Performance Modeling of Epidemic Routing

Ellen(Xiaolan) Zhang, Giovanni Neglia[§], Jim Kurose, Don Towsley
Dept. of Computer Science
University of Massachusetts, Amherst
{ellenz,kurose,towsley}@cs.umass.edu
[§]Università degli Studi di Palermo
giovanni.neglia@tti.unipa.it

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1 Introduction

Epidemic routing [18] has been proposed as an approach for routing in sparse and/or highly mobile networks in which there may not be a contemporaneous path from source to destination. Epidemic routing adopts a so-called "store-carry-forward" paradigm – a node receiving a packet buffers and carries that packet as it moves, passing the packet on to new nodes that it encounters. Analogous to the spread of infectious diseases, each time a packet-carrying node encounters a new node that does not have a copy of that packet, the carrier is said to *infect* this new node by passing on a packet copy; newly infected nodes, in turn, behave similarly. The destination receives the packet when it first meets an infected node. Epidemic routing is able to achieve minimum delivery delay at the expense of increased use of resources such as buffer space, bandwidth, and transmission power. Variations of epidemic routing have recently been proposed that exploit this trade-off between delivery delay and resource consumption, including K-hop schemes [14, 3], probabilistic forwarding [11, 5], and spray-and-wait [17, 16].

Early efforts evaluating the performance of epidemic routing schemes used simulation [18, 6, 11]. More recently, Markovian models have been developed to study the performance of epidemic routing [15, 3, 5], 2-hop forwarding [3], and spray-and-wait [17, 16]. Recognizing the similarities between epidemic routing and the spread of infectious diseases, [15] used ordinary differential equation (ODE) models adapted from infectious disease-spread modeling [2] to study the source-to-destination delivery delay under the basic epidemic routing scheme, and then adopted Markovian models to study other performance metrics.

In this paper, we develop a rigorous, unified framework, based on Ordinary Differential Equations (ODE), to study epidemic routing and its variations. The starting point of our work is [3], where the authors consider common node mobility models (e.g., random waypoint and random direction mobility) and show that nodal inter-meeting times are nearly exponentially distributed when transmission ranges are small compared to the network's area, and node velocity is sufficiently high. This observation suggests that Markovian models of epidemic routing can lead to quite accurate performance predictions; indeed [3] develops Markov chain models for epidemic routing and 2-hop forwarding, deriving the average source-to-destination delivery delay and the number of extant copies of a packet at the time of delivery. An analytical study of such Markov chain models is quite complex for even simple epidemic models, and more complex schemes have defied analysis thus far. Moreover, numerical solution of such models becomes impractical when the number of nodes is large.

We develop ODEs as a fluid limit of Markovian models such as [3], under an appropriate scaling as the number of nodes increases. This approach allows us to then derive closed-form formulas for the performance metrics considered in [3], obtaining matching results. More importantly, we are also able to use the ODE framework to further model the so-called "recovery process" (packet deletion at infected nodes, following the successful delivery to the destination), to study more complex variants of epidemic routing, and to model the performance of epidemic routing with different buffer management schemes under buffer constraints. While different recovery processes are studied also in [15, 16] using Markov chains, model simulation is first needed to determine a number of model parameters. Many of our ODE models can be analytically solved, providing closed-form formulas for the performance metrics of interest; in cases where we resort to numerical solution, the computation complexity does not increase with the number of nodes. The drawback of our ODE models is that they are used to evaluate the moments of the various performance metrics of interest, while numerical solution of Markov chain models can provide complete distributions (e.g., for the number of packet copies in the system). Simulation results show good agreement with the predictions of our ODE models.

Through our modeling studies, we obtain insights into different epidemic routing schemes. In particular, we identify rules of thumb for configuring these schemes, we show the existence of a linear relation between total number of copies sent and the buffer occupancy under certain schemes, and we demonstrate that the relative benefit of different recovery schemes depends strongly on the specific infection process. Finally our analysis of buffer-constrained epidemic routing suggests that sizing node buffers to limit packet loss is not vital as long as appropriate buffer management schemes are used.

The remainder of this paper is structured as follows. Basic epidemic routing and our basic ODE model are described and derived in Section 3, allowing one to characterize the source-to-destination delivery delay, the number of copies made for a packet, and the average buffer occupancy. In Section 4, the model is extended for three important variations of basic epidemic routing: K-hop forwarding, probabilistic forwarding and limited-time forwarding; we use these extended models to characterize the tradeoff between delivery delay and resource (buffer, power) consumption in Section 5. In Section 6, we integrate the ODE models with Markov and fluid queue models to study the effect of finite buffers, and compare different buffer management strategies. Finally in Section 7 we summarize the paper and discuss about future work. Throughout the paper, we compare our work with related efforts, where appropriate.

2 Network Model and Simulation Setting

2.1 Network Model

We study a network made up of $N+1$ mobile nodes moving in a closed area according to a random mobility model. When two nodes come within transmission range of each other, they can forward packets to each other.

We assume the inter-meeting time of any pair of nodes is an exponential random variable with rate β. As the node density is low, we ignore interference among nodes. When two nodes meet, the transmission between them succeeds instantaneously.

There are $N+1$ source-destination pairs, with each node being the source of one flow, and the destination of another flow. Each source generates packets according to Poisson process with rate λ. Each data packet includes a sequence number in its header.

2.2 Epidemic Routing Protocol

We study the performance of a family of epidemic routing protocols. All different variations of the protocol work as follows (as proposed in [18]):

Each node stores and forwards packets destined for other nodes. Along with the data packet, each node maintains a *summary vector* that indicates the set of packets that are stored in its buffer.

When two nodes come within transmission range of each other, they first exchange their summary vectors. Next, based on this information, each node requests packets that are not in its buffer. Finally, they transmit the requested packets to each other.

Under epidemic routing, packets can arrive at the destination out of order. The sequence number allow the destination node to reorder packets and discard duplicates.

2.3 Performance Metrics

We make use of the analogy between epidemic routing and disease spreading: we consider the specific packet as a disease, and call a node that has a copy of a packet an *infected* node, a node that does not have a copy of a packet, but can potentially store and forward a copy, a *susceptible* node. Once a node carrying a copy meets the destination, it deletes the copy and keeps a "packet-delivered" information so that it will not be forwarded the packet again. We call such information *anti-packet* and say that the nodes are *recovered*. The average *lifetime*, L, of a packet is the time from when the packet is generated at the source node to the time when all copies of the packets are removed (i.e, no more infected nodes for this packet in the network).

Three performance metrics, *delivery delay*, *loss probability* and *power consumption*, are studied in the paper. The delivery delay of a packet, T_d, is the duration of the time from when the packet is generated at the source to the time the packet is first delivered to the destination. For the case where nodes have a limited amount of buffer, a packet might be dropped from the network before it is delivered. The loss probability is the probability of a packet being dropped from the network before delivery.

We consider two metrics related to the power consumption: the number of times a packet is copied in its entire lifetime, G; and the number of times a packet is copied at the time of delivery, C. We will use subscript to distinguish these metrics associated with different schemes we consider.

Table 1 summarizes the notations used in this paper.

2.4 Simulation Setting

Throughout the paper, we validate our models through simulation. We directly simulate the random direction mobility model, and use the meeting rate obtained from simulation to drive the models.

In the random direction mobility model [1, 4], each node chooses an initial direction, speed and a travel time, and then travels in that direction with given speed for the duration. When the travel time expires, the node chooses a new direction, speed and travel time at random, independently of all previous directions, speeds and travel times. If a node hits the boundary of the terrain, it appears at the other side of the terrain.

For the simulation results presented throughout the paper, we simulate nodes moving within a 20×20

Parameters	Description
$N+1$	total node number
B	per-node buffer size (in packets)
β	inter-meeting rate of nodes
μ	exponential timeout rate
λ	packet rate of the data flow
T_d	delivery delay
L	average lifetime of a packet
C	number of copies made before the time of delivery
G	number of copies made during a packet's lifetime

Table 1: Model Parameters Definition

terrain. The node speed is chosen uniformly from $[4, 10]$, and the mean trip duration is $1/4$. The resulting pair-wise meeting rate is around $\beta = 0.0047$.

3 ODE models for Basic epidemic Routing

As noted earlier, [3] showed that the pairwise meeting time between nodes is nearly exponentially distributed, if nodes move in a limited region (of area, A) according to common mobility models (such as the random waypoint or random direction model [1]) and if their transmission range (d) is small compared to A, and their speed is sufficiently high. The authors also derived the following formula for estimating the pairwise meeting rate β:

$$\beta \approx \frac{2wdE[V^*]}{A}, \tag{1}$$

where w is a constant specific to the mobility models, and $E[V^*]$ is the average relative speed between two nodes. Under this approximation, [3] showed that the evolution of the number of infected nodes can be modeled as a Markov chain.

We introduce our modeling approach starting from the Markov model for simple epidemic routing. Given $n_I(t)$, the number of infected nodes at time t, the transition rate from state n_I to state $n_I + 1$ is $r_N(n_I) = \beta n_I(N - n_I)$, where N is the total number of nodes in the network (excluding the destination). If we rewrite the rates as $r_N(n_I) = N\lambda(n_I/N)(1 - n_I/N)$ and assume that $\lambda = N\beta$ is constant, we can apply Theorem 3.1 in [10] to prove that, as N increases, the fraction of infected nodes (n_I/N) converges asymptotically to the solution of the following equation[1]:

$$i'(t) = \lambda i(t)(1 - i(t)), \text{ for } t \geq 0 \tag{2}$$

with initial condition $i(0) = \lim_{N\to\infty} n_I(0)/N$. The average number of infected nodes then converges to $I(t) = Ni(t)$ in the sense of footnote 3. The following equation can be derived for $I(t)$ from Eq.(2):

$$I'(t) \quad = \quad \beta I(N - I), \tag{3}$$

[1]Formally, $\forall \epsilon > 0$, $\lim_{N\to\infty}$ Prob$\{|\sup_{s\leq t}\{n_I(s)/N - i(s)\}| > \epsilon\} = 0$

with initial condition $I(0) = Ni(0)$. Such an ODE, which we have shown results as a fluid limit of a Markov model as N increases, has been commonly used in epidemiology studies, and was first applied to epidemic routing in [15] as a reasonable approximation.

