Abstract

When nodes in a mobile network cluster together or move according to common external factors (e.g., cars that follow the road network), the resulting contact patterns become correlated. In this work we address the question of modelling such correlated mobility movements for the analysis of intermittently connected networks. We propose to use the concept of node colouring time to characterise dynamic node contact patterns. We analyse how this model compares to existing work, and demonstrate how to extract the relevant data from actual trace files. Moreover, we show how this information can be used to derive the latency distribution of DTN routing protocols. Our model achieves a very good fit to simulated results based on real vehicular mobility traces, whereas models which assumes independent contacts do not.

1 Introduction

In delay- and disruption-tolerant networks messages are propagated using a store-carry-forward mechanism. Such networks can have applications for disaster area management [3], vehicular networks [19], and environmental monitoring [17]. These systems offer many challenges and have been extensively studied by the research community [1, 23, 25, 29].

Recent results indicate that to the extent that delay-tolerant networks will be found on a larger scale, they will be composed of islands of connectivity, that is, some parts that are well-connected and some parts that are sparse. This in turn implies correlated and heterogeneous contact patterns [2,11]. Most existing analytic delay performance models fail to capture such scenarios, since they assume independent and identical node contacts patterns. Moreover, although there are also more complex mobility models which include correlation [9,10], it is not obvious how one should go about to create such models from real existing traces.

We propose to use the concept of a node colouring process to characterise dynamic and heterogeneous contact patterns. We present a hierarchy of contact modelling models and show that our approach to modelling the system is more
general (models a wider set of mobility patterns) compared to approaches where node contacts are assumed to be independent. Due to the high-level nature of the colouring abstraction, it can be used to analytically study performance properties of message dissemination. We demonstrate how to derive the latency distribution functions (i.e., not just the average case), which allows obtaining more detailed information such as how delivery ratio depends on the time-to-live parameter. We evaluate our theoretical model using synthetic and real-life traces and show that with real mobility, correlation is high which means that our model provides a much better fit compared to earlier work.

There are three main contributions in this paper. First, a novel and yet simple approach of characterising dynamic contact patterns is introduced. Second, a hierarchy of possible connectivity modelling assumptions showing how our approach relates to other connectivity models is presented. Third, a scheme for deriving the routing latency distribution for complex heterogeneous mobility models is provided together with an experimental evaluation and validation of our model. We show that heterogeneous mobility can result in such a high correlation of contacts that theoretical results based on independent inter-contact times are no longer valid whereas a model based on colouring time distributions are able to correctly predict the information dissemination latency.

The rest of the paper is organised as follows. Section 2 describes the system model and the basic assumptions we make. Section 3 presents a model hierarchy of different assumptions on contact patterns. Section 4 describes how to derive the routing latency distribution given knowledge of the colouring rate distribution. This latter distribution is discussed in Section 5 and we explain how it can be determined from mobility traces. Section 6 contains the experimental evaluation. Finally, Section 7 gives an overview of the related work and Section 8 concludes the paper.

2 System model

Consider a system composed of $n$ mobile nodes (some possibly stationary). Nodes can communicate when they are in contact with each other. A contact is defined by a start and an end time between which two nodes have the potential to communicate with each other (through the existence of a link layer connection). We focus on connection patterns and ignore effects of queuing and contentions. Moreover, since we are interested in intermittently connected networks, the time taken to transmit a message is assumed negligible in relation to the time taken to wait for new contacts to be established. We call this assumption A.

2.1 Mobility as a point process

Consider the sequence of contacts between some arbitrary pair of nodes $a$ and $b$. This sequence of events can be mathematically represented as a point process on the time line, which we denote $P^{(a,b)}$. By superimposing all such pairwise
contact events we get a global point process $P^{(\cdot)}$ where all contacts are included. Figure 1 illustrates the general idea.

The pattern of the global point process corresponds to the node meetings in the network, and thus is an abstract representation of the node mobility. In this paper we aim to study how latencies of delay-tolerant routing protocols can be predicted by analysing this sequence of meeting events, and how the analysis is affected by correlation between events. By making assumptions about the characteristics of the contact point process, it is possible to create mathematical models of message dissemination in the network. Since the point process abstractly represents the node mobility, these assumptions implicitly restrict the set of mobility models for which the analysis holds. Therefore, it is desirable that the assumptions are not stronger than necessary, and that they are as realistic as possible.

2.2 Colouring assumption

Our approach to characterising the global contact point process is to introduce a simple colouring process. This concept has been used before to analyse routing latency [23, 25]. The novelty of our approach is to use properties of the colouring process as an abstract representation of mobility. Intuitively this abstract representation captures the rate at which message dissemination could take place in the network which is also closely related to dynamic graph expansion [5].

The basic idea of the colouring process is that if some node $a$ is coloured and subsequently comes in contact with node $b$, then node $b$ will also become coloured at the time of contact (if not already coloured). Formally, a colouring process $C(t_0, o)$ for a given global contact process is characterised by a start time $t_0$ and a source node $o$ from which the colouring process originates (thus, $o$ becomes coloured at time $t_0$). Every contact event where a coloured node comes in contact with an uncoloured node is a colouring event. Figure 2 shows a simple colouring process $C(t_0, a)$ which starts at time $t_0$ by colouring node $a$. The colouring events are the events where a coloured node meets an uncoloured node, which in this case are when nodes $a$ and $b$, and later $b$ and $c$ meet. Note
that the first time $b$ and $c$ meet after the time $t_0$, neither of the nodes are coloured, so this is not a colouring event, whereas the second time they meet, node $b$ is coloured so the second meeting with $c$ is therefore a colouring event.

