Genetic Improvement of Routing in Delay Tolerant Networks*

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ABSTRACT

Routing plays a fundamental role in network applications, but it is especially challenging in Delay Tolerant Networks (DTNs). These are a kind of mobile ad hoc networks made of e.g. (possibly, unmanned) vehicles and humans where, despite a lack of continuous connectivity, data must be transmitted while the network conditions change due to the nodes' mobility. In these contexts, routing is NP-hard and is usually solved by heuristic "store and forward" replication-based approaches, which however produce relatively low delivery probabilities. Here, we genetically improve two routing protocols widely adopted in DTNs, namely Epidemic and PRoPHET, in the attempt to optimize their delivery probability. First, we dissect them into their fundamental components, i.e., functionalities such as checking if a node can transfer data, or sending messages to all connections. Then, we apply Genetic Improvement (GI) to manipulate these components as terminal nodes of evolving trees. We apply this methodology, in silico, to six test cases of urban networks made of hundreds of nodes, and find that GI produces consistent gains in delivery probability in four cases.

CCS CONCEPTS

• Networks → Routing protocols; Ad hoc networks; • Software and its engineering → Genetic programming.

KEYWORDS

Ad hoc network, delay tolerant networks, epidemic routing, PRoPHET, genetic improvement, genetic programming

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1 INTRODUCTION

One of the most important aspects in networking is the concept of *network protocol*, i.e., a set of well-defined data format and rules that allow nodes in a network to communicate with each other. While efficient routing protocols exist for IP networks, routing in mobile ad hoc networks (MANETs) is still a very active area of research. One particularly challenging kind of MANETs is represented by the

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delay tolerant networks (DTNs), also known as disruption tolerant networks, opportunistic networks or intermittently connected wireless networks. In these contexts, routing is NP-hard [2] and as such it is usually solved by heuristic "store and forward" replication-based approaches, where multiple copies of the same message are moved and stored across nodes in the hope that at least one will eventually reach its destination. Still, the sparsity and mobility of the nodes causes unpredictable meeting patterns and frequent disconnections, which result in relatively low data delivery probabilities (i.e., the probability that a message reaches its destination) even with wellestablished protocols such as Epidemic [1] and PROPHET [5].

Here, we consider the *Genetic Improvement* (GI) [4] of these two protocols. Our methodology consists in the following: first, we dissect the two protocols into their fundamental components, i.e., basic network functionalities such as checking if a node can start transferring data, or sending messages to all connections; then, we apply Genetic Programming (GP) to rearrange these components into evolving trees, in the attempt to maximize the data delivery probability. It is worth stressing that, in principle, this methodology can be easily generalized to other protocols and different kinds of networks. To evaluate the proposed methodology, we perform a broad *in silico* experimentation where we improve Epidemic and PROPHET on six test cases of urban networks made of three different kinds of mobile nodes (pedestrians, cars, and trams). Overall, we find that GI consistently produces a gain in delivery probability.

2 METHODS

We used the strongly typed GP (with a custom repair method) provided by the Jenetics library [7]. The candidate GP individuals, represented as tree structures, are obtained by composing the elements in the terminal and non-terminal sets specified in the Appendix online (https://bit.ly/2Nkyyjm). The non-terminals include basic Boolean operators as well as the inequality test, the if and the sequence operators. The terminals, instead, are obtained by "dissecting" the update() method of the baseline protocols into its *main functional components*, which are then rearranged by GP. This is an important aspect of our proposal: rather than evolving from scratch the entire protocol's logic, which would entail an excessively large, hard-to-explore protocol space, we use available knowledge in the form of protocol basic components, for which we then try to identify a better rearrangement by means of GP. See the Appendix for the GP parameters (default values in Jenetics).

3 EXPERIMENTAL SETUP

For the numerical experiments, we used The ONE (Opportunistic Network Environment) [3]. We considered six different test cases, based on three different maps and two different numbers of agents.

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^{*}An extended version of this work appears in [6].

The maps used are those available in The ONE, namely the city center of Helsinki (that in The ONE is identified as the "default" map), the metropolitan area of Helsinki (i.e., Greater Helsinki), and a Manhattan-like map. In the following, we will refer to these three maps as "Default", "Helsinki" and "Manhattan" respectively.