We remark that 1) the initial population of infected nodes must scale with N, and 2) the pairwise meeting rate must scale as $1/N$. Eq.(1) provides insight into the physical interpretation of the meeting rate scaling, in particular one can consider that the area A increases with N, keeping node density constant, then β scales with $1/A$,i.e.,$1/N$. In the following we will consider Eq.(3) with initial condition $I(0) = 1$, which corresponds to an initial fraction of infected nodes $i(0) = 1/N$. Despite the "small" number of initial infected nodes, we'll see via our simulation results that the approximation is a good one. We also note that Eq.(3), as well as other related equations we will derive shortly, can also be obtained in a different manner from Markovian models by neglecting terms related to higher moments (the details are given in Section 8.1).

3.1 Delay under epidemic routing

Let T_d be the packet delivery delay, i.e., the time from when a packet is generated at the source to the time when it is first delivered to the destination, and denote its Cumulative Distribution Function (CDF) by $P(t) = Pr(T_d < t)$. Under the same scaling and approximations considered earlier, we can derive the following equation for $P(t)$: $P'(t) = \lambda i(1 - P)$. In fact, let us consider $P_N(t)$ the CDF of T_d when the number of nodes in the system is $N + 1$, i.e., there are N nodes plus one destination node.

$$
\begin{aligned}
&P_N(t + dt) - P_N(t) = \text{Prob}\{t \le T_d < t + dt\} \\
&= \text{Prob}\{\text{destination meets an infected node in } [t, t + dt] \,|T_d > t\} \\
&= \text{Prob}\{\text{destination meets an infected node in } [t, t + dt] \,\}\, (1 - P_N(t)) \\
&= E\{\text{Prob}\{\text{destination meets one of the } n_I(t) \text{ infected nodes in } [t, t + dt] \,|n_I(t)\}\} \times \\
&\qquad \times (1 - P_N(t)) \\
&\approx E\{\beta n_I(t) dt\}\, (1 - P_N(t)) \\
&= \beta E\{n_I(t)\}(1 - P_N(t))dt = \lambda E\Big\{\frac{n_I(t)}{N}\Big\}(1 - P_N(t))dt.
\end{aligned}
$$

Hence the following equation holds for $P_N(t)$:

$$\frac{dP_N}{dt} \quad = \quad \lambda E\Big\{\frac{n_I(t)}{N}\Big\}(1 - P_N(t)).$$

As N increases $E\{n_I(t)/N\}$ converges to $i(t)$, and $P_N(t)$ converges to the solution of the following equation:

$$P'(t) = \lambda i(t)(1 - P(t)).$$

For a finite population of size N we can consider:

$$P'(t) \quad = \quad \beta I(t)(1 - P(t)). \tag{4}$$

Eq.(4) was proposed in [15], based on an analogy with a Markov process. Solving Eq.(3) and Eq.(4) with $I(0) = 1, P(0) = 0$, we get

$$I(t) = \frac{N}{1 + (N - 1)e^{-\beta N t}}, \qquad P(t) = 1 - \frac{N}{N - 1 + e^{\beta N t}}$$

From $P(t)$, the average delivery delay can be explicitly found in closed form as:

$$E[T_d] = \int_0^\infty (1 - P(t))dt = \ln N/(\beta(N-1)).$$

The average number of copies of a packet in the system when the packet is delivered to the destination, $E[C_{ep}]$, can also be derived, as it coincides with the average number of infected nodes in the system when the packet is delivered (details given in Section 8.3): $E[C_{ep}] = \int_0^\infty I(t)P'(t)dt = \frac{N-1}{2}$.

From the Markov Chain model, [3] obtained the same results for the number of copies, computed the Laplace-Stieltjes Transform (LST) of the delay, and from the LST found the following asymptotic expression for the average delay as $N \to \infty$: $\frac{1}{\beta(N-1)}(\ln N + \gamma + O(\frac{1}{N}))$. We note that derivation is much simpler using our ODE model.

3.2 Recovery from infection

The previous model does not account for the process of deleting packet copies after the packet is delivered to the destination. In this section, after introducing the recovery schemes, we extend the ODE model to model the recovery process, and then study the number of copies sent for a packet and the average storage requirement under these schemes.

[5] first proposed the different recovery schemes we study here, and used Markov Chain to study the corresponding storage requirement. We use same terminologies to refer to the different recovery schemes.

Clearly, once a node delivers a packet to the destination, it should delete the copy from its buffer both to save storage space, and to prevent the node from infecting other nodes. But if the node does not store any information to keep itself from receiving the packet again (i.e., becomes susceptible to the packet), a packet would generally be copied, and the infection would never die out. In order to prevent a node from being infected by a packet multiple times, an anti-packet can be stored in the node when the node delivers a packet to the destination. We refer to this scheme as IMMUNE scheme. With IMMUNE scheme, a node stores a packet copy in the buffer until it meets the destination, often long after the first copy of the packet is delivered. A more aggressive approach to delete obsolete copies is to propagate the anti-packets among the nodes. The anti-packet can be propagated only to those infected nodes (IMMUNE_TX scheme), or also to susceptible nodes (VACCINE scheme).

A Markov model can be used to model the infection and recovery process. In order to derive the limiting equation the number of destinations, n_D, need to scale with the number of nodes N. We first consider IMMUNE scheme. Let $n_R(t)$ denote the number of recovered nodes at time t, then the state can be denoted as $(n_I(t), n_R(t))$. We have the following transition rate: $r_N((n_I(t), n_R(t)), (n_I(t)+1, n_R(t))) = \beta n_I(t)(N - n_I(t) - n_R(t))$, and $r_N((n_I(t), n_R(t)), (n_I(t)-1, n_R(t)+1)) = \beta n_I(t) n_D$.

The transition rates can be similarly written in a "density dependent" form, given that the number of destinations n_D scales in a manner similar to the scaling of the number of initially infected nodes, i.e., $\lim_{N\to\infty} n_D/N = d$. Therefore by Theorem 3.1 in [10], we get as N increases, the fraction of infected nodes (n_I/N) and recovered nodes (n_R/N) converge asymptotically to the solution of the following equations:

$$i'(t) = \lambda i(t)(1 - i(t) - r(t)) - \lambda i(t)d, \text{ for } t \geq 0 \quad (5)$$

$$r'(t) = \lambda i(t)d, \text{ for } t \geq 0 \quad (6)$$

where $d = n_D/N$, and the initial conditions are $i(0) = \lim_{N\to\infty} n_I(0)/N, r(0) = 0$.

The number of infected and recovered nodes then converges to $I(t) = Ni(t), R(t) = Nr(t)$ in the sense of footnote 3. The following equation can be derived for $I(t), R(t)$ from Eq.(5) and Eq.(6):

$$\begin{aligned} I'(t) &= \beta I(N - I - R) - \beta I n_D \quad (7)\\ R'(t) &= \beta I n_D \quad (8)\end{aligned}$$

with initial condition $I(0) = Ni(0), R(0) = 0$. We consider $I(0) = 1, R(0) = 0, D = 1$.

Similarly, ODE models for IMMUNE_TX and VACCINE scheme can be derived from Markov model. For IMMUNE_TX the transition rates are (omitting the dependence from time, t): $r_N((n_I, n_R), (n_I + 1, n_R)) = \beta n_I(N - n_I - n_R)$, and $r_N((n_I, n_R), (n_I - 1, n_R + 1)) = \beta n_I(n_R + n_D)$. The limiting equations are:

$$\begin{aligned} i'(t) &= \lambda i(t)(1 - i(t) - r(t)) - \lambda i(t)(r(t) + d), \text{ for } t \geq 0\\ r'(t) &= \lambda i(t)(r(t) + d), \text{ for } t \geq 0\end{aligned}$$

The following equations can be immediately derived:

$$\begin{aligned} I'(t) &= \beta I(N - I - R) - \beta I(1 + R) \quad (9)\\ R'(t) &= \beta I(1 + R) \quad (10)\end{aligned}$$

For VACCINE we need to specify how many destination nodes have received the packet, let n_{DR} denote this number[2]. We assume that all the destinations have to receive the packets from an infected node[3]. The transition rates are: $r_N((n_I, n_R, n_{DR}), (n_I+1, n_R, n_{DR})) = \beta n_I(N-n_I-n_R)$, $r_N((n_I, n_R, n_{DR}), (n_I - 1, n_R+1, n_{DR})) = \beta n_I(n_R+n_{DR})$ and $r_N((n_I, n_R, n_{DR}), (n_I-1, n_R+1, n_{DR}+1)) = \beta n_I(n_D-n_{DR})$ and $r_N((n_I, n_R, n_{DR}), (n_I, n_R + 1, n_{DR})) = \beta(N - n_I - n_R)(n_R + n_{DR})$. The limiting equations are as follows, where $d_r(t) = \lim_{N\to\infty}(n_{DR}/N)$:

$$\begin{aligned} i'(t) &= \lambda i(t)(1 - i(t) - r(t)) - \lambda i(t)(r(t) + d), \text{ for } t \geq 0\\ r'(t) &= \lambda i(t)(r(t) + d) + \lambda(1 - i(t) - r(t))(r(t) + d_r(t)), \text{ for } t \geq 0\\ d_r'(t) &= \lambda i(t)(d - d_r(t)), \text{ for } t \geq 0\end{aligned}$$

If we consider the average populations ($Ni(t)$,$Nr(t)$ and $Nd_r(t)$), and assume $N_D = 1$, we observe that $Nd_r(t)$ satisfies the same ODE as $P(t)$, and derive the following equations:

$$\begin{aligned} I'(t) &= \beta I(t)(N - I(t) - R(t)) - \beta I(t)(R(t) + 1) \quad (11)\\ R'(t) &= \beta I(t)(1 + R(t)) + \beta(N - I(t) - R(t))(R(t) + P(t)) \quad (12)\\ P'(t) &= \beta I(t)(1 + P(t)). \quad (13)\end{aligned}$$

These ODE models allow us to evaluate the number of times a packet is copied during its lifetime, and the average storage requirement.

[2]There is no such a need for the previous schemes because a destination can recover only an infected node. Hence even if the destination has not received the packet, the destination receives it when it meets the infected node.

[3]Different assumptions can be made, for example a destination could receive the packet from another destination, or a destination could receive the antipacket from a recovered node and propagate it without having received the packet. The latter case is meaningful when we deal with an anycast communication (the packet has to reach at least one of the destinations) or if we can rely on the fact all the destinations will receive a copy of the packet from the destination that started the recovery process. These different assumptions lead to minor differences in the final equations.

3.2.1 Number of times a packet is transmitted

Let $G_{ep}(N)$ denote the number of times that a packet is copied in the network during its entire lifetime. It is a random variable taking value between $[0, \infty]$. The power consumption grows linearly with $G_{ep}(N)$. Our analysis in this section is similar to that of Kermack and McKendrick ([8, 2]) in their derivation of the number of individuals ultimately infected and recovered by an epidemic.

