Extracting Hidden Groups and their Structure from Streaming Interaction Data

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Abstract

When actors in a social network interact, it usually means they have some general goal towards which they are collaborating. This could be a research collaboration in a company or a foursome planning a golf game. We call such groups *planning groups*. In many social contexts, it might be possible to observe the *dyadic interactions* between actors, even if the actors do not explicitly declare what groups they belong too. When groups are not explicitly declared, we call them *hidden groups*. Our particular focus is hidden planning groups. By virtue of their need to further their goal, the actors within such groups must interact in a manner which differentiates their communications from random background communications. In such a case, one can infer (from these interactions) the composition and structure of the hidden planning groups. We formulate the problem of hidden group discovery from streaming interaction data, and we propose efficient algorithms for identifying the hidden group structures by isolating the hidden group's non-random, planning-related, communications from the random background communications. We validate our algorithms on real data (the Enron email corpus and Blog communication data). Analysis of the results reveals that our algorithms extract meaningful hidden group structures.

1 Introduction

Communication networks (telephone, email, Internet chatroom, etc.) facilitate rapid information exchange among millions of users around the world, providing the ideal environment for groups to plan their activity undetected: their communications are embedded (hidden) within the myriad of unrelated communications. A group may communicate in a structured way while not being forthright about its existence. However, when the group must exchange communications to plan some activity, their *need* to communicate usually imposes some structure on their communications. We develop statistical and algorithmic approaches for discovering such hidden groups that *plan* an activity. Hidden group members may have non-planning related communications, be malicious (e.g. a terrorist group) or benign (e.g. a golf foursome). We liberally use "hidden group" for all such groups involved in planning, even though they may not intentionally be hiding their communications.

00	**A→C**	Golf tomorrow? Tell everyone.
05	**C→F**	Alice mentioned golf tomorrow.
06	**A→B**	Hey, golf tomorrow? Spread the word
12	**A→B**	Tee time: 8am; Place: Pinehurst.
13	**F→G**	Hey guys, golf tomorrow .
13	**F→H**	Hey guys, golf tomorrow .
15	**A→C**	Tee time: 8am; Place: Pinehurst.
20	**B→D**	We're playing golf tomorrow.
20	**B→E**	We're playing golf tomorrow.
22	**C→F**	Tee time: 8am; Place: Pinehurst.
25	**B→D**	Tee time: 8am; Place: Pinehurst.
25	**B→E**	Tee time 8am, Pinehurst.
31	**F→G**	Tee time 8am, Pinehurst.
31	**F→H**	Tee off 8am,Pinehurst.

(a)

00	**A→C**
05	**C→F**
06	**A→B**
12	**A→B**
13	**F→G**
13	**F→H**
15	**A→C**
20	**B→D**
20	**B→E**
22	**C→F**
25	**B→D**
25	**B→E**
31	**F→G**
31	**F→H**

(b)

Figure 1: Streaming hidden group with two waves of planning (a). Streaming group without message content – only time, sender id and receiver id are available (b).

The tragic events of September 11, 2001 underline the need for a tool which aides in the discovery of hidden groups during their *planning* stage, before implementation. One approach to discovering such groups is using *correlations* among the group member communications. The *communication graph* of the society is defined by its actors (nodes) and communications (edges). We do not use communication content, even though it can be informative through some natural language processing, because such analysis is time consuming and intractable for large datasets. We use only the time-stamp, sender and recipient ID of a message.

Our approach of discovering hidden groups is based on the observation that the pattern of communications exhibited by a group pursuing a common objective is different from that of a randomly selected set of actors: any group, even one which tries to hide itself, must communicate regularly to plan. One possible instance of such correlated communication is the occurrence of a *repeated communication pattern.* Temporal correlation emerges as the members of a group need to systematically exchange messages to plan their future activity. This correlation among the group communications will exist throughout the planning stage, which may be some extended period of time. If the planning occurs over a long enough period, this temporal correlation will stand out against a random background of communications and hence can be detected.

2 Streaming Hidden Groups

Unlike in the cyclic hidden group setting [9] where all of the hidden group members communicate within some characteristic time period, and do so repeatedly over a consecutive sequence of time periods. A *streaming hidden group* doesn't obey such strict requirements for its communication pattern. Hidden groups don't necessarily display a fixed time-cycle, during which all members of group members exchange messages, but whenever a step in the planning needs to occur, some hidden group member initiates a communication, which percolates through the hidden group. The hidden group problem may still be formulated as one of finding repeated (possibly overlapping) communication patterns. An example of a streaming hidden group is illustrated in Fig. 1(a) with the same group planning golf game. Given the message content, it is easy to identify two "waves" of communication. The first wave (in darker font) establishes the golf game; the second wave (in lighter font) finalizes the game details. Based on this data, it is not hard to identify the group

and conclude that the "organizational structure" of the group is represented in Fig. 2 to the right (each actor is represented by their first initial). The challenge, once again, is to deduce this same information from the communication stream *without* the message contents Fig. 1(b). Two features that distinguish the stream from the cycle model are:

(i) communication waves may overlap, as in Fig. 1(a);

(ii) waves may have different durations, some considerably longer than others.

The first feature may result in bursty waves of intense communication (many overlapping waves) followed by periods of silence. Such a type of communication dynamics is hard to detect in the cycle model, since all the (overlapping) waves of communication may fall in one cycle. The second can be quantified by a propagation delay function which specifies how much time may elapse between a hidden group member receiving the message and forwarding it to the next member; sometimes the propagation delays may be large, and sometimes small. One would typically expect that such a streaming model would be appropriate for hidden groups with some organizational structure as illustrated in the tree in Fig. 2. We present algorithms which discover the streaming hidden group and its organizational structure without the use of message content.

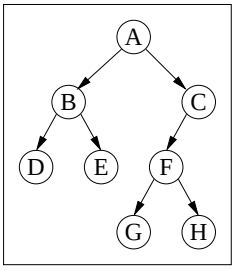


Figure 2: Group structure in Fig. 1

We use the notion of communication frequency in order to distinguish non-random behavior. Thus, if a group of actors communicates unusually often using the same chain of communication, i.e. the structure of their communications persists through time, then we consider this group to be statistically significant and indicative of a hidden group. We present algorithms to detect small frequent tree-like structures, and build hidden structures starting from the small ones.

3 Our Contributions

We present efficient algorithms which not only discover the streaming hidden group, but also its organizational structure *without the use of message content*. We use the notion of communication frequency in order to distinguish non-random behavior. Thus, if a group of actors communicates unusually often using the same chain of communication, i.e. the structure of their communications persists through time, then we consider this group to be statistically anomalous. We present algorithms to detect small frequent tree-like structures, and build hidden structures starting from the small ones. We also propose an approach that uses new cluster matching algorithms together with a sliding window technique to track and observe the evolution of hidden groups over time. We also present a general query algorithm which can determine if a given hidden group (represented as a tree) occurs frequently in the communication stream. Additionally we propose efficient algorithms to obtain the frequency of general trees and to enumerate all statistically significant general trees of a specified size and frequency. Such algorithms are used in conjunction with the heuristic algorithms and similarity measure techniques to verify that a discovered tree-like structure actually occurs frequently in the data. We validate our algorithms on the Enron email corpus, as well as the Blog communication data.

Paper Organization. First we consider related work, followed by the methodologies for the streaming hidden groups and tree mining in Section 5. Next we present similarity measure methods in Section 10. We present experiments on real world data and validation results in Section 10 followed by the summary and conclusions in Section 14.

4 Related Work

Identifying structure in networks has been studied extensively in the context of clustering and partitioning (see for example [3, 7, 8, 14, 4, 11, 16, 17, 20, 22, 23, 24, 25, 30]). These approaches focus on static, non-planning, hidden groups. In [28] Hidden Markov models are the basis for discovering planning hidden groups. The underlying methodology is based on random graphs [10, 21] and some of the results on cyclic hidden groups were presented in [9]. In our work we incorporate some of the prevailing social science theories, such as homophily ([29]), by incorporating group structure. More models of societal evolution and simulation can be found in [12, 13, 19, 34, 35, 31, 32, 26] which deal with dynamic models for social network infrastructure, rather than the dynamics of the actual communication behavior.

Our work is novel because we detect hidden groups by only analyzing communication intensities (and not message content). The study of streaming hidden groups was initiated in [6], which contains some preliminary results. We extend these results and present a general query algorithm which can find if a given hidden group (represented as a tree) occurs frequently in the communication stream, which we extended to algorithm to obtain the frequency of general trees and to enumerate all statistically significant general trees of a specified size and frequency. Such algorithms are used in conjunction with the heuristic algorithms and similarity measures to verify that a discovered tree-like structure actually occurs frequently in the data.

Erickson, [15], was one of the first to study secret societies. His focus was on general communication structure. Since the September 11, 2001 terrorist plot, discovering hidden groups became a topic of intense research. For example it was understood that Mohammed Atta was central to the planning, but that a large percent of the network would need to be removed to render it inoperable [36, 27]. Krebs, [27] identified the network as sparse, which renders it hard to discover through clustering in the traditional sense (finding dense subsets). Our work on temporal correlation would address exactly such a situation. It has also been observed that terrorist group structure may be changing [33], and our methods are based on connectivity which is immune to this trend. We assume that message authorship is known, which may not be true, Abbasi and Chen propose techniques to address this issue, [2].

