GraphSeq: a Graph Matching tool for the extraction of mobility patterns

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Abstract— **Mobile computing systems provide new challenges for verification. One of them is the dynamicity of the system structure, with mobility-induced connections and disconnections, dynamic creation and shutdown of nodes. Interaction scenarios have then to consider the spatial configuration of the nodes as a first class concept. This paper presents GraphSeq, a graph matching tool for sequences of configurations developed in the framework of testing research. It aims to analyze test traces to identify occurrences of the successive spatial configurations described in an abstract scenario. We present the GraphSeq algorithm, as well as first experiments using randomly generated graphs, outputs from a mobility simulator, and test traces from a case study in ad hoc networks.**

Keywords- Algorithm; graph matching; testing; mobile computing systems; scenarios

I. INTRODUCTION

Mobile computing systems involve devices (handset, PDA, laptop, intelligent car…) that move within some physical areas, while being connected to networks by means of wireless links (Blue-tooth, IEEE 802.11, GPRS…). Applications in such systems differ from ones in "traditional" distributed systems in many aspects: frequent connections and disconnections of mobile nodes, communication with unknown partners in a local vicinity, context awareness. These novelties raise new challenges for the testing technology.

One issue is how to express interaction scenarios in mobile settings. Scenario descriptions are quite useful to support various test-related activities, such as the representation of requirements [1], of test purposes [2], of test cases [3], or of execution traces [4]. A number of scenario languages have been proposed in the framework of distributed systems, such as UML Sequence Diagrams [5] or Message Sequence Charts (MSCs) [6]. However, they are not sufficient to account for mobile settings. We, therefore, proposed extensions to fill these gaps [7].

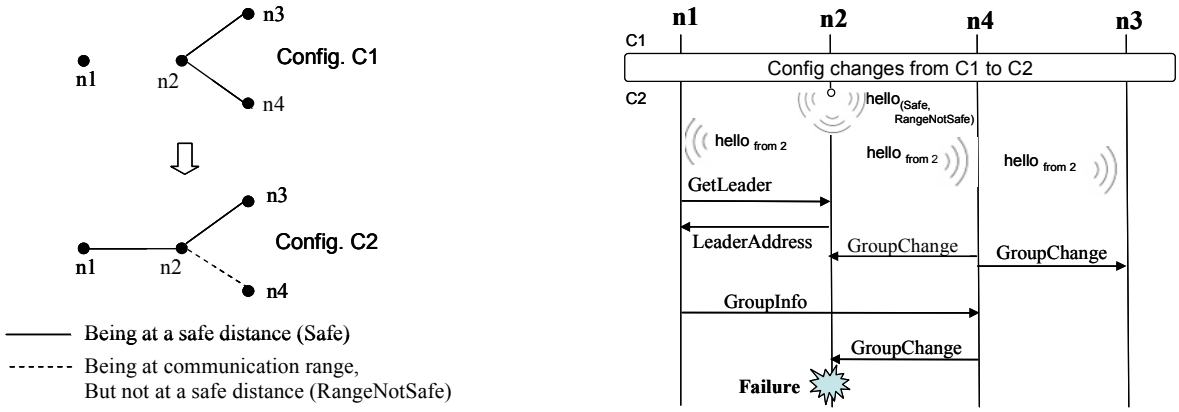
An extension is to consider the spatial relations between nodes as a first class concept. Labeled graphs are used to depict the spatial configurations of a scenario. As a result, the analysis of test traces to identify occurrences of a scenario involves graph matching problems. It led us to develop GraphSeq, a graph matching tool for sequences of configurations.

This paper is organized as follows. Section II explains the background to the development of GraphSeq. Section III introduces the principle of GraphSeq. Based on graph homomorphism building, our tool reasons on sequences of graphs (i.e., sequences of spatial configurations). Then, Section IV presents the algorithms implemented in GraphSeq. First experiments with GraphSeq are reported in Section V, using randomly generated graphs, outputs from a mobility simulator, and test traces from a case study. Section VI concludes the paper.

II. BACKGROUND OF GRAPHSEQ

Scenario languages typically consider interactions in terms of the (partial) orders of communication events. The events are represented by drawing lifelines for the involved entities, and by graphically displaying communication between entities. Some events are ordered while others may interleave in a non-deterministic way, hence yielding partial orders. As argued in [7], when it comes to represent scenarios for mobile computing systems, the focus on event ordering fails to capture other important aspects, such as the spatial configuration of entities.

To illustrate this, let us discuss a case study we performed, a partitionable Group Membership Protocol (GMP) for ad hoc networks [8]. A GMP is a fundamental service lying at the heart of fault-tolerant systems. It aims to maintain a consistent view of who is in the group, in spite of the faults that may affect some nodes. The goal of this GMP is to offer a membership service that accommodates the disconnections induced by mobility (when mobile nodes get out of range). Each group is managed by a leader that may decide to merge with other groups, or to split its group. Decision is based on the notion of safe distance, where the safe distance is strictly lower than communication range. If two nodes are "close enough", this will prevent motion-induced disconnection for some time. A group is then safe if any two members are connected via a path along which all consecutive hosts are at a safe distance (multi-hop communication is allowed). When two groups can merge into a single safe group, they have to do so. When a group is no longer safe, it has to split. Nodes are kept informed about their relative position by "hello" messages that carry location information.