For IMMUNE scheme, Eq.(7) and (8) model the infection and recovery process. Note that as $R(t)$ is a strictly increasing function of t, $I(R)$ is well defined. Dividing Equation (7) over(8) yields:

$$\frac{dI}{dR} = N - I - R - 1.$$

The solution to this ODE with initial condition $I(0) = 1$ is

$$I(R) = (-N + 1)e^{-R} - R + N.$$

As $\lim_{t\to\infty} I(t) = 0$, We can solve $I(R) = 0$ for R to find $\lim_{t\to\infty} R(t)$. For N large enough ($N > 10$), the solution gives $\lim_{t\to\infty} R(t) \approx N$. Since $I(t)+R(t)-(I(0)+R(0)) = I(t)+R(t)-1$ is the number of times a packet is copied in the system by time t, we have $E[G_{ep}(N)] = \lim_{t\to\infty} I(t) + R(t) - 1 \approx N - 1$.

Similarly, for IMMUNE_TX scheme, from Eq.(9) and (10), we can solve $I(R)$ and get:

$$I(R) = \frac{-R^2 + (N-1)R + 1}{R+1}.$$

As $\lim_{t\to\infty} I(t) = 0$, we find $\lim_{t\to\infty} R(t)$ by solving $I(R) = 0$ for R. $I(R) = 0$ has two roots $(N-1\pm\sqrt{N^2-2N+5})/2$. Discarding the negative root, we have $\lim_{t\to\infty} R(t) = (N-1+\sqrt{N^2-2N+5})/2$. Therefore, for IMMUNE_TX scheme, we found

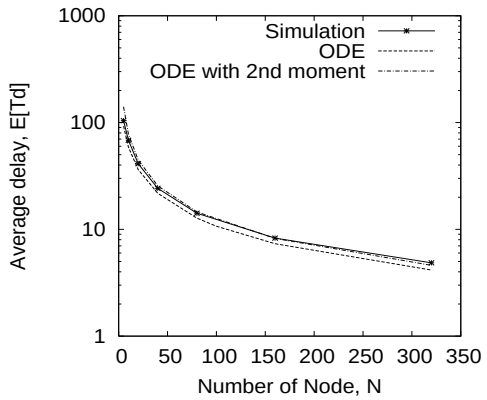
$$E[G_{ep}(N)] = \lim_{t\to\infty}(I(t) + R(t) - 1) = \frac{N - 3 + \sqrt{N^2 - 2N + 5}}{2}.$$

For VACCINE scheme, the ODEs are solved numerically to get the total number of nodes that ever get infected by a packet.

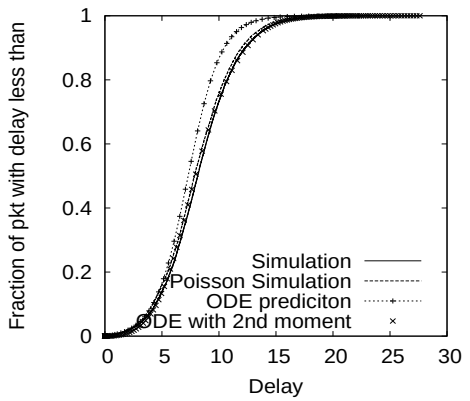
3.2.2 Storage Requirement

We now study the average storage requirement under these different recovery schemes. Suppose L is the average lifetime of a packet (the time from when the packet is generated by the source node to when all copies of the packet are removed from the system), for any random instance during the lifetime of a packet, the average number of copies of this packet in the system is given by $\int_0^\infty I(t)dt/L$, where $I(t)$ is the solution to the corresponding ODEs (e.g. Equation (7) for IMMUNE). Since the total packet arrival rate to the system is $(N+1)\lambda$, the average number of packets in the system is $(N+1)\lambda L$ by Little's law. Therefore the average total buffer occupancy in the whole network, Q_t, is given by

$$E[Q_t] = \frac{\int_0^\infty I(t)dt}{L}(N+1)\lambda L = (N+1)\lambda\int_0^\infty I(t)dt,$$



(a) Average delay for different N



(b) CDF of delay with $N = 160$

Figure 1: Delay under epidemic routing

and per-node buffer occupancy is $E[Q] = \lambda \int_0^\infty I(t)dt$.

Modeling the buffer at a node as an $M/M/\infty$ queue yields the same result, but at the same time shows a useful relation between the average queue length and the average number of copies made for a packet. If on average each packet is duplicated $E[G_{ep}(N)]$ times, each flow generates relay traffic of rate $E[G_{ep}(N)]\lambda$. As there are $N+1$ flows, the total rate of relay traffic in the system is $[G_{ep}(N)]\lambda(N+1)$. This traffic is equally divided among the $N+1$ nodes, therefore for each node, the average arrival rate of relay packets is $E[G_{ep}(N)]\lambda$, resulting in a total packet arrival rate of $\lambda(1 + E[G_{ep}(N)])$.

Let D_r represents the time it takes for a copy to be deleted from a node. For IMMUNE, a packet copy is deleted from the buffer when the packet is delivered to destination, therefore the service rate is given by β, and $E[D_r] = 1/\beta$. For IMMUNE_TX and VACCINE, a packet copy is deleted when the node meets a recovered node or a destination node. On average, each packet has $E[G_{ep}(N)] + 1$ copies, and these copies in the total generate $\int_0^\infty I(t)dt$ occupancy in buffer, so $E[D_r] = (\int_0^\infty I(t)dt)/(E[G_{ep}(N)] + 1)$.

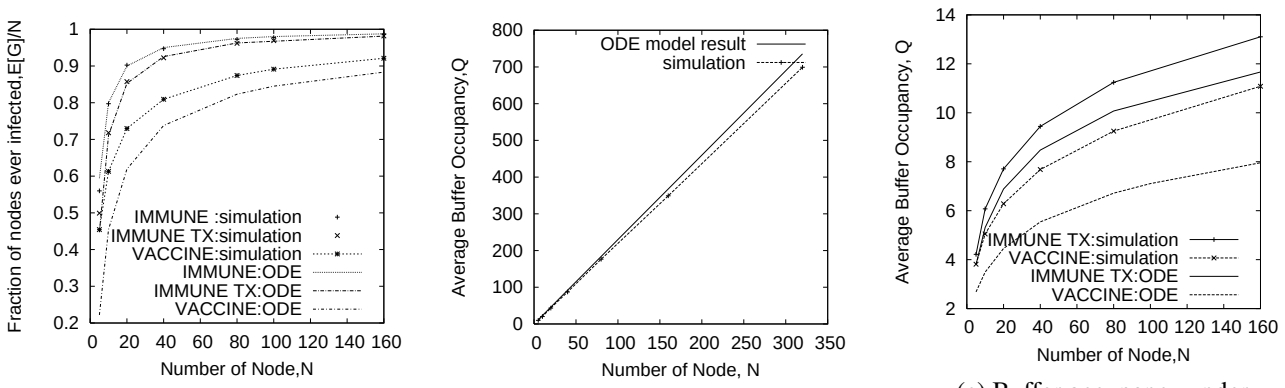
Then the average queue length of the $M/M/\infty$ queue is given by:

$$\lambda(1 + E[G_{ep}(N)]) * E[D_r] = \lambda \int_0^\infty I(t)dt.$$

For IMMUNE, as $E[D_r] = \beta$, therefore the average queue length is linear with $E[G_{ep}(N)]$.

3.3 Model Validation

We perform simulation to validate the modeling result. We vary the number of nodes, N, and let each flow generate packets with Poisson rate $\lambda = 0.01$. The simulation is run long enough so that 100 packets are generated for each flow. The mean and CDF of the delivery delay obtained from the simulation are compared with the model results in Fig.1. We observe that the model is able to accurately predict the delivery delay, capturing the performance trend as N increases, with a slightly larger discrepancy in the CDF. To investigate modeling errors, we ran another set of simulations with nodes meeting according to a Poisson process with rate $\beta = 0.00435$ (i.e., we set the meeting rate in the simulation to exactly match the model's meeting rate) and the results of the two sets of simulations are very close (Fig.1.(b)). We thus conjecture that the



(a) $E[G_{ep}]/N$ (b) Buffer occupancy under IMMUNE (c) Buffer occupancy under IMMUNX_TX and VACCINE

Figure 2: Copies sent and buffer occupancy under epidemic routing

prediction errors are mainly due to the small number of initial infected nodes. We also used a moment-closure technique to derive a ODE system involving second moments ([**?**]). The modified ODE provided a better prediction of average delivery delay and the CDF of delivery delay (Fig.1).

For the different recovery schemes, Fig.2 plots $E[G_{ep}(N)]/N$, and the average buffer occupancy as predicted by the model and obtained from simulation. We find that the ODE models are more accurate for IMMUNE than for VACCINE. In some sense, any error in the infection process modeling is amplified by the exponentially fast recovery of VACCINE. We observe that IMMUNE_TX only slightly reduces the number of copies sent for each packet, while VACCINE further reduces the number of copies sent. The reduction in buffer requirements is similar for IMMUNE_TX and VACCINE.

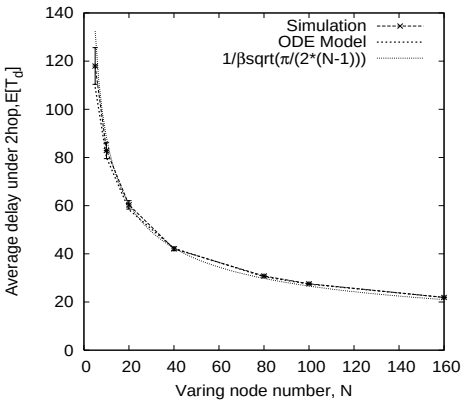
4 Extended Model

The schemes in the previous section differ in the way they counteract the infection after the packet has been delivered to the destination. As we have seen this can lead to substantial differences in terms of buffer and power requirements. However, all of those schemes strive to deliver the packet as soon as possible. Depending on the specific application, it might be preferable to trade off timely delivery for savings in resource consumption. The schemes we are about to describe in this section allow us to achieve such tradeoff. Here we briefly describe them.

