

On analysis of complex network dynamics – changes in local topology

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ABSTRACT

Social networks created based on data gathered in various computer systems are structures that constantly evolve. The nodes and their connections change because they are influenced by the external to the network events. In this work we present a new approach to the description and quantification of patterns of complex dynamic social networks illustrated with the data from the Wrocław University of Technology email dataset. We propose an approach based on discovery of local network connection patterns (in this case triads of nodes) as well as we measure and analyse their transitions during network evolution. We define the Triad Transition Matrix (TTM) containing the probabilities of transitions between triads, after that we show how it can help to discover the dynamic patterns of network evolution. One of the main issues when investigating the dynamical process is the selection of the time window size. Thus, the goal of this paper is also to investigate how the size of time window influences the shape of TTM and how the dynamics of triad number change depending on the window size. We have shown that, however the link stability in the network is low, the dynamic network evolution pattern expressed by the TTMs is relatively stable, and thus forming a background for fine-grained classification of complex networks dynamics. Our results open also vast possibilities of link and structure prediction of dynamic networks. The future research and applications stemming from our approach are also proposed and discussed.

Categories and Subject Descriptors

E.1 [Data Structures]: Graphs and Networks; H.4 [Information Systems Applications]: Miscellaneous; J.4 [Social and Behavioral Sciences]: Sociology;

General Terms

Algorithms, Measurement, Experimentation, Theory, Verification.

Keywords

Complex social networks dynamics, local topology analysis, triad transition matrix.

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The 5th SNA-KDD Workshop '11 (SNA-KDD'11), August 21, 2011, San Diego CA USA. Copyright 2011 ACM 978-1-4503-0225-8...\$5.00.

1. INTRODUCTION

Complex networked systems attract more and more researchers from different fields. Networked structures are present in our everyday life – power grids, transportation networks, social networks, biological and ecological networks. Changes in the structure of these systems can have a wide range of consequences for individuals, groups, whole companies or even countries. In this paper we focus on social networks but the presented methodology for investigation the changes in local topology can be applied to all types of complex networks. Of course the interpretation of the results will vary from one application to another but the technique remains unchanged.

When investigating the topological properties and structure of complex networks we face a number of complexity-related problems. In large social networks, tasks like evaluating the centrality measures, finding cliques, etc. require significant computing overhead. However, the technology-based social networks add a new dimension to the known problems of network analysis [11]. The existence of link is a result of a series of discrete events (like email exchanges, phone calls, posting of blog entries) which have some distribution in time. As shown in [9] for various kinds of human activities related to communication and information technologies, the probability of inter-event times (periods between the events, like sending an email) may be expressed as: $P(t) \approx t^{-\alpha}$ where typical values of α are between 1.5 and 2.5. This distribution inevitably results with series of consecutive events (“activity bursts”) divided by longer periods of inactivity.

These phenomena have serious consequences when we try to apply the classical structural network analysis (SNA) to dynamic networks. The most popular approach to perform SNA on dynamic networks is to divide the time period under consideration into time windows, then run the structural analysis methods on the networks created for each time window separately. This should show how the measures like node centrality, average path length, group partitions etc. change over time, providing an insight into the evolutionary patterns of the network.

However, the bursty behaviour of the users (long inactivity periods mixed with the bursts of communication activities) causes dramatic changes of any measure when switching from one time window to another. There is a trade-off: short windows lead to chaotic and noisy dynamics of network measures, while long windows give us no chance to investigate time evolution of the network [13][14].

In order to address this problem, a number of approaches designed to predict changes in the structure of dynamic networks were

proposed [15][16]. The special case of this family of methods is a so-called link prediction problem – the estimation of probability that a link will emerge/disappear during the next time window [12].

In this work we propose a method of characterizing the dynamic evolutionary patterns of the network by the analysis of changes in the local topology of connections. This approach stems from our previous experience [17] and will be introduced in Sec. 2. Sec. 3 presents the results, showing the possibility of the characterization of network evolutionary schemes with our approach. These concepts are illustrated by the experiments carried on the large e-mail based social networks build from the mail logs of the Wrocław University of Technology e-mail social network.

2. LOCAL TOPOLOGY OF ONLINE SOCIAL NETWORKS

2.1 Triads and network motifs

For the abovementioned reasons, standard approaches exploiting network analysis by means of listing several common properties, like the degree distribution, clustering coefficient, network diameter or average path lengths often fail when applied to dynamic complex networks [18]. In many cases it is possible to use random algorithms (like standard preferential attachment) to construct networks with for example exactly the same degree distribution whose structure and function differ substantially (we'll comment on this issue in the next section). Huge network structures (like social, biological, gene networks) should be investigated with more precise and structure-sensitive methods [1][4].

For complex networks, we experience a general rule that the global properties like network clusters, diameter, node degree distribution emerge from the local interactions, which constitute the local topology of the network (direct neighbourhood of a node in simplest case). Even simple local rules may lead to the emergence of dense groups, phase transitions or non-trivial network topologies [20].

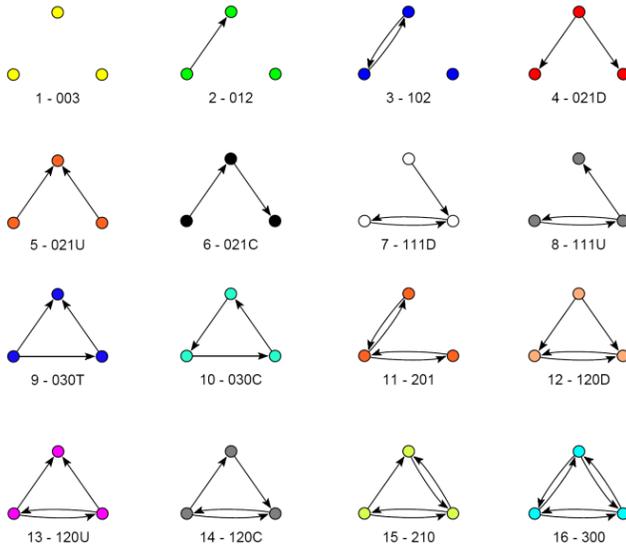


Figure 1 Three-node triads in directed graphs for undistinguishable nodes (picture from [21])

During last years we have experienced the development of a number of methods investigating complex networks by means of their local structure (especially – frequent patterns of connections

between nodes). The simplest, and therefore most popular, way to characterize the network in the context of local connections is to examine the links between the smallest non-trivial subgraphs consisting of three nodes – the triads..