The time between colouring events plays a crucial role in our model. For a given contact point process, let $T_i$ denote the random variable representing the time taken for a randomly chosen colouring process to colour $i$ nodes, and let $f_i(t)$ denote the probability distribution function of $T_i$. Moreover, let $\Delta_i$ denote the random variable that describes the time taken for a randomly chosen colouring process to colour one more node given that $i$ nodes are already coloured. We denote the probability distribution function of $\Delta_i$ as $f_{\Delta_i}(t)$. We can express the time taken for a colouring process to reach $i + 1$ nodes as $T_{i+1} = T_i + \Delta_i$. Since the first node becomes coloured immediately at the start of the colouring process, the time to colour one node is $T_1 = 0$ and the time to colour two nodes is $T_2 = \Delta_1$.

The core assumption of our model which restricts the contact pattern (and thereby constrains the mobility of the nodes) is that the incremental colouring time should be independent from the colouring time so far. More specifically, for any given colouring process, $T_i \perp \Delta_i$ for $2 \leq i \leq n - 1$, where $\perp$ denotes the fact that two random variables are independent (i.e., $X \perp Y \iff P(X \leq x, Y \leq y) = P(X \leq x)P(Y \leq y)$). We call this assumption $\perp_C$. Using this assumption together with the relationship $T_{i+1} = T_i + \Delta_i$ we can characterise the probability distribution function of $T_i$ as the convolution

$$f_{i+1}(t) = (f_i * f_{\Delta_i})(t)$$

In the next section we compare the $\perp_C$ assumption with other assumptions on node connectivity such as that of independent inter-meeting times and show that our assumption is strictly weaker (models a wider set of mobility patterns).
3 Model hierarchy

Our goal in this paper is to mathematically analyse mobility patterns with correlated meeting patterns. However, since we assume that inter-colouring times are independent, it is interesting to analyse how this assumption relates to the more common assumption of independent contact times. The point of this analysis is to properly understand these assumptions and the space of possible modelling choices.

We start by describing a set of five assumptions (actually, the first one is a non-assumption) on the independence of contacts. Each assumption restricts the set of possible point processes (and thereby which mobility patterns that can accurately be modelled with such a point process).

- $\emptyset$ - No assumptions on the properties of the point processes (i.e., arbitrary mobility is allowed)

Having no restricting assumptions on point processes allows all possible contact (and thereby mobility) patterns. Unfortunately, this makes it very hard to do any reasoning about system properties.

- $S$ - Every pairwise meeting process $P^{(a,b)}$ is stationary.

A stationary process is one where the intensity of events is constant over time. It does not mean that events arrive at a constant rate, but rather that the probability of finding a certain number of events in an interval of a given length is independent from the starting time of the interval. Note that a single stationary process cannot model intensity variations over a longer time period (e.g., rush hour and off peak times in a vehicular network).

- $R$ - Every pairwise meeting process is a renewal process: $X^{(a,b)}(i) \perp X^{(a,b)}(j)$ if $i \neq j$, where $X^{(a,b)}(i)$ denotes the time from event $i$ to event $i$ of the process $P^{(a,b)}$ counted after some origin time $t_0$.

In a renewal process the time between two successive events is independent from all other inter-event times. Note that in order for the definition of $X^{(a,b)}(i)$ to be meaningful, the point process needs to be stationary. A special case of the renewal process is when the random variables $X^{(a,b)}(i)$ are exponentially distributed, in which case the resulting point process is a Poisson process.

- $\perp_0$ - Non-overlapping pairs of nodes have independent meeting point processes, $P^{(a,b)} \perp P^{(c,d)}$ if $|\{a, b\} \cap \{c, d\}| = 0$

This assumption basically states that if two node pairs are disjoint (i.e., there are four distinct nodes), then their respective contacts are also independent.
Figure 3: Hierarchy of models characterised by assumptions

- \( \perp_{\leq 1} \) - Two node-pairs of nodes with no more than one node in common have independent meeting point processes: \( P(a,b) \perp P(c,d) \) if \( |\{a, b\} \cap \{c, d\}| \leq 1 \).

This is similar to the previous assumption, but is stronger in the sense that any two node pairs with at most one node in common have independent meeting point processes. For example, node pairs \((a, b)\) and \((b, c)\) are assumed to be independent from each other even if they have node \(b\) in common.

- \( \perp_C \) - For any colouring process the time to colour one more node is independent from the time taken to colour \(i\) nodes, \( T_i \perp \Delta_i \) for \(2 \leq i \leq n - 1\).

This is the assumption that we rely on in our analysis which was explained in Section 2.2. Note that this assumption also requires stationarity of contacts (assumption \(\mathcal{S}\)), since we assume \(T_i\) to be characterisable independently of when the colouring process starts.

Based on these assumptions, we can create a hierarchy of models as shown in Figure 3. The arrows in the figure denote the relative strength of these assumptions. If \(A \rightarrow B\), then all behaviours that are modelled by \(A\) are also modelled by \(B\) (but not vice versa). That is, \(A\) has strictly stronger assumptions on the contact patterns. It is possible to combine two assumptions by assuming both of them to be true in the model (denoted with the logical and symbol \(\land\) in the figure).