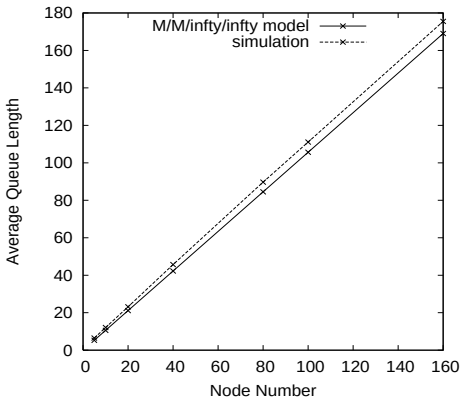
2-Hop forwarding: the nodes infected by the source are able to deliver the packet to the destination, but not to infect other nodes, hence the destination can be reached at most in two hops.

Probabilistic forwarding: each node accepts a realy packet with probability p, or equivalently, each node forwards a packet to relay nodes with probability p.

Limited-Time forwarding: each node starts a timeout timer when it becomes infected, and discards the packet (get recovered) when the timer expires.



(a) average delay



(b) average queue

Figure 3: 2-hop forwarding

4.1 2-hop forwarding

Under 2-hop forwarding, a packet can traverse at most two hops to reach the destination: the source copies the packet to every node it meets until it meets the destination. The relay nodes do not copy the packet to other nodes except the destination. As the packet spreads at a rate proportional to the number of susceptible nodes, we can use the following equations to study the delivery delay:

$$\begin{aligned} \frac{dI}{dt} &= \beta(N-I) \\ \frac{dP}{dt} &= \beta I(1-P) \end{aligned}$$

solving this system with $I(0) = 1, P(0) = 0$, we get

$$\begin{aligned} I(t) &= N - (N-1)e^{-\beta t} \\ P(t) &= 1 - e^{N-1-\beta N t-(N-1)e^{-\beta t}} \end{aligned}$$

An asymptotic expression for the average delay can be evaluated from $P(t)$ (refer to appendix for the calculations):

$$E[T_d] \underset{N\to\infty}{\sim} \frac{1}{\beta}\sqrt{\frac{\pi}{2}}\frac{1}{\sqrt{N-1}}.$$

The average number of copies before the packet is delivered can be evaluated as in Section 3.2.1 and we get:

$$C_{2hop} = \beta N E[T_d] - 1 \underset{N\to\infty}{\sim} \sqrt{\frac{\pi}{2}}\sqrt{N}$$

The same asymptotic expressions were obtained in [3] using a Markov Chain model.

Let $G_{2hop}(N)$ be the number of nodes that ever get infected by a packet. For each packet, the source node copies the packet to every node it meets before it meets the destination. Therefore $G_{2hop}(N)$ equals to the number of nodes the source node meets before meeting the destination. As the inter-meeting times

between pairs of nodes are i.i.d. exponential random variables, the destination node is equally likely to be the i-th node to meet the source node, for $i = 1, ..., N$. Therefore we have $Pr(G_{2hop}(N) = i) = \frac{1}{N}$, for $i = 0, ..., N-1$, and $E[G_{2hop}(N)] = \frac{N-1}{2}$.

With $G_{2hop}(N)$, we can derive the average buffer occupancy using $M/M/\infty$ model. For IMMUNE, the departure rate is β. Figure 3 compares the average delay and queue length under varying number of nodes for 2-hop scheme, showing a good match between the modeling results and simulation results. We also experiment with an ODE model including recovery process, however, it predicts G_{2hop} and average queue length less well.

Notice that with ODE models, one can easily study K-hop scheme where packets can traverse at most K hops to reach the destination.

4.2 Probabilistic Forwarding

Probabilistic forwarding refers to epidemic routing where each node accepts a relay packet with probability p. If $p = 0$, the probabilistic forwarding degenerates to direct source-destination delivery. Varying p in the range $(0, 1)$ allows a trade-off between storage/power consumption and delivery delay. Furthermore, we will see in Section 6.1, when the buffer of a node is constrained, the packet might fail to be copied due to the buffer being full. This situation can be analyzed using probabilistic forwarding with p equal to the probability that the buffer is not full.

We study the delivery delay using the following ODEs:

$$\begin{aligned} \frac{dI}{dt} &= \beta p I(N - I) \\ \frac{dP}{dt} &= \beta I(1 - P) \end{aligned}$$

with $I(0) = 1, P(0) = 0$. Solving this system, we get:

$$\begin{aligned} I(t) &= \frac{N}{1 + (N-1)e^{-p\beta N t}} \\ P(t) &= 1 - (\frac{N}{N - 1 + e^{p\beta N t}})^{1/p} \end{aligned}$$

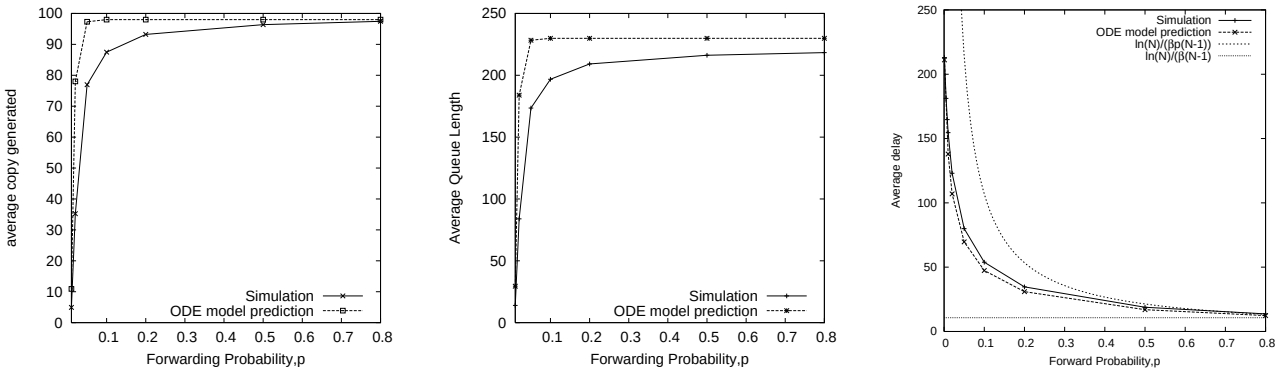
The following bounds hold for the expected delay:

$$\frac{\ln(N)}{\beta(N-1)} \leq E[T_d] \leq \frac{\ln(N)}{\beta p(N-1)}.$$

The average number of copies occurred until the delivery is:

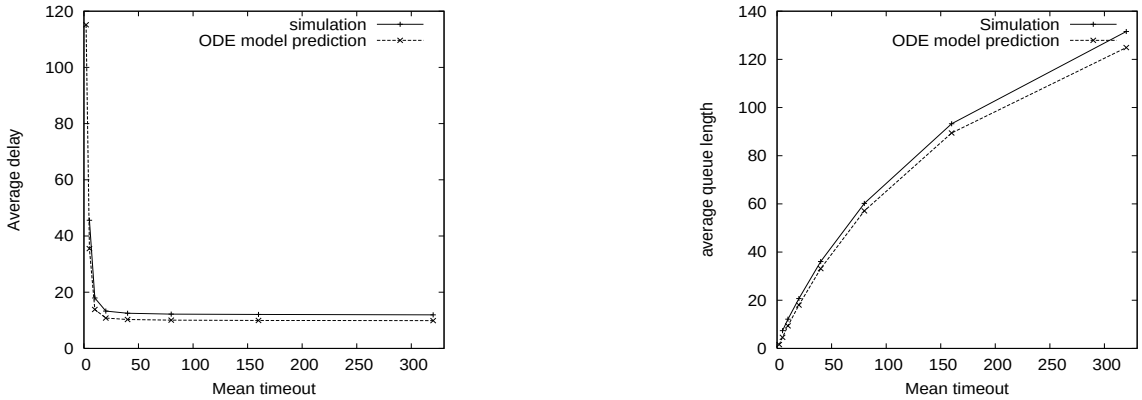
$$C_{prob} = \frac{p(N-1)}{1+p}.$$

Similar to basic epidemic routing case, we have derived ODE model to study G_{prob} and the average buffer occupancy under probabilistic forwarding. Figure 4 plots the average delay, number of copies generated, and the average queue length for probabilistic forwarding, comparing the model prediction with the



(a) Copies transmitted (b) Queue length (c) Average delay

Figure 4: Varying forwarding probability



(a) Average Delay (b) Average Queue

Figure 5: Limited-Time forwarding Model Prediction

simulation result. It shows a worse prediction of the model as $p \to 0$, due to the larger variance (see Section 8.1 in the appendix). In fact as p decreases and approaches 0, the initial infection rate ($p\beta(N-1)$) decreases, while the initial recovery rate remains β. As a result, the average number of infected nodes decreases, leading to larger errors of the continuous first-order ODE models.

4.3 Limited-time Forwarding

We now consider the limited-time forwarding: when a node accepts a copy, it starts a timeout timer. When the timer expires, the copy is deleted from the buffer. The choice of timeout value allows us to trade off the delivery delay against the storage and power each node spends in trying to store and forward a packet. In order to guarantee the delivery of a packet, a node does not time out its source packets. [15] considers a different timeout mechanism, where a global timer is used in order to remove packets from the network.

When a packet copy in a node times out, the node can either store an anti-packet ("packet-seen" information) for the packet, so that it will not be infected by the packet again, or keeps no information, and becomes susceptible to the packet again.

The former scheme can be studied by the following ODE, where $T(t)$ is the number of timed out nodes at time t.

$$\begin{aligned}\frac{dI}{dt} &= \beta I(N-I-T) - \mu(I-1)\\ \frac{dT}{dt} &= \mu(I-1)\\ \frac{dP}{dt} &= \beta I(1-P)\end{aligned}$$

Similar to epidemic routing, the model can be extended to include a recovery process (IMMUNE, IMMUNE_TX, or VACCINE). Figure 5 plots the average delay, and buffer occupancy under different timeout value under IMMUNE recovery. It shows that the model is able to predict the performance of the limited-time forwarding scheme.