5 Problem Statement

A hidden group communication structure can be represented by a directed graph. Each vertex is an actor and every edge shows the direction of the communication. For example a hierarchical organization structure could be represented by a directed tree. The graph in Figure 3 to the right is an example of a communication structure, in which actor A "simultaneously" sends messages to B and C; then, after receiving the message from A, B sends messages to C and D; C sends a message to D after receiving the messages from A and B. Every graph has two basic types of communication structures: *chains* and *siblings*. A *chain* is a path of length at least 3, and a *sibling* is a tree with a root and two or more children, but no other nodes. Of particular interest are chains and sibling trees with three nodes, which we denote *triples*. For example, the chains and sibling trees of size three (triples) in the communication structure above are: $A \to B \to D$; $A \to B \to C$; $A \to C \to D$; $B \to C \to D$; $A \to (B, C)$; and, $B \to (C, D)$. We suppose that a hidden group employs a communication structure that can be represented by a directed graph as above. If the hidden group is hierarchical, the communication graph will be a tree. The task is to discover such a group and its structure based solely on the communication data.

If a communication structure appears in the data many times, then it is

likely to be non-random, and hence represent a hidden group. To discover hidden groups, we will discover the communication structures that appear many times. We thus need to define what it means for a communication structure to "appear". Specifically, we consider chain and sibling triples (trees of size three). For a chain $A \to B \to C$ to appear, there must be communication $A \to B$ at time t_{AB} and a communication $B \to C$ at time t_{BC} such that $(t_{BC} - t_{AB}) \in [\tau_{min}, \tau_{max}]$. This intuitively represents the notion of causality, where $A \to B$ "causes" $B \to C$ within some time interval specified by $[\tau_{min}, \tau_{max}]$. A similar requirement holds for the sibling triple $A \to B, C$; the sibling triple appears if there exists t_{AB} and t_{AC} such that $(t_{AB} - t_{AC}) \in [-\delta\ \delta]$. This constraint represents the notion of A sending messages "simultaneously" to B and C within a small time interval of each other, as specified by δ. For an entire graph (such as the one above) to appear, every chain and sibling triple in the graph must appear using a single set of times. For example, in the graph example above, there must exist a set of times, $\{t_{AB}, t_{AC}, t_{BC}, t_{BD}, t_{CD}\}$, which satisfies all the six chain and sibling constraints: $(t_{BD} - t_{AB}) \in [\tau_{min}, \tau_{max}]$, $(t_{BC} - t_{AB}) \in [\tau_{min}, \tau_{max}]$, $(t_{CD} - t_{AC}) \in [\tau_{min}, \tau_{max}]$, $(t_{CD} - t_{BC}) \in [\tau_{min}, \tau_{max}]$, $(t_{AB} - t_{AC}) \in [-\delta, \delta]$ and $(t_{BD} - t_{BC}) \in [-\delta, \delta]$. A graph appears multiple times if there are disjoint sets of times each of which is an appearance of the graph. A set of times *satisfies* a graph if all chain and sibling constraints are satisfied by the set of times. The number of times a graph appears is the maximum number of disjoint sets of times that can be found, where each set satisfies the graph. Causality requires that multiple occurrences of a graph should monotonically increase in time. Specifically, if t_{AB} "causes" t_{BC} and t'_{AB} "causes" t'_{BC} with $t'_{AB} > t_{AB}$, then it should be that $t'_{BC} > t_{BC}$. In general, if we have two disjoint occurrences (sets of times) $\{t_1, t_2, \ldots\}$ and $\{s_1, s_2, \ldots\}$ with $s_1 > t_1$, then it should be that $s_i > t_i$ for all i. A communication structure which is frequent enough becomes statistically significant when its frequency exceeds the expected frequency of such a structure from the random background communications. The goal is to find all statistically significant communication structures, which is formally stated in the following algorithmic problem statement.

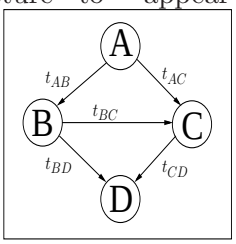


Figure 3: Target group.

Input: A communication data stream and parameters: δ, τ_{min}, τ_{max}, h, κ.

Output: All communication structures of size $\geq h$, which appear at least κ times, where the appearance is defined with respect to δ, τ_{min}, τ_{max}.

Assuming we can solve this algorithmic task, the statistical task is to determine h and κ to ensure that all the output communication structures reliably correspond to non-random "hidden groups". We first consider small trees, specifically chain and sibling triples. We then develop a heuristic to build up larger hidden groups from clusters of triples. Additionally we mine all of the frequent directed acyclic graphs and propose new ways of measuring the similarity between sets of overlapping sets. We obtain evolving hidden groups by using a sliding window in conjunction with the proposed similarity measures to determine the rate of evolution.

6 Algorithms for Chain and Sibling Trees

We will start by introducing a technique to find chain and sibling triples, i.e. trees of type $A \to B \to C$ (chain) and trees of type $A \to (B, C)$ (sibling). To accomplish this, we will enumerate all the triples and count the number of times each triple occurs. Enumeration can be done by brute force, i.e. considering each possible triple in the stream of communications. We have developed a general algorithm for counting the number of occurrences of chains of length ℓ, and siblings of width k. These algorithms proceed by posing the problem as a multi-dimensional matching

problem, which in the case of tipples becomes a two-dimensional matching problem. Generally multi-dimensional matching is hard to solve, but in our case the causality constraint imposes an ordering on the matching which allows us to construct a linear time algorithm. Finally we will introduce a heuristic to build larger graphs from statistically significant triples using overlapping clustering techniques [7].

6.1 Computing the Frequency of a Triple

Consider the triple $A \to B \to C$ and the associated time lists $L_1 = \{t_1 \leq t_2 \leq \ldots \leq t_n\}$ and $L_2 = \{s_1 \leq s_2 \leq \cdots \leq s_m\}$, where t_i are the times when A sent to B and s_i the times when B sent to C. An occurrence of the triple $A \to B \to C$ is a pair of times (t_i,s_i) such that $(s_i - t_i) \in [\tau_{min}$ $\tau_{max}]$. Thus, we would like to find the maximum number of such pairs which satisfy the causality constraint. It turns out that the causality constraint does not affect the size of the maximum matching, however it is an intuitive constraint in our context.

We now define a slightly more general maximum matching problem: for a pair (t_i, s_i) let $f(t_i, s_i)$ denote the score of the pair.

Let M be a matching $\{(t_{i_1}, s_{i_1}), (t_{i_2}, s_{i_2}) \ldots (t_{i_k}, s_{i_k})\}$ of size k. We define the score of M as

$$Score(M) = \sum_{j=1}^{k} f(t_{i_j}, s_{i_j}).$$

The maximum matching problem is to find a matching with a maximum score. The function $f(t, s)$ captures how likely a message from $B \to C$ at time s was "caused" by a message from $A \to B$ at time t. In our case we are using a hard threshold function

$$f(t,s) = f(t-s) = \begin{cases} 1 & \text{if } t - s \in [\tau_{min}, \tau_{max}], \\ 0 & \text{otherwise.} \end{cases}$$

The matching problem for sibling triples is identical with the choice

$$f(t,s) = f(t-s) = \begin{cases} 1 & \text{if } t - s \in [-\delta, \delta], \\ 0 & \text{otherwise.} \end{cases}$$

We can generalize to chains of arbitrary length and siblings of arbitrary width as follows. Consider time lists L_1, L_2, $\ldots$,$L_{\ell-1}$ corresponding to the chain $A_1 \to A_2 \to A_3 \to \cdots \to A_\ell$, where L_i contains the sorted times of communications $A_i \to A_{i+1}$. An occurrence of this chain is now an $\ell - 1$ dimensional matching $\{t_1, t_2, \ldots, t_{\ell-1}\}$ satisfying the constraint $(t_{i+1} - t_i) \in [\tau_{min}\ \tau_{max}]$ $\forall$ $i = 1,\cdots,\ell - 2$.

The sibling of width k breaks down into two cases: ordered siblings which obey constraints similar to the chain constraints, and unordered siblings. Consider the sibling tree $A_0 \to A_1, A_2, \cdots A_k$ with corresponding time lists L_1, L_2, $\ldots$,L_k, where L_i contains the times of communications $A_0 \to A_i$. An occurrence is a matching $\{t_1, t_2, \ldots, t_k\}$. In the ordered case the constraints are $(t_{i+1} - t_i) \in [-\delta\ \delta]$. This represents A_0 sending communications "simultaneously" to its recipients in the order $A_1, \ldots, A_k$. The unordered sibling tree obeys the stricter constraint $(t_i - t_j) \in [-(k-1)\delta, (k-1)\delta]$, $\forall$ i, j pairs, $i \neq j$. This stricter constraint represents A_0 sending communications to its recipients "simultaneously" without any particular order.

Both problems can be solved with a greedy algorithm. The detailed algorithms for arbitrary chains and siblings are given in Figure 4(a). Here we sketch the algorithm for triples. Given two time lists L_1=$\{t_1, t_2, \ldots, t_n\}$ and L_2=$\{s_1, s_2, \ldots, s_m\}$ the idea is to find the first valid match (t_{i_1}, s_{i_1}),

```
1: Algorithm Chain
2: while P_k ≤ ‖L_k‖ − 1, ∀k do
3:   if (t_j − t_i) < τ_min then
4:     P_j ← P_j + 1
5:   else if (t_j − t_i) ∈ [τ_min, τ_max] then
6:     if j = n then
7:       (P_1, ..., P_n) is the next match
8:       P_k ← P_k + 1, ∀k
9:       i ← 0; j ← 1
10:    else
11:      i ← j; j ← j + 1
12:  else
13:    P_i ← P_i + 1
14:    j ← i; i ← i − 1
```

(a)

```
1: Algorithm Sibling
2: while P_k ≤ ‖L_k‖ − 1, ∀k do
3:   if (t_j − t_i) < −(k − 1)δ then
4:     P_j ← P_j + 1
5:   else if (t_j − t_i) > (k − 1)δ, ∀i < j
     then
6:     P_i ← P_i + 1
7:     j ← i + 1
8:   else
9:     if j = n then
10:      (P_1, ..., P_n) is the next match
11:      P_k ← P_k + 1, ∀k
12:      i ← 0; j ← 1
13:    else
14:      j ← j + 1
```

(b)

Figure 4: Maximum matching algorithm for chains and ordered siblings (a); Maximum matching algorithm for unordered siblings (b). In the algorithms above, we initialize $i = 0; j = 1$ (i, j are time list positions), and $P_1, \ldots, P_n = 0$ (P_k is an index within L_k). Let $t_i = L_i[P_i]$ and $t_j = L_j[P_j]$.

which is the first pair of times that obey the constraint $(s_{i_1} - t_{i_1}) \in [\tau_{min}\ \tau_{max}]$, then recursively find the maximum matching on the remaining sub lists $L'_1 = \{t_{i_1+1}, \ldots, t_n\}$ and $L'_2 = \{s_{i_1+1}, \ldots, s_m\}$.