At the top of the hierarchy is the most general model \(\emptyset\) which makes no restrictions on node connectivity patterns. This allows all possible contact patterns, including those that could never appear in a wireless network with mobile
nodes, but makes mathematical analysis difficult. At the bottom of the hierarchy we find $R \land \perp_{\leq 1}$ which has been used extensively as a model when studying intermittently connected networks \cite{1, 23}. This gives tractable closed form analytic expressions, but turns out to be too idealistic. Our model, which is somewhere in between these two, provides a reasonable trade-off between being able to analytically analyse the problem, and still retaining a sufficient level of realism. We believe that it would also be interesting to study the other models (especially those that do not require stationarity) in the hierarchy as well, but it is outside the scope of this paper. Some recent works have modelled pairwise contacts as independent random variables but with heterogeneous rates \cite{21} which would add another dimension to the lattice hierarchy.

We proceed with a brief explanation of how the hierarchy has been derived. Many of the relationships between different independence assumption models are immediate from the respective definitions. We have already explained the fact that $R$ is a stronger assumption than $S$, which we express as $R \rightarrow S$. Moreover, the relation $\perp_{\leq 1} \rightarrow \perp_0$ follows immediately from the respective definitions. Finally, when two assumptions are combined, then the resulting assumption is also by definition stronger than the individual assumptions, so for example $(R \land \perp_0) \rightarrow R$.

The key relation which remains to show is $(S \land \perp_{\leq 1}) \rightarrow \perp_C$, which basically says that the model used in this paper ($\perp_C$) is strictly weaker (i.e., models a wider set of mobility patterns) than the $S \land \perp_{\leq 1}$ model (as well as all stronger models since $\rightarrow$ is a transitive relation). We present this proof in an appendix of the paper.

4 Routing latency

In this section we characterise the routing latency for epidemic and multi-copy routing in intermittently connected networks. We use a number of random variables to describe the colouring and routing processes, Table 1 summarises the most important notation. PDF is an abbreviation for probability density function and CDF stands for cumulative density function, these abbreviations are used throughout the paper. In this analysis we assume that the distribution of the inter-colouring times $\Delta_i$ are known apriori (we will later return to this assumption and discuss how to extract this knowledge from existing mobility traces).

We start by deriving the routing latency for ideal epidemic routing. This corresponds to the optimal performance any routing algorithm can achieve. Thus, these results provide a useful theoretical reference measure on what is good performance for a given mobility model. Such a reference can also be of practical use to decide whether the measured performance in some network is due to the network characteristics or to the protocol implementation. We then present an approximate model for the latency of multi-copy routing, which uses the epidemic routing latency as a base.
Table 1: Notation

| Symbol | Description |
|--------|-------------|
| $n$    | Number of nodes in the system |
| $P(X)$ | Probability of $X$ being true |
| $T_i$  | Random variable, the time taken for a randomly chosen colouring process to colour $i$ nodes |
| $\Delta_i$ | Random variable, the time taken for a randomly chosen colouring process to colour one more node given $i$ coloured nodes |
| $R$    | Random variable, the message delivery latency |
| $f_i(t)$ | PDF of the random variable $T_i$ |
| $F_{\Delta_i}(t)$ | CDF of the random variable $\Delta_i$ |
| $F_R(t)$ | CDF of the random variable $R$ |

### 4.1 Latency of ideal epidemic routing

Consider a randomly chosen time $t_0$, origin node $o$ and destination node $d \neq o$. Let $R$ be the random variable that models the time to route a message from $o$ to $d$ using ideal epidemic routing. We will try to find the CDF of $R$, $F_R(t) = P(R \leq t)$. Clearly, given assumption A in Section 2 (i.e., that the queuing and transmission times can be neglected), this probability is the same as for $d$ being one of the coloured nodes by the colouring process $C(t_0, o)$ after $t$ time units.

Let $C_t$ be the random variable that models the number of coloured nodes after $t$ time units. If $C_t = i$ then the probability that $d$ is coloured after $t$ time units is $(i - 1)/(n - 1)$ since if we remove the source node $o$, there are $i - 1$ coloured nodes and $n - 1$ nodes in total. Thus, we can express $F_R(t)$ as:

$$F_R(t) = P(R \leq t) = \sum_{i=1}^{n} P(C_t = i) \cdot \frac{i - 1}{n - 1} \quad (2)$$

Now let’s consider the probability $P(C_t = i)$ that the number of coloured nodes at time $t$ equals $i$. This is the same as the probability that the time taken to reach $i$ nodes is less than or equal to $t$ minus the probability that $i + 1$ nodes can be reached in this time:

$$P(C_t = i) = P(T_i \leq t) - P(T_{i+1} \leq t) \quad (3)$$

Combining equations (2) and (3), and rewriting gives:

$$F_R(t) = P(T_i \leq t) = \frac{1}{n - 1} \sum_{i=2}^{n} F_i(t) \quad (4)$$

where $F_i(t) = P(T_i \leq t)$ is the CDF of the random variable $T_i$ which denotes the time for a randomly chosen colouring process to reach $i$ nodes. Recall that for the purpose of this analysis we assume that the distribution of the inter-colouring times ($\Delta_i$) are known apriori. Moreover, from Section 2.2 we are able
Listing 1 GetRoutingLatencyDistribution

Input: $f_{\Delta 1}$ : Vector representing the PDF of $\Delta_i$

1. $f_2 \leftarrow f_{\Delta 1}$
2. for $i = 3 \ldots n$
3.     $f_i \leftarrow \text{conv}(f_{i-1}, f_{\Delta i-1})$ /* equation [1] */
4.     $F_i \leftarrow \text{cumsum}(f_i)$
5.     $F_R \leftarrow \frac{1}{n-1} \sum_{i=2}^{n} F_i$ /* equation [4] */
6. return $F_R$

Listing 1 shows an algorithmic representation of how to derive the distribution for $R$ using discrete distributions. The procedure conv and cumsum are standard Matlab functions and compute the convolution between two vectors and cumulative vector sum respectively.

