

Analysis of group evolution prediction in complex networks

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Abstract

In the world, in which acceptance and the identification with social communities are highly desired, the ability to predict the evolution of groups over time appears to be a vital but very complex research problem. Therefore, we propose a new, adaptable, generic, and multistage method for Group Evolution Prediction (GEP) in complex networks, that facilitates reasoning about the future states of the recently discovered groups. The precise GEP modularity enabled us to carry out extensive and versatile empirical studies on many real-world complex / social networks to analyze the impact of numerous setups and parameters like time window type and size, group detection method, evolution chain length, prediction models, etc. Additionally, many new predictive features reflecting the group state at a given time have been identified and tested. Some other research problems like enriching learning evolution chains with external data have been analyzed as well.

Introduction

Network science is a very interdisciplinary domain focusing on understanding the relational nature of various real-world phenomena using for that purpose diverse network models. Commonly, networks consist of smaller, more integrated structures called groups, communities, or clusters. In practice, both the groups and whole networks evolve and change their profiles over time. Hence, their analysis demands advanced computational methods to understand and predict their future behavior. For that reason, group evolution prediction is an essential component of computational network science.

One of the domains explored by network science are biological networks [1–4]. Viruses are as old as life on earth. At the same time, they are very young, as they constantly mutate to change their lethal attributes. Influenza, unlike other viruses which are rather stable, evolves much more rapidly [5,6] and kills up to one million people worldwide every year [7]. We can try to protect ourselves using vaccines. However, the rate of mutation is too rapid to provide an effective cure. What is more, the development of a new drug requires a huge amount of money and lasts from a few to a dozen or so years. Despite these difficulties, new drugs are introduced to the market every year. For example, antagonist drugs (also called blockers) are designed to bind to specific receptors to block the disease's ability to attach to these particular receptors, thereby immunizing the body to the disease. Unfortunately, diseases react to drugs and eventually mutate, creating a variety that will bind to other receptors.

Therefore, we need methods that will be able to track the evolution of the disease, and based on the history of its mutations, will be able to predict the most likely future mutations. To track diseases mutations, we can focus on the group of receptors that it binds to, and observe how such group evolves. Based on the history of changes in the lifetime of this group, we can try to predict what will be the next change. Predicting the direction of the mutation could significantly reduce the amount of time and money needed to study the disease. With such knowledge, we would be able to start preparing the drug in advance and bring it to the market much faster and cheaper.

Another area that widely applies network science, especially its branch called social network analysis (SNA), is marketing, in particular advertising [8–11]. Let us imagine that a start-up company invented a new generation of diapers – *Smart Diapers*, which are extra soft, super absorbing, and additionally, can communicate with parents’ smartphones to notify when their change time comes. The company invested very much in their development, therefore, it has a limited budget to advertise the product. The owners decided to introduce the product to discussion groups on the Facebook platform where parents from different countries/cities create and join independent groups to talk about and comment on new products for babies, share general advice about raising children, sell used clothes, etc. Convincing members (parents) of such relevant, targeted groups to use and buy the new diaper product would be much more effective and cheaper than advertising the broader community using expensive TV commercials. Additionally, the word-of-mouth recommendation is commonly believed to be the most powerful marketing tool [12]. However, the vital question rises here: which Facebook groups the company should invest in its limited resources, i.e., time and money? In the newly created relatively small groups that might be very active and are expanding fast, or in the larger groups that might be not very active in the nearest future? Which of these groups will be still running or growing in a few weeks/months/years and which one will disappear? That is why the knowledge about the history, current state, and future evolution of groups is crucial at decision making on where to allocate the resources.

In 2007, Palla et al. [13] have defined the problem of group evolution identification. In the following years, dozens of solutions to this problem have been proposed. One of them was the highly cited GED method [14]. Existing surveys describe as many as 12 [15] or even over 60 methods [16]. All of them are focused on defining possible events in the community life, hence, tracking the historical changes. This, in turn, has led to emerging a new problem – predicting future changes that will occur in the community lifetime. Some of the first methods concerning prediction of some aspects (e.g., determining lifespan) of the group evolution were: (1) Goldberg et al. [17] – they focused on predicting the lifespan of evolution for a group; (2) Qin et al. [18] – analyzed dynamic patterns to predict the future behavior of dynamic networks; and (3) Kairam et al. [19] – they investigated the possibility of prediction whether a community will grow and survive in the long term.

Note that the methods for tracking group evolution can be also utilized to other similar prediction problems, like link prediction [20], churn prediction [21], as well as to understand evolution of software (Unix operating system networks) [22] or dynamics of social groups forming at coffee breaks [23].

In 2012, we proposed a new concept, in which the historical group changes were utilized to classify the next event in the group’s lifetime [24]. In this first trial, we have used only event type and size of the group to describe its state at a given time. Over the next year, we have investigated the concept and adopted it to two methods for tracking group evolution – the GED [25] method and the SGCI method [26]. This resulted in the first method for group evolution prediction [27]. It was the predecessor of the GEP (Group Evolution Prediction) method described in this paper. Since then, a few more methods have been proposed. At the end of 2013, İlhan et al. presented their

research with several new measures describing the state of the community and a new method for tracking group evolution [28]. In 2014, Takafolli et al. applied the binary approach to classifying the next change that group will undergo [29]. They used 33 measures to describe the state of the community. We have presented new results in 2015, where, apart from new measures, the influence of the length of the history used in the classification was examined [30]. Later the same year, Diakidis et al. adapted the GED method to conduct their research with 10 measures as predictive features [31]. In 2016, İlhan et al. presented new results and proposed a method to select measures, which should be the most useful as predictive features for a given data set [32]. More recently, Pavlopoulou et al. used 19 measures already validated in other works and studied whether employing the temporal features on top of the structural ones improves prediction, as well as what is the impact of using a different number of historical community states on the prediction quality [33].

Unfortunately, all of the methods proposed to this day have some drawbacks (see the Comparison with other methods section) and have been designed to solve a particular problem, hence, their application area is rather narrow. Therefore, in this paper, a new generic and comprehensive method to predict the future behavior of the groups, based on their historical structural changes as well as experienced events, is proposed, evaluated and discussed.

Some of the contributions of this work are: decomposing the group evolution prediction problem, proposing and extensively evaluating the modular method that can be applied to any dynamic network data, proposing new predictive features, performing the features' ranking, proposing a new concept of data set enriching, initial evaluation of the transfer learning technique, an example and discussion on the concept drift problem in group evolution prediction, reviewing all proposed methods in the field.

Methods

Decomposition of the group evolution prediction problem

The crucial matter in developing the modular method predicting group evolution, called *GEP*, was the identification and separation of the components of the entire group evolution prediction problem. The appropriate problem decomposition and information flow between particular components (dependencies) are depicted in Eq 1 and Fig. 1.

$$IS \xrightarrow[S_1]{TWT} TW \xrightarrow[S_2]{NT} TSN \xrightarrow[S_3]{CDM} G \xrightarrow[S_4]{CETM} EC \xrightarrow[S_5]{FE} PF \xrightarrow[S_6]{classification(CH)} Q \quad (1)$$

The data from the input stream *IS* is divided into time windows *TW* using the time window type definition *TWT*. For each time window *TW*, a complex/social network is created using the network type definition *NT*, resulting in the temporal complex/social network *TSN*. Within each time window *TW* in *TSN*, some groups *G* are identified using a community detection method *CDM*. Next, similar and consecutive groups are matched using a community evolution tracking method *CETM*, as well as the transition is labeled with an event type out of the set of possible changes *CH*. The matched groups are combined into evolution chains *EC* that may consist of many successive changes. For each community state in *EC*, the feature extraction process *FE* is applied in order to obtain a set of predictive features *PF* describing the community state at a given time. Using features *PF* in the form of a vector representing each evolution chain *EC*, classification of possible changes *CH* is performed. The classification task (stage *S*₆) is to learn and finally label the next change(s) in community lifetime. The output of the classification process is a set of classification quality (performance) measures *Q*, for

example, F-measure, accuracy, precision, or recall. The identified components were converted into six stages S_1 - S_6 of the GEP method, Fig. 1.

GEP method

The GEP framework consists of six main stages (Fig. 1): (1) time window definition, (2) complex network extraction for the defined periods, (3) community detection in periods, (4) group evolution tracking, (5) evolution chain identification for communities together with feature extraction and computation for each chain and (6) classification, containing classification model learning and testing. Each of them can be implemented by means of different methods and approaches depending on research need and prerequisites, e.g., complexity level. The formal definition of the GEP method is as follows:

Definition 1 *The GEP method is defined as an octuple*

$\langle IS, S_1, S_2, S_3, S_4, S_5, S_6, Q \rangle$, where:

IS is an input stream of activities, e.g., phone calls, linking two actors (network nodes) x, y at time t_i ;

S_1 is a set of considered time windows of the given type TWT;

S_2 is a set of considered approaches to temporal complex / social network TSN creation from IS using time window definitions from S_1 ;

S_3 is a set of considered approaches to community detection methods CDM for each time window in TSN from S_2 ;

S_4 is a set of considered approaches to tracking community evolution methods CETM for communities from S_3 ;

S_5 is a set of considered approaches to feature extraction for evolution chains from S_4 ;

S_6 is a set of considered approaches to classification, including learning, training, validating, undersampling, oversampling, and feature selection techniques;

Q is a set of considered classification quality measures, for example, F-measure, accuracy, precision, recall, estimated based on the classification results from S_6 .

The methods enumerated especially in S_1, S_3, S_4, S_6 also include the space / set of their parameters.

The output of one stage S_i is the input for the next stage S_{i+1} , e.g., communities detected in S_3 are used to discover their evolution in S_4 . All these stages, together with parameters of the methods used, are more in-depth described in S1 File. They also require an appropriate definition of data structures to facilitate hassle-free implementation.

