to stop the epidemic process.

According to the encounter probability, each node calculates the ratio of infection when the packet copies reached the equilibrium point. Then, by using the Markov chain, the node would predict the time when the packet copies reached the equilibrium point. When this time is reached, forwarding node will stop the forwarding process since the packet has been delivered to the destination.

In Figure 1, the numeric which in the circle denotes the number of the infective nodes at current time state. We formulate the numeric as the transition state for the single absorbing Markov chain. The states 1, 2, 3..., n-2, n-1, n denote the transient state in the chain. The D is the single absorbing state of above Markov chain. From the aspect of epidemic theory, every state means the infective node at time t, e.g., the state of x means that at time t, there are x nodes were infected. At the state of n, the network gets to the epidemic spreading equilibrium. For the absorbing state D, it denotes the destination of the packet. In the first sub-process which is based on epidemic theory, each node which has carried
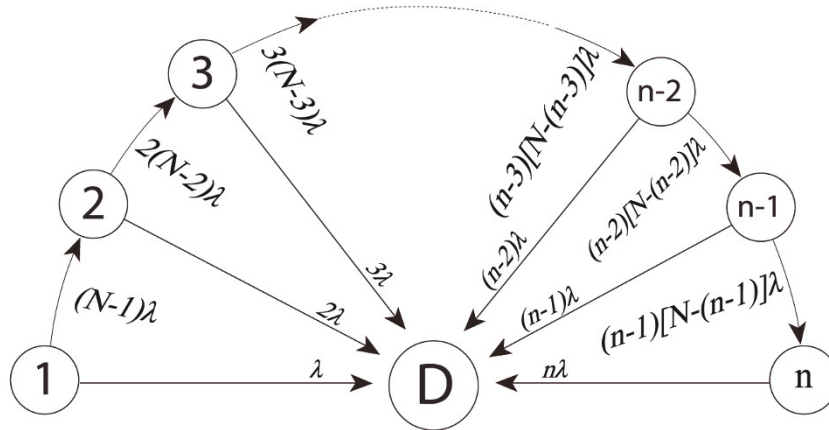
Figure 1 Transition rate of the single absorbing Markov chain.

the duplicate packet will distribute the packet copy to other nodes which do not have this packet when they are within the transmission range. Therefore, when there are x copies of the packet in the network (x nodes are infected), the $x + 1$ copy is generated by the transition rate λx (N-x). At any state x, the transition rate of reaching the destination node for any one infective node could be denoted by λx (transition rate from x to D).

In order to separate the whole forwarding process into two sub-process, we need to let the nodes know that when the forwarding mode should transfer from the first sub-process into the second one. Therefore, we need to know the time when the epidemic forwarding gets to the spreading equilibrium point. According to the above Markov chain, we conclude that when there are i nodes are infected, the inter-meeting time which infected the next $i + 1$ node could denote by the following Equation (12) which is based on the epidemic SIR model. We cumulate the total expected time which from 0 infection node to n_{th} infection node. We define this expected time as T_n.

$$t_{i \to i+1} = \frac{1}{\lambda SI} \tag{12}$$

Denote the expect time from state 1 to n as T_n, we have the following Equation (13) to show the expression of T_n. The parameter n is the local information of node and it is the total number of infection nodes.

$$
\begin{aligned}
T_n &= \frac{1}{(N-1)\lambda} + \frac{1}{2(N-2)\lambda} + \cdots + \frac{1}{n(N-n)\lambda} \\
&= \frac{1}{\lambda N} \sum_{i=1}^{n} \left(\frac{1}{i} + \frac{1}{N-i} \right)
\end{aligned}
\tag{13}
$$

4 Performance modeling for H + 1 hop epidemic forwarding

In wireless intermittently connected mobile ad hoc networks, transmission delay of packet and the amount number of the packet copies are two important performance measurements. In this section, based on the previous mentioned *SIR* epidemic model, we conclude the amount number of the infective nodes at some exact time. Furthermore, formulate the infective nodes into a single absorbing Markov chain and estimate the packet transmission delay when the copy of the original packet reaches the destination node. Also we consider the distribution of the packet transmission and the distribution of the amount number of the packet copies. In order to compute the packet delay, we introduce the Laplace-Stieltjes form to achieve the goal of the computation.

