

Modeling Hop Length Distributions for Reactive Routing Protocols in One Dimensional MANETs

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Abstract— In mobile ad hoc networks (MANETs), packets hop from a source to a series of forwarding nodes until they reach the desired destination. Defining the *hop length* to be the distance between two adjacent forwarding nodes, we observe that the two adjacent forwarding nodes tend to be farther away from each other with a higher probability in a one-dimensional MANET. We derive the probability density functions for the hop lengths to confirm our observation. Applying the developed results, we further formulate the relationship between the mean number of hops and the distance between the source and the destination.

I. INTRODUCTION

Wireless mobile ad hoc networks (MANETs) provide solutions for rapid deployment in areas where infrastructure networks do not exist. MANETs are generally formed by a collection of wireless communications devices commonly known as *nodes*. The packet delivery in a MANET relies on relaying of packets from a source to a series of forwarding nodes until they reach the desired destination. We first define *hop length* to be the distance between two adjacent forwarding nodes, our aim of this paper is to study the characteristics of these hop lengths in a one-dimensional (1-D) MANET implementing a popular reactive routing protocols, such as Dynamic Source Routing (DSR) [1] or Ad-hoc On Demand Distance Vector (AODV) [2].

Our considered 1-D MANET is shown in Fig. 1. This type of networks has been intensively studied recently [3]–[14] with potential applications such as a vehicular network on a freeway, sensor networks deployed along a river, and others. In our considered MANET, the source and the destination is separated by a fixed distance d along a path. Within them, n additional nodes are placed. We consider a uniform placement of nodes.

In the past, we have studied the network connectivity of such a network [6], [7]. It was found that a massive number of nodes is required to achieve a high physical network connectivity. However, having a physical network connectivity, how will a packet travel in such a 1-D MANET with nodes massively deployed within it? To answer this, in this paper, we analyze the hop length distribution and the mean number of hops that a packet travels from the source to the destination for our considered 1-D MANETs. Interestingly, we found that the hop length distribution is not uniformly distributed, instead, two

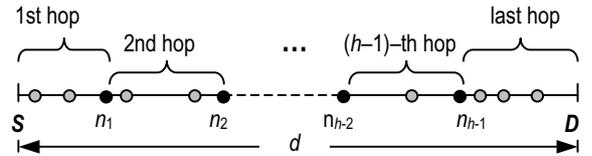


Fig. 1. One dimensional MANET.

adjacent forwarding nodes tend to be farther away from each other with a higher probability.

The paper is organized as follows. Section II briefly describes the route discovery process and reports the observation on the hop lengths. Section III presents the analysis of the hop length distributions. Section IV studies the average number of hops given a certain distance separating the source and the destination. Some important conclusions of this work are drawn in Section V.

II. ROUTE DISCOVERY PROCESS

We consider the 1-D MANET depicted in Fig. 1 with a massive node deployment that leads to a high physical connectivity probability. All nodes are uniformly distributed between the source and the destination. The network implements a certain reactive routing protocol.

In a reactive routing protocol, a source may not have the knowledge of the location of a destination, it must employ a certain mechanism to gather necessary information so as to establish a route to the destination. Broadcasting of Route Request message (RREQ) to the network is a commonly used mechanism for requesting such route information in many popular reactive routing protocols such as DSR or AODV. In this broadcasting procedure, the source first broadcasts a RREQ to its neighboring nodes. All its neighboring nodes will take turn to forward the RREQ if the destination is not within the radio range of the source. Considering the popular IEEE 802.11 protocol implementation for the network, all the neighboring nodes will have an equal probability to gain the access to the wireless channel and forward the RREQ. This RREQ forwarding allows the propagation of RREQ in the network. To prevent massive redundant forwarding of RREQ during its propagation, RREQ detected by a node is strictly

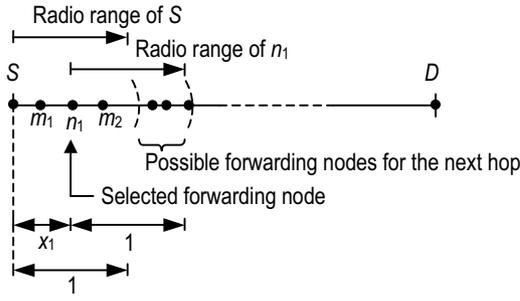


Fig. 2. Illustration of RREQ forwarding node selection.

forwarded once. Duplicate RREQ will be ignored as like it was not detected.