For the limited-time forwarding where a node becomes susceptible after it times out a packet, we study the delivery delay using the following model:

$$\begin{aligned}\frac{dI}{dt} &= \beta I(N-I) - \mu(I-1)\\ \frac{dP}{dt} &= \beta I(1-P)\end{aligned}$$

As usual, $I(t)$ is the average number of infected nodes at time t. The ODE can be solved and asymptotic expresssion for the average delay can be found (see Section 8.2 for details):

$$E[T_d] \underset{N\to\infty}{\sim} \frac{1}{\beta}\frac{\ln(N-\frac{\mu}{\beta})}{N-\frac{\mu}{\beta}}, \quad E[T_d] \underset{\mu\to\infty}{\sim} \frac{\mu - N\beta}{\beta\mu}$$

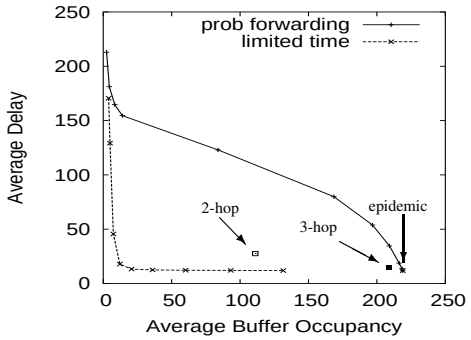
Interestingly the limited-time forwarding can also avoid the need to employ anti-packets and any kind of information at each node. In fact, if $\mu \geq N\beta$ the number of infected nodes goes to zero as $t \to \infty$. The asymptotic delay for $\mu = N\beta$ is equal to $\frac{\pi}{2\beta\sqrt{N-2}}$.

5 Performance Trade-off

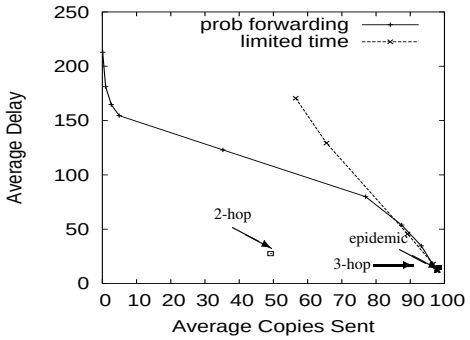
In this section, we employ the models to quantitatively explore the performance trade-off achieved by the different schemes and suggest configuration criteria. The results are mainly based on numerical solution of the previous equations (for $N = 100$, $\beta = 0.00474$, $\lambda = 0.01$), but we also employ asymptotic results for qualitative considerations.

5.1 Performance Trade-off Under IMMUNE

Figure 6 compares the trade-off achieved by different schemes when IMMUNE is employed for recovery. Figure 6.(a) and (b) plots the delay versus queue trade-off (delay/queue curve), delay versus total number of copies sent trade-off (delay/copy curve) respectively. Two curves have been obtained for probabilistic



(a) delay vs buffer occupancy tradeoff



(a) delay vs number of copies sent tradeoff

Figure 6: Comparison with IMMUNE recovery

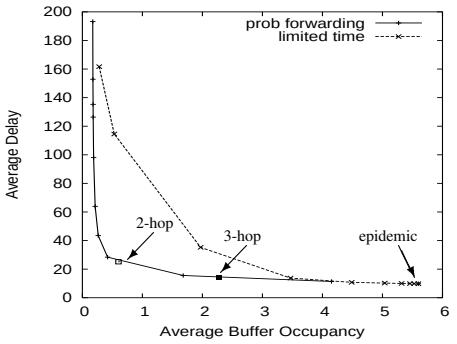
Timeout ($1/\mu$)	Probability (p)
1	0.001
2	0.005
5	0.008
10	0.01
20	0.02
40	0.05
80	0.1
160	0.2
320	0.5
	0.8

Table 2: Settings for Timeout and Probabilistic forwarding

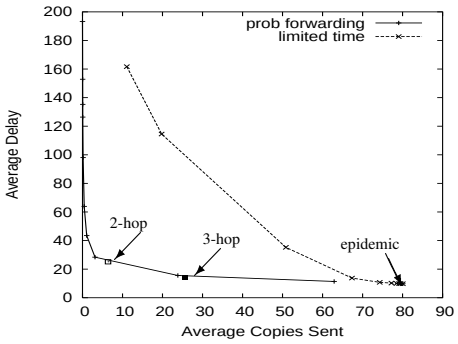
forwarding and limited-time forwarding respectively: each point corresponds to a different value of the probability p and the timeout $1/\mu$ (the values are shown in Table 2). In the figure there are also two points corresponding to the 2-hop and 3-hop forwarding. We could also consider a curve achieved by collecting the performance of the K-hop schemes for $K = 2, 3, 4, ...$ We will refer to this piecewise curve as the K-hop curve, even if in general its points do not correspond to any scheme.

Let us first consider the delay versus queue trade-off. We observe that one can reduce the queue size by decreasing p or $1/\mu$, but at the same time increase the delay. In particular as $p \to 1$ and $1/\mu \to \infty$ the two curves converge to the performance of the original epidemic model, whereas $p \to 0$ and $1/\mu \to 0$ correspond to a no-relaying scenario, where each source node delivers its own packets to the destination (and hence the average delay is $1/\beta$).

Similar considerations hold for delay/copy curve. Note for the probabilistic forwarding and K-hop, the two curves show essentially the same behavior. It follows from the remarks in Section 3.2.2, which show that for these two schemes the number of copies and the queue are mainly proportional. For limited-time forwarding, the delay/copy curve has different behavior than delay/queue curve: as $1/\mu \to 0$, delay/queue curve converges to the point of non-relaying scenario, whereas the number of copies is significantly higher and converges to $N/2$ (which is the average number of nodes the source uselessly infects before meeting the destination).



(a) delay vs buffer occupancy tradeoff



(a) delay vs number of copies sent tradeoff

Figure 7: Comparison with VACCINE recovery

5.2 Performance Improvement by VACCINE

So far, we have compared the trade-off achieved by different schemes under IMMUNE recovery. One might expect similar improvements if VACCINE recovery is deployed. But this is not the case. Figure 7 shows the trade-offs when VACCINE recovery is employed. The figure shows that the performance improvement is more marked for probabilistic forwarding than for limited-time forwarding. This is because limited time forwarding has an intrinsic recovery feature, as a node cannot be reinfected after the timer expires. Therefore, the improvement achieved by VACCINE under limited-time forwarding in buffer occupancy is less significant.

The performance of probabilistic forwarding is improved more by VACCINE than K-hop , even though they have same recovery scheme. To explain this, we can analyze the recovery process which is the outcome of two counteracting processes: the counter-infection due to anti-packets spreading and the ongoing packet infection, hence the net recovery speed depends also on the specific infection process. Let us for example compare probabilistic forwarding and 2-hop forwarding. Figure 8 shows the growth of the number of infected nodes according to the models in Section 4.1 and Section 4.2. The forwarding probability has been chosen so that the two schemes have the same average delay, equal to 25. The vertical line in the figure corresponds to this value. The figure shows that 2-hop forwarding is faster at the beginning of the infection, as at the beginning of the infection it has the same speed as basic epidemic routing with parameter β (This high-speed phase is longer if we consider K-hop schemes with larger K). In contrast, probabilistic forwarding has the same infection speed of the basic epidemic routing with parameter βp. Given that they achieve the same average delay, and $P'(t) = \beta I(t)(1 - P(t))$, the number of infected nodes in the probabilistic forwarding has to overcome at some time the number of infected nodes in the 2-hop scheme. So when the recovery process starts the average number of nodes to be recovered is higher for the probabilistic scheme. Moreover the speed of the ongoing infection after delivery is higher for the probabilistic routing. In conclusion we now expect the recovery process to be "longer" for probabilistic routing leading to a larger queue. Conversely when VACCINE is deployed the recovery process is faster, the queue occupancy is determined mainly by the initial infection process (before the delivery), and the difference becomes much smaller (given that we are comparing two schemes with the same average delay) as it appears from Figure 7.

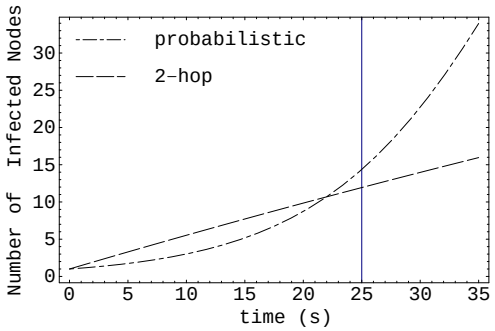


Figure 8: Comparison between 2-Hop and probabilistic forwarding

5.3 Configuration Guidelines

These trade-off figures suggest some criteria to choose and configure the different routing schemes. In particular, time-limited forwarding is a good candidate when the main system constraint is buffer occupancy: in this case for $1/\mu \approx 20$ the delay is near the minimum value but the queue is much smaller than in epidemic routing. By Eq. 3.1, we find the average delay for the epidemic routing to be approximately 10, hence a rule of thumb is to chose $1/\mu \approx 2\ln(N)/(\beta N)$[4]. Note that at this timeout value, limited-time forwarding transmits almost the same number of copies for a packet as the basic epidemic routing, and thus does not provide savings in power consumption.

In order to limit number of copies sent, K-hop schemes can be employed. In the scenario we are considering, the differences in comparison to epidemic routing are significant for $K = 2$. Also in this case we can give some rough indication of the maximum number of hops to be considered in a given scenario. From the expression of the delay for epidemic routing, we can infer that the average number of hops needed to delivery the packet to the destination is about $\ln N$, hence we expect that in general one does not needs to consider $K > \ln N$ in choosing the maximum hop-count in K-hop schemes.

Finally if power consumption is the main consideration, probabilistic forwarding allows one to reach significant gain in comparison to the no relaying case. For example for $p = 0.008$ the decrease of the delay is about 30% and the average number of copies is 3.5. Another advantage of probabilistic forwarding in comparison to K-hop forwarding is that the probability can be tuned continuously.

6 Epidemic Routing under Constrained Buffer

Up to now, we have studied the performance achieved by different relaying schemes under the assumption that each node has sufficient capacity to store all of the packets. This is not a realistic assumption for mobile nodes. One can think about sizing the buffer larger enough to limit the losses, but selecting the right buffer size is hard. For example previous work [5] studied the variability of the buffer occupancy for the purpose of buffer sizing, but their model requires an empirical distribution obtained from simulation.

In this section, we examine the performance of three buffer management strategies: droptail, drophead

[4] As regards the delivery time, it can be proved that the ratio of its standard deviation and its mean goes to zero as N diverges (see Section 8.4), hence good performance are expected also for a higher number of nodes and $1/\mu$ can be even chosen smaller.

and source prioritized drophead under IMMUNE recovery . We observe that with source prioritized drophead, epidemic routing achieves almost the same performance as with an infinite buffer, using a per node buffer far smaller than the average buffer occupancy under infinite buffer. Furthermore, the performance of this scheme smoothly degrades toward that of a non-epidemic scenario as the node buffer decreases. Hence our results mainly show that limiting losses is not necessarily a main requirement, and that significant improvements in the buffer size can be achieved by deleting older copies.