As mentioned previous section, we assume there are N nodes distribute in the network. In general, there always exist multiple packets are transmitting in the network at the same time, in order to explain the forwarding process more clearly, we only consider one packet transmission which is from the source to the destination node. And all other nodes (except the source and destination) could be regarded as relay nodes.

4.1 Definition of the Markov chain model

We denote the λ as the inter-meeting time parameter for any two nodes i and j. And this parameter is determined by the network scale and the number of the nodes. By the following mathematics analysis, we show that packet transmission delay and number of packet copies are the linear function of λ. Therefore, the parameter λ would impact the network performance directly. Here, we denote any two relay nodes as i and j. Before

the packet copy reach the destination, we consider that the relay node i and j could meet n times during the forwarding process and further denote the exact meeting time as $T_{ij}(1)$... $T_{ij}(n)$. In addition, we denote the meeting time interval from n_{th} to $(n + 1)_{th}$ as $\Delta T_{ij}(n \rightarrow n + 1)$.

In this section, we make the following assumption.

For the meeting time processes $\{T_{ij}(n), n \geq 1\}$, we assume the processes are mutually independent and homogeneous Poisson processes with $\lambda > 0$. Also for the meeting time interval $\Delta T_{ij}(n \rightarrow n + 1)$, we assume the processes as mutually independent and exponentially distributed with mean $1/\lambda$. In the latter description, we define the expected packet delay of H + 1 hop forwarding scheme as $E[T]$. It means the time from the packet is generated by the source node to the time when the packet is forwarded to the destination node. For the expected transmission packet copies, we define it as C and it belongs to $\{1, 2,..., N\}$. The expected number of transmission packet copies includes the packet at the destination node but excludes the packet at the source node. In our forwarding scheme, when the first sub-process of transfer to second one, we have n infective node and also means there are n duplicate packet in the network. According to single absorbing Markov chain of Figure 1, the probability of jumping from state i to $i + 1$ is $(N - i)/(N + 1 - i)$. Meanwhile, the probability of jumping from state i to state D (Destination) is $1/(N + 1 - i)$. The sojourn time q_i is exponentially distributed with intensity $\lambda i (N + 1 - i)$ in state i. For $\theta \geq 0$, we have the following expression of Laplace-Stieltjes form. T is the total sojourn time and θ is the parameter of Laplace-Stieltjes form.

$$T^*(\theta) = E\left[e^{-\theta T}\right] \quad (14)$$

4.2 Performance estimate for H + 1 hop epidemic forwarding

In this section, we estimate the expected packet delivery delay and the amount number of the packet copies during the forwarding process through the single absorbing Markov chain. The transition rate of the Markov chain has been shown in Figure 1. In our H + 1 hop forwarding scheme, we think when the forwarding process gets to the epidemic spreading equilibrium point, the forwarding scheme would transfer to the many-to-one mode, the relay nodes which carried packet copy only distribute the packet copy to the destination node. Therefore, in the Markov chain model, there at most exist n states and also means the maximum number of infective nodes is n. Based on the n value, we denote the transition states in the Markov chain as $\{1, 2,..., n\}$,

the destination node is the absorbing state, denoted as D.

By conditioning on the amount number of the infective nodes n, the following Equation (15) is shown.

$$T^*[\theta] = \sum_{i=1}^{n} E\left[\exp\left(-\theta \sum_{j=1}^{i} q_j\right) | N = i\right] P(N = i) \quad (15)$$

The $P(N = i)$ is shown by the following Equation (16) and it is based on the above mentioned single absorbing state Markov chain (see Figure 1).

$$P(N = i) = \frac{1}{N + 1 - j} \prod_{j=1}^{i-1} \frac{N - j}{N + 1 - j} = \frac{1}{N} \quad (16)$$

In Equation (16), we have the detail expression for $P(N = i)$. And furthermore, in order to conclude the result of Equation (15), we show the expression of the former part of Equation (15) by using Laplace-Stieltjes form. It is shown by Equation (17).