A set of 16 triads that do not distinguish between nodes is presented in Figure 1 (Please note that numbers 1, 2, etc will be used further on in this paper when referencing a set of 16 directed triads).

If we want to distinguish between node positions in a triad, there are 64 different triads in a directed graph (Figure 2). In our experiments we distinguish between the nodes, for in our network they are corporate email addresses and, when analysing the connection changes two topologically equivalent subgraphs may in fact represent different behaviour of the users.

Please note the triad ID (the numbers inside the picture of the subgraphs) in Figure 2, as it will be used further on in this paper for identifying the connection patterns. Note also, that there is a correspondence between the IDs and the edit distance between triads – small difference in the ID value *in most cases* suggests small edit distance (the number of link removal/addition operations needed to transform one triad into another).

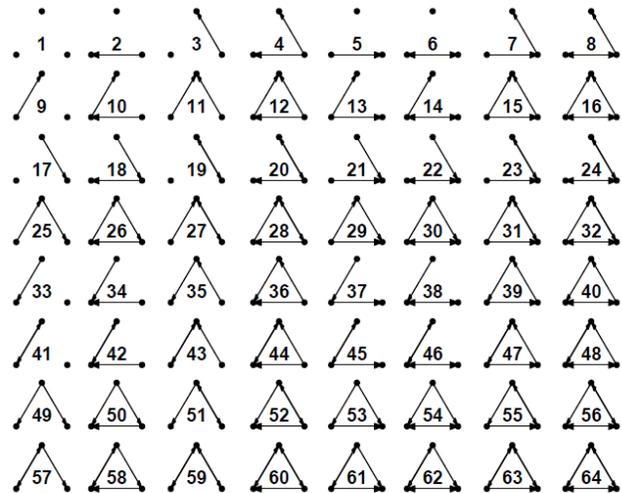


Figure 2 Three-node triads in a directed graph

The basic method utilizing such subgraphs is the well-known triad census, which is enumeration of all triads in the network, allowing to reason about the functional connection patterns of the nodes [18]. Last years have seen the development of more sophisticated approaches, among them *motif analysis* which aims to characterize the network by the difference between its structures and an ensemble of random networks of the same size and degree distribution. A biased distribution of local network structures (subgraphs) is widely observed in complex biological or technology-based networks. Motif analysis stems from bioinformatics and theoretical biology [1][3], where it was applied to the investigation of huge network structures like transcriptional regulatory networks, gene networks or food webs [4][5]. Although the global topological organization of metabolic networks is well understood, their local organization is still not clear. At the smallest scale, network motifs have been suggested to be the functional building blocks of network biology. So far several interesting properties of large biological network structures were reinterpreted or discovered with the help of motif analysis. There was also one more conclusion: although the properties like node degree distribution, clustering or diameter of real-life networks and their randomly generated counterparts may agree, the local

topology shows distinctive features which are quite different (like the general motif profile of the network expressed by so-called triad significance profile – TSP – a vector of the Z-score measures of the motifs) [6][7][8].

Motif analysis offers low computational overhead and opportunity to gain an insight into the local structure of huge networks which otherwise would require prohibitive computations to investigate. Moreover, the discovered motifs and their numbers enable to assess which patterns of communication appear often in the large social networks and which are rather rare.

In our former research we have investigated the local structure of numerous technology-based networks, among them an e-mail social network of Wrocław University of Technology (WUT), consisting of more than 5 800 nodes and 140 000 links [2][17]. Our aim was to check if the known properties of local topology in social networks (known on the basis of motif analysis conducted for small non-technology social networks [4]) are also present in large email-based social structures, and if there are some distinct features characteristic to the email communication. The most important conclusion from these experiments was that the TSP of the network is stable over long periods of time. This was confirmed even for periods like summer holidays when the number of links in the university network dropped by 50% and for different link weight thresholds [17]. Summing up – the investigated complex network show statistically stable pattern of connections as a whole, despite the fact that average stability of a single link is quite low: 59% in our case (which means that 41% of the connections will not be present in the next time window). This statement is even more important when we consider that it generally holds regardless of the width of the time window (the link stability of 67% was measured for 30-day time windows). It may be explained by the cumulative effect of the users’ activity – for longer time windows the chance that the communication between users will be noticed obviously grows, but on the other hand there are links which will appear only in one of the shorter time windows. Some of the users use their email accounts only occasionally, for example, in our dataset 16% of the users exchanged only one email during the analysed period.

The above observations taken together with the former results cited led to the idea of characterizing the evolutionary patterns of the network by means of the changes in elementary subgraphs, in this particular case – directed triads.

In the next section we introduce the Triad Transition Matrix (TTM) as a basic structure used in our experiments to measure the changes in local topology patterns of the network.

2.2 Triad Transition Matrix

The idea behind the Triad Transition Matrix is to use the data about the history of the network (recorded during past time windows) to derive the probabilities of transitions between triads (patterns of local connections).