(a) Spatial view (b) Event view

Figure 1. Example of scenario for the GMP case study

Fig. 1 provides a representation of a fail scenario found by testing the GMP [9]. The representation resembles a classical scenario, but with some extensions to account for the mobile setting. Note that the syntax used in Fig. 1 is unimportant, we focus here on the concepts.

The event view (Fig. 1b) shows a specific interleaving of split and merge operations of the protocol. The scenario is triggered by the "hello" message broadcasted by n2 after a change in spatial configuration. Specifically, n2 is no longer at a safe distance from n4, while getting close to n1. The configuration change is shown in Fig. 1a. Both the "GetLeader" message from n1 (initiating a merge) and the "GroupChange" message from n4 (performing the split) are causally related to the "hello" message: when receiving the location data from n2, the other nodes get aware of a change in the topology. At the end of the scenario, a violation of a property of the GMP occurs on node n2. Without entering into the details of the scenario, let us insist on the fact that both the ordering of messages and the topology of nodes are important for the failure to occur. In particular, it is important that:

> The change in spatial configuration breaks the transitive safe path between n4 and n3 (it is precisely the inconsistent treatment of n3 in the group change operations received by n2 that will induce the property violation);
>
> When asked about its leader address, n2 replies before being informed about the split.

As can be seen from Fig. 1, the description of such a scenario needs two connected views, a spatial view (describing the successive topological configurations of the system nodes) and an event view (describing communication and configuration change events). The spatial view consists of a set of labeled graphs, where labels attached to vertices and edges represent relevant attributes of system nodes and of communication links between nodes. In the example, nodes are merely characterized by their id, but tuples of labels may be allowed for applications needing a richer representation of contextual attributes. The event view makes it explicit which communication event occurs in which spatial configuration. It offers special symbols to represent broadcast in a local vicinity (see the hello message). Configuration change events are introduced as global synchronization points.

In our work, scenario descriptions are intended to allow the off-line analysis of execution traces, collected on a test platform with simulation and instrumentation facilities [7, 9]. The comparison of scenarios and traces may serve different objectives, depending on the role of the scenario. For example, requirements scenarios are used to check whether key properties are violated during testing. This offers an automated solution to the test oracle problem, namely how to determine acceptance or rejection of the test outputs. Test purposes are used to check whether desired fragments of behavior are covered at least once during testing. Such treatments are classical when testing distributed systems, and involve comparing the orders of events in the scenario and the trace. In our case, graph algorithms are also needed to identify occurrences of a target scenario. This is due to the need to determine whether the physical nodes appearing in the trace can match symbolic nodes appearing in the spatial view of the scenario. We, therefore, have developed GraphSeq to fulfill this need.

III. PRINCIPLE OF GRAPHSEQ

GraphSeq takes as input two sequences of graphs:

> A sequence $P_0, \ldots, P_{m-1}$ of m graphs coming from a scenario description, called pattern graphs,
>
> A sequence $C_0, \ldots, C_{n-1}$ of n graphs extracted from an execution trace, called concrete configuration graphs.

It computes the set of all matches, where a match identifies a subset of concrete nodes that exhibit the searched sequence of patterns for a certain interval of time. Fig. 2 gives the visual intuition of this. P_0 occurs as

a subgraph of the system in concrete configurations C_1, C_2. Then, there is a system configuration change yielding P_1, and finally P_2 occurs until the system changes to concrete configuration C_7. Note that a given pattern may persist for several successive concrete configurations. The temporal window computed by GraphSeq will be later used when processing the event view of the scenario. For example, if a scenario description involves a communication message *msg* while in configuration pattern P_2 of Fig. 2, we know that *msg* is to be searched in the system subtrace starting at the date of configuration change event C_3->C_4, and ending at the date of C_6->C_7. The match let us also know which concrete nodes should be the sender and receiver of *msg*.

The computation of matches requires a core functionality to compare two graphs, e.g., to determine whether P_0 occurs as a subgraph of C_1. Technically, this calls for graph homomorphism building, a problem well studied in the literature.

Based on such a facility, there is a need to reason on *sequences* of graphs, as illustrated in Fig. 2: this is the specific contribution of GraphSeq. Before introducing the principle of the sequential reasoning, we recall the definition of graph homomorphism and briefly present an existing tool that GraphSeq uses as a core facility for its computation.

A. *Graph homomorphism building*

Let L_V and L_E denote sets of labels for vertices and edges, and let $G = (V, E, \lambda, \ )$ denote a graph structure, where:

V is the set of vertices,

$E \subseteq V \times V$ *is the set of edges,*

$\lambda : V \rightarrow L_V$ is a function assigning labels to vertices,

$: E \rightarrow L_E$ is a function assigning labels to edges.

A graph homomorphism is a mapping between two graphs that respects their structure. It can be defined as follows.

Definition. Let $G_1 = (V_1, E_1, \lambda_1, \ _1)$ and $G_2 = (V_2, E_2, \lambda_2, \ _2)$ be two graphs. An injective function $f : V_1 \rightarrow V_2$ is a graph homomorphism from G_1 to G_2 if:

$\lambda_1(v_1) = \lambda_2(f(v_1))$ for all $v_1 \in V_1$,

For any edge $e_1 = (v_{1s}, v_{1e}) \in E_1$, there exists an edge $e_2 = (f(v_{1s}), f(v_{1e}))$ such that $\ _1(e_1) = \ _2(e_2)$.