$$
\begin{aligned}
E\left[\exp\left(-\theta \sum_{j=1}^{i} q_j\right)\right] &= \int_0^\infty e^{-\theta x} d\left(1 - e^{-\lambda j(N+1-j)x}\right) \\
&= \lambda j(N + 1 - j) \int_0^\infty e^{-\theta x} e^{-\lambda j(N+1-j)x} dx \\
&= \lambda j(N + 1 - j) \int_0^\infty e^{-(\theta + \lambda j(N+1-j))x} dx \\
&= -\frac{\lambda j(N + 1 - j)}{\theta + \lambda j(N + 1 - j)} \int_0^\infty e^{-(\theta + \lambda j(N+1-j))x} d[-\theta + \lambda j(N + 1 - j)]x \\
&= -\frac{\lambda j(N + 1 - j)}{\theta + \lambda j(N + 1 - j)} \cdot e^{-(\theta + \lambda j(N+1-j))x} \big|_0^\infty \\
&= \frac{\lambda j(N + 1 - j)}{\lambda j(N + 1 - j) + \theta}
\end{aligned}
\quad (17)
$$

By multiplying the Equations (16) and (17), we have the following Equation (18).

$$T^*[\theta] = \frac{1}{N} \sum_{i=1}^{n} \prod_{j=1}^{i} \frac{\lambda j(N + 1 - j)}{\lambda j(N + 1 - j) + \theta} \quad (18)$$

By using the Laplace-Stieltjes form and exponential, we evaluate the expected packet delivery delay and it is shown by the following Equation (19).

$$
\begin{aligned}
E[T] &= \frac{-dT^*[\theta]}{d\theta} \Big|_{\theta=0} \\
&= \frac{1}{N} \sum_{i=1}^{n} \prod_{j=1}^{i} \frac{\lambda j(N + 1 - j)}{(\lambda j(N + 1 - j) + \theta)^2}
\end{aligned}
\quad (19)
$$

Since the θ is the parameter of Laplace-Stieltjes form, in order to conclude the final expression of expected packet delivery delay, we let the parameter θ to be 0.

Then we have the final result for delivery delay and it is shown in Equation (20).

$$
\begin{aligned}
E[T] &= \frac{1}{N} \sum_{i=1}^{n} \prod_{j=1}^{i} \frac{1}{\lambda j (N + 1 - j)} \\
&= \frac{1}{\lambda N} \sum_{i=1}^{n} \prod_{j=1}^{i} \frac{1}{j(N + 1 - j)} \\
&= \frac{1}{\lambda N (N + 1)} \sum_{i=1}^{n} \sum_{j=1}^{i} \left(\frac{1}{j} + \frac{1}{N + 1 - j} \right) \\
&= \frac{1}{\lambda N} \sum_{j=1}^{n} \frac{1}{j}
\end{aligned}
\tag{20}
$$

4.3 Number of the duplicate copy

We denote the expected number of the duplicate packet copy as C_n and it is shown by the following Equation (21).

$$
C_n = \sum_{i=1}^{n} \frac{i}{N} = \frac{n(n + 1)}{2N}
\tag{21}
$$

5 Performance evaluation

In this section, we validate the H + 1 hop forwarding scheme shows the better performance on packet delivery delay and the average delivery ratio, compared with the basic epidemic and Spray and Wait. We implement the simulation in the two dimensional random direction mobility model. The random direction mobility model is commonly adopted in the mobile sensor and ad hoc networks for simulation. In the random direction model, every node is assigned an initial moving direction ϕ, speed S with the maximum is S_{max} and minimum is S_{min}, the travel time interval is finite and it is denoted as τ. In all our evaluation results, we think the sensed field is fixed and constant, the packet size is 20 KB for sending and forwarding, every mobile node is equipped with 512 KB buffer. Each simulation lasts for one simulated hour. If there is no special noted, we run at least 20 times for getting each data point.

As for the intermittent connected ad hoc and sensor networks, traditional performance metrics include average message delivery ratio and end-to-end message latency. Therefore, we choose the two metrics to evaluate the performance.