CPM method

The Clique Percolation Method (CPM) proposed by Palla et al. [34] is the most widely used algorithm for extracting overlapping communities. The CPM method works locally, and its primary idea assumes that the internal edges of a group have a tendency to form cliques as a result of high density between them. Oppositely, the edges connecting different communities are unlikely to form cliques. A complete graph with k members is called k -clique. Two k -cliques are treated as adjoining if a number of shared members is $k-1$. Lastly, a k -clique community is the graph achieved by the union of all adjoining k -cliques. Such an assumption is made to represent the fact that it is a crucial feature of a group that its nodes can be attained through densely joint subsets of nodes.

Infomap method

The Infomap method proposed by Rosvall and Bergstrom [35] uses the information-theoretic approach to cluster nodes within a network. It focuses on

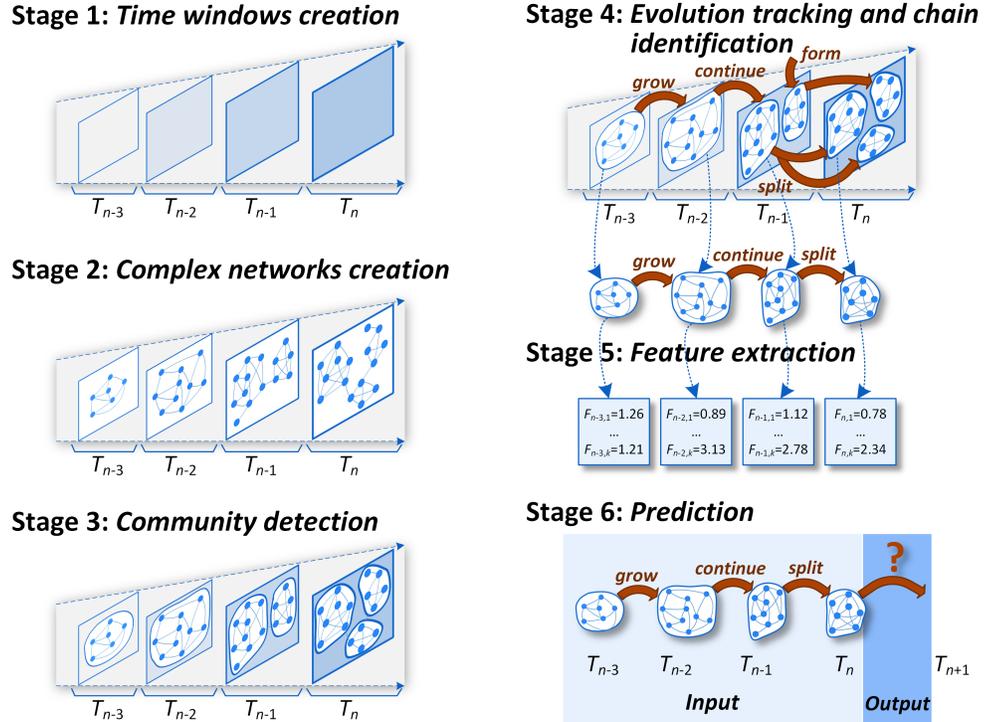


Fig 1. The concept of the GEP method. **Stage 1:** Data set is divided into time windows. **Stage 2:** A complex network for each time window is created. **Stage 3:** Groups are extracted within each time window using any community detection method. **Stage 4:** The evolution of communities is tracked with any group evolution tracking method, and the evolution chains are created. **Stage 5:** Features describing the previous group profile such as size, density, cohesion, etc. are calculated to capture community state at a given time. **Stage 6:** Supervised machine learning approach is applied to learn and predict the forthcoming event in the group's lifetime.

information diffusion across the graph and compression of the information flow description obtained from a random walker, which is chosen as a mean of information diffusion. Infomap changes the problem of finding the best cluster structure into finding the partition with the minimum description length of an infinite random walk. It follows the intuitive idea that if the community structure is present, the random walker will spend more time inside the community because of its higher edges density. It means that the transition to another cluster will be less likely.

GED method

The Group Evolution Discovery (GED) method [25] is one of the best methods for tracking community evolution [36]. It uses inclusion measure to match similar communities from neighboring time windows. This measure takes into account both the quantity and quality of the group members. The quantity is reflected by the first part of the inclusion measure, i.e., what portion of the members from group G_1 also belongs to group G_2 . The quality is expressed by the second part of the inclusion measure, namely, what contribution of important members from group G_1 is in G_2 . It provides a balance between the groups that contain many of the less important members and groups with only few but key members. The inclusion measure and the group size

determine the type of community change. The authors defined seven possible event types: forming, dissolving, continuing, growing, shrinking, merging, and splitting. The method can work with any community detection method and with any group similarity measure, thus, providing great flexibility.

İlhan et al. method

The İlhan et al. method [32] works with the disjoint type of communities and utilizes the function by Hopcroft et al. [37] to calculate the similarity between two communities. The event types that can occur in the community lifetime and also the classes being classified are: survive, growth, shrink, merge, split, and dissolve. The measures used as predictive features are divided into two categories: structural and temporal community measures. In total, nine features per timeframe are used, i.e., number of nodes and edges, intra and inter measure of community edges, betweenness, degree, conductance, aging, and activeness. If one calculates four network measures beforehand (average path length, betweenness, clustering coefficient, embeddedness), the method can also identify features that should be the most prominent for a given network profile.

Results

Suitable decomposing the problem of group evolution prediction (see the Methods section and Fig. 1) was crucial in solving the problem. It allowed to analyze distinct phases of the process and to propose multiple solutions for each phase. The GEP method was extensively analyzed on fifteen real-world data sets (see S1 File for their profiles), for which more than 1,000 different temporal networks were created, and in total, more than 5,000,000 individual classification tasks were performed. However, to keep the article clear and concise, only selected results are presented for each stage.

Stage 1: Time windows creation

At first, the data is divided into time windows. Three main approaches can be considered in this context: (1) equal length periods – the events and relations are segmented based on their timestamp; (2) the same number of relations in each time window; (3) the arbitrary division, based on the data context. Additionally, the type and size of time windows have to be decided, which may be a challenging task. There are three most common types of time windows: disjoint, overlapping, and increasing.

A proper choice of the time window type and size has a direct impact on the following GEP stages, especially on the number of evolution chains discovered by the tracking method (Stage 4). If relations between individuals in a data set have a tendency to change rapidly, then disjoint time windows would be a poor choice since there may not be too many relations lasting between two consecutive time windows. As a result, the tracking method will not provide any events (Stage 4), so there will be no input to a classifier resulting in no event to predict (Stage 6). The too large size of the time window, in turn, might lose some information about community changes that occurred in the meantime.

So far, there is no formula which determines the right type and size of the time window, but a few guidelines can be provided based on our extensive experiments:

- If the network is sparse or changes rapidly, the overlapping time window should be used. Usually, the offset equal to 30% of the time window size is enough to obtain a reasonable number of events between the consecutive time windows;

- The time window type and size should be adjusted to the context of the given data set, e.g., the co-authorship network, referring to researchers who often publish only once a year, should evolve smoothly with the 1-year disjoint time windows;
- If the persistent groups are the goal of analyses, the increasing time window should be utilized, as it provides mostly the continuing and growing events;
- If relations between individual nodes are recurrent and the network is rather dense, one may try using disjoint time windows to lower the computational cost;
- It is acceptable and even preferable to repeat the selection of the time window type and size several times to see which approach yields the best results.

The most common choice in our studies was the overlapping time windows with the offset between 30% - 50% of their size.

Stage 2: Formation of networks

The parameters that can be adjusted at the creation of networks for each time window is the set of edge attributes, in particular, their weights and direction. The weighted/unweighted, as well as directed/undirected profile of the network, did not yield a significant impact on computational complexity nor classification accuracy. Some community detection methods, however, may be incompatible with the networks of particular characteristics or may ignore some attributes, e.g., weights. The CPM [34] and Infomap [35] methods, used in the experimental studies, are capable of handling the most important network attributes.

Stage 3: Community detection

Some community detection methods can produce both disjoint and overlapping communities, but there are only a few methods for tracking the evolution (Stage 4) that can deal with the overlapping groups. Overall, the methods extracting disjoint communities perform faster than the ones providing overlapping groups. In some extreme cases, when the network is very large, the CPM method is unable to extract groups due to its enormous memory requirements. It is hard to compare two types of the grouping methods in terms of their impact on the classification accuracy, as each type of clustering delivers a different set of communities resulting in a different distribution of evolution events. Besides, the profile of the groups may be diverse, e.g., networks grouped with the CPM method tend to have a single giant component with many small overlapping groups alongside. This method also inclines to leave out nodes that do not belong to any clique, thus, excluding them from further consideration. If the network is sparse, a major fraction of the network may be omitted. In the most extreme case, the CPM method neglected even as many as 97% of network nodes, what resulted in a deficient number of communities and evolutions (Fig. 2A), and eventually in very low classification accuracy, Fig. 2B. At the same time, the Infomap method performed very well, identifying a large number of communities. Furthermore, the overlapping groups are likely to generate more merging and splitting events in Stage 4, since there are plenty of similar and overlapping communities in the consecutive time windows. On the other hand, the Infomap method tends to produce many communities having only 2 or 3 nodes. In general, while considering which type of grouping method to use the data context should be a crucial factor.