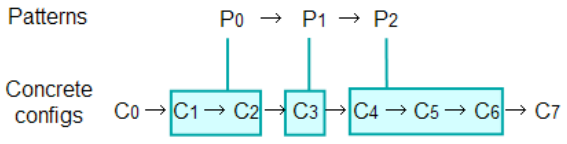


Figure 2. Matching sequences of graphs.

This definition captures the idea of G_1 being matched by a subgraph of G_2. For us, G_1 is expected to be a pattern graph from a scenario, and G_2 a concrete configuration graph from an execution trace. Note that our internal encoding of graphs considers disconnection as an edge with a specific label, so that vertices that are unconnected in a pattern must also be unconnected in a matching concrete configuration.

Classical algorithms for graph homomorphism building can be found in [10, 11]. However, the basic definitions of graph structure and graph homomorphism need to be extended to fulfill our needs. First, it is convenient to assign tuples of labels to vertices in order to allow a richer representation of node attributes. Second, we need label variables in pattern graphs. For example, a node has symbolic id *n1* in a scenario description, and we may detect a matching by a physical node "140.93.130.95", using substitution n1:= "140.93.130.95". To accommodate label variables, a graph homomorphism has now the form *(f, val)*, where *f* is a mapping and *val* a valuation that consistently unifies the labels.

To fulfill these needs, *GraphSeq* uses an existing graph homomorphism tool developed by colleagues at LAAS [12]. Their work addresses the specification of dynamically reconfigurable architectures [13]. Like in our case, this induced matching concerns for graphs with multiple and symbolic labels. The resulting tool is implemented in C++ and can be reused for our purposes. It provides us with facilities to encode graphs with constant labels, variable labels and wildcards (for edges). We made a slight extension to have wildcards for vertices as well.

The syntax of our pattern graphs is exemplified by Fig. 3. Vertices have at most three labels. The first one is mandatory; it is a symbolic id to be matched by the concrete id of a physical node. The other two labels may be used to represent additional attributes of integral types (integers, or enumerated types). Their form may be:

A constant value from the type. In Fig. 3, the attributes of node *id2* have constant values 1 and 2.

A variable name, denoting a value from the type. For example, the first optional attribute of nodes *id1* and *id3* must be identical, but their precise value is let unspecified (variable *v1*).

A wildcard indicating a don't care value, see e.g. the last attribute of node *id1*.

Edges can be labeled by constant values or wildcards.

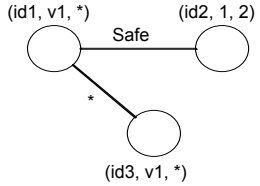


Figure 3. Graph with various forms of label.

In Fig. 3, the connection type is {Safe, RangeNotSafe}. Nodes *id1* and *id2* have a safe distance connection; nodes *id2* and *id3* are disconnected; we do not care about the connection of nodes *id1* and *id3*.

The syntax of concrete configuration graphs is simpler, because only constant labels are allowed. Concrete node ids are strings, while the other labels must be values from the appropriate integral type.

The graph homomorphism tool accommodates the above syntax, and allows us to identify instances of a pattern graph in a concrete configuration graph. It also provides convenient facilities to manage the valuation of pattern graphs. Two supplied functions will be mentioned later:

> MATCHGRAPHS (G_1: Graph, G_2: Graph) that returns the list of all homomorphisms *(f, val)* from G_1 to G_2.
>
> VALUATEGRAPH (G: Graph, V: Valuation) that returns a copy of G with the vertex labels rewritten according to the valuation V.

GraphSeq uses these functions as core facilities to search for matches in the case of *sequences* of graphs.

B. Comparing sequences of graphs

While the problem of comparing two graphs has been extensively studied, there has been relatively little work on the comparison of sequences of graphs (see [14] for a survey on graph matching). Existing work cannot be directly reused for our purposes, because it addresses simpler matching problems (e.g., search for graph subsequence *"g1 g2"* in *"g0 g1 g2 g3"*) or different ones (e.g., infer predictions from the analysis of past time series of graphs). Examples of different problems in the field of dynamic network analysis can be found in [15]. The closest work we found is for the analysis of video images. In [16], the authors search for sequences of patterns (called pictorial queries) into a sequence of graphs extracted from video images. A difference with our work, however, is that the patterns do not involve label variables, and that a pattern node corresponds to at most one object in an image. Hence, to the best of our knowledge, the sequential reasoning implemented by GraphSeq is a new contribution.

In our case, there may be several instances of pattern P_i in concrete configuration C_j, each corresponding to a different valuation of P_i variables. In particular, there may be several instances of the first pattern P_0. Each candidate valuation for P_0 may in turn yield several possibilities for the rest of the sequence, with alternative valuations for the variables that are new in P_1, …, P_n. Variables that are not new are expected to keep the same value as previously. The key of the sequential reasoning is to explore all possibilities, while retaining consistent valuation choices across the sequence, and properly identifying the transition from one pattern to the next. Let us present the properties expected from the search results.