Since the intermittent connected wireless networks could be operated in many different environments and further could be applied in many traditional mobility model. We implement the H + 1 hop forwarding scheme in the random direction model. In the future studies, we will implement our scheme in the random

waypoint model and random walker model. In our simulation for random direction model, we think the nodes are moving slowly to match the practical application scenario. The velocity of the nodes are between 0.5 and 2 m/s. And further, since when any two nodes meet each other, the nodes need the sojourn time to exchange information. Therefore, we define the sojourn time is between 10 to 100 s. For the random direction model, the sense field is 3 km by 3 km. And also for the each node, the transmission range is fixed by 250 m.

To demonstrate the effectiveness of H + 1 hop forwarding scheme and also guarantee the fairness for basic and Spray and Wait, we perform two groups of simulations on the random direction mobility models. In order to illustrate how each of the protocols (basic epidemic, Spray and Wait and H + 1 hop forwarding scheme) reacts to changes in node density, we increase the number of nodes starting from 30 to 240. To illustrate how each protocol reacts to varying network loads, we vary the per node offered load by adjusting the number of messages sent per minute per source from 1 (lower load), to 5 (higher load).

As for the first group of simulation, in Figure 2, we illustrate the performance of packet delivery ratio on the random direction model. At the start point of the H + 1 hop forwarding and Spray and Wait, the two protocols almost have the same delivery ratio. However, according to the increasement of the number of nodes, the gap between H + 1 scheme and Spray and Wait is becoming larger. From Figure 2, we can notice that when the number of nodes increased from 30 to 60, the delivery ratio is also increased suddenly. Since the density of the network is becoming adequate for delivery ratio. It is easy to see that the basic epidemic shows the poor performance compared with another two protocols.
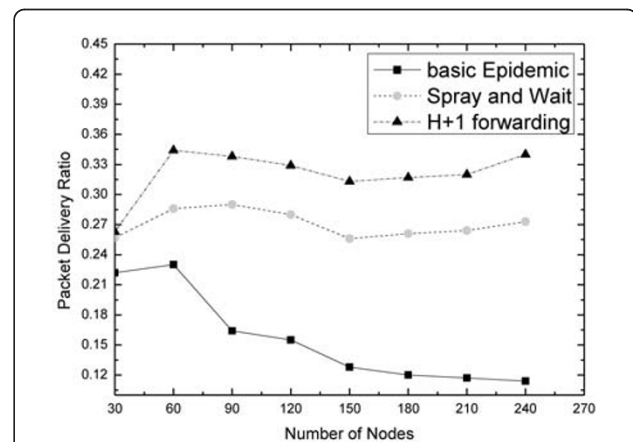

Figure 2 Number of nodes increased versus Packet delivery ratio.

As for the average delivery delay (illustrated by Figure 3), Spray and Wait performs the better performance than basic epidemic. When the number of nodes is less than 100, the Spray and Wait also performs a little better than H + 1 hop forwarding scheme. However, according to the increasement of the number of nodes from 100, the average delay of H + 1 forwarding is becoming a little better than Spray and Wait.
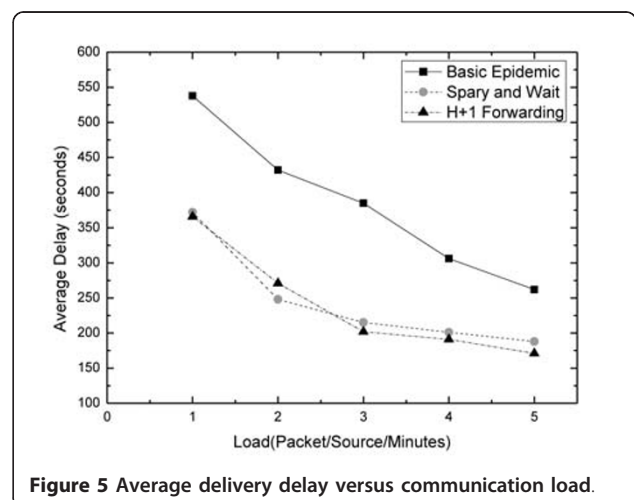
In the second group of simulation, we vary the network communication load from 1 to 5 messages per source node and per minute in the random direction mobility model. In this group of simulations, we also compare the performance of packet delivery ratio and delivery delay. In the aspect of packet delivery ratio (see Figure 4), When the communication load is varied, the basic epidemic shows poor performance compared to another two protocols. As for Spray and Wait protocol and H + 1 forwarding scheme, the gap between them is small. This is because the Spray and Wait protocol also control the amount of the duplicate copies. Also because of the buffer limitation, the performance of delivery ratio for all the three protocols are becoming lower according to the variation of the communication load.