The case of general chains and ordered sibling trees is similar. The first valid match is defined similarly. Every pair of entries $t_{L_i} \in L_i$ and $t_{L_{i+1}} \in L_{i+1}$ in the maximum matching must obey the constraint $(t_{L_{i+1}} - t_{L_i}) \in [\tau_{min}\ \tau_{max}]$. To find the first valid match, we begin with the match consisting of the first time in all lists. Denote these times $t_{L_1}, t_{L_2}, \ldots, t_{L_\ell}$. If this match is valid (all consecutive pairs satisfy the constraint) then we are done. Otherwise consider the first consecutive pair to violate this constraint. Suppose it is $(t_{L_i}, t_{L_{i+1}})$; so either $(t_{L_{i+1}} - t_{L_i}) > \tau_{max}$ or $(t_{L_{i+1}} - t_{L_i}) < \tau_{min}$. If $(t_{L_{i+1}} - t_{L_i}) > \tau_{max}$ (t_{L_i} is too small), we advance t_{L_i} to the next entry in the time list L_i; otherwise $(t_{L_{i+1}} - t_{L_i}) < \tau_{min}$ ($t_{L_{i+1}}$ is too small) and we advance $t_{L_{i+1}}$ to the next entry in the time list L_{i+1}. This entire process is repeated until a valid first match is found. An efficient implementation of this algorithm is given in Figure 4. The algorithm for unordered siblings follows a similar logic.

The next theorem gives the correctness of the algorithms.

Theorem 1. *Algorithm-Chain and Algorithm-Sibling find maximum matchings.*

Proof. By induction. Given a set of time lists $L = (L_1, L_2, \ldots, L_n)$ our algorithm produces a matching $M = (m_1, m_2, \ldots, m_k)$, where each matching m_i is a sequence of n times from each of the n time lists $m_i = (t_1^i, t_2^i, \ldots, t_n^i)$. Let $M^* = (m_1^*, m_2^*, \ldots, m_{k^*}^*)$ be a maximum matching of size k^*. We prove that $k = k^*$ by induction on k^*. The next lemma follows directly from the construction of the Algorithms.

Lemma 1. *If there is a valid matching our algorithm will find one.*

Lemma 2. *Algorithm-Chain and Algorithm-Sibling find an earliest valid matching. Let the first valid matching found by either algorithm be $m_1 = (t_1, t_2, \ldots, t_n)$, then for any other valid matching*

$m' = (s_1, s_2, \ldots, s_n)$ $t_i \leq s_i \ \forall \ i = 1, \cdots, n$.

Proof. Proof by contradiction. Assume that in m_1 and m' there exists a corresponding pair of times $s < t$ and let s_i, t_i be the first such pair. Since m_1 and m' are valid matchings, then s_i and t_i obey the constraints: $\tau_{min} \leq (t_{i+1} - t_i) \leq \tau_{max}$, $\tau_{min} \leq (t_i - t_{i-1}) \leq \tau_{max}$ and $\tau_{min} \leq (s_{i+1} - s_i) \leq \tau_{max}$, $\tau_{min} \leq (s_i - s_{i-1}) \leq \tau_{max}$.

Since $s_i < t_i$, then $\tau_{min} < (t_{i+1} - s_i)$ and $\tau_{max} > (s_i - t_{i-1})$. Also because $s_{i-1} \geq t_{i-1}$, we get that $\tau_{min} \leq (s_i - t_{i-1})$ and since $(s_{i+1} - s_i) \leq \tau_{max}$, then $(min(t_{i+1}, s_{i+1}) - s_i) \leq \tau_{max}$ as well. But if s_i satisfies the above conditions, then m_1 would not be the first valid matching, because the first matching m_f would contain $m_f = (t_1, t_2, \ldots, t_{i-1}, s_i, min(t_{i+1}, s_{i+1}), min(t_{i+2}, s_{i+2}), \ldots, min(t_n, s_n))$.

Let us show this by induction on the number of pairs p of the type $min(t_{i+j}, s_{i+j})$, where $s_i < t_i$ and $j \geq 1$.

If $p = 1$, then $j = 1$, and since $\tau_{min} \leq (s_{i+1} - s_i) \leq \tau_{max}$ and $\tau_{min} < (t_{i+1} - s_i)$, then $\tau_{min} < (min(t_{i+1}, s_{i+1}) - s_i) \leq \tau_{max}$ as well, and therefore satisfies the matching constraints.

Let the matching constraints be satisfied up to $p = m$, such that in the matching $m^* = (t_1, t_2, \ldots, t_{i-1}, s_i, min(t_{i+1}, s_{i+1}), \ldots, min(t_{i+m}, s_{i+m}), \ldots, min(t_n, s_n))$ the sequence of elements of m^* up to $min(t_{i+m}, s_{i+m})$ satisfy the matching constraints. Then we can show that $min(t_{i+m+1}, s_{i+m+1})$ is also a part of the matching. Since m_1 and m' are both valid matchings, then $\tau_{min} \leq (t_{i+m+1} - t_{i+m}) \leq \tau_{max}$ and $\tau_{min} \leq (s_{i+m+1} - s_{i+m}) \leq \tau_{max}$, from which we get that $\tau_{min} \leq (min(t_{i+m+1}, s_{i+m+1}) - min(t_{i+m}, s_{i+m})) \leq \tau_{max}$. Therefore, $min(t_{i+m+1}, s_{i+m+1})$ is also a part of the matching.

Thus, we get a contradiction since m_f would be an earlier matching if there exists a pair of times $s_i < t_i$. Therefore, Algorithm-Chain and Algorithm-Sibling find an earliest valid matching. □

If $k^* = 0$, then $k = 0$ as well. If $k^* = 1$, then there exists a valid matching and by Lemma 1 our algorithm will find it.

Suppose that for all sets of time lists for which $k^* = M$, the algorithm finds matchings of size k^*. Now consider a set of time lists $L = (L_1, L_2, \ldots, L_n)$ for which an optimal algorithm produces a maximum matching of size $k^* = M + 1$ and consider the first matching in this list (remember that by the causality constraint, the matchings can be ordered). Our algorithm constructs the earliest matching and then recursively processes the remaining lists. By Lemma 2, our first matching is not later than optimal's first matching, so the partial lists remaining after our first matching contain the partial lists after optimal's first matching. This means that the optimal matching for our partial lists must be M. By the induction hypothesis our algorithm finds a matching of size M on these partial lists for a total matching of size $M + 1$. □

For a given set of time lists $L = (L_1, L_2, \ldots, L_n)$ as input, where each L_i has a respective size d_i, define the total size of the data as $\|D\| = \sum_{i=1}^{n} d_i$.

Theorem 2. *Algorithm-Chain runs in $O(\|D\|)$ time.*

Theorem 3. *Algorithm-Sibling runs in $O(n \cdot \|D\|)$ time.*

6.2 Finding all Triples

Assume the data are stored in a vector. Each component in the vector corresponds to a sender id and stores a balanced search tree of receiver lists (indexed by a receiver id). And let S be the whole set of distinct senders. The algorithm for finding chain triples considers sender id s and its list of receivers $\{r_1, r_2, \cdots, r_d\}$. Then for each such receiver r_i that is also a sender, let $\{\rho_1, \rho_2, \cdots, \rho_f\}$ be

the receivers to which r_i sent messages. All chains beginning with s are of the form $s \to r_i \to \rho_j$. This way we can more efficiently enumerate the triples (since we ignore triples which do not occur). For each sender s we count the frequency of each triple $s \to r_i \to \rho_j$.

Theorem 4. *Algorithm to find all triple frequencies takes $O(\|D\| + n \cdot \|D\|)$ time.*

6.3 General Scoring Functions for $2D$-Matching

One can observe that for our $2D$-matching we are using a so called "Step Function", which returns 1 for values between $[\tau_{min}, \tau_{max}]$, and gives 0 otherwise. Such a function represents the probability delay density which is the distribution of the time it takes to propagate a message once it is received.

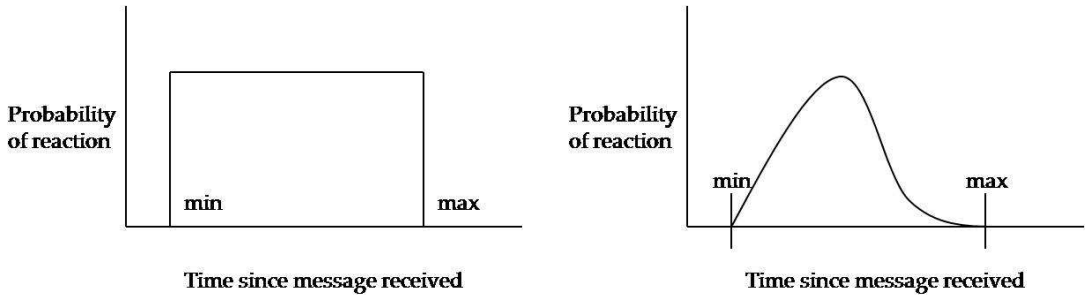


Figure 5: Step function on the left and a General Response Functions for 2D Matching on the right

Here we extend our matching algorithm to be able to use any general propagation delay density function, see Figure 5.