Given two graph sequences $P_0, ..., P_{m-1}$ and $C_0, ..., C_{n-1}$ to be compared, GraphSeq computes the set of all matches, where a match has the following data structure:

```
Match : Valuation val
        int index[0..m]
```

The valuation *val* assigns a concrete value to every label variables appearing in the sequence of pattern graphs. It is a set of pairs *(varName, value)* such that each variable name appears in exactly one pair. In particular, each symbolic identifier of a system node is assigned a unique value by a match.

The index table encodes the temporal window *[start date, end date]* for each pattern. It is defined as follows:

> *index[0]* is the start date of the matching for P_0. That is, the matching starts at $C_{index[0]}$.
>
> For $i > 0$, *index[i]* is the end date of the matching for P_{i-1}. That is, the matching ends after $C_{index[i]}$.

For example, the duration of patterns in Fig. 2 is encoded as follows:

	start date for P_0	end date for P_0	end date for P_1	end date for P_2
index:	1	2	3	6

The encoding means that P_0 starts when the system exhibits configuration C_1 and ends after the system leaves C_2. The start date for pattern P_1 is implicit: it can be retrieved as *1 + end date of* P_0, i.e. *3*. The end date for P1 is then explicitly given, yielding a temporal window *[3, 3]*. Likewise, the temporal window for P_2 is *[4, 6]*.

Let M be a match returned by GraphSeq. Let $[s_i, e_i]$ be the temporal window for each pattern P_i, as indicated by *M.index*. Obviously, we expect that each concrete configuration C_{Si}, ..., C_{ei}, contains the instance of P_i determined by valuation *M.val*.

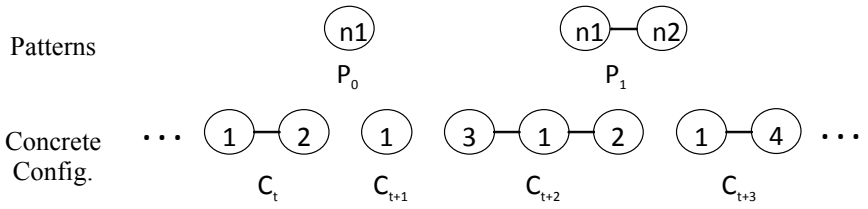


Figure 4. Matching sequences of graphs.

Property 1 – $\forall i \in [0, m\text{-}1]$, $\forall k \in [s_i, e_i]$, there exists a mapping *f* such that:
MATCHGRAPHS (Valuate (P_i, *M.val*), C_k) = *{(f,∅)}*

Note that for each pair *(i, k)*, we are comparing two graphs without label variables, hence the empty valuation for the resulting homomorphism. Also, if *f* exists then it is necessarily unique because the valuation of nodes ids leaves no choice for the homomorphism.

A consistent valuation of variables, and more specifically of symbolic node ids, must also account for nodes that dynamically appear and disappear. Fig. 4 shows an example of patterns with node creation. For the sake of simplicity, the vertices of the graphs are labeled by their id, and we omit all other labels. Pattern P_1 introduces a new node, with id *n2*, that was not present in P_0. The valuation of *n2* must correspond to a concrete node that never showed up in previous configurations matching P_0. For example, the following match should not be retained (although it satisfies Property 1):

val:	{ (n1,“ 1”), (n2, “2”) }		
Index:	t	t+1	t+2

Here, concrete node “2” cannot play the role of a new node *n2*. However, the following match is OK:

val:	{ (n1,“ 1”), (n2, “2”) }		
Index:	t+1	t+1	t+2

The sequential reasoning must thus introduce consideration for nodes that are forbidden in certain configurations. Let F_Id_i be the set of concrete values (determined from *M.val*) for symbolic node ids that do not appear in P_i but appear in some $P_j, j \neq i$.

Property 2 – $\forall i \in [0, m\text{-}1]$, $\forall k \in [s_i, e_i]$, C_k has no vertex with id label in F_Id_i.

Finally, we require that each temporal window for pattern matching is maximal, that is, $s_i\text{-}1$ would not be a start date with valuation *M.val*, and $1+e_i$ would not be an end date. The following match is not maximal, because the temporal window for P_0 could start earlier:

val:	{ (n1,“ 1”), (n2, “3”) }		
Index:	t+1	t+1	t+2

Property 3 – $\forall i \in [0, m\text{-}1]$, let P_i' = Valuate (P_i, *M.val*). Temporal window $[s_i, e_i]$ is maximal, that is:

$s_i = 0$, or there is no homomorphism from P_i' to $C_{Si\text{-}1}$, or $C_{Si\text{-}1}$ contains a vertex with id in F_Id_i.

$e_i = n\text{-}1$, or there is no homomorphism from P_i' to C_{1+ei}, or C_{1+ei} contains a vertex with id in F_Id_i.

Property 3 implies that start and end dates really correspond to configuration change events. A scenario with two successive identical patterns would yield no match. Transition from P_i to P_{i+1} must be triggered by a change in connectivity or attributes of concrete nodes, the introduction of a node, the suppression of a node, or any combination of these.