The forwarding of RREQ is repeated until it reaches the destination. A Route Reply message (RREP) will be returned in the reverse direction of the path that the RREQ traveled from the source. After the return of the RREP, all nodes that participate in that particular RREQ forwarding will be used as the forwarding nodes for the future packet delivery. It is common that the destination receives several RREQ messages, the reaction of the destination depends on routing protocols. For example, in AODV, the destination replies only to the first arriving RREQ which automatically favors the least congested route [15]. Whereas, in DSR, all received RREQ messages will be replied by the destination and the source chooses the shortest route [15]. Detailed descriptions of the route discovery process can be found in [1], [2], [15].

Observation from this RREQ broadcasting mechanism in reactive routing protocols has led to an interesting finding. We discovered that the next forwarding node tends to be farther away from the current forwarding node. In the following, we shall use an example depicted in Fig. 2 to explain this side effect of the broadcasting mechanism.

Considering node S as the source which broadcasts the first RREQ, this RREQ will reach the three nodes located within its radio range. We assume that n_1 gained the channel access right earlier than others and forwarded the RREQ. Two possible events may occur within the radio range of S : (i) If m_1 forwards its RREQ after n_1 , since all nodes have already detected the RREQ either from S or n_1 , none of the nodes will forward the duplicate RREQ for m_1 . Consequently, route request from m_1 fails, and m_1 can never become the next hop of S in this case. In fact, m_1 can be located at any location between S and n_1 ; (ii) if m_2 forwards its RREQ after n_1 , since from S , m_2 is located farther away compared to n_1 , thus m_2 may still find some of its neighboring nodes which may not have detected the RREQ from n_1 . They may forward the RREQ with a chance to form a path. Thus, m_2 remains as a potential candidate for the next forwarding node of S . Evaluating the two cases given above, we conclude that if a node has forwarded the RREQ for the current forwarding node, all nodes located between the two adjacent forwarding nodes will be excluded from becoming the next forwarding node if they have not performed their RREQ forwarding. Hence

the nodes located farther from the current forwarding node are more likely to become the next forwarding node. This phenomenon shall be referred to as *Phenomenon-1*.

Continuing with the above example, after n_1 has performed the RREQ forwarding, its neighboring nodes will take turn to forward the RREQ to establish the second hop. However, not all of n_1 's neighboring nodes will forward the RREQ, only those detected RREQ the first time may forward, which are those within the radio range of n_1 but outside the radio range of S . Hence the potential next forwarding nodes would be located farther from n_1 , and this distance depends on the separation between n_1 and S ¹. This phenomenon shall be referred to as *Phenomenon-2*.

Combining the two described phenomena, it is obvious that the next forwarding node will occur at a longer distance away from the current forwarding node with a higher probability. In the following subsection, we shall establish an evidence to illustrate this phenomenon by deriving the cumulative distribution functions for the distance between two adjacent forwarding nodes.

III. HOP LENGTH ANALYSIS

A. The Model

Let X_i be a random variable (r.v.) describing the distance between two adjacent forwarding nodes n_{i-1} and n_i , where $i = 1, 2, \dots$. The probability density function (pdf) and the cumulative distribution functions (cdf) of X_i are $f_{X_i}(\cdot)$ and $F_{X_i}(\cdot)$ respectively. Distances are normalized to the radio range, r . That is, $r = 1$. According to the RREQ broadcasting mechanism and the observation discussed in the previous subsection, we see that the first hop exhibits only Phenomenon-1.

To capture Phenomenon-1, we derive $f_{X_1}(x_1)$ based on conditioning and unconditioning on the location of the node which transmitted the first RREQ for the source. Let G be the r.v. describing the location of the node transmitted the first RREQ for the source, and $g(\cdot)$ be the pdf of G . For the first hop, all nodes within the radio range of the source have equal probability to transmit the first RREQ. Hence, $g(k) = 1$ where $0 < k \leq 1$.