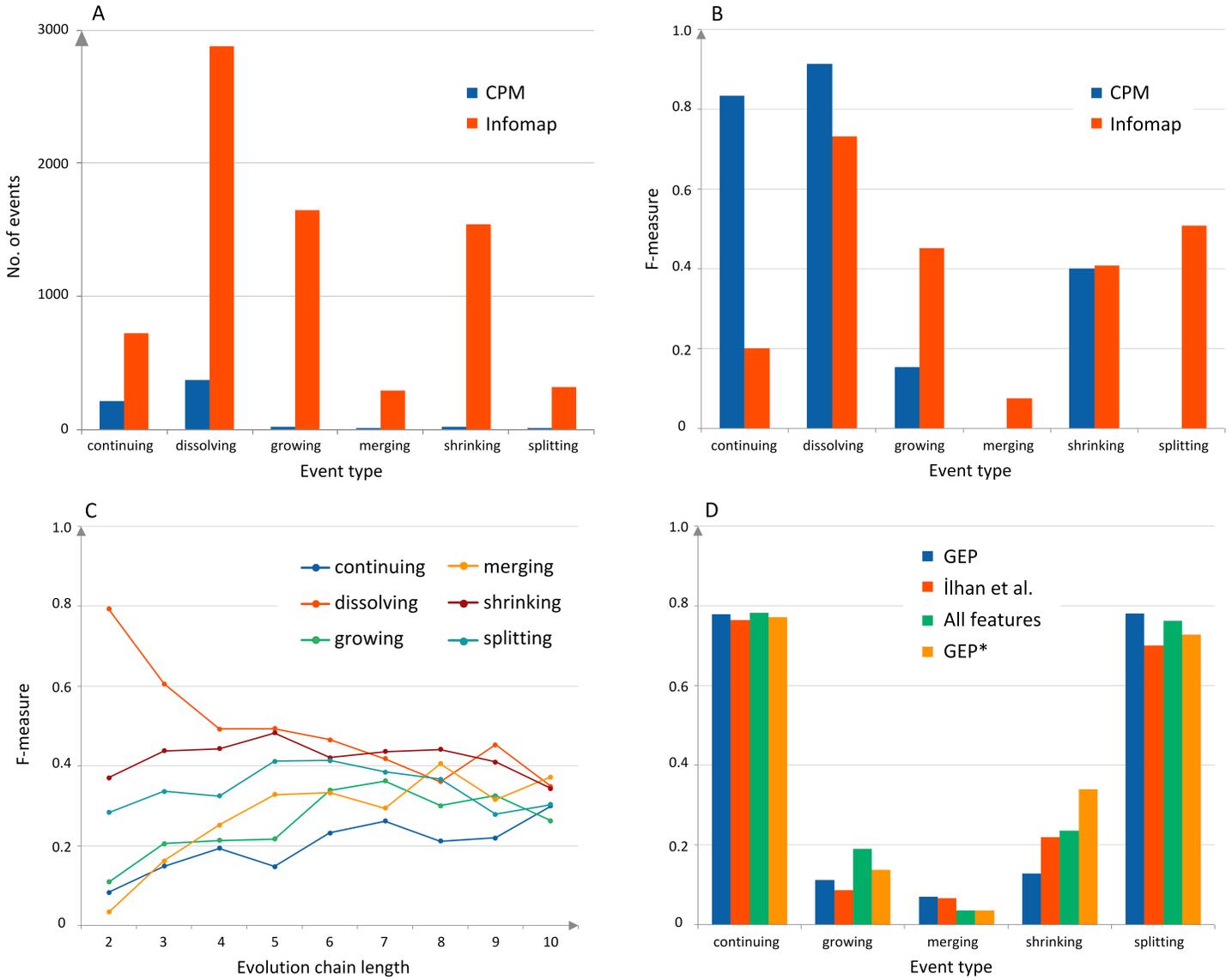


Fig 2. (A) CPM vs. Infomap. The number of events tracked with the GED method for groups obtained with two different community detection methods applied to the Digg data set. The CPM method leaves out even 97% of nodes that do not belong to any clique, hence the small number of groups and events. **(B) CPM vs. Infomap.** The F-measure values achieved for the events presented in Fig. 2A. The results reflect the distribution of events. **(C) Chain length.** The F-measure values for different lengths of the evolution chains for the Facebook data set. For most of the events, the F-measure value was increasing with the increase of the chain length up to 6 or even 7 states (the continuing and growing events). Beyond that point, the number of evolution chains of the particular types dropped below 50 which was insufficient to train the classifier properly; **(D) GEP vs. İlhan et al.** The F-measure values for the 9-state evolution chains obtained from the Slashdot data set with the different set of predictive features: only from the GEP method (GEP) - see S1 File, from the İlhan et al. method, combined from both GEP and İlhan et al. methods (All features), and from the GEP method, but only for the last 3 states out of all 9 states (GEP*). The GEP* and "All features" scenarios achieved slightly better overall scores.

Stage 4: Stepwise evolution tracking and chain identification

Regardless of the method, tracking the evolution of community is a computationally demanding task. The method has to iterate over all time windows and compare all the

communities in order to detect similar ones. Although the methods for tracking group evolution can be very distinct, especially while defining the possible event types, our earlier study showed that the selection of the method has no significant impact on classification accuracy [30]. In this evaluation, we use the GED method [25] since, in the last evaluation of existing community evolution tracking method, it was selected as the one giving the most satisfying results [36].

The parameters of the selected method might influence the classification results, e.g., the alpha and beta parameters of the GED method have a direct impact on the number of evolution events discovered – the lower the threshold, the more events obtained (see S1 File for details). In the experimental studies, the most common value for the alpha and beta parameters was 50%. If the network is dense and relations are recurrent, the alpha and beta might be even increased to 70%. On the other hand, when the method provides a small number of the evolution events, the alpha and beta should be reduced to, e.g., 30%. Apart from the selection of the evolution tracking method, the length of the evolution chain has to be decided. The longer the evolution chain, the more predictive features for the classifier in Stage 6, hence, the higher computational complexity. Nevertheless, the results presented in Fig. 2C revealed that it is worth dedicating some more time and resources to extract longer chains since it can boost classification accuracy. The overall score achieved with the evolution chains containing six community states was 32% higher than the results achieved with shorter 2-state chains. In case of limited time or resources, the chains with the length of 2-3 states should be reasonably good.

Stage 5: Feature extraction

In order to predict the future evolution of the group, we need to describe its recent and historical states by means of predictive features. Based on these features and previous evolutionary changes used to learn the model, we are able to forecast the next changes. The crucial features that are at our disposal are structural network measures computed for the previous group states. Calculation of all measures may be a very demanding task since they need to be evaluated for every community state in the evolution chain. Additionally, some measures, e.g., betweenness centrality, require finding all shortest paths for each pair of nodes in the community or network. The experiments revealed, Fig. 2D, Fig. 3 that the set of predictive features has a significant impact on classification accuracy, as they are used to build the classification model, see also S1 File, Feature Selection section. Therefore, it is highly recommended to compute as many predictive features as possible to deliver to the classifier a wide variety of descriptions to choose from.

To significantly enhance the already existing approaches, many new predictive features are proposed in this paper (see S1 File, Predictive Features section). We have clustered structural features into three general types: (1) *microscopic* – calculated for individual nodes, e.g., node degree, (2) *mesoscopic* – quantifying single groups, e.g., group size - no. of nodes, and (3) *macroscopic* – describing the whole network, e.g., network density. Mesoscopic features also include normalized group measures like the group size divided by the network size. Besides, node-based (microscopic) measures can be aggregated (usually averaged) at either *local* (group) or *global* (network) level resulting in *microscopic local* or *microscopic global* features, respectively.

All computed features were thoroughly evaluated in terms of usefulness for the classifier and rankings of the most prominent features were built, see S1 File, Feature Selection section, especially Tab. 5-9. For the evolution chains of a variable length, different rankings were obtained. For the shortest 1-state evolution chains, only macroscopic (network) features were helpful, which may result from the fact that communities with a short history are considered unstable and vulnerable to the

environment they are a part of. For the evolution chains with the increasing time windows, the features describing the local structure, especially the centrality- and distance-based measures, were more informative for the classifier, as the changes between the consecutive increasing time windows were delicate and occurred at the microscopic rather than macroscopic level. The neighborhood-based features were among the most valuable features for the longest 8- and 9-state chains, which lead to believe that for the long-lasting communities, the relations with their surroundings are a better predictor of the forthcoming change than, e.g., the macroscopic features. In general, the variations of the eigenvector-, eccentricity-, and closeness-based features were present in most of the selective rankings, which suggests that centrality- and distance-based measures obtained on the node level are the most prominent ones. Hence, in case of limited computational capacity, these features should be respected before any other. However, out of all features considered by the classifiers, the Backward Feature Elimination selected only up to 34% of them as prominent, i.e., used by the classifier to make a decision, Fig. 3A.

Additionally, it turned out that usually over 90% of the selected prominent features were obtained from the last three community states, Fig. 3A1. For example, when the evolution chain length was 8, and the next change was classified, all the prominent features were from the 8th, 7th, and 6th group profiles. It means that the most recent history of the community has the most significant impact on its next change. This is an extremely useful conclusion if one has limited computational capabilities and cannot calculate community profiles for all states or does not possess data about older history. The number of features has a direct impact on the duration of the entire learning process, Fig. 3C.

Stage 6: Prediction

In the last stage, the machine learning techniques, such as oversampling, undersampling, feature selection, and first of all, model training and adjustment are applied to achieve the highest possible prediction quality. The common problem with the training data is an imbalanced distribution of output classes, Fig. 2A. In extreme cases, when one class greatly dominates over the other ones, a trained model tends to assign the dominant class to most observations. Then, the solution is to apply additional preprocessing techniques like oversampling and undersampling to generate additional observations or to filter out predominant ones, thus providing a distribution closer to flat. Another common problem is overfitting the classifier by providing too many features or observations. In order to prevent from such case, feature elimination technique may be applied, which unfortunately is very expensive in terms of computational complexity.