From the modeling point of view, we couple the forwarding models with models of the queue (Markovian or fluid). The coupling involves some common parameters, so that in general a fixed point problem has to be solved.

6.1 droptail

Under droptail, when the buffer of a node is full, the node will not accept any packet. If the probability that the buffer of a node is full is P_d, then with probability P_d, a source packet generated at a node finds a full buffer and is lost; otherwise, it is stored at the source node until delivered. Therefore the loss probability under droptail is given by P_d.

To estimate P_d, we model the buffer at a node as an $M/M/B/B$ queue, where B denotes the buffer size. The service rate is β, the rate that the node meets the destination. The arrival rate is the sum of the source packet rate, λ, and the relay packet rate. The total rate of relay packets is $(N-1)\lambda(1-P_d)$, as there are $N-1$ relay flows each of rate λ, with each packet being lost at the source with probability P_d. We find P_d by solving a fixed point problem: given arrival rate of $\lambda(1+(N-1)(1-P_d))$, and service rate of β, the loss probability P_d can be calculated by Erlang's loss formula.

We use the probabilistic forwarding ODE model with forwarding probability $1-P_d$ to evaluate the delivery delay.

6.2 drophead

For drophead, when a node receives a new packet (source or relay) and its buffer is full, it pushes the oldest packet out from the buffer, and the node does not accept the pushed-out packet in the future. Let G_{dh} be the number of times a packet is copied in the system, and $\overline{G}_{dh}$ be its expected value. As the average packet arrival rate to a node is given by $(\overline{G}_{dh}+1)\lambda$, the packets in the buffer is pushed to the head of the buffer with this rate.

We use the following ODE to study the spreading of a packet. Let $S(t)$ denote the average number of susceptible nodes, $I_i(t)$ denote the average number of infected nodes where the copy of the packet is the i-th newest packet. $D(t)$ is the average number of nodes that have deleted the packet (and would not accept the packet in the future) at time t. The following equations can be used to model the infection spreading process.

$$\frac{dS}{dt} = -\beta S \sum_{1\le i\le B} I_i$$

$$
\begin{aligned}
\frac{dI_1}{dt} &= \beta S \sum_{1\le i\le B} I_i - (\overline{G}_{dh}+1)\lambda I_1 \\
\frac{dI_j}{dt} &= (\overline{G}_{dh}+1)\lambda(I_{j-1}-I_j), 2\le j\le B \\
\frac{dD}{dt} &= (\overline{G}_{dh}+1)\lambda I_B \\
\frac{dP}{dt} &= \beta \sum_{1\le i\le B} I_i(1-P)
\end{aligned}
$$

The initial conditions are: $S(0)=N-1, I_1(0)=1, I_j(0)=0$, for $j=2,...B$, $D(0)=0, P(0)=0$.

If all copies of a packet are pushed out of the buffers before its delivery to the destination, the packet is lost. We estimate the loss probability as $\lim_{t\to\infty} P(t)$.

We find $\overline{G}_{dh}$ by solving a fixed point problem: given $\overline{G}_{dh}$, we numerical solve the full ODE model (obtained by adding recovery process to the above ODEs) and calculate the amount of flow from state S to I_1, i.e. $S(0)-S(\infty)=\overline{G}_{dh}$. We perform a binary search algorithm to find the fixed point $\overline{G}_{dh}$.

6.3 drophead high priority for source packet

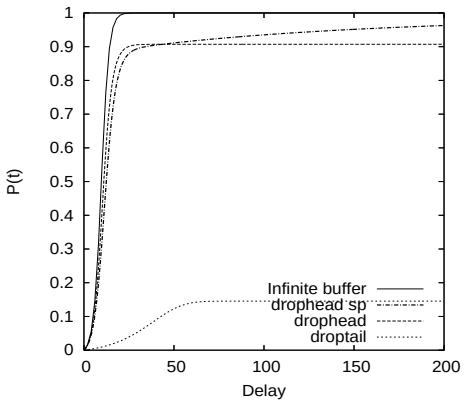
Finally, we consider the drophead_sp scheme, i.e., drophead with high priority for source packet. Under this scheme, if a source packet arrives to a node with a full buffer, the node will first try to drop oldest relay packets, then the oldest source packets. If a relay packet arrives to a full buffer, the node finds the oldest relay packets and delete it from the buffer; if all packets in the buffer are source packets, the relay packet is not accepted.

We first calculate P_f, the probability that a node's buffer is filled with its own source packets. Source packets arrive to a node with rate λ, and when the node encounters the destination of these packets (with rate β), all of them are delivered and deleted from the buffer. We use a Markov chain to model the number of source packets in the buffer, and calculate the stationary distribution p_i (probability that there are i source packets in the buffer), and get:

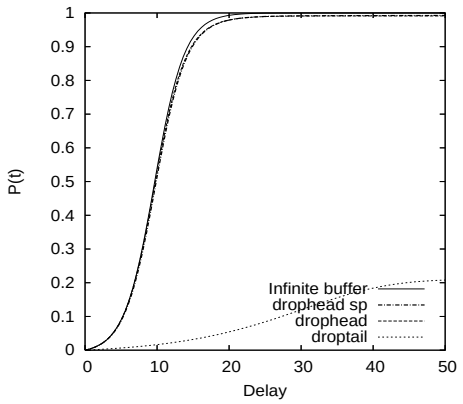
$$
P_f = p_B = \frac{\frac{\lambda}{\beta}(\frac{\lambda}{\lambda+\beta})^{B-1}}{1+\frac{\lambda}{\beta}-(\frac{\lambda}{\lambda+\beta})^{B-1}}.
$$

Given P_f, the effective infection rate is $\beta(1-P_f)$. The following ODE is used to study the delivery delay, here $I_j^s(t)$ denotes the probability of source node's copy of the packet is the j-th newest source packet in the buffer.

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta(1-P_f)S \sum_{1\le i\le B} (I_i^s + I_i) \\
\frac{dI_1}{dt} &= \beta(1-P_f)S \sum_{1\le i\le B} (I_i^s + I_i) - (\overline{G}_{dhs}+1)\lambda I_1
\end{aligned}
$$



(a) $B = 5$



(b) $B = 10$

Figure 9: $P(t)$ under $B = 5, 10$

$$
\begin{aligned}
\frac{dI_j}{dt} &= (\overline{G}_{dhs} + 1)\lambda(I_{j-1} - I_j), \quad 2 \leq j \leq B \\
\frac{dI_1^s}{dt} &= -\lambda I_1^s \\
\frac{dI_j^s}{dt} &= \lambda(I_{j-1}^s - I_j^s), \quad 2 \leq j \leq B \\
\frac{dD}{dt} &= (\overline{G}_{dhs} + 1)\lambda I_B + \lambda I_B^s \\
\frac{dP}{dt} &= \beta \sum_{1 \leq i \leq B} (I_i^s + I_i)(1 - P)
\end{aligned}
$$

The initial conditions are given by: $S(0) = N - 1$, $I_j(0) = 0$, for $j = 1, ..., K$, $I_1^s = 1$, $I_i^s = 0$, for $i = 2, ...B$, $D(0) = 0$, $P(0) = 0$.

Similar to drophead, we find $\overline{G}_{dhs}$ by solving a fixed point problem using the extended ODEs (taking into consideration the recovery).

6.4 Comparisons of different schemes

We have simulated these dropping schemes considering IMMUNE recovery, using the usual setting of $N = 100, \lambda = 0.01$. The meeting rate is, as before, $\beta = 0.0047$. We varied the buffer size: $B = 5, 10, 20$. Figures 9 plot the delay distributions predicted for $B = 5, 10$, in the range $[0, 200]$ and $[0, 50]$ respectively so that the difference between schemes can be seen. Table 3 tabulates the loss probabilities for varing buffer size. We observe that the ODE models provide good predictions on the loss probabilities. A closer comparasion of the $P(t)$ against the delay distribution obtained from simulation shows that ODE model correctly characterizes the different performance achieved by different dropping schemes.

Figures 9 show that a naive droptail scheme performs badly. Drophead allows fast infection, as relay packets are always accepted by a node. On the other hand, significant packet losses start to occurr for $B \leq 10$. With drophead_sp, the infection process is slower than the drophead scheme, for when a node has B source packets in its buffer, it does not accept relay packets. On the other hand, it allows more packets to

Buffer size	sim/model	droptail	drophead	drophead_sp
5	simulation	0.9696	0.2234	0.0536
	model	0.8544	0.0928	0.0079
10	simulation	0.9471	0.0315	0.0
	model	0.7891	0.0088	0.0
20	simulation	0.899	0.0016	0.0
	model	0.7011	0.0	0.0

Table 3: Loss Probability under different buffer sizes

be delivered. If the flow rate is so high that the buffer can only hold its own source packets, then no relaying takes place, and drophead_sp degenerates to source-destination transmission scheme.

Observe that under infinite buffer assumption, the average buffer occupancy for this setting is over 200 (see Figure 2.(b). in Section 3.2.2). Here we show that we can achieve same performance with a much smaller buffer, $B = 20$, using drophead and drophead_sp.

One can imagine a scheme that combines drophead_sp with VACCINE or IMMUNE_TX should perform even better, as VACCINE allows the source packet to be deleted from the buffer much faster, leading to higher infection process.

7 Summary

In this paper, we proposed a unified framework based on ODEs to study the performance of basic epidemic routing and its variations. Using these models, we obtained a rich set of quantitative results regarding the packet-delivery delay, number of copies sent, and buffer requirements (and the tradeoffs among these performance metrics) under various epidemic routing schemes. We further considered the buffer-constrained case, and showed that with appropriate buffer management schemes, a much smaller buffer can be used with negligible effect on delivery performance. In the future, we plan to study the overhead of storing and transmitting anti-packets, and investigate schemes for deleting anti-packets. We are also interested in the performance of these schemes when bandwidth is constrained.

8 Appendix

8.1 Derivation of ODEs from Markov Chain

In this section, we show how the mean field approximation ODE model can be derived from Markov Chain model by ignoring variability. A way to deal with variability involves the derivation of differential equations for the higher moments [20]. For a nonlinear system such as ours, this set of equations is not closed, as the equations for the lower order moments involve higher order moments. The moment closure technique [12] can be applied to truncate this system of equations at certain order.

We consider the generic epidemic routing with a pair-wise infection rate of β, and per-node recovery rate of γ. Under the basic epidemic routing, we have $\beta = \gamma$; for probabilistic forwarding, we have $\gamma = p\beta$.