Usage of these various functions may uncover some additional information about the streaming groups and their structure which the "Step Function" missed.

Unfortunately, the matching problem with an arbitrary function, unlike in the case with the "Step Function" which can be solved in linear time, cannot be solved so efficiently.

First we provide an efficient algorithm to find a $2D$ maximum matching which satisfies a causality constraint (a maximum weight matching which has no intersecting edges). Additionally we will provide an approach involving the Hungarian algorithm to discover a maximum weighted $2D$-matching, which does not obey the causality constraint (edges involved in the maximum matching may intersect).

Given the two time lists $L_1 = \{t_1, t_2, \ldots, t_n\}$ and $L_2 = \{s_1, s_2, \ldots, s_m\}$ and a general scoring function $f(\cdot)$ over the specified time interval $[\tau_{min,\tau_{max}}]$ we would like to find a maximum weighted $2d$ matching between these two time lists, such that the matching has no intersecting edges. No intersecting edges intuitively guaranties the causality constraint. To solve this problem we will employ the dynamic programming approach. Let $M_{i,j}$ be a maximum matching with the respective weight $w(M_{i,j})$, obeying the causality constraint, involving up to and including the t_i'th item of the list L_1 and up to and including the s_j'th item in the list L_2. Thus, the matching $M_{n,m}$ will hold the maximum weighted matching for the entire lists L_1 and L_2. When we compute the matching, we attempt to improve it from step to step by adding only the edges(matches) which do not intersect any of the edges already present in the matching. The following description of the algorithm will show why it is the case.

We will illustrate now that if we have correct solutions to subproblems $M_{i-1,j}$, $M_{i,j-1}$ and $M_{i-1,j-1}$, then we can construct a maximum matching $M_{i,j}$, which obeys the causality constraint by considering the following two simple cases:

1: **Algorithm Match-Causality**
2: Compute $\{M_{1,1}, M_{1,2}, \ldots, M_{1,n}\}$ and $\{M_{1,1}, M_{2,1}, \ldots, M_{m,1}\}$
3: **for** $i = 2$; $i \leq n$; $i++$ **do**
4: **for** $j = 2$; $j \leq m$; $j++$ **do**
5: $M_{i,j} = max\{w(M_{i-1,j-1} \cup (t_i, s_j)), w(M_{i-1,j}), w(M_{i,j-1})\}$
6: Store a direction for backtracking
7: Start at $M_{m,n}$ and backtrack to retrieve the edges of the matching

Figure 6: Algorithm to discover a maximum weighted matching which obeys the causality constraint. In the algorithm above, we initialize $i = 0; j = 0$ (i, j are time positions in lists $L_1 = \{t_1, t_2, \ldots, t_n\}$ and $L_2 = \{s_1, s_2, \ldots, s_m\}$.

1. Either the elements t_i and s_j are both matched to each other in the matching $M_{i,j}$, in which case $M_{i,j} = M_{i-1,j-1} \cup (t_i, s_j)$. Obviously the edge (t_i, s_j) does not intersect any of the previous edges of $M_{i-1,j-1}$ so we maintain the causality constraint;

2. Or, the elements t_i and s_j are not matched to each other in the matching $M_{i,j}$. Then, one of the t_i or s_j is not matched (see Lemma 4), which means that $M_{i,j} = max\{M_{i,j-1}, M_{i-1,j}\}$. No edges are added to the matching in this case.

We initialize our algorithm by computing in linear time the base set of matches $\{M_{1,1}, M_{1,2}, \ldots, M_{1,n}\}$ (the bottom row) and $\{M_{1,1}, M_{2,1}, \ldots, M_{m,1}\}$ (the left most column) of the two-dimensional array of subproblems (of size $n \cdot m$) that is being built up. The matchings $\{M_{1,1}, M_{1,2}, \ldots, M_{1,n}\}$ are constructed by taking the first element s_1 from the list L_2 and computing all of the weights of the edges $w(t_i, s_1)$, s.t. $w(M_{1,1}) = \{f(s_1 - t_1)\}$ (contains edge (t_1, s_1), if its not 0), $w(M_{1,2}) = max\{f(s_1 - t_1), f(s_1 - t_2)\}$ (contains the heavier of two edges (t_1, s_1), (t_2, s_1)) up to $M_{1,n} = max\{f(s_1 - t_1), f(s_1 - t_2), \ldots, f(s_1 - t_n)\}$ (contains the edge of maximum weight considered over all t_i's). We similarly compute the set of matchings $\{M_{1,1}, M_{2,1}, \ldots, M_{m,1}\}$. Next we are ready to fill in the rest of the two-dimensional array of subproblems starting with $M_{2,2}$, since $M_{1,1}$, $M_{1,2}$ and $M_{2,1}$ are all available. The pseudo code of the algorithm is given in Figure 6.

Lemma 3. *The matching constructed by algorithm Match-Causality, obeys the causality constraint (contains no intersecting edges).*

Proof. By construction of our algorithm, during the computation of every $M_{i,j}$ a new edge is added to the matching only if the $(M_{i-1,j-1} \cup (t_i, s_j))$ is picked as maximum. But since t_i and s_j are the very last two elements for the matching $M_{i,j}$, they can't intersect any of the edges. Thus, since at each step our algorithm consistently adds edges which do not intersect any of the previously added edges, the final matching will contain no intersecting edges. □

Lemma 4. *If the items t_i and s_j are not matched to each other in the matching $M_{i,j}$, then one of the t_i, s_j is not matched at all.*

Proof. Let us assume for the sake of contradiction that both t_i and s_j are matched with some nodes. This automatically implies that t_i must be matched with some $s_{j'}$, which appears before the s_j in the list L_2; and s_j is matched with some $t_{i'}$, which occurs before the t_i in the list L_1. But this means that the edges $(t_i, s_{j'})$ and $(t_{i'}, s_j)$ intersect, a contradiction. □

Theorem 5. *Algorithm Match-Causality correctly finds a maximum weighted matching.*

Proof. Proof by induction. For the base case lets consider the case where $\|L_1\| = 1$ and $\|L_2\| = 1$, in this case the algorithm will trivially match t_1 (the only element of L_1) with s_1 (the only element of L_2) as long as the $f(s_1 - t_1) > 0$, otherwise the matching would be empty.

For the inductive step we assume that if our algorithm finds all of the maximum weighted matchings ,which obey the causality constraint, correctly up to and including $M_{i,j-1}$, then the algorithm correctly finds the maximum matching which obeys the causality constraint for $M_{i,j}$ (the very next position it considers after $M_{i,j-1}$). By our assumption we know that our algorithm correctly found the matchings $M_{i,j-1}$, $M_{i-1,j-1}$ and $M_{i-1,j}$, which all obey the causality constraint, since all of them occurred before the computation of $M_{i,j}$. If so, then our algorithm by construction will pick the maximum weight matching from the set of 3 possible matchings $\{(M_{i-1,j-1} \cup (t_i, s_j)), M_{i-1,j}, M_{i,j-1}\}$, which guaranties the $M_{i,j}$ to be maximum weight and obey the causality constraint. □

Theorem 6. *Algorithm Match-Causality runs in $O(n \cdot m)$ time.*

The general propagation delay function $f(\cdot)$ can have any shape, and one can wonder if it is possible to find an algorithm which will perform faster then $O(n \cdot m)$ for some special case of the general propagation delay function. Let us consider one of the most intuitive scenarios where the propagation delay function is monotonically decreasing. We prove that there does not exist an algorithm which can construct the maximum weight matching in less then $O(n \cdot m)$ time, which obeys the causality constraint.

Theorem 7. *Algorithm which finds exactly the maximum weight matching for a propagation delay function which is strictly monotonically decreasing (not a "step" function) and obeys the causality constraint, requires at least $O(n \cdot m)$ time.*

Proof. Consider the two time lists $L_1 = \{t_1, t_2, \ldots, t_n\}$, $L_2 = \{s_1, s_2, \ldots, s_m\}$, where every time $s_j > t_n$, and a strictly monotonically decreasing function $f(\cdot)$, s.t. $f(s_m - t_1) > 0$. The first observation to make is that t_n must be a part of the matching. If $t_{n'}$ is the last matched item and t_n is not matched, where $n' < n$, then the matching can be improved by replacing $t_{n'}$ with t_n, since $f(\cdot)$ is a strictly monotonically decreasing function and $n' < n$.

If the matching obeys the causality constraint, then the maximum weight matching can be $\{f(s_1 - t_n)\}$ or $\{f(s_2 - t_n) + f(s_1 - t_{n-1})\}$ or ... or $\{f(s_1 - t_1) + f(s_2 - t_2) + \ldots + f(s_m - t_n)\}$, order of $O(n \cdot m)$ combinations. And since the function is any strictly monotonically decreasing function, one can't guaranty the optimality of the discovered matching without having to consider all of the mentioned $O(n \cdot m)$ permutations. Thus an algorithm which finds exactly the maximum weight matching for a propagation delay function which is strictly monotonically decreasing (not a "step" function) and obeys the causality constraint, requires at least $O(n \cdot m)$ time. □

Additionally we present a method to discover a maximum weight matching for a general propagation delay function, which doesn't have to obey the causality constraint (we allow the intersection of edges in the matching). The general idea is to use a Hungarian algorithm to find a maximum weighted $2d$-matching for a pair of time lists.

First, given two time lists $L_1 = \{t_1, t_2, \ldots, t_n\}$ and $L_2 = \{s_1, s_2, \ldots, s_m\}$ and a general scoring function $f(\cdot)$ over the specified time interval $[\tau_{min,\tau_{max}}]$, we construct the bipartite graph, where on the left we have the set of n nodes, where each node represents a respective time from $\{t_1, t_2, \ldots, t_n\}$ and on the right we have a set of m nodes representing each of $\{s_1, s_2, \ldots, s_m\}$ times respectively. Each pair of nodes t_i and s_j is connected by an edge, where the weight on the edge equals to $f(s_j - t_i)$ (0 if outside the $[\tau_{min,\tau_{max}}]$ bounds).