After a node located at k has transmitted the first RREQ for the source, due to Phenomenon-1, all nodes in the range $[0, k]$ will fail in the route request. Potential forwarding nodes will then be located in the range $(k, 1]$, and each of these nodes has a probability of $\frac{1}{1-k}$ to become the next forwarding node. Thus, by unconditioning on k , the pdf of the first hop length can be formulated as

$$f_{X_1}(x_1) = \int_0^{x_1} \frac{1}{1-k} g(k) dk = -\ln(1-x_1) \\ F_{X_1}(x_1) = \int_0^{x_1} f_{X_1}(x) dx = x_1 - (x_1-1) \ln(1-x_1) \quad (1)$$

where $0 < x_1 \leq 1$. With this condition, the hop length cannot be zero. When the hop length is zero, the previous and the

¹Strictly speaking, this distance also depends on whether there are nodes such as m_1 transmitted before n_1 . If m_1 transmitted before n_1 , the distance between n_1 and the potential next forwarding nodes will then depend on the separation between n_1 and m_1 . In our analysis, we did not consider this effect as the influence of this effect will be small.

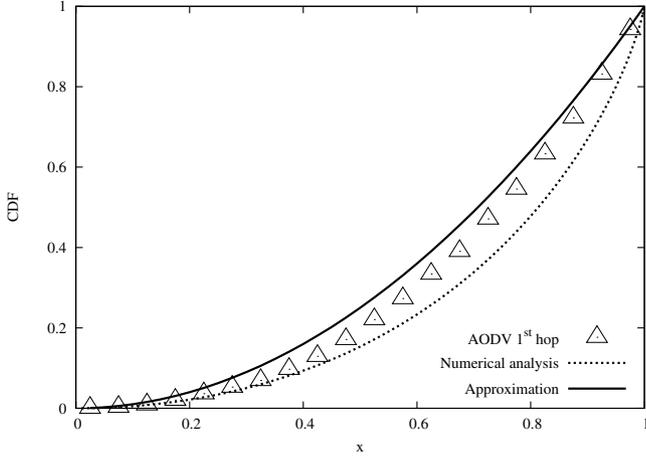


Fig. 3. Distribution of the first hop length.

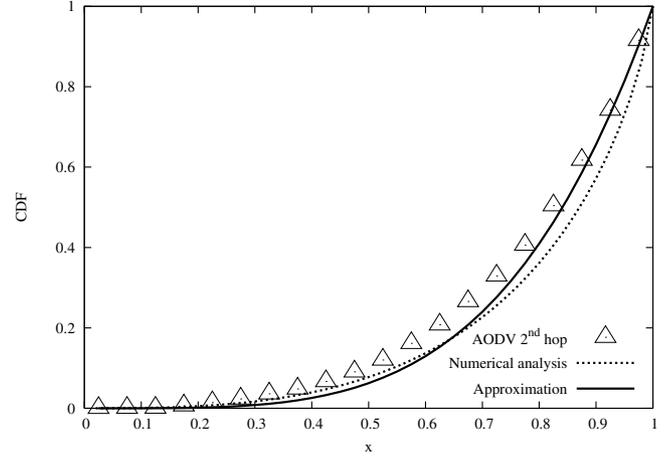


Fig. 4. Distribution of the second hop length.

current forwarding nodes are located at the same place. As they share the same neighboring nodes, all possible next forwarding nodes will have detected a duplicate RREQ when the current forwarding node transmitted the RREQ. Consequently, none of the neighboring nodes will decide to forward the RREQ, and the route establishment fails.

The second hop length appears to be more complex because both the Phenomenon-1 and Phenomenon-2 take place. To model both the phenomenons, we first derive $X_2|X_1$ to capture Phenomenon-1, then perform unconditioning to include Phenomenon-2. According to Fig 2, n_2 will be selected² randomly from those detected the RREQ for the first time. This mean that only nodes located at the range $(1, 1+x_1]$ away from the source can participate in the next RREQ forwarding. In other words, those nodes will have a distance in the range $(1-x_1, 1]$ away from n_1 , i.e. $1-x_1 < x_2 \leq 1$. As Phenomenon-1 governs the selection of the next forwarding nodes, using the similar approach for modeling Phenomenon-1 given in the previous subsection, the pdf of $X_2|X_1$ can be determined by

$$f_{X_2|X_1}(x_2|x_1) = \int_{1-x_1}^{x_2} \frac{1}{1-k} \frac{1}{x_1} dk = -\frac{1}{x_1} \ln \frac{1-x_2}{x_1}. \quad (2)$$