Note that by knowing $R$ we can easily deduce the delivery ratio of a protocol given a certain time-to-live (TTL) for each packet. The probability that a message with TTL of $T$ will reach its destination is simply $F_R(T)$ (i.e., the probability that the message will be delivered within time $T$).

4.2 Latency of multi-copy routing

In the previous analysis we considered ideal epidemic routing, where nodes propagate and multiply messages without discrimination. In real networks, such a strategy results in severe congestion and poor performance. The other extreme, when the system keeps a single copy of the message at any point in time, can result in very long message latencies unless additional knowledge can be used (e.g., geographic forwarding). Between these two, there is a middle way where multiple active copies are disseminated. There are several ways of regulating the number of active copies, including having the maximum number of copies as a parameter, the Spray and Wait protocol by Spyropoulos et al. [26] probably being the most well-known such protocol.

In this section we describe how the colouring model of mobility can be used also to approximate multi-copy routing latency. Our main objective is not to extensively analyse multi-copy routing which has been done commendably elsewhere [23]. Rather, our goal is to demonstrate that the colouring model of correlated mobility can also be used to analyse more advanced routing protocols than just ideal epidemic routing.

To make this approximation, we introduce two new node states as shown in Figure 4. In addition to a node being coloured or uncoloured, we say that a
coloured node can also be active, and that an uncoloured node can be solitary. The basic intuition is that active nodes are those which hold one of the message copies, and solitary nodes are such nodes which seldom interact with any other nodes.

The way we derive the final routing latency distribution is similar to the process for epidemic routing. Thus, we first analyse how long it would take a hypothetical colouring process to colour all the nodes, and then use this information to derive the time taken to reach the a given destination node. However, instead of directly using the colouring distribution functions for $\Delta_i$, we consider a new colouring process $C'(t_0, o, a)$ with inter colouring times $\Delta'_i$ where at most $a$ active nodes are allowed to colour other nodes. The real-world interpretation is that a coloured node is a node such that if it had been the destination of the message, then the message would be delivered. So a node which meets an active node becomes coloured.

In order to determine the distribution function for $\Delta'_i$, we take advantage of the fact while we do not know exactly the characteristics of the point process $C'(t_0, o, a)$, we might know properties of a point process containing a super set of the events in $C'(t_0, o, a)$. Figure 5 illustrates the basic idea. The time between colouring two events in this figure is the same as the time of $k$ events.
to happen in the super set process. In general, the probability that \( \Delta'_i \) is less than \( t \) is (which amounts to the cumulative distribution function \( F_{\Delta'_i}(t) \)) can be expressed as:

\[
F_{\Delta'_i}(t) = \sum_k P(i, k) F(i, k, t)
\]  

(5)

where given \( i \) coloured nodes, \( P(i, k) \) represents the probability that \( k \) meetings of the super set process are needed for a colouring event to occur, and \( F(i, k, t) \) represents the probability that, given \( i \) coloured nodes, the time for \( k \) events to occur in the super set process is less than \( t \). We will now proceed to find reasonable approximations for \( P(i, k) \) and \( F(i, k, t) \). These approximations will partly rely on assumptions of independence which will reduce the fidelity of the model. However, by introducing these assumptions at a late stage in the process we still retain important characteristics about the node mobility. As a result, our approximate model still provides good results in a scenario with correlated mobility as we demonstrate in Section 6.

Due to the nature of multi-copy routing we split the approximation of \( F_{\Delta'_i}(t) \) in three phases. The first phase when there are less than \( a \) active nodes is similar to epidemic routing. In the second phase \( a \) active nodes is colouring the non-solitary nodes. In the final phase the solitary nodes become coloured. Solitary nodes are such nodes which seldom interact with any other nodes. Such behaviour is seldom considered in homogeneous models, but can be seen in the inter-colouring time distributions. If there are no solitary nodes, then there is a symmetry \( \Delta_i = \Delta_{n-i} \) (colouring the first few nodes take equally long as colouring the last few nodes), whereas if there are solitary nodes then \( \Delta_i \ll \Delta_{n-i} \) for small values of \( i \). That is, it takes much longer to colour the last few nodes, than to colour the first few nodes. For the purpose of this approximation we define the number of solitary nodes \( s \) as the largest \( i \) so that \( \Delta_i < 2\Delta_{n-i} \).

1. Initial phase: In this phase there are no more than \( a \) coloured nodes \((1 \leq i \leq a)\), so the spreading process is essentially the same as epidemic routing. Therefore, we let \( F_{\Delta'_i}(t) = F_{\Delta_i}(t) \)

2. Middle phase: In this phase, there are more than \( a \) coloured nodes, but the colouring has not yet reached the solitary nodes \((a \leq i \leq (n-s))\). We assume that the likelihood of an active node meeting a solitary node is much less than the probability of meeting a non-solitary node. Moreover, if the chance of meeting a coloured node and uncoloured node is proportional to the number of respective nodes, the probability that \( k \) meetings are needed to meet an uncoloured node is:

\[
P(i, k) = \frac{n-s-i}{n-s-a} \left( \frac{i-a}{n-s-a} \right)^{k-1},
\]

where the first part of the expression is the probability of meeting an uncoloured node and the second part is the probability of \( k-1 \) consecutive meetings happening meeting only coloured nodes. Finally, the probability that the time to meet \( k \) nodes is less than \( t \) can be approximated with
\( F(i, k, t) = (F_{\Delta a}(t))^k \), since there are \( a \) nodes that actively colour other nodes and there need to be \( k \) such colouring events.