A bivariate Markov chain as illustrated in Figure 10 can be used to model the infection and the IMMUNE recovery process, with state $(S(t), I(t))$ denotes a state where there are $S(t)$ susceptible nodes, and $I(t)$ infected nodes at time t, given that $S(0) = N - 1, I(0) = 1$.

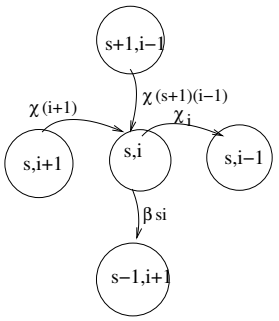


Figure 10: Markov Chain for epidemic routing

Define the state probabilities: $P_{s,i}(t) = Pr\{S(t) = s, I(t) = i | S(0) = N - 1, I(0) = 1\}$. The Kolmogorov forward equation for the process is :

$$\begin{aligned} \frac{dP_{s,i}(t)}{dt} &= -P_{s,i}(t)(\gamma i + \beta si) + P_{s,i+1}(t)\gamma(i+1) \\ & \quad P_{s+1,i-1}(t)\beta(s+1)(i-1) \end{aligned}$$

Multiplying the above equation with $e^{\theta_1 s + \theta_2 i}$, and summing over all possible s, i, we get:

$$\frac{\partial M}{\partial t} = \gamma(e^{-\theta 2} - 1)\frac{\partial M}{\partial \theta_2} + \beta(e^{\theta_2 - \theta_1} - 1)\frac{\partial^2 M}{\partial \theta_1 \partial \theta_2},$$

where $M(\theta_1, \theta_2, t) = E[e^{\theta_1 s + \theta_2 i}]$ is the *moment generating function*.

We define the *cumulant generating function*, $K(\theta_1, \theta_2, t) := \log M(\theta_1, \theta_2, t)$, and observe that the following equations hold:

$$\begin{aligned} \frac{\partial K}{\partial t} &= \frac{1}{M}\frac{\partial M}{\partial t} \\ \frac{\partial K}{\partial \theta_1} &= \frac{1}{M}\frac{\partial M}{\partial \theta_1} \\ \frac{\partial^2 K}{\partial \theta_1 \partial \theta_2} &= -\frac{\partial K}{\partial \theta_1}\frac{\partial K}{\partial \theta_2} + \frac{1}{M}\frac{\partial^2 M}{\partial \theta_1 \partial \theta_2} \end{aligned}$$

Substitute these equations into Equation (14), we get:

$$\frac{\partial K}{\partial t} = \gamma(e_2^{\theta} - 1)\frac{\partial K}{\partial \theta_2} + \beta(e^{\theta_2 - \theta_1} - 1)\left(\frac{\partial^2 K}{\partial \theta_1 \partial \theta_2} + \frac{\partial K}{\partial \theta_1}\frac{\partial K}{\partial \theta_2}\right) \tag{14}$$

By taking partial derivatives of θ_1 and θ_2 respectively on this equation and setting $\theta_1 = \theta_2 = 0$, we can get the following ODE system.

$$\frac{d\bar{S}}{dt} = -\beta(\bar{I}\bar{S} + C_{IS})$$

$$\frac{d\bar{I}}{dt} = -\gamma\bar{I} + \beta(\bar{I}\bar{S} + C_{IS})$$

If we ignore covariance of $I(t)$ and $S(t)$, and set $C_{IS} = 0$, we get:

$$\frac{d\bar{S}}{dt} = -\beta\bar{I}\bar{S} \tag{15}$$

$$\frac{d\bar{I}}{dt} = -\gamma\bar{I} + \beta\bar{I}\bar{S} \tag{16}$$

$$\tag{17}$$

This is exactly the first-order ODE we've been used.

We could derive ODEs for second-order moments by taking second order partial derivatives of θ_1 and θ_2 respectively on this equation and setting $\theta_1 = \theta_2 = 0$:

$$\begin{aligned}
\frac{dV_S}{dt} &= \beta(\bar{I}\bar{S} + C_{IS}) - 2\beta(T_{SSI} + V_S\bar{I} + \bar{S}C_{IS}) \\
\frac{dV_I}{dt} &= \gamma\bar{I} - 2\gamma V_I + \beta(C_{IS} + \bar{I}\bar{S}) + 2\beta(T_{SII} + C_{IS}\bar{I} + \bar{S}V_I) \\
\frac{dC_{IS}}{dt} &= -\gamma C_{IS} - \beta(C_{IS} + \bar{I}\bar{S}) - \beta T_{SII} - \beta C_{IS}\bar{I} - \beta\bar{S}V_I + \beta T_{SSI} + \beta V_S\bar{I} + \beta\bar{S}C_{IS}
\end{aligned}$$

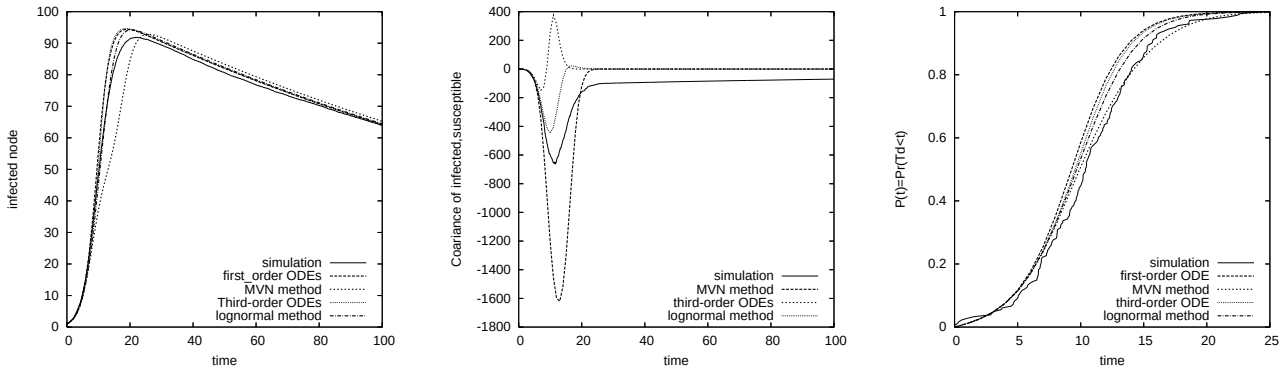
where $\bar{S}(t) = E[S(t)], \bar{I}(t) = E[I(t)], V_s(t) = Var(S(t)), V_I(t) = Var(I(t)), C_{IS}(t) = Cov(S(t), I(t))$, and T_{SII}, T_{SSI} are the third central moments: $T_{SII} = E[(S - ES)(I - EI)^2], T_{SSI} = E[(S - ES)^2(I - EI)]$.

One could keep on this procedure to derive ODEs for the third and higher moments, but eventually a moment closure technique is needed to truncate the equations at certain order. We experiment with three different methods [7, 13, 12].

- MVN (Multi-Variate Normal) method: setting third central moments to zero. This is equivalent to assuming a multi-variate normal distribution of the state variables $(S(t), I(t))$.
- Lognormal method: if we assume a lognormal distribution for the state variables, then the third moments can be expressed in terms of the lower moments
- third-order moment: truncate the equations by setting fourth-order moments to zero.

In order to compare the performance of these different methods, we simulate probabilistic forwarding for forwarding probability in the range between 0.001 to 1.0, with a total number of $N + 1 = 101$ nodes, and compare the model predictions with the simulation results.

For the basic epidemic routing, i.e., $P = 1.0, \gamma = \beta$ case, Figure 11 plots the average infected node number, the covariance of infected node number of susceptible node, and the CDF of delay, comparing simulation results with the prediction of different moment equations. We observe that third-order ODEs gives similar result as first-order ODEs, with slight improved match with simulation results. Like first and third order ODEs, lognormal equations under estimates the covariance, and therefore over predicts the infection spreading process, and under predicts the delivery delay. On the other hand, MVN method over



(a) $I(t)$ (b) $COV(I(t), S(t))$ (c) $P(t)$

Figure 11: Comparison of different moment equations for the case $p = 1.0$

estimates the covariance, and under estimates the spread of the infection. For this case, MVN method performs best in prediction of delivery delay as shown also in the Figure 1 in Section 3.

However, MVN method has a drawback. For P in the range $[0.01, 0.3]$, the MVN ODEs have no stable equilibrium, i.e., the solution diverges. [12] observed this drawback of MVN method (under a different model), and attributed it to the large variability under the scenario considered.

8.2 Delay Asymptotic Results

Here we are going to derive the different bounds and asymptotic values we presented in the paper. For each of the forwarding schemes we have been considering, closed-form expressions can be derived for the number of infected nodes $I(t)$ and for the cumulative distribution $P(t) = Pr(T_d < t) = 1 - Q(t)$. The expected delay can be evaluated as $E[T_d] = \int_0^\infty Q(t)dt$, so we are going to show how this integral can be approximated in the different cases.

- 2-hop forwarding without timeout (Section 4.1)

  The expected delay is equal to:

$$E[T_d] = \frac{1}{\beta}\int_0^\infty e^{-t}e^{(N-1)(1-t-e^{-t})}dt$$

  $e^{(N-1)(1-t-e^{-t})}$ has a single maximum for $t = 0$, hence according to the saddle point approximation when $N \to \infty$ we can consider:

$$e^{-t}e^{(N-1)(1-t-e^{-t})} \approx e^{-0}e^{-(N-1)t^2/2}$$

  hence

$$E[T_d] \approx \frac{1}{\beta}\int_0^\infty e^{-(N-1)t^2/2}dt = \frac{1}{\beta}\sqrt{\frac{\pi}{2}}\frac{1}{\sqrt{N-1}}$$

- Probabilistic routing (Section 4.3). In this case

$$Q(t) = \left(\frac{N}{e^{N\beta pt} + N - 1} \right)^{\frac{1}{p}}.$$

This expression can be easily bounded:

$$\frac{N}{e^{N\beta t} + N - 1} \leq Q(t) \leq \frac{N}{e^{N\beta pt} + N - 1}.$$

Note that these bounds correspond to compare the probabilistic forwarding with epidemic routing with inter-meeting rates equal to β and βp: probabilistic forwarding is slower than the first one, but faster than the second one.

If we integrate the previous inequality, we get:

$$\frac{\ln(N)}{\beta(N-1)} \leq E[T_d] \leq \frac{\ln(N)}{\beta p(N-1)}$$

- Timeout scheme (Section 4.3) In this case:

$$Q(t) = \frac{(a_2 - a_1)e^{-a_1\beta t}}{(a_2 - 1) + (1 - a1)e^{(a2-a1)\beta t}},$$

where a_2 and a_1 are respectively the positive and the negative solution of the equation $\beta I(N - I) - \mu(I - 1) = 0$ (to be solved for I), obtained by imposing $\frac{dI}{dt} = 0$.