Evaluating the relationship between (1) and (2), it is found that the pdf and the cdf of $X_2|X_1$ can be expressed as

$$\begin{aligned} f_{X_2|X_1}(x_2|x_1) &= \frac{1}{x_1} f_{X_1}\left(\frac{x_2-(1-x_1)}{x_1}\right) \\ F_{X_2|X_1}(x_2|x_1) &= F_{X_1}\left(\frac{x_2-(1-x_1)}{x_1}\right) \end{aligned} \quad (3)$$

which clearly shows the effect of Phenomenon-1.

The cdf of X_2 can be determined by unconditioning on X_1 in the range $(1-x_2, 1]$. This range will ensure that n_1 can reach n_2 . To be precise,

$$F_{X_2}(x_2) = \int_{1-x_2}^1 F_{X_1}\left(\frac{x_2-(1-x_1)}{x_1}\right) f_{X_1}(x_1) dx_1 \quad (4)$$

²A node that forwards the RREQ for the current forwarding node will become the next forwarding node. We use the term *select* to describe this distributed decision making instead of that the current forwarding node chooses the next forwarding node.

and the pdf of X_2 can be calculated by $f_{X_2}(x_2) = F'_{X_2}(x_2)$, where $0 < x_2 \leq 1$.

Using the same approach, the cdf of $X_3|X_2$ can be obtained by

$$F_{X_3|X_2}(x_3|x_2) = F_{X_1}\left(\frac{x_3-(1-x_2)}{x_2}\right) \quad (5)$$

and $f_{X_3}(x_3) = F'_{X_3}(x_3)$. The cdf of X_3 can then be computed by

$$F_{X_3}(x_3) = \int_{1-x_3}^1 F_{X_1}\left(\frac{x_3-(1-x_2)}{x_2}\right) f_{X_2}(x_2) dx_2. \quad (6)$$

From the above result, it is not difficult to see that the cdf of X_i can be generalized as

$$F_{X_i}(x_i) = \int_{1-x_i}^1 F_{X_1}\left(\frac{x_i-(1-x_{i-1})}{x_{i-1}}\right) f_{X_{i-1}}(x_{i-1}) dx_{i-1} \quad (7)$$

and $f_{X_i}(x_i) = F'_{X_i}(x_i)$, where $i = 2, 3, \dots$

B. Hop Length Distributions

We first plot $F_{X_1}(x_1)$ in Fig. 3. We include the simulation results of AODV³ obtained from NS-2 [16] to illustrate our observation. The reported results clearly indicate that a node farther away from the source has a higher probability to become the next forwarding node which is due to Phenomenon-1.

In Fig. 4, numerical results for $F_{X_2}(x_2)$ and the simulation results are presented. A comparison between $F_{X_1}(x_1)$ and $F_{X_2}(x_2)$ shows that the combination of the two phenomenons in the second hop has made the farther nodes even more favorable as the next forwarding nodes compared with that of the first hop governed by only Phenomenon-1.

Likewise, in Figs. 5-6, we present the third and fourth hop length cdfs from the numerical computation and computer simulation. The same observation that farther nodes is more favorable to become the next forwarding nodes due to the

³The choice of AODV is mainly because our model best describes AODV. Another popular routing protocol, DSR, tends to choose the shortest route. Since this is not considered in our model, the comparison is not given.

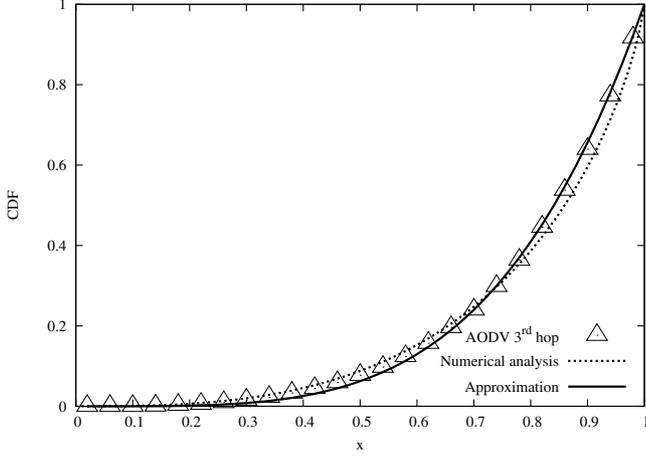


Fig. 5. Distribution of the third hop length.