Additionally, the proper classifier should be selected, and its parameters need to be accordingly adjusted. In the experimental study, fifteen different classifiers were compared in terms of the classification accuracy, Fig. 4. The tree-based classifiers and meta-classifiers (equipped with decision trees) performed best. Many classifiers could not efficiently handle imbalanced data, so the undersampling and oversampling techniques were applied, resulting in notably better prediction quality, Fig. 4B. On the balanced data set, a classifier focuses on the predictive features computed for the community states instead of focusing on the event distribution.

The Friedman statistical test [38] with the Shaffer post-hoc multiple comparisons [39] was performed to obtain rankings of classifiers on the imbalanced and balanced data sets (cf. S1 File, Tab. 10). In both cases, the Bagging classifier (with the REPTree classifier) was the winner, and the Random Forest classifier was ranked second. What is essential, the p-values confirmed that the results were statistically significant.

Furthermore, classifiers often have their parameters to tune them accordingly, which can substantially affect the classification accuracy, cf. S1 File for detailed discussion.

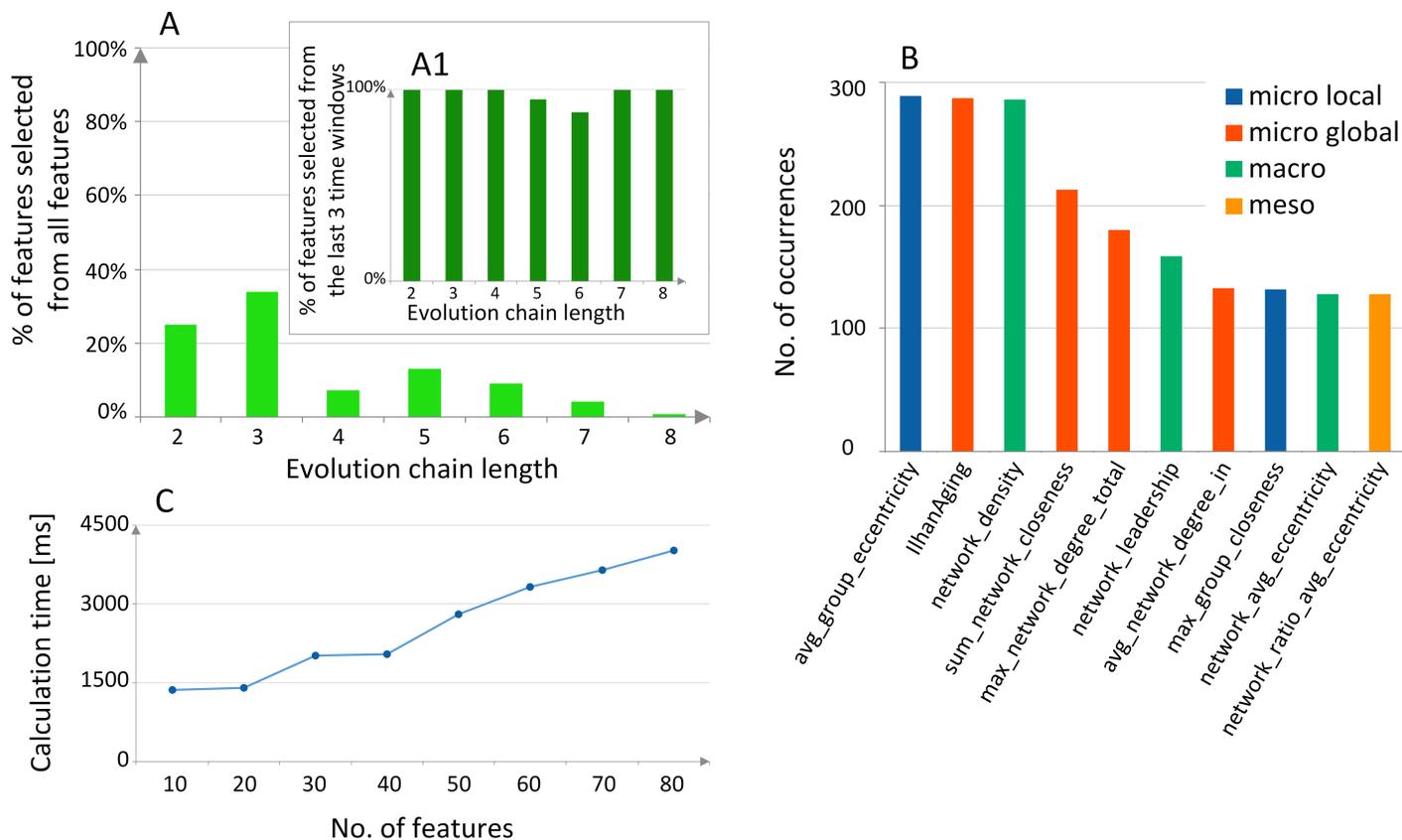


Fig 3. (A) Feature selection. Important features selection obtained by the Backward Feature Elimination for the DBLP data set. The total number of features increases with every state by 91, e.g., the 3-state evolution chain has $91 \cdot 3 = 273$ features in total, out of which 34% were selected as prominent. **(A1)** Features selected only from those related to the last 3 time windows. **(B) Feature ranking.** The most frequently selected features for the 1-state evolution chains. All kinds of information are important to achieve a satisfactory prediction; microscopic features are focused on nodes, mesoscopic on groups, and macroscopic on entire network parameters. The ranking obtained by analyzing eight data sets and repeating feature selection 1000 times. **(C) Computational efficiency.** The time required to train a single Random Forest classifier in relation to the number of descriptive features used as the input data. The results obtained for the IrvineMessages data set.

For example, the logarithmic correlations were observed between the number of bagging iterations for the Bagging classifier and the average F-measure value, as well as between F-measure and the number of generated trees by the Random Forest classifier. The results prove that the process of adjusting the classifier parameters should always be performed, as long as the computational time and resources are available.

Comparison with other methods

The GEP method was compared to other approaches. The existing methods for group evolution prediction were additionally analyzed, and many of their drawbacks have been identified. The most severe were: a narrow application area, methodological issues (e.g., inappropriate computation of the conditional probability), insufficient validation of the methods (e.g., a single sampling into two folds instead of the 10-fold cross-validation), superficial descriptions of the methods and conducted experiments (often insufficient to repeat and validate the experiments), and lack or unreliable comparisons with other

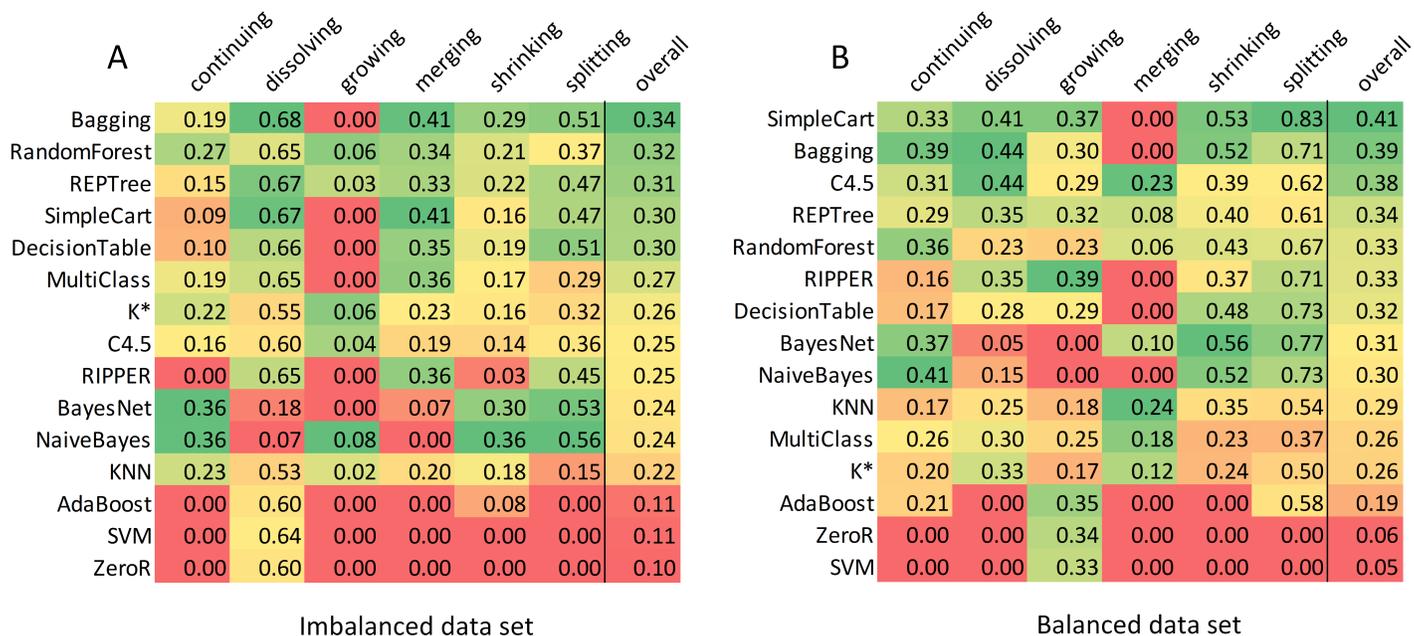


Fig 4. The rankings of classifiers. The heat-maps of the F-measure results for the 1-state evolution chains obtained from the Twitter data set. Classifiers are ordered by the overall score. The Bagging classifier and the SimpleCart classifier achieved the highest overall scores but failed to predict the growing and the merging events. Therefore, the tree-based classifiers are the best choice as all the events are successfully classified and the overall score is insignificantly lower.

methods.