The TTM is a $g_\Delta \times g_\Delta$ matrix, where g_Δ is the number of considered subgraphs. For directed triads in our experiments $g_\Delta = 64$ (see Fig.1, however if we decide not to distinguish between the nodes, there will be only 16 possible triads).

The values of TTM entries are defined as follows:

$$TTM_t(i,j) = P(g_i[t] \rightarrow g_j[t+1]) \quad (1)$$

$TTM_t(i,j)$ is the probability (estimated on the basis of the full subgraph enumeration for networks created from data gathered in time windows $[t-1, t]$ and $[t, t+1]$), that a connection pattern g_i detected during $[t-1, t]$ will transit into g_j during $[t, t+1]$. In large complex networks (like the one analysed in our experiments) we may expect the occurrence of huge numbers of the triads of all

kinds – typically the network comprising of thousands of nodes contains at least million triads.

Our goal was to check if the local network structures (the triads – discussed in the former subsection) show distinguishable evolutionary patterns.

2.3 Size of the Time Window

Selecting the right time window for analysis of network dynamics is a very challenging process, for the reasons briefly presented in the introductory section. There are two standard approaches to split data into time periods:

a) Moving window – length of the time window (e.g. x) and the time interval that is used to move the window (e.g. y) are defined. In order to extract time periods, the time frame of the length x is moved by the factor y . In consequence the whole timeframe under consideration is divided into partially overlapping periods. Note that, the time window and time interval need to be specified in the way that the period from the start date to end date should be completely covered.

b) Equal, separate periods – number of periods e.g. k is set and then the data are divided into k separate, equal periods according to the dates of activity occurrence.

The concepts of both procedures are presented in the Figure 3.

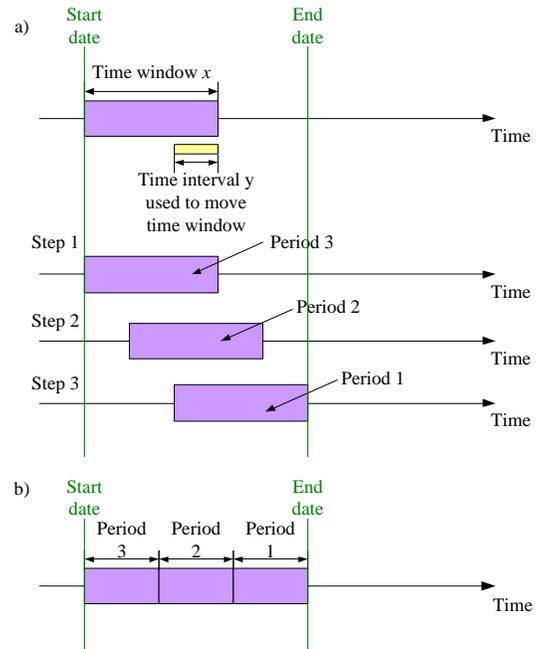


Figure 3 The division of analysed data into time periods using a) the concept of moving window, b) the concept of equal, separate periods.

The most challenging part of both procedures is to decide what should be the length of time window. In this paper, second approach with equal, separate periods has been used, because overlapping windows would make it difficult to uniformly assign the changes in the triad connections to the given time period. Four different time frames have been chosen (1, 3, 7, and 30 days long) and analyses were performed to investigate the influence of time window size on the discovered patterns.

3. EXPERIMENTS

3.1 Data Preparation

The experiments were carried out on the logs from the Wrocław University of Technology (WUT) mail server, which were pruned to contain only the emails originated from (or: sent to) the staff

members registered at the mail server of the university. First, the data has to be cleansed by removal of spam and unification of duplicated email addresses. There are 5834 active email addresses on the server, which implied that even for the shortest time window of 1 day, there were on average ~2000 active network nodes. For our experiments we used data from a period of 100 days, starting on the 5th of March 2010.

3.2 Experiment Setup

The dataset has been divided into time windows in the following

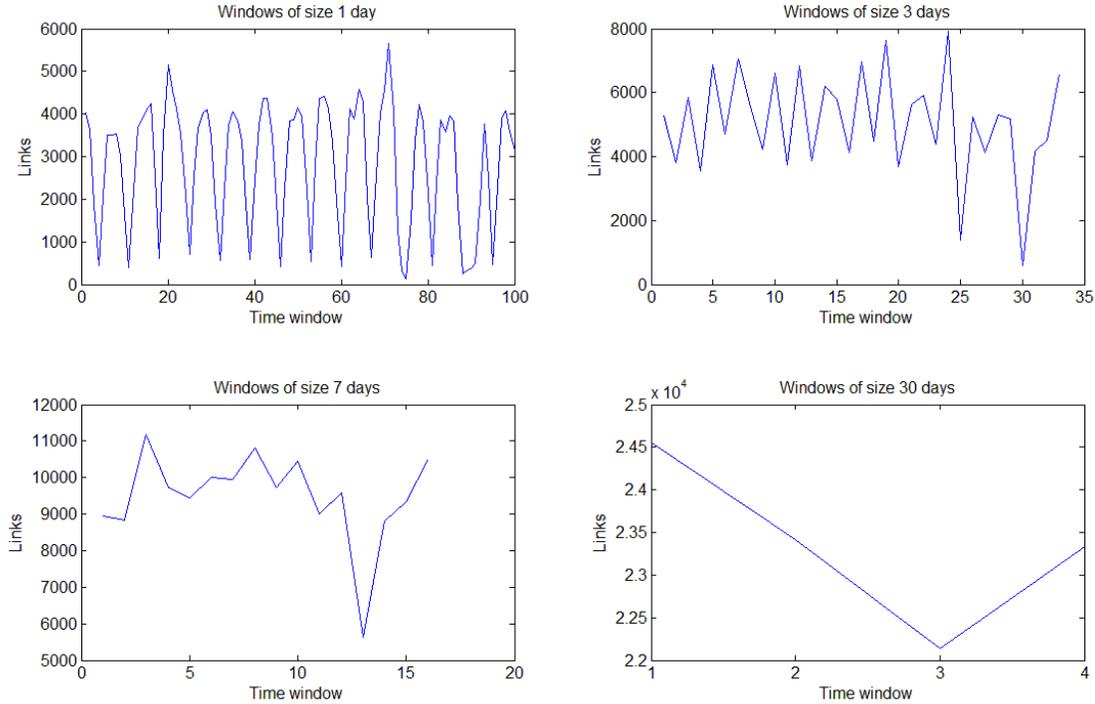


Figure 4 Number of edges for specific time windows

way (note that the length of time windows not always sums to 100 days, but we decided to maintain equal timespans of the windows in order to exclude the possible influence on the results):