Once we have constructed the bipartite graph we are ready to run the Hungarian algorithm. The produced matching M is of maximum weight, but does not take into account the causality constraint (some of the edges of M may intersect). This algorithm runs in cubic time.

We use ENRON data to test general propagation delay functions against the "step" function. The results of our experiments are presented in Section 13. It turns out that in most of the cases there is not much added value from the more general propagation delay function in practice. Thus, the more efficient function seems adequate.

7 Statistically Significant Triples

We determine the minimum frequency κ that makes a triple statistically significant, using a statistical model that mimics certain features of the data: we model the inter-arrival time distribution and receiver id probability conditioned on sender id, to generate synthetic data and find all randomly occurring triples to determine the threshold frequency κ.

7.1 A Model for the Data

We estimate directly from the data the message inter-arrival time distribution $f(\tau)$, the conditional probability distribution $P(r|s)$, and the marginal distribution $P(s)$ using simple histograms (one for $f(\tau)$, S for $P(r|s)$ and S for $P(s)$, i.e. one conditional and marginal distribution histogram for each sender, where S is the number of senders). One may also model additional features (e.g. $P(s|r)$), to obtain more accurate models. One should however bear in mind that the more accurate the model, the closer the random data is to the actual data, hence the less useful the statistical analysis will be - it will simply reproduce the data.

7.2 Synthetic Data

Suppose one wishes to generate N messages using $f(\tau)$, $P(r|s)$ and $P(s)$. First we generate N inter-arrival times independently, which specifies the times of the communications. We now must assign sender-receiver pairs to each communication. The senders are selected independently from $P(s)$. We then generate each receiver independently, but conditioned on the sender of that communication, according to $P(r|s)$.

7.3 Determining the Significance Threshold

To determine the significance threshold κ, we generate M (as large as possible) synthetic data sets and determine the triples together with their frequencies of occurrence in each synthetic data set. The threshold κ may be selected as the average plus two standard deviations, or (more conservatively) as the maximum frequency of occurrence of a triple.

8 Constructing Larger Graphs using Heuristics

Now we discuss a heuristic method for building larger communication structures, using only statistically significant triples. We will start by introducing the notion of an overlap factor. We will then discuss how the overlap factor is used to build a larger communication graph by finding clusters, and construct the larger communication structures from these clusters.

8.1 Overlap between Triples

For two statistically significant triples (A, B, C) and (D, E, F) (chain or sibling) with maximum matchings at the times $M_1 = \{(t_1, s_1), \ldots, (t_k, s_k)\}$ and $M_2 = \{(t'_1, s'_1), \ldots, (t'_p, s'_p)\}$, we use an overlap weighting function $W(M_1, M_2)$ to capture the degree of coincidence between the matchings M_1 and M_2. The simplest such overlap weighting function is the extent to which the two time intervals of communication overlap. Specifically, $W(M_1, M_2)$ is the percent overlap between the two intervals $[t_1, s_k]$ and $[t'_1, s'_p]$:

$$W(M_1, M_2) = \max\left\{\frac{\min(s_k, s'_p) - \max(t_1, t'_1)}{\max(s_k, s'_p) - \min(t_1, t'_1)}, 0\right\}$$

A large *overlap factor* suggests that both triples are part of the same hidden group. More sophisticated overlap factors could take into account intermittent communication but for our present purpose, we will use this simplest version.

8.2 The Weighted Overlap Graph and Clustering

We construct a weighted graph by taking all significant triples to be the vertices in the graph. Let M_i be the maximum matching corresponding to vertex (triple) v_i. We define the weight of the edge e_{ij} to be $\omega(e_{ij}) = W(M_i, M_j)$, producing an undirected complete graph (some weights may be 0). By thresholding the weights, one could obtain a sparse graph. Dense subgraphs correspond to triples that were all active at about the same time, and are a candidate hidden group. We want to cluster the graph into dense possibly overlapping subgraphs. Given the triples in a cluster we can build a directed graph, consistent with all the triples, to represent its communication structure. Cluster containing multiple connected components implies the existence of some hidden structure connecting them. Below is an outline of the entire algorithm:

1: Obtain the significant triples.
2: Construct a weighted overlap graph (weights are overlap factors between pairs of triples).
3: Perform clustering on the weighted graph.
4: Use each cluster to determine a candidate hidden group structure.

For the clustering, since clusters may overlap, we use the algorithms presented in [7, 8].

9 Algorithm for Querying Tree Hidden Groups

We describe efficient algorithms for computing (exactly) the frequency of a hidden group whose communication structure is an arbitrary pre-specified tree. We assume that messages initiate from the root. The parameters $\tau_{min}, \tau_{max}, \delta$ are also specified. Such an algorithm can be used in conjunction with the previous heuristic algorithms to verify that a discovered tree-like structure actually occurs frequently in the data.

Let L be an adjacency list for the tree T, D a dataset in which we will query this tree. The first entry in the list L is the *root communicator* followed by the list of all its children (receivers) the *root* sends to. The next entries in L contain the lists of children for each of the receivers of L_{root} until we reach the leaves, which have no children.

After we have read in D, we process L and use it to construct the tree, in which every node will contain: *node id*, *time list* when its parent sent messages to it, and a *list of children*. We construct such tree by processing L and checking each communicator that has children if it is present in D as

```
1: Algorithm Tree-Mine(T,D)
2: D_rem ← D
3: while M = TRUE do
4:    (M, t') = FindNext(T, D_rem)
5:    if M then
6:       Store Match
7:       Increment List Pointers; get D_rem
```

```
1: Algorithm FindNext(T, D_rem)
2: Initialize all truth_j ← 0
3: return Findnext_rec(NULL, root)
```

```
1: Algorithm FindNext_rec(t, *node i)
2: (⋆)Run Algorithm-Sibling from current time list pointers to get m = (t_1, ..., t_n)
3: if m ∼ t then
4:    for j = n to 1 do
5:       if (truth_j = 1 & prev_j < t_j) or truth_j = 0 then
6:          (truth_j, prev_j) = FindNext_rec(t_j, *node j)
7:          if truth_j = 0 then
8:             Increase t_j pointer, GOTO(⋆)
9:       else
10:         return (truth_j,t)
11: if m < t then
12:    Increase t_j pointer, GOTO(⋆)
13: if m > t then
14:    return (0, t)
```

Figure 7: Algorithms used for Querying a Tree T in the data D. In the algorithms above, D_{rem} represents D in an way that allows the Tree-Mine Algorithm to efficiently access the necessary data.

a *Sender*, and if its children are present in D in the list of its *Receivers*. During the construction, if a node that has children is not present in D as a *Sender*, or some child is not on the list of *Receivers* of its parent, then we know that the given tree does not exist in the current data set D and we can stop our search.

For a tree to exist there should be at least one matching involving all of the nodes (lists). We start with *root* and consider the time lists of its children. We use Algorithm-Sibling to find the first matching $m_1 = (t_1, t_2, \ldots, t_n)$, where t_i is an element of the i's child time list and n is the number of time lists. After the first matching m_1 we proceed by considering the children in the matching m_1 from the rightmost child to the left by taking the value t_i, which represents this node in the matching and passing it down to the child node. Next we try to find a matching $m_2 = (s_1, s_2, \ldots, s_k)$ for the k child time lists. There are three cases to consider:

1. Every element s_j of the matching m_2 also satisfies the chain-constraint with the element t_i: $\tau_{min} \leq s_j - t_i \leq \tau_{max}$, $\forall s_j \in m_2$, $j = k, \ldots, 1$. In this case we say $m_2 \sim t_i$ (m_2 matches t_i) and proceed by considering all children. Otherwise consider the rightmost $s_j \in m_2$. The two cases below refer to s_j.

2. If $s_j < t_i + \tau_{min}$, in which case we say $m_2 < t_i$, we advance to the next element in child j's time list and continue as with Algorithm-Sibling to find the next matching $(s'_1, s'_2, \ldots, s'_k)$. This process is repeated as long as $m_2 < t_i$. Eventually we will find an m_2 with $m_2 \sim t_i$ or we will reach the end of some list (in which case there is no further matching) or we come to a matching $m_2 > t_i$ (see case below).

3. If $s_j > t_i + \tau_{max}$, in which case we say $m_2 > t_i$, we advance t_i to the next element in i's time list on the previous level and proceed as with Algorithm-Sibling to find the next matching in the previous level. After this new matching $(t'_1, t'_2, \ldots, t'_n)$ is found, the chain constraints have to be checked for these time lists $(t'_1, t'_2, \ldots, t'_n)$ with their previous level and the algorithm proceeds recursively from then on.

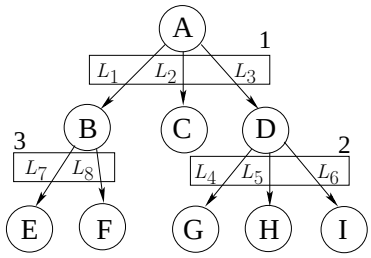


Figure 8: Example of a communication tree structure

The entire algorithm for finding a complete matching can be formulated into two steps: find the first matching; recursively process the remaining parts of the time lists. What we have described is the first step which is accomplished by calling the recursive algorithm $FindNext_{rec}(NULL, root)$ that is summarized in the Figure 7. If this returns $TRUE$, the algorithm has found the first occurrence of the tree, which can be read off from the current time list pointers. After this instance is found, we store it and proceed by considering the remaining part of the time lists starting from the *root*.