With the introduction of new nodes, the computation of start and end dates may become tricky. For example, in Fig. 4, if concrete node “1” plays the role of *n1*, the end date of P_0 may be *t+1* (before appearance of concrete nodes “2” or “3”), *t+2* (before appearance of “4”) or later. Depending on which choice is taken, candidate start dates for P_0 may, or not, yield a maximal temporal window.

The purpose of GraphSeq is to explore alternative choices, so as to build the set of all matches satisfying properties 1, 2 and 3.

IV. ALGORITHM OF GRAPHSEQ

The implementation of GraphSeq is about 2K lines of C++ code (not including the graph homomorphism tool). A detailed presentation of the algorithm can be found in a technical report [17]. For space constraints, we only provide a high-level view of the algorithm in this paper. We then discuss complexity issues.

A. High-level view of the search for matches

In order to gradually build matches, *GraphSeq* uses an intermediate data structure called *PartialMatch*:

```
PartialMatch :   Valuation val
                 int index[0..m]
                 int depth
```

PartialMatch is thus like *Match*, but with an additional *depth* field. The depth value gives the number of patterns that have been successfully matched so far. A depth of *i* indicates that patterns $P_0, \ldots, P_{i-1}$ have been matched, but $P_i, \ldots, P_{m-1}$ are still to be processed. Back to the example in Fig. 4, a partial match could be:

val:	{ (n1,“ 1”)}		
index:	t+1	t+1	-1
depth:	1		

The valuation *val* assigns a value only to variables of the processed patterns. In *index*, the spurious value -1 means that end dates of unmatched patterns are not determined yet.

A partial match of depth *i* is extended by the processing of the next P_i, yielding a partial match of depth *i+1*. When a partial match has been extended up to depth *m*, then a complete match has been found.

GraphSeq uses depth-first search (DFS) to extend partial matches. That is, if a partial match has several possible extensions, the tool will explore as far as possible along each branch before backtracking. The DFS control structure is shown in Fig. 5. The algorithm involves steps

indicated in bold characters: preprocessing of pattern data, creation of partial matches of depth *1*, extension of partial matches, final check before retaining a match.

```
Preprocess pattern data
Let L be an empty stack of PartialMatch elements
For (s=0; s≤n-m; s++)
  build all partial matches of depth 1 with
  start date s, push each of them in L
  While L is not empty
    Let pm = pop (L)
    If (pm.depth < m)
       Build all one step extensions of pm,
       push each of them in L
    Else   // found
      If (FINALCHECK(pm))
        Write pm.val and pm.index in output file
      Endif
    Endif
  End While
End For
```

Figure 5. DFS control structure of GraphSeq.

B. Steps for searching matches

A preprocessing step is performed before the search is entered. Its first task is to identify nodes that are forbidden in some configurations, hence preparing the checking of Property 2. They can be nodes that already appeared in the past or will appear for the first time in the future. For the example in Fig. 4, the analysis determines that configurations matching P_0 should not contain the node playing the role of *n2* in the future. The second task of the preprocessing step is to analyze the differences between two successive patterns. It is used to facilitate the determination of start and end dates of the patterns (see Property 3). The analysis distinguishes two classes of transitions $P_i \rightarrow P_{i+1}$:

after the transition, concrete configurations matching P_{i+1} cannot match P_i.

after the transition, concrete configurations matching P_{i+1} can match P_i as well.

In the first class, there is only one possible end date for P_i: the date j such that C_{j+1} no longer matches P_i. The second class occurs when the appearance of a node is possibly the only trigger of the transition. Then, the search must consider a set of candidate end dates, namely all intermediate dates before P_i ceases to be matched. For example, in Fig. 4, P_0 could end at $t+1$, $t+2$ or later.

When the search is entered, we first build partial matches of depth 1. The corresponding algorithm is described in Fig. 7a, with auxiliary functions in Fig. 7b. Given a candidate start date s, the search is initialized by looking at all possible instances for P_0. Deciding whether s is really a start date depends on ForbiddenNodes (0), the forbidden nodes at P_0. If this set is empty, we do not retain s as a candidate start date if C_{s-1} already matched P_0 with the proposed valuation. But if the set is not empty, we always retain s. For example, in Fig. 4, $s=t+1$ is retained as a candidate start date for a partial match with valuation *{(n1, 1)}* because ForbiddenNodes (0) is not empty. Decision of whether s fulfills Property 3 will be taken by the final check (see the general control structure in Fig. 5), when all symbolic ids have a valuation in ForbiddenNodes (0), and in particular node *n2*. As regards the end date, the preprocessing step tells us whether one or several dates should be considered. The function COMPUTEENDDATE() detects an end of matching when it is no longer possible to find an homomorphism. Note that the last two parameters of the function would also allow end-of-matching detection in the following case: a concrete configuration graph contains forbidden nodes. This detection mode will be used when computing the one-step extensions of a partial match. It is not used here (the relevant parameters are set to ∅ and NULL by the call statement), because no concrete id of forbidden nodes is known at this stage. A different partial match is built for each date, e.g., $s=t+1$ and valuation *{(n1, 1)}* yield several partial matches with end date $t+1$, $t+2$, …

The search then gradually extends a partial match of depth d to produce partial matches of depth $d+1$, until $d=m$ or the extension fails. Here, the start date is fixed: it comes just after the end of matching of the previous pattern. The processing of the end date is as already explained above. The extension accounts for forbidden nodes. Their concrete id is known if they appeared in the previous patterns, and it is ensured that they are not present in concrete configurations matching the current pattern. Also, if the current P_d introduces new nodes to valuate, it is checked that they never showed up since the start date of P_0.