- Setup 1: 100 windows – each window 1 day long
- Setup 2: 33 windows – each window 3 days long
- Setup 3: 16 windows – each window 7 days long
- Setup 4: 4 windows – each window 30 days long

In Figure 4 the number of edges for each time window has been presented. The biggest variations in number of links can be observed in the case of time windows of size 1, which corresponds to the phenomena mentioned in Introduction. In particular, the visible drop in the number of links observed every seven days clearly corresponds with Sundays (or, in general, the weekends), when the activity at the university freezes. The situation stabilises when larger time windows are considered. However, the sudden drop of number of links that is visible in windows 25 and 30 (for window size of 3 days), and also for window 13 (for window size of 7 days) and finally window 3 (for window size of 30 days), cannot be properly identified when windows of length 1 day are considered (although it may be associated with student celebration days practically resulting in a few extra holidays in May).

3.3 Frequency of Triad Occurrence

First experiments were performed to check if and how the number of specific triads changes in different windows that are of different size (Figure 5). In this (and *only* this) analysis we were not distinguishing between the nodes in the triads, which implies that there are only 16 possible directed triads to be considered.

Obviously, the most dynamic changes occur when the time window of size 1 day is investigated. However it can be noticed for 1 day window, that the changes have periodical character. Again, the changes repeat within the cycles which last 7 days

each.

This pattern is still visible when analysing three-day periods but is flatter than in the previous case, since normal communication overlaps with the free time. Analysis of the three-day periods revealed that the number of motifs drops significantly in windows 25 and 30 in comparison to other windows.

Looking at the time windows of the length of 7 days, further flattening of dynamics is clearly visible and it is even more clear for time window of size 1 month.

Figure 5 suggests that in the analysed network one can observe the stability of triad connection pattern. The pattern that covers 7 days and repeats periodically, reflects the changes that occur within the network structure although the rules of these changes can be perceived as stable.

3.4 TTM for different windows size

The number of triads enumerated in the networks derived from different time windows varies from 1.3 million (for 1 day windows) up to 2.2 million (for 30 day windows). The changes in the connections within these triads were used to compute the transition probabilities which constitute the entries of the TTMs.

In Figure 6 the TTM derived on the basis of 4 time windows of size 30 days each are presented (from this point, all results are for

the triads in which the nodes are distinguished from each other, which results in 64 connection schemes between 3 nodes connected by directed links). We may notice that the triad transition probabilities have distinctive form (the distribution of transition probabilities is not flat and looks stable) which reveals some variation but holds the general shape which may be called *the evolutionary pattern of the network* under consideration –the TTM’s entries computed for neighbouring time windows have similar values.

First of all, the value of TTM(1,1) reflects the fact that the network is sparse (the link density is below 1%) which means that

The last important observation is that some triads are special as they show clearly bigger values in their columns of TTM, which means that they are “sinks” of the evolution patterns of connections.

High probability of the fact that triads number 4, 13, and 49 (Figure 1) will not change shows that they may be called *stable triads* in the analysed network. It reveals the specific characteristic of email networks where many departments exist and there is a lot of broadcast communication (which is not answered) from one person (e.g. secretary) to the large number of recipients.