To illustrate how the Algorithm Tree-mine works, consider the example tree T in Figure 8. Let node A to be a *root* and let $L_1, \ldots, L_8$ be the time lists. Refer to (L_1, L_2, L_3) as the $phase_1$ lists,

(L_4, L_5, L_6) as the $phase_2$ lists and (L_7, L_8) as the $phase_3$ lists. Let $m_1 = (t_1, t_2, t_3)$, $m_2 = (s_1, s_2, s_3)$ and $m_3 = (r_1, r_2)$ be the first matchings of the $phase_1, phase_2$ and $phase_3$ lists respectively. If $m_2 \sim t_3$ and $m_3 \sim t_1$, we have found the first matching and we now recursively process the remaining time lists. If $m_2 < t_3$ (eg. $s_2 < t_3 + \tau_{min}$), then we move to the next matching in the $phase_2$ lists. If $m_2 > t_3$ then we move to the next matching in $phase_1$ lists and reconsider the $phase_2$ matching and the $phase_3$ matching if necessary. If $m_2 \sim t_3$ we then similarly check m_3 with t_1. Since node C is a leaf, it need not be further processed.

Theorem 8. *Algorithm Tree-Mine correctly finds the maximum number of occurrences for a specified tree T.*

Proof. Proof by contradiction. Given a set of time lists $L = (L_1, L_2, \ldots, L_n)$ that specify a tree, our algorithm produces a matching $M = (m_1, m_2, \ldots, m_k)$, where each matching m_i is a sequence of n times from each of the n time lists $m_i = (t_1^i, t_2^i, \ldots, t_n^i)$. Let $M^* = (m_1^*, m_2^*, \ldots, m_{k^*}^*)$ be a maximum matching of size k^*. The next lemma follows directly from the construction of the Algorithms.

Lemma 5. *If there is a valid matching our algorithm will find one.*

Lemma 6. *Algorithm Tree-Mine finds an earliest valid matching(occurrence). Let the first valid matching found by our algorithm be $m_1 = (t_1, t_2, \ldots, t_n)$, then for any other valid matching $m' = (s_1, s_2, \ldots, s_n)$ $t_i \leq s_i \ \forall \ i = 1, \cdots, n$.*

Proof. Proof by contradiction. Assume that in m_1 and m' there exists a corresponding pair of times $s < t$ and let s_i, t_i be the first such pair. Since m_1 and m' are valid matchings, then s_i and t_i obey the chain constraints: $\tau_{min} \leq (t_i - t_p) \leq \tau_{max}$ (where t_p is a time passed down by the parent node), $\tau_{min} \leq ((t_{children} - t_i) \leq \tau_{max}$ (where $t_{children}$ are times of children of t_i), similarly $\tau_{min} \leq (s_i - s_p) \leq \tau_{max}$, $\tau_{min} \leq (s_{children} - s_i) \leq \tau_{max}$; and obey the sibling constraint: $\tau_{min} \leq (t_{i+1} - t_i) \leq \tau_{max}$, $\tau_{min} \leq (t_i - t_{i-1}) \leq \tau_{max}$ (where t_{i-1} and t_{i+1} are matched times of neighboring siblings of t_i) and similarly $\tau_{min} \leq (s_{i+1} - s_i) \leq \tau_{max}$, $\tau_{min} \leq (s_i - s_{i-1}) \leq \tau_{max}$.

Since $s_i < t_i$, then $\tau_{min} < (t_{i+1} - s_i)$ and $\tau_{max} > (s_i - t_{i-1})$. Also because $s_{i-1} \geq t_{i-1}$, we get that $\tau_{min} \leq (s_i - t_{i-1})$ and since $(s_{i+1} - s_i) \leq \tau_{max}$, then $(min(t_{i+1}, s_{i+1}) - s_i) \leq \tau_{max}$ as well. By similar reasoning since $s_i < t_i$, then $\tau_{min} < (t_{children} - s_i)$ and $\tau_{max} > (s_i - t_p)$; also since $s_p \geq t_p$, we get that $\tau_{min} \leq (s_i - t_p)$ and since $(s_{children} - s_i) \leq \tau_{max}$, then $(min(t_{children}, s_{children}) - s_i) \leq \tau_{max}$ as well. But if s_i satisfies all of the chain and sibling constraints, then m_1 would not be the first valid matching as has already been proven for algorithms chain and sibling triples, because the first matching m_f would contain $m_f = (t_1, t_2, \ldots, t_{i-1}, s_i, min(t_{i+1}, s_{i+1}), min(t_{i+2}, s_{i+2}), \ldots, min(t_n, s_n))$. Thus, algorithm Tree-Mine finds the earliest possible matching(occurrence). □

Now let us for the purpose of contradiction assume that Tree-Mine does not find a maximum number of occurrences of a specified tree T, s.t. $k < k^*$.

The situation where $k < k^*$ can only appear if M^* discovers an occurrence of T before the Tree-Mine does, s.t. some occurrence m_i^* which is earlier then its respective occurrence m_i. But such a situation can not happen, since, given the set of time lists (or the remainder of them, if we already processed some of them) which define the tree T, Tree-Mine guaranties to find the earliest valid match by Lemma 6. Thus, we obtain a contradiction. This proves that Tree-Mine correctly finds the maximum number of occurrences of a specified tree T. □

Theorem 9. *Algorithm Tree-Mine runs in $O(d_{max} \cdot \|D\|)$.*

9.1 Mining all Frequent Trees

Here we propose an algorithm which allows us to discover the frequency of general trees and to enumerate all statistically significant general trees of a specified size and frequency. The parameters $\tau_{min}, \tau_{max}, \delta$ and κ must be specified. Additionally you can specify the min and the max tree size to bound the size of the trees of interest. The parameter κ in this algorithm represents the minimal frequency threshold, and is used to discard the trees which occur fewer times then the specified threshold.

As for any tree mining problem, there are two main steps for discovering frequent trees. First, we need a systematic way of generating candidate trees whose frequency is to be computed. Second, we need efficient ways of counting the number of occurrences of each candidate in the database D and determining which candidates pass the threshold. To address the second issue we use our *Algorithm Tree-Mine* to determine the frequency of a particular tree. To systematically generate new candidate trees we inherit the idea of an *Equivalence Class-based Extensions* and the *Rightmost Path Extensions* proposed and described in [38, 37].

The algorithm proceeds in the following order:

(i) Systematically generate new candidates, by extending only the frequent trees until no more candidates can be extended;

(ii) Use *Algorithm Tree-Mine* to determine the frequency of our candidates;

(iii) If the candidate's frequency is above threshold - store the candidate.

The main advantage of equivalence class extensions is that only known frequent elements are used for extensions. But to guaranty that all possible extensions are considered, the non-redundant tree generation idea has to be relaxed. In this way the canonical class (considers candidates only in canonical form) and equivalence class extensions represent a trade-off between the number of isomorphic candidates generated and the number of potentially frequent candidates to count.

Theorem 10. *Mining all of the tress on the current level requires* $O(n^2 \cdot d_{max} \cdot \|D\| \cdot (v + log(d_{max})))$ *operations.*

10 Comparing Methods

To compare methods, we need to be able to measure similarity between sets of overlapping clusters. We will use the *Best Match* approach proposed in [18], which we briefly describe here.

We formally define the problem as follows:

- Let $C_1 = \{S_1, S_2, \ldots, S_n\}$ and $C_2 = \{S'_1, S'_2, \ldots, S'_m\}$ be the two clusterings of size n and m respectively, where S_i and S'_j are the groups that form the clusterings. A group does not contain duplicates.
- Let $D_{(C_1,C_2)}$ be the distance, between the clusterings C_1 and C_2.
- The task is to find $D_{(C_1,C_2)}$ efficiently, while ensuring that $D_{(C_1,C_2)}$ reflects the actual distance between the network structures that C_1 and C_2 represent.

The *Best Match* algorithm determines how well the clusterings represent each other. That is when given $C_1 = \{S_1, S_2, \ldots, S_n\}$ and $C_2 = \{S'_1, S'_2, \ldots, S'_m\}$ it will determine how well C_2 represents C_1 and vice-versa.

We begin by considering every group $S \in C_1$ and finding a group $S' \in C_2$ with the min distance $d_{(S,S')}$ between them. The best match algorithm can run with any set difference measure which

measures the distance between two sets S, S'. We define the distance $d_{(S,S')}$ between the two groups S and S' as the number of moves(changes) necessary to convert S into S':

$$d_{(S,S')} = |S| + |S'| - 2|S \cap S'|$$

Note, that alternatively we can also define $d_{(S,S')}$ as:

$$d_{(S,S')} = 1 - \frac{|S \cap S'|}{|S \cup S'|}$$

As we step through C_1, we find for each group $S_k \in C_1$ the closest group $S'_l \in C_2$ with a minimal distance $d_{(S_k,S'_l)}$:

$$d_{(S_k,C_2)} = \min_{l=1,\ldots,m}(d_{(S_k,S'_l)})$$

Next we sum up all such distances. For the purposes of normalization one can normalize the obtained sum by the total number of distinct members T_{C_1} in C_1 to obtain $D_{(C_1,C_2)}$:

$$D(C_1, C_2) = \frac{\sum_{k=1}^{n} d_{(S_k,C_2)}}{T_{C_1}},$$

$$T_{C_1} = \| \cup_{k=1}^{n} S_k \|;$$

this normalization computes a distance per node. One can also normalize by $\|C_1\|$ and $\|C_2\|$.

So far we successfully found the distance measure $D_{(C_1,C_2)}$ of how well the groups in C_1 are represented in C_2. If this *asymmetric* measure of the distance is considered adequate, one may stop the algorithm here. However, since in most of the cases we want the measure to be *symmetric* with respect to both clusterings, we also want to know how well C_1 represents C_2. We will thus repeat the same calculation for each group in C_2 with respect to the groups in C_1 and normalize the sum of distances using one of the normalization methods. Finally, the *Best Match* symmetric distance between a pair of clusterings C_1 and C_2 defined as:

$$D_{BestMatch}(C_1, C_2) = \frac{D_{(C_1,C_2)} + D_{(C_2,C_1)}}{2}$$

This result can be viewed as a representation of the average number of moves per distinct member (or set) necessary to represent one clustering by the other.