When we get a complete match, Properties 1 and 2 are ensured by construction. For Property 3, we still need to verify the start date for P_0: this is done by the final check. The final check is shown in Fig. 6. In the case where P_0 has forbidden nodes (like in Fig. 4), the search algorithm retained potential start dates s even if C_{s-1} already matched P_0. We must now decide whether or not s is a real start date. Decision will be negative if C_{s-1} matches P_0 and does not contain any of the forbidden nodes. Back to the example in Fig. 4, the final check will accept $t+1$ as a start date for a match with *n2*:= "2", but not for *n2*:= "3" or *n2*:= "4". It ensures that the temporal window of P_0 is indeed maximal.

```
Boolean FINALCHECK (PartialMatch pm)
   If (pm.index[0]=0 || ForbiddenNodes(0)=∅)
      return (true)
   Else
      Let P' = VALUATEGRAPH (P0, pm.val)
      Let H= NEWMATCHGRAPHS (P', C pm.index[0]-1,
       ForbiddenNodes(0), pm.val)
      If (H is empty)
         Return (true)
      Else return (false)
      Endif
   Endif
End FINALCHECK
```

Figure 6. Final check befor outputting.

```
// build all partial matches of depth 1
// with start date s,
// push each of them in L
Let H = MatchGraphs (P0, Cs)
While H is not empty
  Extract h from H
  Let P' = ValuateGraph (P0, h.val)
  // Can s be a start date for P0?
  Let start_OK = true
  If (s > 0 && ForbiddenNodes (0)= ∅)
    Let H' = MatchGraphs (P', Cs-1)
    If (H' is not empty)
         // previous config did match
         // --> not a start date
      start_OK = false
    Endif
  Endif
  // Now, check the end date
  If (start_OK = true)
    Let end = ComputeEndDate(P', s, ∅,NULL)
    If (StopBefore(0))
    // can stop at an intermediate date
      For (j=s; j<=min(end,n-m); j++)
        let pm = CreatePartialMatchD1(h.val,s,j)
        push pm in L
      End for
    Else If (end ≤ n-m)
         // end date is not too late
      let pm = CreatePartialMatchD1 (h.val,s,end)
      push pm in L
    Endif
  Endif
End While
```

(a) Core algorithm for building the matches

```
ListOfHomomorphisms NewMatchGraphs
(Graph G1, Graph G2,SetOfStrings ForbidIds,
Valuation v)
   // None of the forbidden ids in G2?
   For each f in ForbidIds
     Let concreteId be the value v(f)
     If (concreteId exists in G2)
         Return (empty list)
     End if
   End For
   Return (MatchGraphs (G1, G2))
End NewMatchGraphs

int ComputeEndDate (Graph G, int start,
            SetOfStrings ForbidIds, Valuation v)
   Let i = 1
   Repeat
     Let H = NewMatchGraphs (G, Cstart+I,ForbidIds,v)
      If (H is not empty) then
         i = i+1
      Endif
   until (H is empty or start+i = n)
   return (start+i-1)
End ComputeEndDate

PartialMatch CreatePartialMatchD1 (Valuation v,
                                   int start, int end)
   Let pm be a Partial match
   pm.val = v
   pm.index[0] = start
   pm.index[1] = end
   For (i=2; i≤m; i++)
      pm.index[i] = -1
   End For
   pm.depth = 1
   return (pm)
End CreatePartialMatchD1
```

(b) Auxiliary functions

Figure 7. Partial matches of depth 1 starting at date s.

C. Complexity of GraphSeq algorithm

Graph homomorphism building is an NP-complete problem. Let *Np* be the number of nodes of a pattern graph, and *Nc* be the number of nodes of a concrete configuration graph. In the worst case, when every pattern node can be mapped to every concrete node, function MatchGraphs () has an exponential complexity $O(Nc^{Np})$. In the favorable case when every pattern node can be mapped to at most one concrete node, complexity is only quadratic in *Np* and N_C.

Let us now discuss the complexity added by the sequential reasoning. We are comparing a sequence of *m* patterns to a sequence of *n* concrete configurations.
Generally speaking, the cost of auxiliary treatments (pre-processing, final check) exhibits an increase that is at most quadratic in the number and size of the graphs. Complexity problems only come from the repeated calls to MatchGraphs (). For the sake of simplicity, let us abstract the cost of a call by *H* (as explained above, H is actually a function of the compared graphs, and may range from quadratic to exponential complexity class). Two cases can be distinguished for the sequential search: 1) there is no node creation in the sequence of patterns, and 2) there are node creations.

In the first case, for each candidate start date *s*, the valuation of P_0 assigns a concrete id to every nodes. Every subsequent comparison of graphs yields at most one possibility for the mapping of nodes. The total cost is then dominated by the cost of comparing P_0 to each C_s, yielding complexity $O(nH)$.

In the second case, the impact of node creation is twofold. First, when P_{i+1} is processed, we must investigate a valuation for node ids that are new with respect to $P_0, \ldots, P_i$.