3. End phase: In the final phase we assume that all non-solitary nodes have been coloured, and only the solitary nodes remain \((n - s) \leq i \leq (n - 1)\). Considering the meetings between coloured and uncoloured nodes, the probability that a coloured node is active is \( a/i \) so the probability that \( k \) attempts are required is \( P(i, k) = \frac{a}{i} \left( \frac{i-a}{i} \right)^{k-1} \). The CDF for the time of \( k \) meetings between coloured and uncoloured nodes to occur can be expressed as \( F(i, k, t) = (F_{\Delta i}(t))^k \).

These three steps together with equation (5), gives us the cumulative distribution function \( F_{\Delta i}(t) \). By using equation (4), we can then calculate the latency distribution function for multi-copy routing in the same way as we did for epidemic routing.

5 Colouring rate

Having derived the routing latency distribution based on knowledge of the distribution of the incremental colouring time \( \Delta_i \) we now proceed to show how to find the distribution function \( f_{\Delta_i}(t) \) based on analysing existing mobility traces.

We consider two cases, when the mobility is homogeneous, and the more interesting heterogeneous case. By homogeneous we mean that the pairwise inter-contact times (i.e., the time between contacts) are identical and independently distributed (often abbreviated iid). The homogeneous case is not really novel in this context and is provided here briefly in order to explain the baselines we have used and to show that this case is also covered by our general approach.

5.1 Homogeneous mobility

For the particular case of homogeneous mobility we adopt the model \((R \land \perp_{\leq 1})\) which states that all pair-wise contact point processes should be stationary, renewal, and independent (see Section 3 for details).

Now consider a set of coloured nodes that wait for a new contact to appear so that a new node can become coloured. The time they have to wait is the smallest of all pairwise waiting times for all pairs where one node in the pair is coloured and one node is uncoloured. If \( i \) nodes are coloured, then there are \( i(n-i) \) such pairs. Given the assumption of independence, we can express the CDF of \( \Delta_i \) as:

\[
F_{\Delta i}(t) = P(\Delta_i \leq t) = 1 - (1 - F_{\tau}(t))^{i(n-i)}
\]

where \( F_{\tau}(t) \) is the cumulative distribution of the residual inter-contact time between two nodes. We refer to Karagiannis et al. [12] for further explanation and

\(^1\)The residual inter-contact time refers to the time left to the next contact from a randomly chosen time \( t \), as opposed to the time to the next contact measured from the previous contact time.
how to derive the residual distribution from the inter-contact distribution. If the inter-contact time is exponentially distributed with rate $\lambda$, then the residual waiting time is also exponentially distributed with the same rate and the incremental colouring time $\Delta_i$ will be exponentially distributed with rate $\lambda(n - i)$.

### 5.2 Heterogeneous mobility

If node contacts are not independent, then deriving an expression for the colouring distribution $\Delta_i$ will be more challenging. We now proceed to present a first simple model for approximating it from real heterogeneous traces.

In order to explain the rationale behind the model we first show some data from a real-life trace based on the movement of taxis in the San Francisco area. The trace was collected by Piorkowski et al. [22] based on data made available by the cabspotting project during May 2008 and we used a subset of the first 100 vehicles from the trace. In the simulation each taxi was assumed to have a wifi device with a range of 550m.

Fig. 6 shows the Complementary Cumulative Distribution Function (CCDF) of each $\Delta_i$ (recall that $i$ corresponds to the number of already coloured nodes) for the San Francisco cab scenario. We obtained this data by running 700 of colouring processes on the contact trace and logging the time taken to colour the next node. The plot uses a logarithmic scale on both axes to highlight the characteristics of the distribution. This shows that they exhibit an exponential decay (i.e., it approaches 0 fast, indicated by the sharp drop of the curves.).

The second phenomena that we have observed is that due to clustering of nodes, it is often the case that the next node can be coloured without any waiting time at all. Based on these two basic principles we conjecture that the colouring time can be modelled as either being zero with a certain probability, or with a waiting time that is exponentially distributed.

If $i$ nodes have been coloured, then we let $Con(i)$ denote the probability that one of those $i$ nodes is in contact with an uncoloured node (thereby allowing
an immediate colouring of the next node). Further we let $f_{\text{Exp}}(t, \lambda_i)$ denote the PDF of the exponential distribution with rate $\lambda_i$. Then, we let the PDF of the simple colouring distribution model be expressed as:

$$f_{\Delta i} = \begin{cases} 
Con(i) & \text{if } t = 0 \\
(1 - Con(i)) \ast f_{\text{Exp}}(t, \lambda_i) & \text{otherwise}
\end{cases}$$

(7)

While this is clearly a simple model, it can be seen as a first step towards modelling the colouring distribution and seems to work well enough for the scenarios we have studied. We believe that further work is needed to better understand how the colouring distribution is affected by different mobility conditions. Note also that our general scheme is not tied to this particular model and allows further refinements.

6 Evaluation

To validate our routing latency estimation model from Section 4 and to test whether it actually provides any added value compared to existing models we performed a series of simulation-based experiments. We used three different mobility models, the random waypoint mobility model, a model based on a map of Helsinki and a real-world trace from the cabs in the San Francisco area. After explaining the experiment setup we give the details and results for these models, first for epidemic routing, and then multi-copy routing. Finally, we relate our findings on the effects of heterogeneity for these cases.