We consider three different asymptotic values: for $N \to \infty$, for $\mu \to \infty$ and for $N = \frac{\mu}{\beta} \to \infty$.

As regards the first bound, we proceeded in the following way: we considered a function $Q_{a,N}(t) > 0$ which approximates $Q_N(t)$ (we have stressed the dependence from N), and for which we can closely evaluate $\int_0^\infty Q_{a,N}(t)dt$. This is an asymptotic value for the expected delay if:

$$\lim_{N\to\infty} \frac{\int_0^\infty Q_N(t)dt - \int_0^\infty Q_{a,N}(t)dt}{\int_0^\infty Q_{a,N}(t)dt} \to 0$$

In order to prove it, we proved that $\frac{Q_N(t) - Q_{a,N}(t)}{Q_{a,N}(t)}$ converges uniformly to zero as N diverges:

$$\frac{Q_N(t) - Q_{a,N}(t)}{Q_{a,N}(t)} \xrightarrow[N,\infty]{u} 0.$$

In fact in this case for all $\epsilon > 0$, $\exists\, n_\epsilon$ such that

$$\frac{|Q_N(t) - Q_{a,N}(t)|}{|Q_{a,N}(t)|} < \epsilon$$

hence:

$$\frac{|\int_0^\infty Q_N(t) - Q_{a,N}(t)dt|}{|\int_0^\infty Q_{a,N}(t)|} \leq \epsilon.$$

The asymptotical behavior of a_2 and a_1 as $N \to \infty$ ($\lim_{N\to\infty} a_2 = +\infty$, $\lim_{N\to\infty} a_1 = 0$) suggests to consider:

$$Q_{a,N}(t) = \frac{a_2 - a_1}{(a_2 - 1) + (1 - a_1)e^{a_2\beta t}}$$

which can be easily integrated.

$$\left|\frac{Q_N(t) - Q_{a,N}(t)}{Q_{a,N}(t)}\right| = \frac{(1 - e^{a_1\beta t})}{e^{a_1\beta t} + \frac{(1-a_1)}{a_2-1}e^{a_2\beta t}} \leq \frac{(1 - e^{a_1\beta t})}{\frac{(1-a_1)}{a_2-1}e^{a_2\beta t}}$$

We can easily evaluate the maximum of the right expression, and we get:

$$\left|\frac{Q(t)_N - Q_{a,N}(t)}{Q_{a,N}(t)}\right| \leq \frac{-a_1(a_2 - 1)}{(1 - a_1)(a_2 - a_1)} \left(\frac{a_2}{a_2 - a_1}\right)^{-\frac{a_2}{a_1}}$$

The maximum converges to 0 when N diverges, hence the convergence is uniform.

The asymptotic value is:

$$\int_0^\infty Q_{a,N}(t)dt = 1/\beta \frac{a_2 - a_1}{(a_2 - 1)a_2} \ln\left(\frac{a2 - a1}{1 - a_1}\right)$$

which behaves asymptotically as:

$$\frac{1}{\beta}\frac{\ln(N - \frac{\mu}{\beta})}{N - \frac{\mu}{\beta}}$$

In the same way we have found the second bound as $\mu \to \infty$. In this case $\lim_{\mu\to\infty} a_2 = 1$, $\lim_{\mu\to\infty} a_1 = -\infty$, and we consider

$$Q_{a,\mu}(t) = e^{-a_2\beta t}.$$

$$\left|\frac{Q_N(t) - Q_{a,N}(t)}{Q_{a,N}(t)}\right| = \frac{1}{\frac{a_2-a_1}{(a_2-1)(1-e^{-(a2-a1)\beta t})} - 1}$$

The supremum is achieved for $t \to \infty$ and is equal to:

$$\frac{a_2 - 1}{1 - a_1}$$

which converges to 0 as μ diverges.

The asymptotic value is:

$$\int_0^\infty Q_{a,\mu}(t)dt = \frac{1}{\beta a_2} \underset{\mu\to\infty}{\sim} \frac{\mu - N\beta}{\beta\mu}$$

Finally, as regards the third bound, a closed form can be found for $E[T_d]$, considering $N = \mu/\beta$:

$$E[T_d] = \frac{2\,\mathrm{arccot}\sqrt{\frac{\sqrt{N-1}+1}{\sqrt{N-1}-1}}}{\beta\sqrt{N-2}},$$

and

$$E[T_d] \underset{N\to\infty}{\sim} \frac{\pi}{2\beta\sqrt{N-2}}.$$

8.3 Number of Copies

In this section we show how the results about the average number of copies occurred until the delivery (C_d) can be derived.

First note that for the all the considered schemes, except the timeout one, the number of copies (excluding the copy to the destination) coincides with the average number of infected node in the system when the packet is delivered minus one. Hence:

$$C_d = \int_0^\infty I(t)P'(t)dt - 1,$$

where $I(t)$ is the number of infected nodes at time t, given that the packet has not been delivered at time t.

The following two different expressions can be derived (respectively replacing $P'(t)$ and integrating by parts):

$$\int_0^\infty I(t)P'(t)dt = \beta \int_0^\infty I^2(t)Q(t)dt \quad (18)$$

$$= \int_0^\infty I'(t)Q(t)dt + 1 \quad (19)$$

By replacing $I'(t)$ according to the equation of the specific schemes and considering that $\int_0^\infty \beta I(t)Q(t)dt = P(\infty) - P(0) = 1$, we can get the following results, respectively for epidemic routing, 2-hop and probabilistic routing.

$$C_{ep,d} = \frac{N-1}{2} \quad (20)$$

$$C_{2hop,d} = \beta N E[T_d] - 1 \underset{N\to\infty}{\sim} \sqrt{\frac{\pi}{2}}\sqrt{N} \quad (21)$$

$$C_{prob,d} = \frac{p(N-1)}{1+p} \quad (22)$$

8.4 Variance of the delivery time

In this section we show that, for the basic epidemic routing, the delivery time converges to a constant as N diverges, namely that the ratio of its standard deviation and its mean goes to zero.

Let us evaluate the second moment of the delivery time, it holds:

$$E[T_d^2] = \int_0^\infty t^2 P'(t)dt = \int_0^\infty 2tQ(t)dt = -\frac{2\,\mathrm{Li}_2(1-N)}{N(N-1)},$$

where Li_2 is the dilogarithm function [19] and we considered $\beta = 1$ without loss of generality.

From the asymptotic formulae in [21]:

$$\mathrm{Li}_2(1-N) \underset{N\to\infty}{\sim} -\frac{(\ln(N-1))^2}{2}.$$

It follows that:

$$\lim_{N\to\infty} \frac{E[T_d^2]}{E[T_d]^2} = 1,$$

and hence:

$$\lim_{N\to\infty} \frac{Var\{T_d\}}{E[T_d]^2} = 0.$$

References

[1] C. Bettstetter. Mobility modeling in wireless networks: categorization, smooth movement, and border effects. In *ACM SIGMOBILE Mobile Computing and Communications Review*, volume 5, Issue 3, July, 2001.

[2] D.J. Daley and J. Gani. *Epidemic Modelling*. Cambridge University Press, 1999.

[3] R. Groenevelt, P. Nain, and G. Koole. The message delay in mobile ad hoc networks. In *Performance*, October 2005.

[4] R. Gurin. Channel occupancy time distribution in a cellular radio system. In *IEEE Transactions on Vehicular Technology*, volume Vol. vt-36, No. 3, pp. 89-99, August 1987.

[5] Z. J. Haas and T. Small. A new networking model for biological applications of ad hoc sensor networks. To appear in IEEE/ACM Transactions on Networking.

[6] P. Juang, H. Oki, Y. Wang, M. Martonosi, L.-S. Peh, and D. Rubenstein. Energy-efficient computing for wildlife tracking: Design tradeoffs and early experiences with zebranet. In *ASPLOS-X*, 2002.

[7] Matt J. Keeling. Multiplicative moments and measures of persistence in ecology. *Journal of Theoretical Biology*, 205, 2000.

[8] W.O. Kermack and A.G. McKendrick. A contribution to the mathematical theory of epidemics. In *Proc. Royal Society of London*, volume A 115, 700-721.

[9] A. Khelil, C. Becker, J. Tian, and K. Rothermel. An epidemic model for information diffusion in manets. In *Proceedings of MSWiM (the International Workshop on Modeling, Analysis and Simulation of Wireless and Mobile Systems)*, 2002.

[10] T. G. Kurtz. Solutions of ordinary differential equations as limits of pure jump markov processes. *Journal of Applied Probabilities*, pages 49–58, 1970.

[11] A. Lindgren, A. Doria, and O. Schelen. Probabilistic routing in intermittently connected networks. In *ACM Mobicom (poster session)*, 2003.

[12] A. L. Lloyd. Estimating variablity in models for recurrent epidemics: assessing the use of moment closure techniques. *Theoretical Population Biology*, 2004.

[13] Ingemar Nåsell. An extension of the moment closure method. *Theoretical Population Biology*, 64:233–239, 2003.

[14] G. Sharma and R. R. Mazumdar. Delay and capacity tradeoffs for wireless ad hoc networks with random mobility. Submitted for publication.

[15] T. Small and Z. J. Haas. The shared wireless infostation model - a new ad hoc networking paradigm. In *Mobihoc*, 2003.

[16] T. Small and Z. J. Haas. Resource and performance tradeoffs in delay-tolerant wireless networks. In *ACM workshop on Delay Tolerant Networking*, 2005.

[17] T. Spyropoulos, K. Psounis, and C. S. Raghavendra. Spray and wait: an efficient routing scheme for intermittently connected mobile networks. In *ACM workshop on Delay-tolerant networking*, 2005.

[18] A. Vahdat and D. Becker. Epidemic routing for partially connected ad hoc networks. Technical Report CS-200006, Duke University, April 2000.

[19] Eric W. Weisstein. Dilogarithm. From MathWorld – A Wolfram Web Resource. http://mathworld.wolfram.com/Dilogarithm.html.

[20] P. Whittle. On the use of normal approximation in the treatment of stochastic processes. *J.R. Stat. Soc. B*, 19:268–281, 1957.

[21] David Wood. The computation of polylogarithms. Technical Report 15-92*, University of Kent, Computing Laboratory, Canterbury, UK, June 1992.