This may involve several candidate mappings, defining different extensions of the current partial match. Second, given a valuation for new node ids, the algorithm must consider many candidate end dates if transition P_i-> P_{i+1} is triggered solely by the new nodes, yielding again different partial match extensions. Combining these effect, a pessimistic complexity estimate is $O(n^m H^m)$. In

the worst case for H, we thus have an exponential increase in both the number and size of patterns.

It is obvious that GraphSeq could not process large sequences of (large) graphs. However, we argue that it still is practically useful for its purpose, namely the analysis of test traces against graphical scenarios.

Graphical scenarios typically involve few entities, the interactions of which are the focus. For example, the scenarios we derived from the GMP case study (from the analysis of requirements, or from the analysis of failures observed during testing) never involved more than five symbolic nodes. This is comparable to what can be seen in other work, and anyway the graphical representation could not accommodate a very large number of lifelines. Similarly, it is expected that the number of successive patterns in scenarios remain tractable (e.g., typically two or three successive patterns in a GMP scenarios).

The size and number of concrete configurations is much less critical to the complexity of the analysis. Note that in-house testing rarely involves very large experimental settings. For example, in [18, 19, 20, 21, 22], the experimental configurations involve from 5 to 50 nodes. The duration of a test run range from 28s to 15 minutes. First experimentation with GraphSeq shows that such configurations are well in the reach of the tool.

V. VALIDATION AND EXPERIMENTS OF GRAPHSEQ

GraphSeq has been validated by using hundreds of randomly generated sequences of graphs. We also report on first experiments demonstrating the usage of *GraphSeq* to extract mobility patterns. They involve the analysis of test traces from the GMP case study, and of outputs from a mobility simulator.

A. Validation of GraphSeq

We performed a number of tests to validate *GraphSeq*. We first started with small examples that were manually produced (e.g., the example in Fig. 4 was included as one test case), but quickly came to the conclusion that we would need an automated solution for both the generation of graph sequences and the analysis of results. We developed a tool that produces random sequences of graphs P_i and C_j such that, by construction, C_j contains at least one match. The *GraphSeq* results can then be automatically analyzed and a fail verdict is issued if the expected match is not found. Note that *GraphSeq* may find several matches, but the test verdict only concerns the one known to be there by construction.

The random generation can be parameterized, and we produced about 900 test cases exhibiting various characteristics:

- Number of patterns for each sequence from 1 to 5,
- Number of concrete configurations from 1 to 100,
- Number of nodes in patterns from 1 to 5,
- Number of nodes in concrete configurations from 1 to 25,
- For each individual P_i, duration of a matching from 1 to 20 steps in the concrete configurations.
- The transitions from P_i to P_{i+1} may involve a change in a node label, in an edge label, a node that appears, that disappears, or any combination (up to 5 changes).

The test tool proved very useful to debug *GraphSeq*, and to perform regression verification after changes in the C++ code.

B. GraphSeq applied to the GMP case study

The purpose of GraphSeq is to allow us to identify all occurrences of a scenario in a test trace. The graph matching part corresponds to the processing of the spatial view, to be supplemented by an analysis of the events occurring in the temporal window of the match, for the identified nodes. The principle of scenario extraction can be exemplified using the GMP case study mentioned in Section 2.

In this case study [9], our test experiments reported numerous violations of the protocol requirements defined in [8]. It was not possible to manually examine all of them, but a sample of 164 fail cases were selected and analyzed. The scenario shown in Fig. 1 is one of the outcomes from this analysis. Note that some observed failures could correspond to the same scenario occurring several times during the runs.

Manual analysis was tedious, and we now demonstrate how automated scenario extraction can be performed with the help of GraphSeq. In order to show an example of patterns with node creation, we investigate a variant of the previous scenario that should yield exactly the same failure. This variant differs in the spatial view (Fig. 8). Node n1 does not exist in the initial configuration. It then wakes up at a safe distance from n2, while n2 gets away from n4. After the configuration change event, communication events are like in Fig. 1b.

TABLE I. PARAMETERS FOR THE GMP RUNS

Parameters	Value
Number of nodes	Random in [6..15]
Start date of nodes	Random in [0..300] s
Death date of nodes	Random in [StartDate..300] s
Transmission range	300 m
Safe Distance	140 m
Maximal speed	10 $m.s^{-1}$
Mobility model	Random movement at maxi speed
Duration of a run	5 minutes

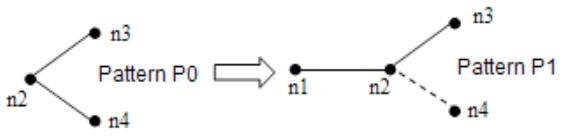


Figure 8. Spatial view of the scenario variant.

TABLE II. PARAMETERS USED FOR THE SIMULATION RUN

Parameters of the mobility model	Value
Simulation duration (1 simulation step / second)	15 minutes
Number of nodes	15
Acceleration (Max Speed/10)	4 $m.s^{-2}$
Max Speed	40 $m.s^{-1}$
Map: Number of freeways Number of lanes	 2 6
Distance SD	40 m

The experiments consist in testing the GMP implementation, recording execution traces, and searching for occurrences of the scenario variant. A total number of 100 test runs were generated with parameters in Table 1.