Despite GEP is so flexible and has so many options, it is competitive with other approaches, designed to deal with a specific problem or data set. For example, a special version of the GEP method, in which only features from the last three states (out of all 8 or 9 states) were used as an input for the classifier, performed noticeably better than the method by İlhan et al. [32], Fig. 2D.

After all, it needs to be emphasized that none of the existing methods is as adjustable and versatile as the GEP method.

Discussion

Across its six stages, the GEP method utilizes various approaches, methods, and techniques, which can be adjusted with respect to a given data set and a particular study purpose. These approaches, methods, and techniques are considered as the GEP method parameters. To provide a concise summary of their impact on overall computational complexity, and first of all on the final classification accuracy, the crucial parameters were listed in Tab. 1 and discussed throughout the article.

Many different classifiers were evaluated on various data sets. The tree-based classifiers and meta-classifiers (equipped with decision trees) performed best. Many classifiers could not handle imbalanced data sets, so the undersampling and oversampling techniques were applied. Balancing data sets notably improved the results confirming the usefulness of the undersampling and oversampling methods. The experimental studies showed that adjusting the classifier parameters can significantly improve classification accuracy. The logarithmic correlations were observed between the number of bagging iterations in Bagging classifier and the average F-measure value, as

Table 1. The GEP method parameters and their impact on computational complexity and classification accuracy.

Parameter group	Parameter	Parameter value	Impact on computational complexity	Impact on classification accuracy
time window	window division	timestamp / relations count / arbitrary	none	low
	window size	time unit or number of relations	medium	low
	window type	disjoint / overlapping / increasing	medium	medium
network type	edge attributes	directed / undirected, weighted / unweighted	low	low
methods	group type	disjoint / overlapping	medium	low
	grouping method	a method	high	medium
	tracking method	a method	medium	low
	GED alpha and beta	(10%, 100%]	none	low
	GED social position measure	a measure	medium	low
classification	classifier used	a classifier	medium	medium
	machine learning techniques	undersampling, oversampling, feature selection	high	high
other	evolution chain length	number of community states	medium	medium
	predictive features	a set of features	high	high

well as between the number of generated trees by the RandomForest classifier and the average F-measure value. The confidence factor parameter of the J48 classifier was found also correlated with the average F-measure value. The maximum improvement in average F-measure value achieved by adjusting the classifier parameter was 17%, and it was obtained by increasing the number of generated trees by the RandomForest classifier. The results prove that the process of adjusting the classifier parameters should always be performed, as long as the computational time and resources are not limited.

The GEP method enables us to consider different new scenarios, which are hardly available without this generative framework like transfer learning, class balancing by adding external data, or decreasing the concept drift effect.

The transfer learning technique was adapted to the problem of group evolution prediction for the first time in this field. Its main idea is to learn the classification model on one data set and test it on another one. Such an attempt was quite successful, and the preliminary results were satisfactory. The key to success is finding a data set with a likewise profile. Moreover, in some cases, learning the transferred model on the balanced data set can boost the classification quality for the data set to which the model is adapted. The initial experiments also suggest that the underlying similarity of two data sets (e.g., the same habits of actors or ideally the same set of actors) can help to create a model that if transferred can outperform the primary model built for a given data set.

Very promising results, although at an early stage, were achieved at enriching the learning phase of the classification model with additional evolution chains from a different data set. By partially balancing the original training set with extra evolution chains from another external data set, it was possible to improve the model and thus produce better results for minority classes, without affecting the outcome for the dominating classes, Fig. 5A. This phenomenon is especially important because the existing techniques of balancing a data set always affect the classification results of the dominating classes.

Another way to enhance the classification model, initially considered, is an

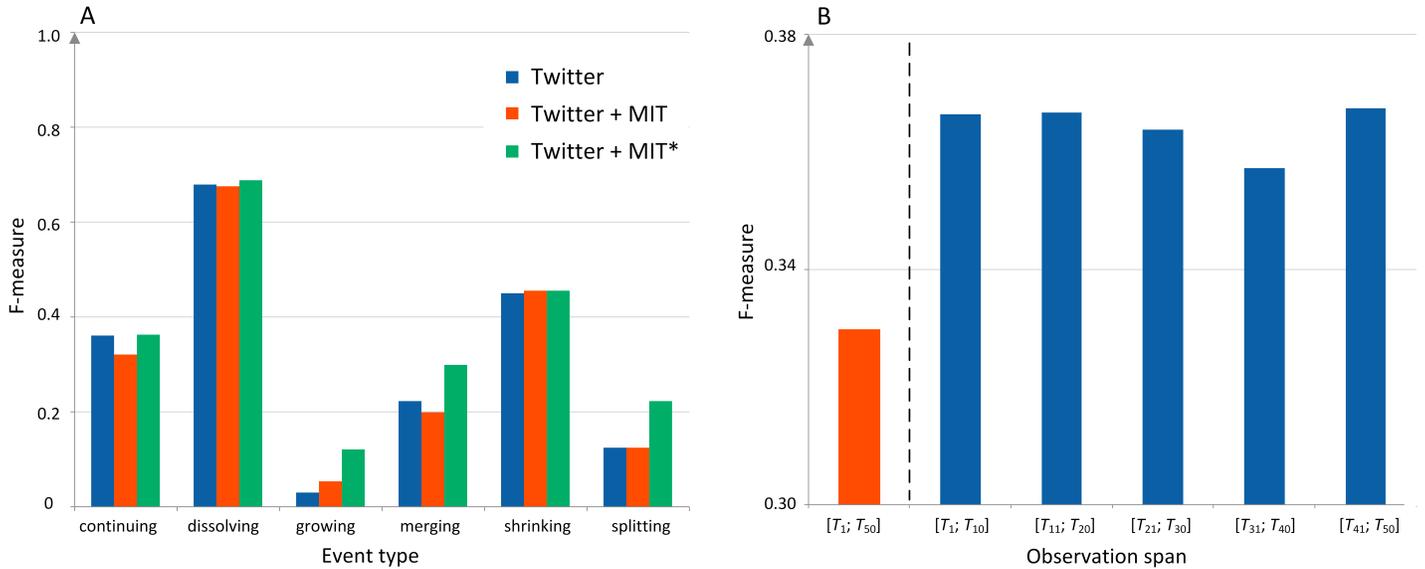


Fig 5. Application of the GEP method. (A) Enriching the classification model by partially balancing the original training set (Twitter) with extra evolution chains taken from another full external data set (MIT) or with chains from only selected event types, i.e. growing, merging and splitting (MIT*); chains with these classes were the worst classified events for the original Twitter data – they had the lowest F-measure values. The results for these selectively enriched event types were significantly improved without worsening classification for other classes (green vs. blue bars). Data enriching was performed only for learning, not for testing. **(B) Concept drift.** Classification quality for the Facebook data from one longer period $T_1 - T_{50}$ (the red bar); alternatively, the data was split into five smaller periods and separate classification models were built to catch concept drift phenomena between periods (blue bars). Independent models learned for smaller periods are better adapted to the changing environments.

appropriate selection of the observation time span to reduce the effect of non-stationarity of data – a.k.a concept drift. Our preliminary research shows that for a network spanning over a long period or changing rapidly, updating the classification model every once in a while might improve the results, as the model reflects the current characteristics of the network in the better and more up to date way, Fig. 5B. Nevertheless, in order to rebuild the model every now and then, the number of observations (evolution chains) extracted from such shorter time span must be high enough.

The GEP framework can be applied to any dynamic network data, i.e., to any complex network changing over time. In this paper, we have explored popular social network data, see Table 2 in the Supporting information section. However, the entire GEP method, its stages and component solutions may be used for diverse complex networks [40, 41] like evolving clusters of web pages [42], co-citation and bibliographic coupling networks extracted from citations between scientific papers [43, 44], biological and medical networks [45, 46], linguistic networks linking word meanings - WordNets [47], multimedia networks [48] and many more.

Conclusion

The main subject studied in this paper is group evolution prediction in social/complex networks. Its primary goal is to foresee a change like shrinking, growing, splitting, merging, or dissolving that the recently existing community will experience in the

nearest future. To be able to perform any prediction, the most common approach is to process a temporal complex network TSN extracted from the stream of user activity traces. Communities and their changes are identified and predicted within such TSN . However, the existing methods are often limited to operate on a particular data set or to solve a specific problem, which makes them useful only in a particular and narrow domain.

Therefore, a new generic method called Group Evolution Prediction (GEP) has been proposed in this paper. The GEP method has a modular structure, which makes it very flexible and allows us to successfully apply it to any data set and under any specific requirements. The method consists of several stages; each of them involves a suitable selection of methods, algorithms, and attributes – the GEP method parameters. The evaluation process of the GEP method included: (1) analysis of numerous parameters (time window type and size, community detection method, evolution chain length, classifier used, set of features, and more), (2) comparative analysis against other existing methods, (3) adaptation of the transfer learning concept to group evolution prediction, (4) enriching the classification model with evolution chains from a different data set, and (5) enhancing the classification model with a more appropriate training set.

Regarding the time window types and sizes, the main finding is that for rapidly changing or sparse social networks a shorter overlapping time windows (in relation to the context of the data) are a better choice than longer or disjoint periods. On the contrary, if relations between individuals are recurrent and the network is rather dense, one may try disjoint time windows to obtain more concise results and to lower the computational cost. If long-lasting, persistent communities are the goal, then the increasing type of time window is the best choice as it generates a high number of the continuing, growing, and shrinking events.

Two most commonly used community detection approaches were analyzed: the CPM method detecting the overlapping communities, and the Infomap method identifying the disjoint communities. It turned out that the CPM method was not a proper choice for sparse networks, as it left out nodes that did not belong to any clique. However, if a network is not so sparse, then generating overlapping communities may be a better choice, especially if the context of the data suggests overlapping communities. For example, when the nodes tend to belong to more than one community at a given time. The Infomap method, however, performs better if computational complexity is an essential factor, and computational time is limited.