Intuitively the *Best Match* algorithm is a relative measure of distance, and reflects how well two clusterings represent each other, and how similar/different are the social networks formed by these clusterings. This approach is not sensitive to having clusterings of different size or having overlapping sets. Refer to [18] for more details.

11 Enron Data

The Enron email corpus consists of emails released by the U.S. Department of Justice during the investigation of Enron. This data includes about 3.5 million emails sent from and to Enron employees between 1998 and 2002. The list of approximately 150 employees mailboxes constitute the Enron dataset. Although the dataset contains emails related to thousands of Enron employees, the complete information is only known for this smaller set of individuals. The corpus contains detailed information about each email, including sender, recipient(s) (including To, CC, and BCC fields), time, subject, and message body. We needed to transform this data into our standard input format (sender, receiver, time). To accomplish this, for each message we generated multiple entries (sender, receiver1, time), ... (sender, receiverN, time), for all N recipients of the message.

12 Weblog (Blog) Data

This data set was constructed by observing Russian livejournal.com blogs. This site allows any user to create a blog at no cost. The user may then submit text messages called *posts* onto their own page. These posts can be viewed by anyone who visits their page. For the purposes of our analysis we would like to know how information is being disseminated throughout this blog network. While data about who accessed and read individual home pages is not available, there is other information with which we can identify communications. When a user visits a home page, he or she may decide to leave *comments* on one or more posts on the page. These comments are visible to everyone, and other users may leave comments on comments, forming trees of communications rooted at each post. We then must process this information into links of the form (sender, receiver, time). We make the following assumptions for a comment by user a at time t in response to a comment written by user b, where both comments pertain to a post written by user c: a has read the original post of c, hence a communication (c, a, t) if this was the earliest comment a made on this particular post. c reads the comments that are made on his site, hence a communication (a, c, t); a read the comment to which he is replying, hence the communication (b, a, t); b will monitor comments to his comment, hence the communication (a, b, t); Fig. 9 shows these assumed communications. Note that the second post by user a only generates a communication in one direction, since it is assumed that user a has already read the post by user c.

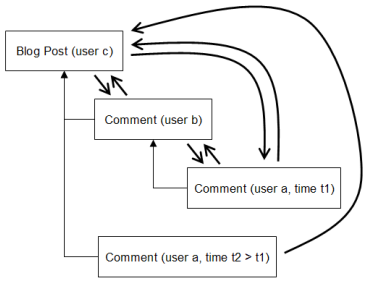


Figure 9: Communications inferred from weblog data.

In addition to making comments, LiveJournal members may select other members to be in their "friends" list. This may be represented by a graph where there is a directed edge from user a to user b if a selects b as a friend. These friendships do not have times associated with them, and so cannot be converted into communication data. However, this information can be used to validate our algorithms, as demonstrated in the following experiment.

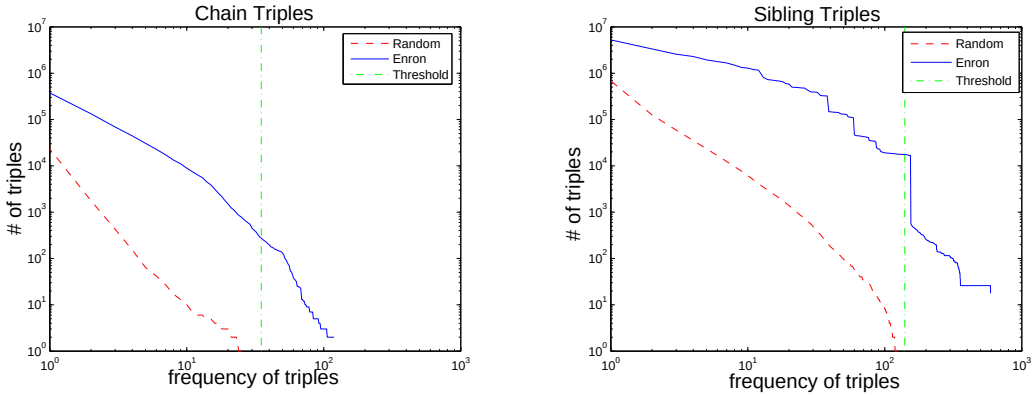
The friendship information may be used to verify the groups that have been discovered by our algorithm. If the group is indeed a social group, the members should be more likely to select each other as a friend than a randomly selected group. The total number of members in the friendship network is 2,551,488, with 53,241,753 friendship links among them, or about 0.0008 percent of all possible links are friendship links. Thus, we would expect about 0.0008 percent of friendship links to be present in a randomly selected group of LiveJournal members.

13 Experimental Results

13.1 Triples in Enron Email Data

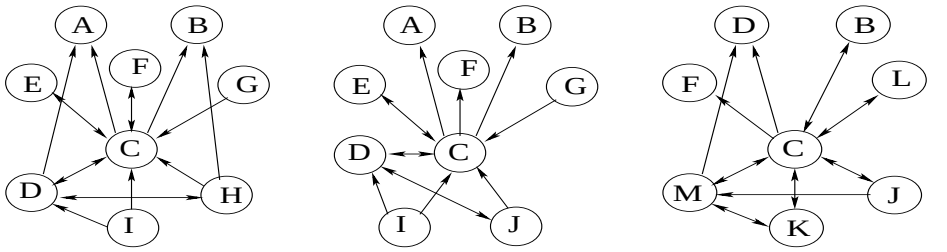
For our experiments we considered the Enron email corpus (see Section 10). We took τ_{min} to be 1 hour and τ_{max} to be 1 day. Fig. 10 compares the number of triples occurring in the data to the number that occur randomly in the synthetically generated data using the model derived from the Enron data. As can be observed, the number of triples in the data by far exceeds the random triples. After some frequency threshold, no random triples of higher frequency appear - i.e., all the triples appearing in the data at this frequency are significant. We used $M = 1000$ data sets to determine the random triple curve in Fig. 10.

The significance thresholds we discover prove that the probability of a triple occurring at random above the thresholds is in practice very close to zero. In other words, the observed probability B of a random triple occurring above the specified threshold is 0, however the true probability T of a random triple occurring above the threshold is not 0. Thus to put a bound on the true probability T, we use the Chernoff bound: $P(T < \epsilon) \geq 1 - e^{-2 \cdot n \cdot \epsilon^2}$, where n is the number of random sets we generated ($M = 1000$) and ϵ would be an error tolerance. Setting $\epsilon = 0.05$, we have that the probability of $P(T < 0.05) \geq 0.9933$.



(a) (b)

Figure 10: Abundance of triples occurring as a function of frequency of occurrence. (a) chain triples; (b) sibling triples



Sept. 2000 - Sept. 2001 Mar. 2000 - Mar. 2001 Sept. 2001 - Sept. 2002

Figure 11: Evolution of part of the Enron organizational structure from 2000 - 2002. Note: actors B, C, D, F present in all three intervals. Here is who they are: B - T. Brogan, C - Peggy Heeg, D - Ajaj Jagsi and F - Thresa Allen.

13.2 Experiments on Weblog Data

Similar experiments were run on the Weblog data to obtain communication groups (see Section 12 for a description of the Weblog data). As a validation we used a graph of friendship links, which was constructed from friendship lists of people who participated in the conversations during that period. Fig. 12 shows one of the groups found in the Weblog data and the corresponding friendship links between the people who participated in that group. The fraction of friendship links for this group of 24 actors is 2.5%, again well above the 0.0008% for a randomly chosen group of 24 actors.

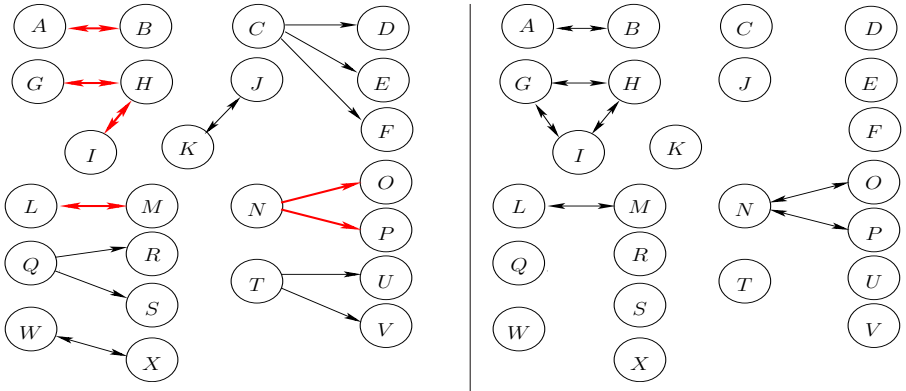


Figure 12: Validation of Weblog group communicational structure on the left against actual friendship links on the right.

13.3 General Scoring Functions vs. "Step" Function Comparison

Here we would like to present a comparison of a general scoring function and a "step" function. We will compare a given general propagation delay functions G_1, G_2, G_3 and G_4, to a "best fit" step function, see Figure 13.

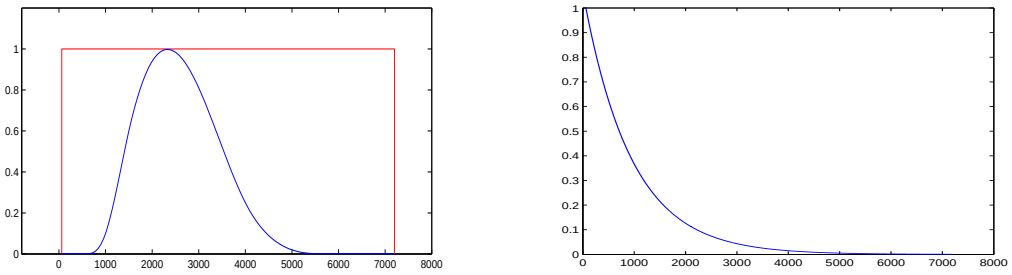


Figure 13: Step function H and a General Response Function G_1 for $2D$ Matching on the left and Exponential Decay Response Function G_4 on the right.