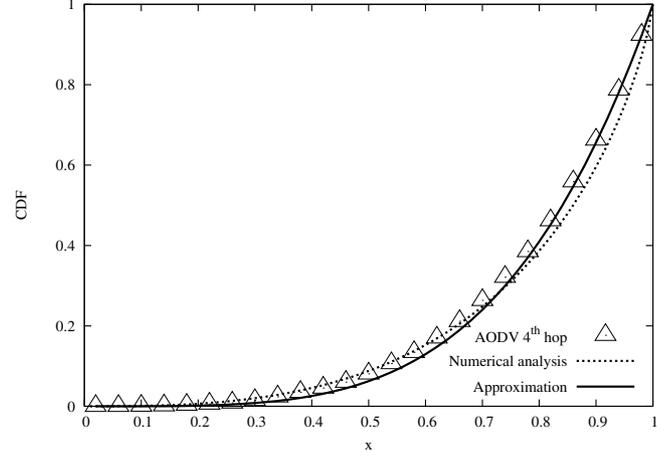


Fig. 6. Distribution of the fourth hop length.

two phenomenons is clearly shown. Similar behavior is further extended to the subsequent hop lengths although we did not show all results.

Although the above formulas allow straightforward numerical computation, they cannot be expressed in simple form which limits the study of the results. In the following, we shall propose an approximation.

We first rewrite $F_{X_1}(x_1)$ into a polynomial using the Maclaurin Series for $\ln(1-x)$, as

$$F_{X_1}(x_1) = x_1 - (x_1 - 1) \sum_{i=1}^{\infty} \frac{-x_1^i}{i}. \quad (8)$$

If we aggressively truncate the Maclaurin Series for $\ln(1-x)$ to its first order expansion⁴, after algebraic manipulation, $F_{X_1}(x_1)$ can be reduced to $\hat{F}_{X_1}(x_1) = x_1^2$, where $\hat{F}_{X_1}(x_1)$ is the approximation of $F_{X_1}(x_1)$ after the truncation. Hence, $\hat{f}_{X_1}(x_1) = 2x_1$. We compare the differences between $F_{X_1}(x_1)$ and $\hat{F}_{X_1}(x_1)$ in Fig. 3.

By using the above approximation, (4) can be simplified into

$$F_{X_2}(x_2) \approx (3x_2^2 - 2x_2) - 2(1-x_2)^2 \ln(1-x_2).$$

We may again truncate the Maclaurin Series for $\ln(1-x)$ to a certain order expansion to further simplify $F_{X_2}(x_2)$. We found that the expansion to the first order generates a significant error. To maintain a certain accuracy in our approximation, here we choose to truncate the Maclaurin Series for $\ln(1-x)$ to its second order expansion⁵. This approximation leads to the following simple form of $\hat{F}_{X_2}(x_2) = x_2^4$ and hence $\hat{f}_{X_2}(x_2) = 4x_2^3$.

In Fig. 4, numerical results for $F_{X_2}(x_2)$, $\hat{F}_{X_2}(x_2)$ and the simulation results are compared. Accuracy of our analysis and approximation are demonstrated.

Continuing the study for the subsequent hop length distributions, we first define $\hat{F}_{X_i}(x_i)$ to be the approximated

⁴ $\ln(1-x) \approx -x + R_1(x)$, where $R_1(x) = 0$.