The simulation time of each DTN simulation is 12 hours (with an update interval of 0.1 seconds), starting after a warm-up period of 1000 seconds of simulation time needed to allow the node mobility to reach steady state conditions. The simulated DTNs are made of three types of mobile nodes (referred to as hosts): pedestrians, cars and trams. Hosts are further divided into 6 groups: two groups of pedestrians, one group of cars and three groups of trams. The groups of pedestrians and cars are composed of 40 or 100 hosts each (depending on the experiments), while in all the experiments the groups of trams are composed of 2 hosts each. During the simulations, a new message of size 500KB-1MB is generated every 25-35 seconds (both the message size and the interval are uniformly sampled in these ranges), with source and destination randomly chosen among all the hosts in the network. Each group has different networking parameters and mobility behaviors, which are specified in the settings file and have been set according to the default parameters of The ONE. As for the mobility behavior, the hosts are randomly placed on the map at the beginning of the simulation, and the destination of each host is chosen randomly between a set of available target points. Pedestrians and cars use the ShortestPathMapBasedMovement mobility model, while trams use the MapRouteMovement model available in The ONE.

4 EXPERIMENTAL RESULTS

In Table 1, we report the comparative results (median across 10 simulations) of the delivery probability obtained by the baseline Epidemic protocol vs that obtained by the best evolved protocol on each test case. We consider as best evolved protocol the one showing the highest delivery probability across 10 runs of GP, and the lowest number of nodes in case of equal delivery probability. For each pairwise comparison, we report also the p-value of the Wilcoxon rank-sum test ($N = 10, \alpha = 0.05$). From the table, it can can observed that GP is able to obtain statistically significant improvements of the delivery probability (p-value $\leq \alpha$) in the Default and Helsinki cases. Finally, the analysis of the fitness trends shown in the Appendix (mean \pm std. dev. of the best delivery probability found at each generation across 10 runs of GP) reveals that in 5 out of 6 test cases the initial GP population shows an average delivery probability lower than the corresponding baseline (median across 10 simulations, shown as a dashed blue line). In all cases, the average delivery probability quickly increases during the evolutionary process.

The same analysis has been performed comparing the PRoPHET routing protocol, as baseline, and the best evolved protocol for each test case, see Table 2. The corresponding fitness trends are shown in the Appendix. The results reveal that also in this case GP is able to obtain statistically significant improvements of the delivery probability (p-value $\leq \alpha$) in all cases except the two Manhattan test cases. As for the fitness trends, it can be noted that in the two Default test cases the average delivery probability of the initial GP population is approximately equal to that of the baseline, while in the remaining cases it is quite lower.

Table 1: Comparison on the delivery probability of Epidemic routing vs the corresponding best evolved protocol.

| Test case | Epidemic | GP | p-value |
|-----------------------|----------|--------|---------|
| Default (40 hosts) | 0.2542 | 0.3342 | 0.005 |
| Default (100 hosts) | 0.2041 | 0.3764 | 0.005 |
| Helsinki (40 hosts) | 0.1910 | 0.2467 | 0.005 |
| Helsinki (100 hosts) | 0.1798 | 0.2887 | 0.005 |
| Manhattan (40 hosts) | 0.1685 | 0.1654 | 0.574 |
| Manhattan (100 hosts) | 0.1774 | 0.1664 | 0.139 |

Table 2: Comparison on the delivery probability ofPRoPHET vs the corresponding best evolved protocol.

| Test case | PRoPHET | GP | p-value |
|-----------------------|---------|--------|---------|
| Default (40 hosts) | 0.2673 | 0.3281 | 0.005 |
| Default (100 hosts) | 0.2307 | 0.3829 | 0.005 |
| Helsinki (40 hosts) | 0.2047 | 0.2447 | 0.005 |
| Helsinki (100 hosts) | 0.2078 | 0.2887 | 0.005 |
| Manhattan (40 hosts) | 0.1719 | 0.1647 | 0.333 |
| Manhattan (100 hosts) | 0.2092 | 0.2109 | 0.646 |

5 CONCLUSIONS

We applied Genetic Programming to improve two replication-based routing protocols widely adopted in intermittently connected networks, namely Epidemic and PRoPHET. In four out of six test cases, GP was able to find protocol implementations that produced significantly better delivery probabilities w.r.t. the two baseline protocols. In the two Manhattan-like test cases, on the other hand, no significant improvement was obtained. In the full paper [6] we also show that: 1) A similar difference in performance is observed when comparing our improved PRoPHET protocols against three variants of PRoPHET proposed in the recent literature; 2) The evolved protocols are in general characterized by a reduced overhead yet larger latencies w.r.t. the baseline protocols; 3) Apart from the Manhattan cases the evolved protocols could generalize across test cases.

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