The results yield that evolution chains with more community states (longer chains) provide better classification results. However, there seems to be a threshold of the number of states, which make the evolution chains too short, resulting in a lack of possibility of improving the accuracy level.

Even over 70% of the most prominent features were obtained from the last three community states. It means that the most recent history of the community has the highest impact on its next change. This is an extremely useful conclusion if one has limited computational capabilities and cannot calculate community profiles for all states. Additionally, many new predictive features are proposed in this paper. In particular, some aggregations of node measures were used to compute the local and global microscopic features. Network structural measures were adopted as macroscopic features, and ratios of community measures to network measures were utilized as mesoscopic features. In general, the variations of the eigenvector-, eccentricity-, and closeness-based features were present in most of the selective rankings, which suggests that centrality- and distance-based measures obtained on the node level are the most valuable features.

The GEP method flexibility enabled us to investigate some other interesting scenarios, i.e., (1) adapting the transfer learning technique to the group evolution

prediction problem, (2) enriching the classification model with evolution chains from a different data set, (3) appropriate selection of the observation time span to reduce the concept drift effect. All of them appeared to be quite successful.

Even though the GEP method is a flexible, generic framework, it is competitive with other approaches often dedicated to a specific problem or data set.

Supporting information

S1 File. Supporting information file. Contains additional results and discussion.

Authors Contributions

Conceptualization: SS, PB, PK.

Data Curation: SS.

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Funding Acquisition: PK.

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Methodology: SS, PB, MK, PK.

Project Administration: SS.

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Supervision: PB, PK.

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Analysis of group evolution prediction in complex networks - supplementary information

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Example of a social group on Facebook

The Facebook platform allows to perform various social activities like discussion in groups, content sharing, commenting, expressing opinions and emotions. One of the platform's tools allows to create and join independent discussion groups devoted to a specific topic. For example, there are groups intended for mothers living in Singapore, which purpose is to talk about and comment on new products for babies, share general advices about raising children, sell used clothes, etc.

By obtaining and processing data of a single discussion group we are able to create its social network graph, and furthermore, we can track its evolution. Depending on what we are trying to achieve, we would process data in a different way. In the simplest case we can assume that one post (content posted to the discussion group) and all interactions to this post (likes, comments, shares) reflect a social group at a particular time. By obtaining social groups for each post we can create a temporal social network of the considered discussion group and analyze its activeness over time. In a more complex scenario, we can analyze the content of the comments and types of interactions within each post to discover two or more groups with different opinions, e.g. recommending and criticizing a new product for babies.

Group Evolution Prediction methods

The summary of the most relevant methods for group evolution prediction known from the literature confronted with GEP, which is described in this paper, can be found in Tab. A.

Data sets used

Fifteen real-world data sets were analyzed in the iterative process of evaluating and improving the GEP method. Nonetheless, the results presented in this work refer to ten out of fifteen analyzed data sets. The limitation was made to keep the paper clear and concise. The data sets were selected in such way, that the networks created from them had diverse characteristics, see Tab. B. During the experimental studies, the parameters of the GEP method and its components (algorithms, methods, tools) were adjusted based on the literature review, authors suggestion, previous results and experience, and sometimes as a result of repeating the experimental study endless number of times.

Table A. Methods for group evolution prediction.

Method name	Time window type	Type of communities	Community evolution tracking method	No. of predictive features per group state	No. of classifiers analyzed	No. of real-world data sets analyzed	Prediction goal
GEP	any	any	any	91	15	15	next event (6 classes), several forthcoming events, community measure
Ilhan et al. [1, 2]	increasing	disjoint	included in the method	9	10	4 + 40 synthetic	next event (6 classes)
Takaffoli et al. [3]	disjoint	disjoint	MODEC	33	9	2	next event (3 classes), size, cohesion
Diakidis et al. [4]	overlapping	overlapping	GED	10	7	1	next event (4 classes)
Goldberg et al. [5, 6]	disjoint	overlapping	included in the method	20 (average)	1	2	length of community lifetime
Kairam et al. [7]	disjoint	unknown	unknown	8	1	1	community growth rate and longevity (binary classification)

Table B. Characteristics of the data sets used in the research

Data set name	Source	Nodes	Edges	Avg. degree	Time span	Directed	Short description
DBLP	[8]	1,314,050	18,986,618	28.9	20 years	no	co-authorship of articles from the DBLP bibliography
Digg	[9]	30,398	87,627	5.8	15 days	yes	replies between users on the Digg online platform
Facebook	[10]	46,952	876,993	37.4	1 year	yes	posts to other user's wall on the Facebook social platform
Infectious	[11]	410	17,298	84.4	8 hours	no	face-to-face contacts during an exhibition
IrvineForum	[12, 13]	899	33,700	74.0	164 days	no	students activity on the UC Irvine discussion forum
IrvineMessages	[12]	1,899	59,835	63.0	6 months	yes	private messages between students of the UC Irvine
Loans	[14]	89,269	3,394,979	76.1	1 year	yes	loans between users of the prosper.com platform
MIT	[15]	96	1,086,404	22.6	9 months	no	face-to-face contacts between students of the MIT
Slashdot	[16]	51,083	140,778	5.5	32 months	yes	replies between users on the Slashdot online portal
Twitter	[13, 17]	18,500	61,200	6.0	48 days	no	retweets between users on the Twitter social platform

Evolution chain duplication

Let's consider creating evolution chains of length 2 for the exemplary community evolution depicted in Fig. A. The list of evolution chains would contain five unique pairs

of following states, see Tab. C. As one can observe, some evolution chains are partially duplicated, e.g., state ST_2 and event EV_2 of chain EC_1 are the same as state ST_1 and event EV_1 of chain EC_2 , chains EC_2 and EC_3 have the same state ST_1 and event EV_1 , chains EC_4 and EC_5 share the same state ST_2 and event EV_2 , and so on. The number of duplicated states and events would be even higher for a longer evolution chains. The partial duplication is a result of mixing (crossing) lifetimes of several groups, as the splitting and merging events involve at least two communities from the same time window: $G_{1,3}$ and $G_{2,3}$ in this example.

Even partially duplicated chains might be a problem, as they may affect the classification results. For example, if chains EC_2 and EC_4 would be in the training set, used to learn a classifier, and chains EC_3 and EC_5 would be in the test set, used to evaluate the classification model, the classification accuracy for chains EC_3 and EC_5 could be falsely improved, because the classifier might assign the correct event type based on “remembering” the data, rather than learning from them. One may try to remove the partially duplicated chains by applying procedure similar to the “group by” SQL command. However, this will always result in losing some information as well. In this example, grouping chains on state ST_2 and event EV_2 would result in removing chain EC_5 .

A better solution is to use single-state chains, see Tab. D for the set of chains obtained from the considered exemplary evolution. Single-state chains can also contain duplicated states, e.g., when a method for tracking evolution will assign two different event types to the same community, but it is a rare case, and such duplication can be easily removed. Throughout this paper, the process of removing partially duplicated chains is called “removing duplicates.”

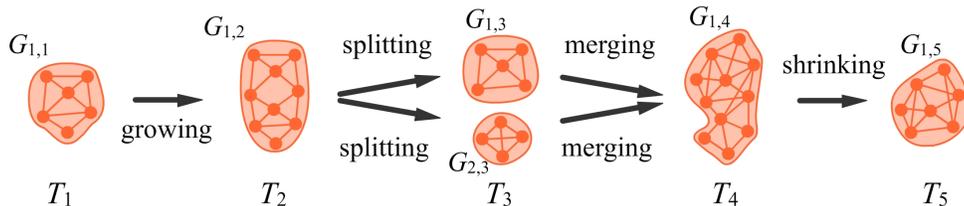


Fig A. An example of community evolution containing five states and four events.

Table C. Evolution chains of length 2 created from the community evolution presented in Fig. A.

Evolution chain	Group state ST_1 in T_i	Event type EV_1	Group state ST_2 in T_{i+1}	Event type EV_2
EC_1	$G_{1,1}$	growing	$G_{1,2}$	splitting
EC_2	$G_{1,2}$	splitting	$G_{1,3}$	merging
EC_3	$G_{1,2}$	splitting	$G_{2,3}$	merging
EC_4	$G_{1,3}$	merging	$G_{1,4}$	shrinking
EC_5	$G_{2,3}$	merging	$G_{1,4}$	shrinking

Feature selection

Feature extraction is an essential step that needs to be performed prior to the classification. Various measures can be used to represent the characteristic of the community at any given time step. Much effort has been made by various researchers to propose such measures, leading to their abundance. However, the high number of features is not always beneficial in the classification process. It can lead to the necessity

Table D. Single-state evolution chains created from the community evolution presented in Fig. A.

Evolution chain	Group state ST_1 in T_i	Event type EV_1
EC_1	$G_{1,1}$	growing
EC_2	$G_{1,2}$	splitting
EC_3	$G_{1,3}$	merging
EC_4	$G_{2,3}$	merging
EC_5	$G_{1,4}$	shrinking

of obtaining more data for training, which is not always feasible. Not all classifiers are resilient to the presence of uninformative features, which can weaken their performance. Finally, feature extraction can be a time consuming procedure, during both training and evaluation of the model. Due to abovementioned factors, the number of utilized features should ideally be kept to the minimum, as long as it does not lead to loss in performance.