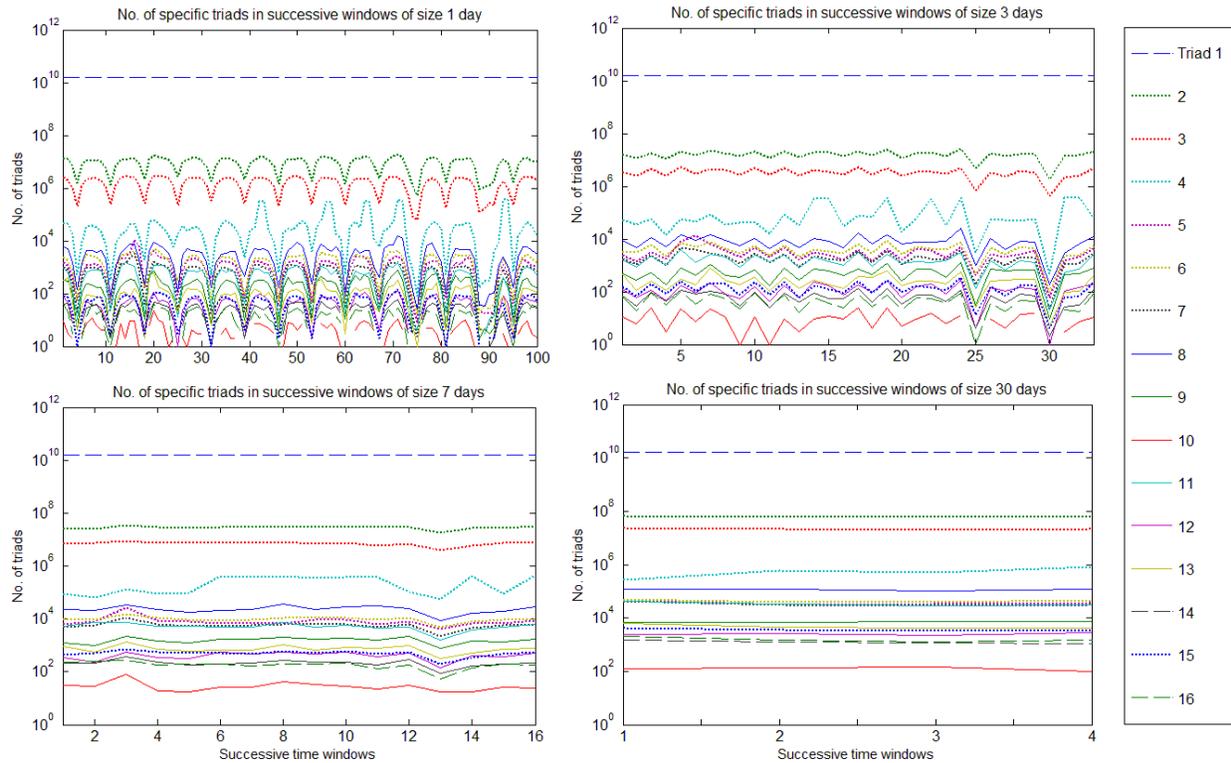


Figure 5 Number of specific motifs (from Figure 1) in successive windows

most of the possible triads contain no edges. As the result most of the “empty” triads always remain in this state, which gives us a relatively high value of TTM(1,1) for all TTM matrices.

We should also note the high values in the first column of the TTM. This means that when it comes to disappearing of the links, the probability of resetting the entire triad to zero-connection state is relatively high.

On the other hand, it is also visible, that the values on the diagonal of TTM are bigger than most values in their neighbourhood, which shows that the already-formed triads tend (in general) to stay in their current state.

Interesting situation can be observed in the case of windows of size 1 day. Although most of TTMs are similar to those presented above there is an interesting outlier that reoccur every 7 windows (Figure 7). These Triad Transition Matrices show that almost all network triads disappear as it was pointed out previously. It can reflect the day-off where almost nobody sends emails. The rest of the triads, which do not disappear totally, degenerate to weakly connected triads, e.g. triad number 62 changes into triad number 33.