We used the ONE Simulator [14] to empirically find the ideal epidemic routing latency distribution and the routing latency of Spray and Wait (which is an instance of a multi-copy routing protocol) for the three different mobility models. For each mobility model we ran the simulation 50 times. For the first 40000 seconds a new message with random source and destination was sent every 50 to 100 seconds. The simulation length was sufficiently long for all messages to be delivered. We used small messages of size 1 byte, and channel bandwidth of 10Mb/s.

In addition to the simulated results we used two different theoretical models to predict the latency distribution:

**Colouring Rate:** This model uses equation (7) from Section 5.2 to model the colouring times. The necessary parameters $Con(i)$ and $\lambda_i$ are estimated from the trace file by sampling.

**Homogeneous:** This model assumes independent and exponentially distributed inter-contact times which are used to compute $f_{\Delta i}$ as described in Section 5.1. This has been a popular model for analysing properties of delay-tolerant networks [23, 25, 29].

2We also obtained nearly identical results when estimating the inter-contact distribution from the mobility trace, which we have excluded for lack of space.
In order not to get a biased value for the inter-contact time distributions due to a too short sampling period, we analysed contacts from 200,000 seconds of simulation. To further reduce the effect of bias we use Kaplan-Meier estimation as suggested by Zhang et al. [29].

6.1 Epidemic routing

Random Waypoint Mobility. In order to validate our model against already known results, we start with considering the random waypoint mobility model. Despite its many weaknesses [2, 28], this model of mobility is still very popular model for evaluating ad hoc communication protocols and frameworks. The network was composed of 60 nodes moving in an area of $5\text{km} \times 5\text{km}$, each having a wireless range of 100 m. The speed of nodes was constant 10 m/s with no pause time.

Helsinki Mobility. We now turn to a more realistic and interesting mobility model, the Helsinki mobility model as introduced by Keränen and Ott [13]. The model is based on movements in the Helsinki downtown area. The 126 nodes is a mix of pedestrians, cars, and trams, and the move in the downtown Helsinki area (4500x3400 m). We used a transmission range of 50 meters for all devices. Fig. 8 shows the results. Again both theoretical models achieve reasonable results. However, due to the partly heterogeneous nature of the mobility model, the homogeneous model differs somewhat more from the simulated result. In particular, we see that the s-shape is sharper compared to the observed
data. We further discuss possible explanations for this in Section 6.3.

San Francisco Cabs. Finally, the last mobility trace we have analysed is a real-life trace based on the movement of taxis in the San Francisco area as explained in Section 5.2. Fig. 9 shows the results. In this case the homogeneous model fails to capture the routing latency that can be observed in simulation. However, the heterogeneous model based on equation (7) is still quite accurate. We were surprised to find such a big difference between the simulated data and the homogeneous model. Something is clearly very different in this trace compared to the synthetic mobility models. An estimate of the fraction of messages being delivered within an average latency of 2500s in such a scenario would be misleadingly optimistic by 20%.
6.2 Multi-copy routing

In Section 4.2 we proposed an approximate model to predict the latency distribution of multi-copy routing, which was based on our basic method of modelling correlated connectivity patterns. We now proceed to validate this model in the same manner as for epidemic routing. We used a replication factor of 10, both in the simulation and in calculations (i.e., the parameter \( a \)). The results from the Helsinki and San Francisco cabs mobility models are shown in figures 10 and 11 (the results for RWP all follow the simulated line closely so we omit this curve). Clearly, the results are structurally similar to those of ideal epidemic routing, but routing takes longer time (about twice the time). This is expected since we exclude the effects of limited bandwidth which otherwise significantly reduces the performance of epidemic routing (due to congestion).

![Figure 10: Spray and Wait with Helsinki Mobility](image)

In terms of the ability of the theoretical model to predict the results achieved in simulation, we can again observe that the model which assumes homogeneous, independent mobility, works reasonably well, for syntactic mobility, but not very well for the trace based on real vehicular movements. However, when using a colouring-based connectivity model the routing latency distribution closely matches the simulated results, despite the fact our analysis of multi-copy routing was only approximate.

6.3 The effects of heterogeneity

We have seen that the accuracy of the homogeneous model is high for the random waypoint model, but is lower for the Helsinki model and completely fails for the San Francisco cab trace. In this subsection we present our investigation into why this is the case. We proceed by identifying four different aspects of how this model differs from reality.

**Correlation.** We begin with the most striking fact of the results presented so far. The homogeneous model is way off in predicting the routing latency distribution in the San Francisco case. There are a number of different ways
that one can try to explain this, but we believe that the most important one has to do with correlation (i.e., non-independence) of events. The main assumption that makes equation (6) possible, and thereby the homogeneous model is that the contacts between different pairs of node are independent from each other. However, this seems to be a false assumption.

We analysed the contact patterns of the three different mobility models by considering the residual inter-contact times for each node during a period of 20000 seconds. Fig. 12 shows the percentage of nodes for which the average correlation among their contacts is higher than a given value (i.e., it is the complementary CDF of nodes having a given average correlation). If the pairwise contacts are independent, they will have no (or very low) average correlation and we would expect to see a sharp decay of the curve in the beginning of the graph. This is also what we see for the random waypoint model. Since the nodes move around completely independently from each other, the contacts also become independent. The Helsinki trace shows a higher degree of correlation,
but not as significant as for the San Francisco cab case. In this case 40% of the nodes have an average correlation of their contacts which is higher than 0.2 (a correlation of 1 would mean that all contacts are completely synchronised). This shows a high degree of dependence and we believe provides an explanation of the result we have seen in Section 6.1.