To address this issue, feature selection process [18] can be performed prior to classification. Feature selection is a procedure of automatically selecting a subset of features from the larger set, possibly containing irrelevant or mutually redundant features. The aim of such task is twofold: to improve the performance of the trained model, as well as to reduce the evaluation time during its testing. However, feature selection does not address the issue of long training time. On the contrary, based on the chosen method of selection, training can be significantly prolonged. Furthermore, feature selection might itself require large amounts of data to lead to meaningful results, instead of overfitting to the task at hand. Finally, feature selection by itself gives little insight into the problem. Selected features may or may not generalize well to the other, related problems, which is uncertain when the selection is performed on a single dataset.

In the experiment described in this section, we implemented a slightly different task – feature ranking, with the aim of providing more insight about all considered measures. Given a large number of benchmark datasets, we tried to evaluate which measures lead to the best performance during the classification. To this end, we performed a feature selection based on the evolutionary algorithm [19]. This procedure was repeated for various datasets and random data partitionings. Finally, we constructed a feature rankings based on the frequency of the occurrence of the given feature in the final selection. Because the feature selection strategy aims to optimize the classification performance, we postulate that the produced rankings indicate the quality of the features in the group evolution prediction task, with the quality being defined as an expected performance on the problems from the same domain. To the best of our knowledge, such evaluation has not been done before in the context of social group prediction. In the remainder of this section, we describe the proposed method more in-depth along with the most significant results.

Method

The goal of the feature selection procedure is selecting a subset of features maximizing classification performance, at the same time minimizing the cost (most often computational) of producing the final subset. Given specific performance and cost measures, as well as the weights associated with both of these factors, in principle, it is possible to find the optimal feature subset, at least with regard to the available data. However, individually valuable features, i.e. the ones leading to the highest performance if used as the only predictor, will not necessarily be a part of the optimal subset. It has been shown [18] that the feature useless by itself can improve performance significantly when taken with others, and that the presence of highly correlated features can negatively affect the performance. Therefore, finding the optimal feature subspace

was possible, a distinction between high-quality features (those included in the optimal subset) and low-quality features (the remaining ones) can be made. However, as the number of the available features grows larger, evaluating all of the possible subsets becomes infeasible. Instead of the optimal feature subset, one has to rely on its approximation produced by the feature selection procedure. If numerous such approximations can be produced, one can associate feature quality with the frequency of the occurrence of the feature in the selected subset. Similarly, the optimality can be discussed only with regard to the available data, which is only an approximation of the underlying distribution. By selecting different data sample, we obtain a different feature subset, which is only an approximation of the optimal one.

We propose associating individual feature quality with the fraction of time it appears in the selected feature subset. On the data level, we provide diversity in the produced feature subsets by performing 5×2 -fold partitioning [20] on the original dataset. Furthermore, we perform a non-deterministic feature selection using basic evolutionary algorithm [21] and repeat it multiple times with a random initialization. The goal of the evolutionary algorithm is selecting a feature subset optimizing the defined fitness function.

Let us denote the original data by a tuple (X, y) , with X being a $n \times d$ dimensional matrix of n observations consisting of d features each, and y being a vector of n class labels associated with observations. Furthermore, let us denote a d -dimensional binary mask encoding which features are present in the selected subset by \hat{s} , with \hat{s}_i indicating the presence of the i th feature. Finally, let us denote by $X^{(\hat{s})}$ the subselection of the observations, consisting only of the features encoded in \hat{s} . Given the partitioning of (X, y) into the training data (X_{train}, y_{train}) , validation data (X_{val}, y_{val}) and test data (X_{test}, y_{test}) , we denote the weighted F_1 score obtained by training the classifier on subselection $(X_{train}^{(\hat{s})}, y_{train})$ and evaluating its performance on subselection $(X_{val}^{(\hat{s})}, y_{val})$ as $F_1(\hat{s})$. We can then define the final fitness function, optimized by the evolutionary algorithm, as

$$f(\hat{s}) = \gamma \times F_1(\hat{s}) - \delta \times \frac{\sum_{i=1}^d \hat{s}_i}{d}, \quad (1)$$

with γ being the coefficient assigned to the classification performance, and δ – the coefficient assigned to the number of the selected features. The evolutionary algorithm using such fitness function performs a multi-objective optimization, with the objectives: maximize the classification performance and minimize the number of selected features, and the weight associated to the objectives based on the choice of γ and δ .

For the experiments, the values of γ and δ have been set to 0.8 and 0.2, respectively. They were chosen to keep the number of features in a given selection relatively small, with the exact value dependent on the dataset. The Random Forest was chosen as the classifier used to evaluate the classification performance of a given feature subset. The original data has been split into the training, validation and test partitions in the proportion of 0.375, 0.125 and 0.5, respectively. Finally, the following parameters of the evolutionary algorithm have been used: number of generations of 100, population size of 500, probability of mutation of 0.02, probability of crossover of 0.7, and the tournament selection with the size of 3. For each of the 5×2 folds, the evolutionary algorithm has been run 100 times, leading to 1000 feature subsets, based on which the final feature rankings have been computed.

During the conducted experimental study, all GEP features (Tab. L), and additionally the features proposed by İlhan et al. in [2] were analyzed. The features were obtained from 7 real-world data sets: Digg, Facebook, Infectious, IrvineMessages, Loans, MIT, Slashdot, see Tab. B. The Infomap method was applied to obtain the disjoint communities, which evolution was then tracked by means of the GED method with the alpha and beta parameters set to 50%. Time windows of various type and size,

as well as the evolution chains of various length, were used to evaluate abovementioned data sets, which led to 28 separate rankings. See Tab. E for the detailed information about the data setup parameters. For each configuration from Tab. E, a separate ranking was created. However, to draw more general conclusions some rankings were merged together by averaging occurrences of features in separate rankings. Only rankings containing the same set of features can be merged, thus, the same length of the evolution chain is required. Therefore, the merged rankings were obtained from the evolution chains of the following lengths: all 1-state evolution chains - Tab. F (ids 1-12 in Tab. E), all 2-state evolution chains - Tab. G (ids 13-18 in Tab. E), all 3-state evolution chains - Tab. H (ids 19-24 in Tab. E), and all 9-state evolution chains - Tab. I (ids 26, 27, 28 in Tab. E).

Table E. The configuration of parameters utilized to obtain 28 feature quality rankings

Ranking id	Evolution chain length	Time window type	Data set	Time window size	No. of time windows
1	1 state	disjoint	Infectious	s=15min	32
2		overlapping	Facebook	s=28days; o=14days	27
3		overlapping	IrvineMessages	s=2days; o=1day	192
4		overlapping	IrvineMessages	s=7days; o=3days	47
5		overlapping	IrvineMessages	s=14days; o=7days	26
6		overlapping	IrvineMessages	s=28days; o=14days	12
7		overlapping	Loans	s=30days; o=15days	23
8		overlapping	MIT	s=7days; o=3days	57
9		overlapping	MIT	s=30days; o=15days	14
10		increasing	Digg	s=2days	10
11		increasing	MIT	s=30days	10
12		increasing	Slashdot	s=36days	10
13	2 states	disjoint	Infectious	s=15min	32
14		overlapping	IrvineMessages	s=7days; o=3days	47
15		overlapping	IrvineMessages	s=14days; o=7days	26
16		overlapping	IrvineMessages	s=28days; o=14days	12
17		overlapping	Loans	s=30days; o=15days	23
18		overlapping	MIT	s=30days; o=15days	14
19	3 states	overlapping	Facebook	s=28days; o=14days	27
20		overlapping	IrvineMessages	s=2days; o=1day	192
21		overlapping	MIT	s=7days; o=3days	57
22		increasing	Digg	s=2days	10
23		increasing	MIT	s=30days	10
24		increasing	Slashdot	s=36days	10
25	8 states	increasing	Digg	s=2days	10
26	9 states	overlapping	Facebook	s=28days; o=14days	27
27		overlapping	MIT	s=7days; o=3days	57
28		increasing	Slashdot	s=36days	10

In summary, the rankings of the most prominent features were different between various data sets and types of the time window, since the characteristics of the obtained temporal social networks were different. However, it was possible to identify a few measures, which appeared more often in the top ten features of various rankings. The variations of the eigenvector-, eccentricity-, and closeness-based measures were present in most of the presented shortlisted rankings, which suggests that centrality- and distance-based measures, obtained at the node level, are more informative predictors for the classifier. Surprisingly, measures describing the community in the most straightforward way, e.g., the community size or density, did not occur in the shortlisted

Table F. The top ten features of the merged rankings for all 1-state evolution chains (ids 1-12 in Tab. E). Bolded features are newly proposed.

Rank	Feature	Occurrences	Feature type
1	IlhanAging	258	microscopic
2	network_density	242	macroscopic
3	network_leadership	216	macroscopic
4	avg_group_eccentricity	185	microscopic local
5	sum_network_closeness	178	microscopic global
6	min_group_eigenvector	164	microscopic local
7	max_network_degree_total	162	microscopic global
8	network_reciprocity	146	macroscopic
9	max_group_closeness	146	microscopic local
10	max_network_closeness	145	microscopic global

Table G. The top ten features of the merged rankings for all 2-state evolution chains (ids 13-18 in Tab. E). Bolded features are newly proposed.

Rank	Feature	Occurrences	Feature type
1	avg_group_eccentricity T_{n-1}	312	microscopic local
2	beta T_{n-1}	293	mesoscopic
3	alpha T_{n-1}	261	mesoscopic
4	group_coefficient_global T_{n-1}	259	mesoscopic
5	network_ratio_coefficient_global T_{n-1}	258	mesoscopic
6	sum_group_closeness T_{n-1}	251	microscopic local
7	sum_group_betweenness T_{n-1}	243	microscopic local
8	network_density T_{n-1}	242	macroscopic
9	avg_group_closeness T_{n-1}	222	microscopic local
10	max_group_closeness T_{n-1}	218	microscopic local

Table H. The top ten features of the merged rankings for all 3-state evolution chains (ids 19-24 in Tab. E). Bolded features are newly proposed.