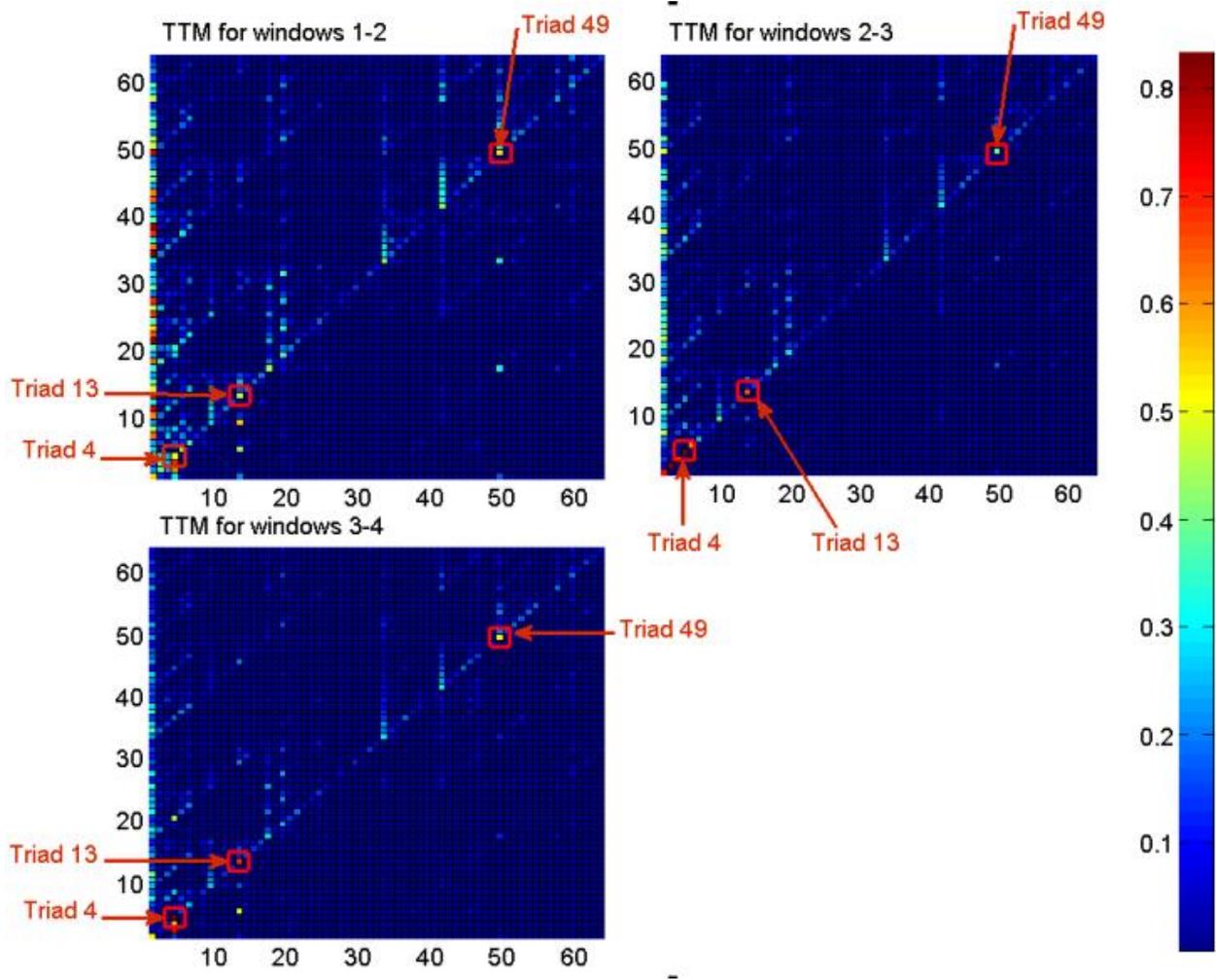


Figure 6 TTM between windows of size 30 days

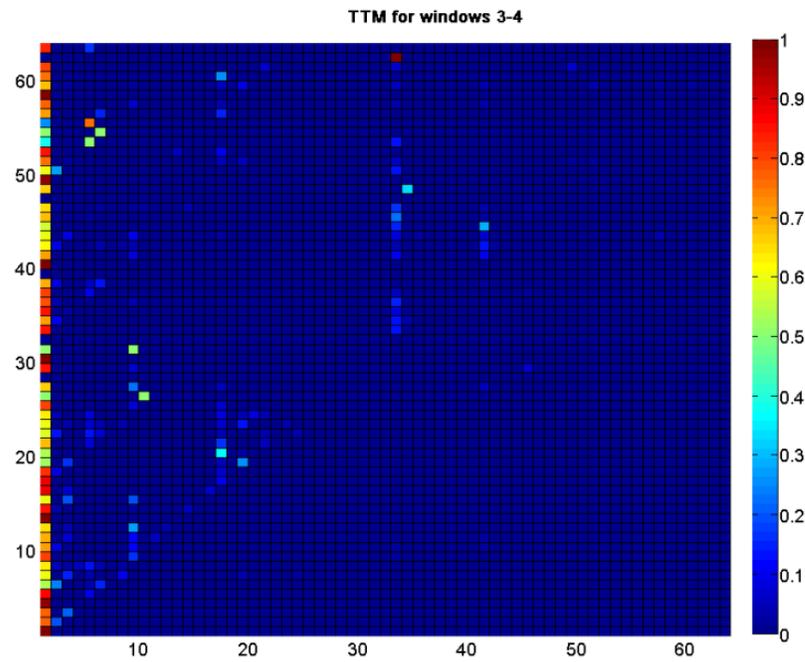


Figure 7 TTM between windows 3 and 4 (1 day time windows)

3.5 Similarity between the TTMs

The analysis of each of the TTM separately is very complex. Thus one of the methods that can be applied to compare TTMs was to calculate the degree to which two Triad Transition Matrices are similar to each other. First step of this approach is to subtract one matrix from another. Then all absolute values of elements from the resulting matrix are summed up. The obtained value is normalised by dividing by the largest possible value – 128 (when two matrices are completely different – the result will be denoted by $inv_sim(TTM_1, TTM_2)$). Finally, the similarity between the matrices, $sim(TTM_1, TTM_2)$, is calculated as:

$$sim(TTM_1, TTM_2) = 1 - inv_sim(TTM_1, TTM_2) \quad (2)$$

The calculated similarities between 99 TTMs created for time windows of size 1 day are presented in the top-right corner of Figure 8. It can be seen that a repeating pattern can be found. Starting from TTM number 3 and then every 7 days the TTMs are similar to each other. These TTMs (3rd, 10th, 17th, etc.) although

very similar to each other are less similar to the rest of the Triad Transition Matrices.

Similarities between TTMs for 3 days' time windows also feature some patterns but they are not as visible as in the case of TTMs for 1 day window. Interesting situation can be observed in the case of time windows of size 3, where the TTMs between window 24 and 25 as well as between 29 and 30 are not similar to other TTMs. It shows that in these TTMs the sudden change of local structure has occurred.

Finally the similarity matrix for TTMs for 7 days time window shows that they are very similar, so the fluctuations in triad profile can be hardly observed.

Next step of the TTMs analysis focused on investigation of the mean and variance of the TTM entries for different sizes of time windows.

The mean values for all experimental setups look very similar (Figure 9). The highest mean values occur in the diagonal and also in the case of loosely connected triads (triads' number 1, 2, 3, 4) of each matrix presented in Figure 9.