In terms of average delivery delay, as the communication load increases (see Figure 5), since the buffer limitation and too much duplicate copies for basic epidemic, the average delay is higher than Spray and Wait and H + 1 hop forwarding scheme. Before the communication load is varied to 3 packets per source per minute, the H + 1 forwarding is a little higher than Spray and Wait. According to the communication load is increased, the average delay of H + 1 hop is better than Spray and Wait, even the gap between the two protocols is close, the figure still can illustrate the performance improvement.

Figure 4 Packet delivery ratio versus communication load.
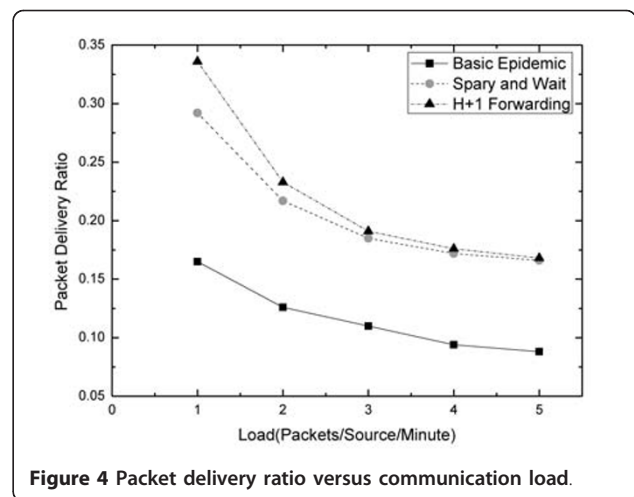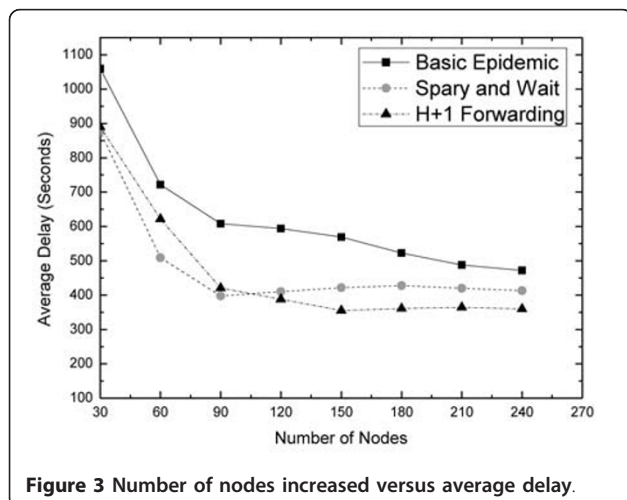
6 Conclusion

In intermittently connected mobile ad hoc and sensor networks, routing packet from the source to the destination is critically important. Since the inherent character, how to guarantee the efficiently and effectively routing performance is an interesting topic. In this article, we introduce a novel forwarding algorithm based on the epidemic. Our study combines the advantage of 2-hop and multi-hop forwarding which are based on the basic epidemic theroy. Through the classical SIR model of epidemic theory, we conclude the equilibria point for the spreading process of the packet. By using the single absorbing state Markov chain, we evaluate the two important metrics, delivery delay and number of the copies, to describe the advantage of H + 1 hop forwarding scheme. In order to validate the performance, we make the simulation for getting the results of delivery ratio and delay. The results demonstrate that compared to basic epidemic and Spray and Wait routing protocols,

Figure 3 Number of nodes increased versus average delay.

Figure 5 Average delivery delay versus communication load.

H + 1 forwarding scheme shows the better performance for intermittently connected wireless networks.

Author details
[1]Department of Information and Computer Science, Keio University, Japan
[2]School of Computer Science and Techology, Huazhong University of Science and Technology, China [3]Department of Computer Science, St. Francis Xavier University, Antigonish, Canada

Competing interests
The authors declare that they have no competing interests.

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