Functions G_2 and G_3 are respectively linear monotonically increasing and linear monotonically decreasing functions, while G_4 is generated using a well known exponential distribution of the form $(y = \lambda \cdot e^{-\lambda \cdot x})$. We generated G_1 using a cubic splines interpolation.

For the purposes of this experiment we used an Enron dataset, where we looked at the data which represents approximately one year of Enron communications and consists of $753,000$ messages. We obtained a set of triples of H for the step function and a set of triples of G_1, G_2, G_3 and G_4 for the general propagation functions with causality constraint and G_1', G_2', G_3' and G_4' without causality constraint. Next we used our distance measure algorithms to measure the relative distance between these graphs. Figure 14 shows the discovered relative distances.

The results indicate that functions H, G_3 and G_4 produce very similar sets of triples, which is explained by the fact that the most of the captured triples occur "early" and therefore are discovered by these somewhat similar functions. Also we can notice that G_1 and G_2 find different sets of triples, while G_1 still has a significant overlap with H, we can explain this behavior by the fact that G_1 and G_2 have peaks in different time intervals and thus capture triples occurring in those intervals.

	H	G_1	G_2	G_3	G_4
G_1	0.63	-	0.34	0.66	0.67
G'_1	0.64	0.98	0.34	0.65	0.67
G_2	0.22	0.34	-	0.33	0.18
G'_2	0.23	0.34	0.97	0.34	0.18
G_3	0.94	0.66	0.33	-	0.88
G'_3	0.95	0.67	0.34	0.96	0.89
G_4	0.90	0.67	0.18	0.88	-
G'_4	0.92	0.67	0.19	0.89	0.97

Figure 14: Relative similarity between the groups of H, Gs and G's.

In the current setting we showed that functions with peaks at different points will discover different triples. Most of the times in real data there seems to be no practical need for this added generality, however having this ability at hand may prove useful in certain settings. Also, since the difference is small compared to the rate of group change in the Enron data, hence there is not much value added by a general propagation delay function to justify the increase in computation cost from linear to quadratic time.

13.4 Tracking the Evolution of Hidden Groups

For chains the significance threshold frequencies were $\kappa_{chain} = 30$ and $\kappa_{sibling} = 160$. We used a sliding window of one year to obtain evolving hidden groups. On each window we obtained the significant chains and siblings (frequency $> \kappa$) and the clusters in the corresponding weighted overlap graph. We use the clusters to build the communication structures and show the evolution of one of the hidden groups in Fig. 11 without relying on any semantic message information. The key person in this hidden group is actor C, who is Peggy Heeg, Senior Vice President of El Paso Corporation. El Paso Corporation was often partnered with ENRON and was accused of raising prices to a record high during the "blackout" period in California [1, 5].

13.5 Estimating the Rate of Change for Coalitions in the Blogosphere

Next we would like to show how the approaches of distance measure, presented in this thesis, can be used to track the evolution and estimate the rate of change of the clusterings and groups over time. As our example we studied the social network of the Blogosphere (Live Journal). We found four clusterings C_1, C_2, C_3 and C_4 by analyzing the same social network at different times. Each consecutive clustering was constructed one week later than the previous. The task of this experiment is to find the amount of change that happened in this social network over the period of four weeks. The sizes of the clusterings C_1, C_2, C_3 and C_4 are 81348, 82056, 82132 and 80217 respectively, while the average densities are 0.630, 0.643, 0.621 and 0.648.

We can see in the Fig. 15 that the *Best Match* and the *K-center* algorithms imply that the rate of change of groups in the blogosphere is relatively high and the groups change very dynamically

	C_1 - C_2	C_2 - C_3	C_3 - C_4	Average Change
Best Match	4.31	5.01	4.83	4.72

Figure 15: The rate of change of the clusterings in Blogosphere over the period of four weeks.

from one week to another.

	C'_1 - C'_2	C'_2 - C'_3	C'_3 - C'_4	Avg. Change
Best Match	0.3	0.23	0.24	0.26

Figure 16: The rate of change of the clusterings in the Enron organizational structure from 2000 - 2002.

13.6 Estimating the Rate of Change for Groups in the Enron Organizational Structure

Another experiment we conducted, using the proposed distance measures, is estimating the rate of change for groups in the Enron organizational structure. We used Enron email corpus and the approach proposed in [6] to obtain clusterings with statistically significant persistent groups in several different time intervals.

On each window we first obtained the significant chains and siblings and then the clusterings in the corresponding weighted overlap graph. The clusterings C'_1, C'_2, C'_3 and C'_4 with average densities 0.65, 0.7, 0.71 and 0.67 respectively, were computed based on the intervals Sept. 1999 - Sept. 2000, Mar. 2000 - Mar. 2001, Sept. 2000 - Sept. 2001 and Mar. 2001 - Mar. 2002.

Next we used the *Best Match* and *K-center* algorithm to track the rate of change in the network. Fig. 16 illustrates the rate of change as well as the average rate of change of the clusterings. Notice that the rate of change in the email networks over a 6 month period are significantly lower than the rate of change in Blogs over a 1 week period. Blogs are a significantly more dynamic social network which should be no surprise.

The Fig. 11 illustrates the structure of a single group in each of the clusterings as well as it gives a sense of its evolution from one time interval to next.

The ability to account for the overlap and evolution dynamics is the underlying reason why the distance found by the *Best Match* and *K-center* algorithms is relatively low for groups in the ENRON dataset.

As a conclusion we would like to point out that Blogs and ENRON are two completely different social networks. ENRON represents a company network, which has the underlying hierarchy of command, which is unlikely to change quickly over time, while Blogosphere is a much more dynamic social network, where groups and their memberships can change rapidly. This behavior is well reflected in the experiments described above.

13.7 Tree Mining Validation

Additionally for the purpose of validation, we used the tree mining approach in conjunction with the heuristic algorithms , in order to verify that a discovered tree-like structure actually occurs frequently in the data. For the experiment, we once again used the ENRON email corpus and the

	C_1 - T_1	C_2 - T_2	C_3 - T_3	C_4 - T_4
Best Match	0.323	0.321	0.294	0.389

Figure 17: The similarity between the trees and the clusterings in the Enron organizational structure from 2000 - 2002.

time intervals Sept. 1999 - Sept. 2000, Mar. 2000 - Mar. 2001, Sept. 2000 - Sept. 2001 and Mar. 2001 - Mar. 2002. For each interval were found significant chains and siblings and performed the

clustering on the weighted graph of overlapping triples. The clusterings C_1, C_2, C_3 and C_4 were found. Next we performed tree mining in order to extract exact tree like communication patterns for the same intervals and obtained T_1, T_2, T_3 and T_4. The same significance threshold frequencies were used $\kappa_{chain} = 35$ and $\kappa_{sibling} = 160$ when we found C_1, C_2, C_3 and C_4.

	C'_1 - T'_1	C'_2 - T'_2	C'_3 - T'_3	C'_4 - T'_4
Best Match	0.411	0.407	0.414	0.41

Figure 18: The similarity between the trees and the clusterings in the Blogosphere over the period of 4 weeks

We also performed the same experiment on the Blogosphere, where we randomly picked the set of 4 consecutive weeks and discovered groups by performing our heuristic clustering approach to obtain clustering C'_1, C'_2, C'_3 and C'_4. Next we found exact tree like communication structures T'_1, T'_2, T'_3 and T'_4 for each week respectively.

We used the *Best Match* and the *K-center* algorithms to measure the amount of similarity between these two sets. You can find the results of these measurements in the Fig. 17 and 18. The groups which we find using a heuristic clustering approach compare well to the actual tree-like structures present in the data.

Additionally we would like to bring your attention to the Fig. 15 and 18 to point out that despite the rapid and dynamic rate of change in the Blogosphere as a system, the relative distance which is found between respective T's and C's remained low. This suggests that our algorithms for discovering planning hidden groups are able to perform well for very dynamic systems as Blogosphere as well as the more stable systems as ENRON. Notice that the slightly higher similarity in the ENRON data could be caused by the fact that the underlying hierarchy like structure of the ENRON company resembles the tree like patterns much more then a chaotic Blogosphere. Nevertheless the discovered similarity for the groups in the Blogosphere data is still suggesting that the groups we discover using our heuristic approach are similar in their nature to the groups discovered by performing tree mining. Thus this section provides yet another prove of that our algorithms find real and meaningful groups in the streaming communication data by using no message content.

14 Conclusions

In this work, we described algorithms for discovering hidden groups based only on communication data. The structure imposed by the need to plan was a very general one, namely connectivity. Connectivity should be a minimum requirement for the planning to take place, and perhaps adding further constraints can increase the accuracy or the efficiency.

In our algorithms there is no fixed communication cycle and the group's planning waves of communications may overlap. The algorithm first finds statistically significant chain and sibling triples. Using a heuristic to build from triples, we find hidden groups of larger sizes. Using a moving window and matching algorithms we can track the evolution of the organizational structure as well as hidden group membership. Using a tree querying algorithm one can query a hierarchical structure to check if it exists in the data. The tree mining algorithm finds exactly all of the frequent trees and can be used for verification purposes. Our statistical algorithms serve to narrow down the set of possible hidden groups that need to be analyzed further.

We validated our algorithms on real data and our results indicate that the hidden group algorithms do indeed find meaningful groups. Our algorithms don't use communication content and don't differentiate between the natures of the hidden groups discovered, for example some of the

hidden groups may be malicious and some may not. The groups found by our algorithms can be further studied by taking into account the form and the content of each communication, to get a better overall result and to identify the truly suspicious groups.

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