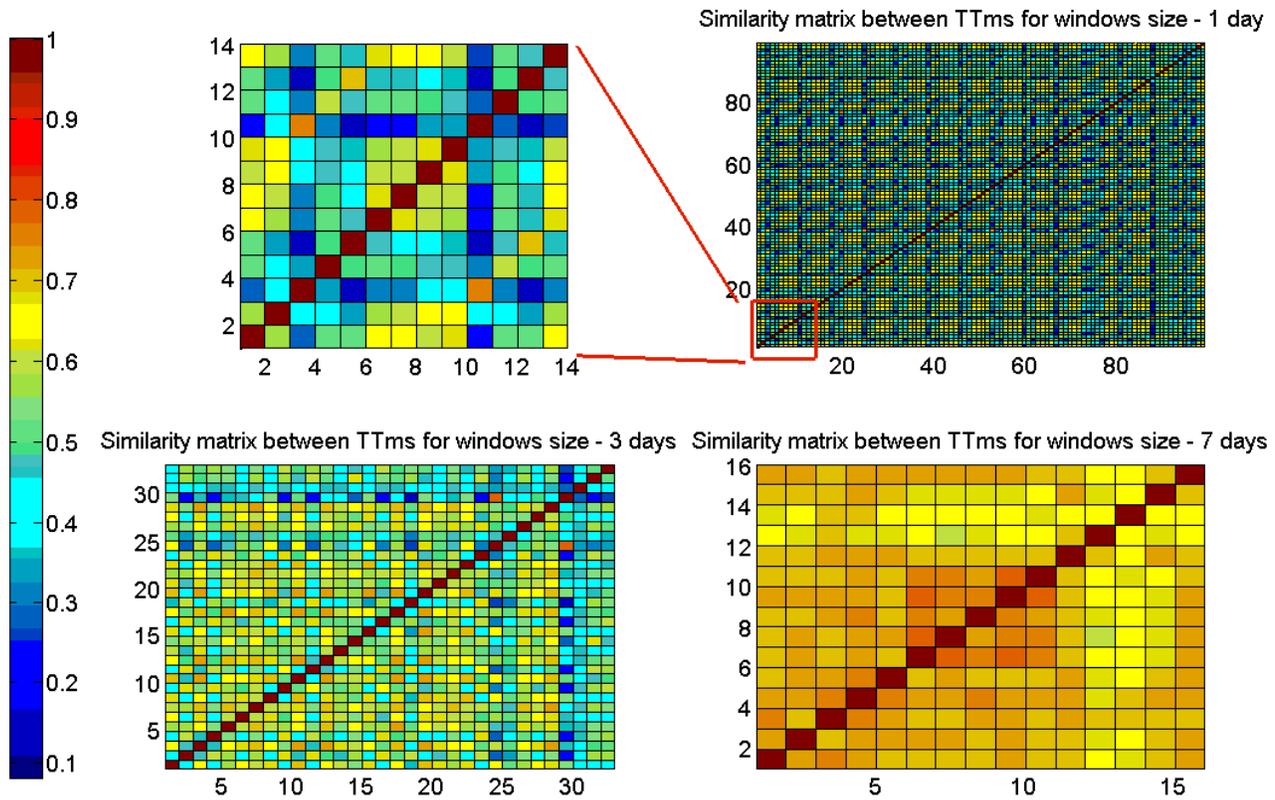


Figure 8 Similarity matrices between TTMs for different sizes of time window

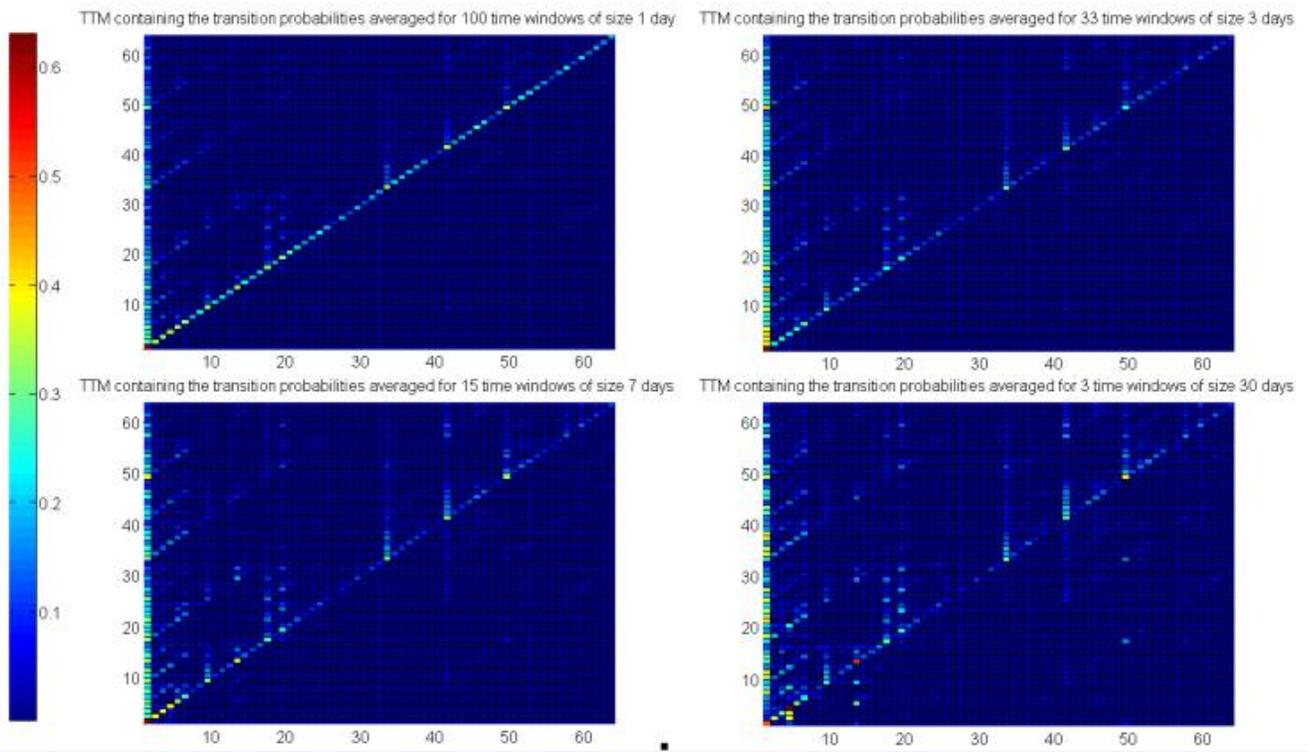


Figure 9 TTMs containing the transition probabilities averaged for number of time windows in a specific setup.