⁵ $\ln(1-x) \approx -x - 0.5x^2 + R_2(x)$, where $R_2(x) = 0$.

cdf of $F_{X_i}(x_i)$ where $i \geq 3$. In Fig. 5, it is found that x_3^4 appears to be a better cdf describing $F_{X_3}(x_3)$, and this cdf is also used to approximate $F_{X_2}(x_2)$. According to (7), the cdf of a particular hop length depends on the cdfs of the first hop length and the previous hop length. Given the $\hat{F}_{X_1}(x_1) = x_1^2$ and $\hat{F}_{X_2}(x_2) = x_2^4$, we found that the third hop length cdf can be approximated as $\hat{F}_{X_3}(x_3) = x_3^4$ which has an identical distribution to its previous hop length. Recursively, we expect the same distribution for the fourth's, fifth's, and so on. Consequently, $\hat{F}_{X_i}(x_i)$ can be approximated as $\hat{F}_{X_i}(x_i) = x_i^4$, $i \geq 2$. The results shown in Fig. 6 have confirmed this, where x_4^4 remains an accurate cdf to describe $F_{X_4}(x_4)$.

IV. HOP COUNT ANALYSIS

One of the main factor affecting the performance of packet delivery in MANETs is the number of hops involved in relaying a packet commonly known as *hop count*. The number of hops depends on how a forwarding node is selected during the route establishment. Our analysis in the above subsection has concluded that using the common RREQ forwarding mechanism, neighbors nodes of farther distance away from the current RREQ forwarder has a higher probability to be selected as the next RREQ forwarder. Using the approximated hop length CDFs, the mean distance between the two adjacent forwarders can be easily determined by $E[X_1] = \frac{2}{3}$ and $E[X_i] = \frac{4}{5}$, $i \geq 2$.

Given that the RREQ is transmitted $h-1$ times including the transmission from the source, based on the above results, the RREQ would have reached an average distance of $E[X_1] + (h-2)E[X_i]$ away from the source. The average hop length of the final hop depends on the location of the destination. If the distance between the source and the destination is a constant value d , and the destination is located at the next hop after the $(h-1)th$ hop, then the average hop length for the final hop is

$$E[X_h] = d - (E[X_1] + (h-2)E[X_i]) \quad (9)$$

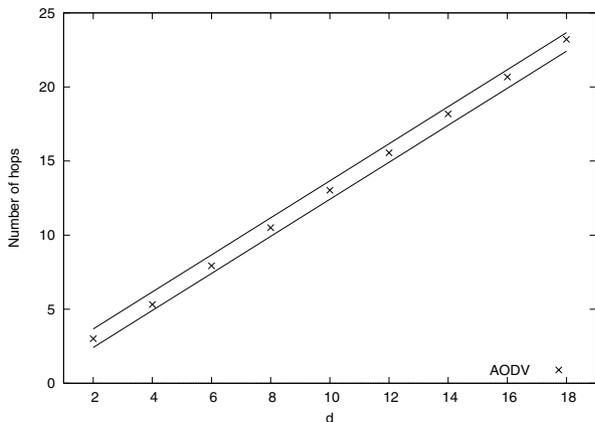


Fig. 7. Average number of hops versus the distance between the source and the destination.

where h must satisfy the condition that $0 < E[X_h] \leq 1$. After algebraic simplification, we get

$$\frac{5}{4}d - \frac{1}{12} \leq h < \frac{5}{4}d + \frac{14}{12}. \quad (10)$$

The very last result tells us that given a certain distance d between a source and a destination, the average number of hops that a packet travels is bounded by (10). In Fig. 7, we compare (10) with the simulation to show the accuracy of our formula.

Based on the above result, it is found that except for the first hop, the expected next forwarding node is located at $0.8r$ from the current forwarding node where r is the radio range. The average number of hops grows linearly at the rate 1.25 as the distance between the source and the destination increases. Given this result, one can evaluate the reliability of a particular network. For instance, a network of highly mobile nodes may easily trigger link breakage as two adjacent forwarding nodes are located near to the border of each radio range. In this case, a redesign of route discovery process such as one proposed in [17] may be necessary.

V. CONCLUSIONS

In this paper, we have reported an interesting observation on the commonly used route discovery process. We found that nodes farther from the current RREQ forwarding node are more favorable to become the next RREQ forwarding node. Modeling and analysis were performed to confirm this finding.

Precisely, we developed the pdf and cdf of the hop length. Approximations were employed leading to the possible study of the average number of hops. It was found that the average distance between two adjacent forwarding nodes is 0.8 of the radio range. It was found that the hop count grows linearly at the rate 1.25 as the distance between the source and the destination increases. The reported observation and results will be useful for the routing protocol enhancement and network design.

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