Note that correlated mobility does not necessarily lead to slower message propagation, in fact there are results indicating the contrary [9]. What we have seen is that the prediction of the latency becomes too optimistic when not taking correlation into account. If the model assumes that contacts are “evenly” spread out over time, whereas in reality they come in clusters, the results of the model will not be accurate.

Lack of Expansion. The second prominent effect is what we choose to call lack of expansion (motivated by the close connection to expander graphs [5]). This means that the rate of the colouring process seems not to correspond to the number of coloured nodes. Fig. 13 shows the expected time to colour one more node for the San Francisco trace. The x-axis represents the number of nodes already coloured (up to half the number of nodes). We can see that the homogeneous model predicts that the time decreases (i.e., the rate of colouring increases) as the number of coloured nodes increase. On the other hand, the data based on sampling the distribution of $\Delta_i$ from the mobility trace file (indicated as “From trace” in the figure) shows that after the first 5-10 nodes have been coloured, the rate is more or less independent from the number of coloured nodes. We believe that this is partly due to the fact that most of the node mobility is relatively local and that nodes are often stationary for long periods of time.

Slow Finish. Another effect that can be observed is that in some rare cases it can take a very long time for a message to reach its destination. For example in Fig. 9 even after 10000 seconds not all messages have been delivered to their destinations. This has to do with the fact that the time to colour all nodes is significantly longer than to colour almost all the nodes. The models
based on independent contacts predict that it takes the same amount of time to colour the second node as it takes to colour the last node. In both cases there are \( n - 1 \) possible node pairs that can meet and result in a colouring. However, we have seen that in reality colouring the last node takes significantly longer (on average). Fig. 14 shows the effect for the Helsinki trace, by plotting the expected colouring time as a function of the number of coloured nodes. While the homogeneous model is completely symmetrical around the middle, the actual data shows that it takes roughly three times longer to reach the last node than to reach the second node.

![Graph showing expected colouring time vs nodes](image)

Figure 14: Time to colour one more node with the Helsinki mobility model

**Fast Start.** Finally, we consider why the homogeneous model predict a lower probability for delivering messages fast. This can be seen in both the Helsinki and San Francisco cases, but is more distinct in the former case. It can be seen visually in Fig. 8 in that the homogeneous model has a slightly flatter start compared to the other curves. This is because there is a chance that when a message is created, the node at which it is created has a number of neighbours. Thus, the message will not need to wait any time at all before being transmitted. Or if we express it as a colouring process, the time to colour the second node is sometimes zero. For a model based on inter-contact times, this is not considered.

Fig. 15 shows the CDF of \( T_2 \), (i.e., the time taken to colour the second node) for the Helsinki case with the colouring rate and homogeneous model. We see that both curves are similar (the expected value for \( T_2 \) is the same for both models) but that the start value differs. That is, in the homogeneous model, it is predicted that the chance that the second node is immediately coloured is zero, whereas in fact it is roughly 0.3. Recall that the colouring time only reflects the contact patterns of the mobility and does not consider message transmission delays.

In this section we have seen how heterogeneous mobility causes correlated contacts and how that affects predictions of routing latency. Our model which is based on colouring rate of nodes was the only model able to accurately predict...
the routing latency distribution in these cases.

7 Related works

There is a rich body of work discussing detailed analytic models for latency and delivery ratio in delay-tolerant networks. The work ranges from experimentally grounded papers aiming to find models and frameworks that fit to observed data to more abstract models dealing with asymptotic bounds on information propagation. Many of these approaches are based on or inspired by epidemiological models [15]. We have previously characterised the worst-case latency of broadcast for such networks using expander graph techniques [6]. In a preliminary version of this paper we developed the basic framework for deriving the latency of ideal epidemic routing [4]. This paper extends the latter work by incorporating an analysis of multi-copy routing as well as presenting a more rigorous mathematical basis with a hierarchy of connectivity models.

Closest to our work in this paper is that of Resta and Santi [23], where the authors present an analytical framework for predicting routing performance in delay-tolerant networks. The authors analyse epidemic and two-hops routing using a colouring process under similar assumptions as in our paper. The main difference is that our work considers heterogeneous node mobility (including correlated inter-contact times), whereas the work by Resta and Santi assumes independent exponential inter-contact times.

Zhang et al. [29] analyse epidemic routing taking into account more factors such as limited buffer space and signalling. Their model is based on differential equations also assuming independent exponentially distributed inter-contact times. A similar technique is used by Altman et al. [1], and extended to deal with multiple classes of mobility movements by Spyropoulos et al. [27].

Kuiper and Nadjm-Tehrani [16] present a quite different approach for analysing performance of geographic routing in large scale. Their framework can be used
based on abstract mobility and protocol models together with extracting distributions for arbitrary mobility models and protocols from simulation data (in smaller scale). The main application area for this model is geographic routing where waiting and forwarding are naturally the two modes of operation in routing.

The assumption of exponential inter-contact times was first challenged by Chaintreau et al. [8] who observed a power law of the distribution for a set of real mobility traces (i.e., meaning that there is a relatively high likelihood of very long inter-contact times). Later work by Karagiannis et al. [12] as well as Zhu et al. [30] showed that the power law applied only for a part of the distributions and that from a certain time point, the exponential model better explains the data. Pasarella and Conti [20] present a model suggesting that an aggregate power law distribution can in fact be the result of pairs with different but still independent exponentially distributed contacts. Such heterogeneous but still independent contact patterns have also been analysed in terms of delay performance by Lee and Eun [18].