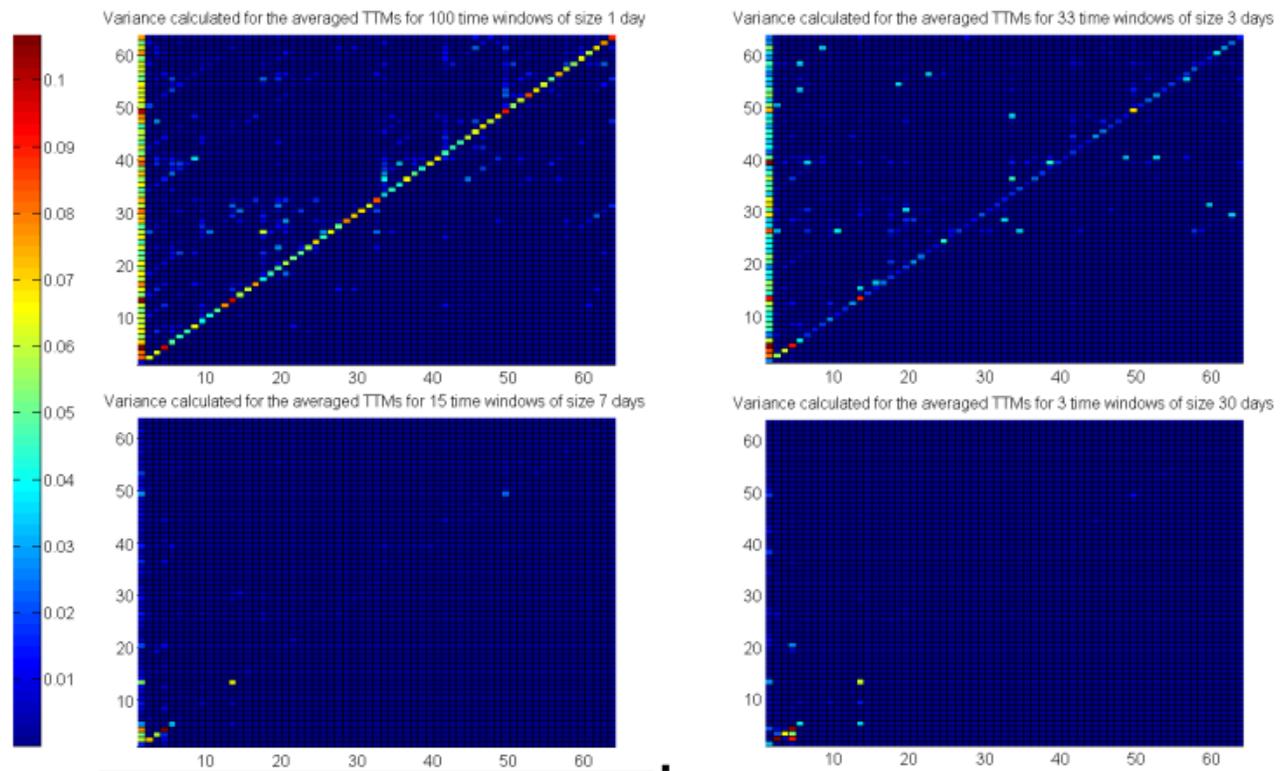


Figure 10 Variance calculated for TTMs containing the transition probabilities averaged for number of time windows in a specific setup.

The variance informs how far the set of numbers lie from the mean (expected value). In Figure 10 a specific variances for corresponding matrices in Figure 9 are presented. As it can be seen the variance is the biggest in the case of TTMs created for windows of size 1 day. However please note that the variance is from the range (0; 0.11) so it is small in general. The variance for TTMs where time windows were either 7 days long or 30 days long is 0 for most of the matrices cells. The variations from mean value exist only in the case of loosely connected triads.

The last fact clearly shows, that for longer time windows the network is still dynamic, there are constant transitions between the connection patterns, however the dynamic changes follow a well-defined pattern.

It is worth to note that although the evolutionary pattern of the network is stable, the links are not, as mentioned in the preceding sections. Thus our approach offers a way to statistically describe the evolutionary patterns in the network and to show that these patterns are relatively stable, even while the links and (in consequence) traditional structural measures of the network are not.

4. CONCLUSIONS AND FUTURE WORK

The approach presented in this paper allows the statistical description of evolutionary patterns of complex networks and shows that, for the complex and dynamic social network based on everyday communication in a large company these patterns show stability in spite of link instability. From the other hand, the periodical fluctuations resulting from external events (like weekends, holidays etc.) are also detectable and may be used to quantitatively describe the life of the network.

The results shown in this work open also vast possibilities for future research and building more sophisticated models, allowing also interesting applications. The most interesting and prospective possibilities are:

1. Link and structure prediction: knowing the evolutionary patterns of the network one can predict its future topology, on the level of single link (link prediction) or even global connectivity and cluster structure. Our next step will be the application of the TTMs to link and structure prediction. Our approach seems to be especially promising in the second case, while the triads – topologically - lie between links and network groups. In consequence the TTMs embrace part of group behaviour patterns and may be used to characterize group dynamics as well.
2. Including link weight issues in the analysis. The network analysed in this work was unweighted, but, obviously, not all triads consist of the links of the same intensity. The information about weights may be used as complementary and may help to estimate the triad transition probabilities
3. Reducing the complexity of our method in order to be used to analyse huge networks (like telecom graphs coming from logs of mobile phone operators, who may use the predictions to evaluate the marketing strategies, make customer churn predictions, learn about user behaviour patterns and so on). In practice, for the network of the size used in our experiments the computations were not prohibitive and were made on a state-of-the-art PC (it should be also noted that the method may be easily parallelized, which is not a challenge for algorithms involving triad counting).

4. Network classification according to evolutionary patterns. It will be checked if the complex networks emerging in different areas show stable TTMs and if they can be classified according to them. We have obtained preliminary results showing that the similar patterns (expressed by the stable values of TTMs) exist in other dynamic complex networks – like in communication graphs formed by source-to-destination communication by the computers in distributed systems. We are planning to test the applicability of our approach for the detection of traffic anomalies and network attacks.
5. Tuning of the method by including the periodicity of the changes in TTM entries for consecutive time windows (visible in 1-day windows in our experiments).

5. ACKNOWLEDGMENTS

This work was supported by the Polish Ministry of Science and Higher Education, grant no. N N516 518339.

The research leading to these results has received funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement no. 251617.

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