GraphSeq returns 75 matches of the spatial view in the execution traces. This allowed us to extract the subtraces of communication events occurring during the matches. Note that, at the date of the writing of this paper, the analysis of communication events has not been automated yet. We thus had to compare manually the events in the scenario and the subtraces. In 48 cases, the communication events did not match. The remaining 27 corresponded to occurrences of the scenario. The GMP exhibited the expected failure in each of these cases. This allowed us not only to confirm our diagnosis of the problem, but also to discriminate between fail cases that match or do not match the identified scenario.

C. *Connection to a mobility simulator*

The GMP case study used a very simple management of node movement, with GPS stubs delivering random coordinates for each node. However, more realistic test platforms would include a mobility simulator.

Mobility simulators manage the relative positions of nodes according to some mobility models, and produce contextual data (e.g., location-based data) needed by applications. Examples of test platforms with a mobility simulator can be found in [23, 24]. The data produced at each simulation step may be used to identify the configurations of the tested system. To demonstrate the concept, we experimented with the connection of *GraphSeq* to a simulation tool.

We chose a mobility simulator developed at the University of Southern California, USA, as part of the IMPORTANT (Impact of Mobility Patterns On Routing proTocol in the mobile Ad hoc NeTworks) framework [25]. The tool is freely available on the web[1]. It offers a rich set of parameterized mobility models, including Reference Point Group, Freeway and Manhattan mobility models. The generated traces are compatible with the ns-2 network simulator.

The connection of *GraphSeq* to such a mobility simulator requires the development of an interfacing component (see Fig. 9) that abstracts the raw simulation data into a sequence of configuration graphs. In our experiments, the raw data are the position of nodes at each simulation step. Then, the abstraction consists in assigning edge labels according to the distance of nodes, like in the GMP case study.

We made trials with various mobility models, different parameterizations of the models and different patterns to be searched. We describe here an example of run using the freeway model.

This model emulates the motion behavior of vehicles in a freeway. It has the following characteristics:

- Each mobile node is restricted to its lane on the freeway.
- The velocity of a mobile node is temporally dependent on its previous velocity.
- If two mobile nodes on the same freeway lane are within a distance SD, the velocity of the following node cannot exceed the velocity of the preceding node.

Table 2 provides the parameters used for the example run. The map was built using predefined fragments of freeways and lanes, available in the simulation environment.

Our format translator extracts 345 different configuration graphs from the simulation trace. The concrete ids of mobile nodes are labeled "N0", "N1", "N2",… The edges representing the spatial relations between two mobile nodes depend on their distance *d* and are defined as follows:

- $0 < d < 140$m: edge = 1,
- $140 \leq d \leq 300$m: edge = 2,
- $d > 300$m: nodes are disconnected (300 m is thus the transmission range).

The pattern graphs are as in Fig. 1a, with *Safe* =1 and *RangeNotSafe* = 2.

GraphSeq searches for the sequence of patterns in the 345 concrete configurations, and returns 11 matches. Their manual extraction would have been unfeasible.

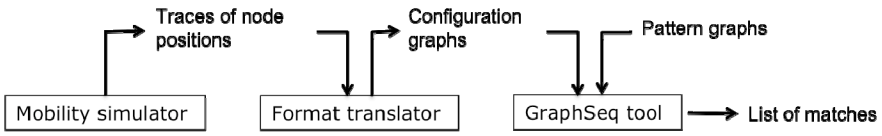


Figure 9. Connecting *GraphSeq* to a mobility simulator

[1] http://nile.usc.edu/important/

VI. CONCLUSION AND PERSPECTIVES

This paper has presented GraphSeq, a graph matching tool developed to process the spatial view of interaction scenarios in mobile settings. The spatial view explicitly represents the dynamically changing topology of system nodes, with mobility induced connections and disconnections, as well as dynamic creations and shutdowns of nodes.

GraphSeq takes as inputs two sequences of labeled graphs, intended to come respectively from a scenario and a trace, and generates the set of all matches. The corresponding algorithm uses existing facilities for graph homomorphism building, taken from another graph tool developed by colleagues at LAAS. Here, the novelty of our tool consists in reasoning on sequences of spatial configurations. Specifically, the accounting for scenarios where nodes dynamically appear and disappear proved a tricky issue. We thoroughly validated GraphSeq by challenging test cases that were manually designed, and then by hundreds of randomly generated graph sequences. We also started proof-of-concept experiments to demonstrate the usage of GraphSeq in connection with a mobility simulator, and in relation with a case study that is representative of mobile computing problems.

Our work will now tackle the integrated processing of the spatial and event views of scenarios. Joint work with the Technological University of Budapest has defined a UML profile for sequence diagrams in mobile settings, as well as a semantics for them [17]. This will allow us to complete the automated analysis of test traces by matching the communication events.

ACKNOWLEDGMENT

This work was partially supported by the ReSIST network of Excellence (IST 026764) and the HIDENETS project (IST 26979) funded by the European Union under the Information Society Sixth Framework Program. We wish to thank Khalil Drira, Karim Guennoun and Ismael Bouassida for having made their graph tool available to us, and for having spent time to respond to our questions.

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