Our work on the other hand, suggests that the exact characteristic of the inter-contact distribution is less relevant when contacts are not independent. Correlated and heterogeneous mobility and the effect on routing have recently been discussed in several papers [7, 6, 9, 11], but to our knowledge, we are the first to provide a framework that accurately captures the routing latency distribution for real traces with heterogeneous and correlated movements.

8 Conclusions

Node mobility is often one of the most important factors to determine the performance of wireless multi-hop communication. However, the disparity of different application scenarios, and the difficulty of obtaining representative large-scale mobility traces have often forced the research community to use coarse and idealistic models for their analyses. In this paper we proposed to model node connectivity as a colouring process in the analysis of message dissemination protocols. Such model of colouring times is strictly weaker in assumptions on the contact patterns compared to the case where node pairs are assumed to meet independently of other node pairs. Moreover, this basic model of node connectivity can be used to derive the full routing latency distribution of ideal epidemic routing as well as to accurately approximate the routing latency distribution of multi-copy routing. At a more general level, we believe that this approach could also be valid for information dissemination in social computing applications where individual actors interact in more complex patterns.

Complex node mobility requires complex models of connectivity. When modelling node connectivity as a set of inter-colouring distributions, we need to collect more parameters from the mobility trace than just the contact rate. Moreover, the calculations proposed in the paper requires computer power to convolute the distributions. However, given the complexity of the underlying systems, it is not surprising that computer power is needed to provide good mod-
els. The key insight that we try to convey is that node contact patterns should be modelled with a sufficient level of fidelity to account for complex node interactions. We believe that the colouring rate model for node connectivity provides a good trade-off between abstraction and fidelity.

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A Proofs

In this appendix we present a semi-formal proof of the proposition that $\perp_C$ models a strictly wider set of contact point processes than the $(S \land \perp_{\leq 1})$ model as discussed in Section 3. We first show that if $(S \land \perp_{\leq 1})$ is true for some point process, it follows that $\perp_C$ is also true. We then proceed to show that the opposite is not true.

**Theorem 1.** $(S \land \perp_{\leq 1}) \Rightarrow \perp_C$

**Proof.** Consider a set of nodes whose contact events constitute a multivariate point process for which $(S \land \perp_{\leq 1})$ is true, meaning that the contact events for each pair of nodes is independent from every other pair of nodes, and the processes are stationary. Moreover, consider an arbitrary colouring process $C(t_0, s)$ and its associated sequence of inter-colouring times $\Delta_0, \Delta_1, \ldots$, we will now prove that for any $i$ the sum $T_i = \sum_{j=1}^{i-1} \Delta_j$ is independent from the next inter-colouring time: $T_i \perp \Delta_i$.

Figure 16 shows an arbitrary colouring process where $i$ nodes have been coloured. The time to colour one more node $\Delta_i$ will depend on all future meeting events $(x, y)$ such that either $x$ or $y$ has been previously coloured but not both. (In the particular case of the figure the first such contact event is between nodes

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3We try to avoid a too heavy use formal notation since it would require first presenting an extensive mathematical framework
Note that since at least one of the nodes in all relevant contact events \((x, y)\) one node is not coloured whereas all previous colour events contain only coloured nodes, we know from the assumption \(\bot_{\leq 1}\) stated in section 3 that all point processes \(P^{(x, y)}\) are independent from all point processes whose events are part of the colouring process up to the \(i\)th colouring. Since the event \((j, k)\) thus is independent from all previous events in the colouring process (including meetings \((a, b)\) and \((g, h)\)), then the time \(\Delta_i\) will also be independent from the time from event \((a, b)\) to \((g, h)\), so \(T_i \perp \Delta_i\).

**Theorem 2.** \(\bot_C \not\Rightarrow (S \wedge \bot_{\leq 1})\)

**Proof.** We will prove this with a counterexample of a contact process that fulfils \(\bot_C\), but not \(\bot_{\leq 1}\). Consider a set of three nodes \(a, b, c\). Assume that contacts always occur according to the following infinite sequence:

\[
\ldots, (a, b), (b, c), (c, a), (a, b), \ldots
\]

Moreover, assume that the time between two such contacts is independent and identically distributed with an exponential distribution. However, the pairwise contacts are clearly not independent of each other since they are ordered, so \(\bot_{\leq 1}\) is not true.

What remains is to show that \(\bot_C\) is true. Any colouring process in this system will have only two inter-colouring times: \(\Delta_1\) and \(\Delta_2\), so \(T_1 = 0, T_2 = \Delta_1, T_3 = \Delta_1 + \Delta_2\). For \(\bot_C\) to hold we need to show that \(T_1 \perp \Delta_1\) (follows immediately, since \(T_1 = 0\)) and \(T_2 \perp \Delta_2\), which is the same as \(\Delta_1 \perp \Delta_2\).

The length of \(\Delta_1\) depends on at what point in the contact sequence the colouring process starts and if the next meeting involves the only coloured node or not (see Figure 17). The next inter-colouring time \(\Delta_2\) is always exactly equal to the time between the next two contacts in the system. By the assumptions of our counterexample this time is independent from all other inter-colouring times. Since \(\Delta_1\) is only decided by the start time and the previous contact times it follows that \(\Delta_1 \perp \Delta_2\), which means that \(\bot_C\) holds. Thus, we have identified an example where \(\bot_C\) is true and \(\bot_{\leq 1}\) is false.

\[\square\]
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