Rank	Feature	Occurrences	Feature type
1	beta T_{n-1}	590	mesoscopic
2	avg_group_eccentricity T_{n-1}	403	microscopic local
3	min_group_eigenvector T_{n-1}	374	microscopic local
4	beta T_{n-2}	344	mesoscopic
5	network_ratio_eccentricity T_{n-1}	342	mesoscopic
6	avg_network_degree_total T_{n-1}	322	microscopic global
7	avg_group_eigenvector T_{n-1}	307	microscopic local
8	IlhanInter T_{n-1}	300	microscopic local
9	avg_network_degree_in T_{n-1}	290	microscopic global
10	max_group_closeness T_{n-1}	287	microscopic local

rankings, usually taking place in the second half of the rankings. Furthermore, the macroscopic features, especially the network density, were important only when the history of the community was very short (1-2 states). Thus, when there were more historical data available, classifiers preferred past microscopic and mesoscopic features over the recent macroscopic features. What is more, the predictive features proposed by İlhan et al. in [2] were ranked rather low, except the IlhanAging feature, which was the most commonly used in case of the 1-state evolution chains (Tab. F) and was usually also among the top 30 features in other rankings.

Table I. The top ten features of the merged rankings for all 9-state evolution chains (ids 26, 27, 28 in Tab. E). Bolded features are newly proposed.

Rank	Feature	Occurrences	Feature type
1	min_group_eigenvector T_{n-1}	521	microscopic local
2	network_ratio_eccentricity T_{n-1}	433	mesoscopic
3	sum_network_eigenvector T_{n-1}	428	microscopic global
4	avg_network_eigenvector T_{n-1}	427	microscopic global
5	neighborhood_out T_{n-1}	411	mesoscopic
6	avg_group_eccentricity T_{n-1}	403	microscopic local
7	sum_network_betweenness T_{n-1}	399	microscopic global
8	neighborhood_all T_{n-1}	398	mesoscopic
9	neighborhood_in T_{n-1}	395	mesoscopic
10	avg_network_degree_in T_{n-1}	395	microscopic global

Reproducibility

Experiment described in this section has been implemented in the Python programming language. Existing implementations of the classification algorithms from scikit-learn [22] and evolutionary algorithms from DEAP [23] have been used. Code sufficient to repeat the experiment has been made publicly available at¹, whereas the necessary data, especially its partitioning used during the experiment, has been provided at [24].

Classifiers used in the experiments

In this experimental study 15 different classifiers, implemented in WEKA Data Mining Software [25], were compared in term of the average F-measure value. They were gathered into six more general types.

Rule classifiers

- **ZeroR** is the simplest classification method, which relies on the target and ignores all predictors. ZeroR classifier simply classifies the majority category (class). Although there is no predictability power in ZeroR, it is useful for determining a baseline performance as a benchmark for other classification methods.
- **RIPPER** (JRip) is a propositional rule learner, also called Repeated Incremental Pruning to Produce Error Reduction (RIPPER), which was proposed by Cohen [26].
- **DecisionTable** builds a simple decision table majority classifier [27]. It evaluates the feature subsets using a best-first search and can use a cross-validation for the evaluation.

Function classifier

- **Support Vector Machine** (SVM) performs classification by finding the hyperplane that maximizes the margin between classes. The vectors (cases) that define the hyperplane are the support vectors [28].

¹<https://github.com/michalkoziarski/SocialNetworkFeatureRanking>

Tree classifiers

- **REPTree** is a fast decision tree learner, which builds a decision/regression tree using the information gain/variance and prunes it using a reduced-error pruning (with backfitting). It only sorts values for the numeric attributes once, and the missing values are dealt with by splitting the corresponding instances into pieces.
- **RandomForest** is a well-known classifier for constructing a forest of random trees [29].
- **C4.5 (J48)** is a classic classifier generating a pruned or unpruned C4.5 decision tree [30].
- **SimpleCart** is a classifier implementing the minimal cost-complexity pruning [31].

Bayes classifiers

- **NaiveBayes** is a simple classifier using estimator classes; numeric estimator precision values are chosen based on analysis of the training data [32].
- **BayesNet** is a factored representation of the probability distributions that generalize the naive Bayesian classifier and explicitly represent statements about independence [25].

Lazy classifiers

- **KNN (IBk)** is a simple algorithm that stores all available cases and classifies new cases based on a similarity measure, e.g., distance functions [33].
- **K*** KStar is an instance-based classifier, that is the class of a test instance is based upon the class of those training instances similar to it, as determined by some similarity function. It differs from other instance-based learners in that it uses an entropy-based distance function [34].

Meta-classifiers

- **AdaBoost** (with DecisionStump) is a classifier for boosting a nominal class classifier using the Adaboost M1 method [35]. DecisionStump [36] performs the classification based on entropy; missing values are treated as a separate value.
- **Bagging** (with REPTree) bags a classifier to reduce the variance. Can do classification and regression depending on the base learner [37].
- **MultiClassClassifier** (with Logistic) is a meta-classifier for handling multi-class data sets with 2-class classifiers. This classifier is also capable of applying error correcting output codes for increased accuracy. Logistic is a classifier building a multinomial logistic regression model with a ridge estimator [38].

Statistical tests of classifiers

In order to statistically compare classifiers the Friedman test [39] with the Shaffer post-hoc multiple comparisons [40] was utilized. The non-parametric statistical analysis was computed with the KEEL software tool [41]. The Friedman procedure was applied two times, once on the results obtained from the imbalanced data sets, and once on the results obtained from the data sets balanced with the equal size sampling technique.

Tab. J presents the average ranks obtained by applying the Friedman procedure. The test conducted on the imbalanced data sets produced p-value= $5.25 * 10^{-5}$, while the test on the balanced data sets provided p-value= $1.1 * 10^{-3}$. Since both p-values are much lower than 0.05, the results can be considered statistically significant.

In both cases, the Bagging classifier achieved the best ranks, and the RandomForest classifier was ranked second, while the ZeroR, AdaBoost and SVM classifiers performed worst. However, the Friedman test compares only the average F-measure values obtained for all event types, it does not take into account the fact that some of the events were not classified by the particular classifier, which may be crucial if a successful classification of all event types is the goal. For instance, the Bagging classifier, which achieved the highest ranks, was not able to classify: (1) the growing event for the imbalanced Twitter data set (Fig. BA), (2) the merging event for the balanced Twitter data set, and (3) the splitting event for the imbalanced Facebook data set. At the same time, the RandomForest classifier was able to classify all event types within data sets analyzed in this experiment (Fig. BB).

However, the post-hoc comparison revealed that the difference between the Bagging and RandomForest classifiers was not statistically significant. In fact, the difference between any tree classifier and the Bagging classifier was not statistically significant.

Table J. The average ranks of classifiers obtained by applying the Friedman procedure

Imbalanced data sets		Balanced data sets	
Algorithm	Avg. Ranking	Algorithm	Avg. Ranking
Bagging	1.00	Bagging	3.00
RandomForest	3.75	RandomForest	4.00
REPTree	3.75	BayesNet	5.50
C4.5	5.50	DecisionTable	5.75
MultiClassClassifier	5.50	REPTree	6.00
DecisionTable	6.75	SimpleCart	6.00
K*	6.75	NaiveBayes	6.75
SimpleCart	7.00	KNN	6.75
BayesNet	7.75	MultiClassClassifier	7.25
KNN	9.75	C4.5	7.75
RIPPER	10.50	K*	9.00
NaiveBayes	10.50	RIPPER	10.25
LibSVM	13.00	AdaBoost	13.25
AdaBoost	13.50	LibSVM	14.00
ZeroR	15.00	ZeroR	14.75

Adjusting classifiers parameters

A final step in the process of applying the machine learning is tuning the classifiers' parameters. This allows us to adjust the model to a given problem – data set, however, it also requires a lot of efforts to run thousands of iterations slightly modifying one parameter at a time. Therefore, only the top-ranked classifiers, i.e., the Bagging, RandomForest and C4.5 classifiers, were chosen for this experimental study and only one parameter per classifier was evaluated.

The result of tuning the Bagging classifier is presented in Fig. CA. The correlation between the number of bagging iterations and the average F-measure demonstrates a logarithmic tendency. The average F-measure value increased substantially from 0.305 with one bagging iteration to 0.360 with 50 bagging iterations. However, the additional bagging iterations are very costly in terms of computational time. It took over 24 hours

to obtain the classification results for the Bagging classifier with 50 bagging iterations and for this reason it was not further increased. Nonetheless, since the correlation between the number of bagging iterations and the average F-measure value has a logarithmic nature, it is enough to set the parameter to 10 (default value) or 20 in order to obtain a score close to the results obtained with 50 bagging iterations.

The number of generated trees by the RandomForest classifier also reveals the logarithmic correlation to the average F-measure value, Fig. CB. The overall classification score achieved with just one tree was 0.291, while the result obtained with 100 generated trees was as high as 0.350. Again, increasing the parameter value required a much longer computational time. Therefore, the experiment was discontinued for higher values. Based on the results, the parameter set to 50 seems to be a reasonable choice between the average F-measure value and the computational cost required to generate more trees. The overall score achieved with 50 trees was higher by 0.018 in comparison to the result obtained with the default parameter value (10 trees).

The confidence factor parameter of the C4.5 classifier was also correlated with the average F-measure value, see Fig. CC. Increasing the parameter value resulted in only a slight decrease of the overall score. The highest observed F-measure value was 0.326 and it was achieved with the confidence factor equal to 0.01, while the lowest overall score was 0.297, obtained with confidence of 0.99. The difference between the result achieved with the default parameter value (0.25) and the best result obtained with the parameter value set to 0.01 was 0.026.

In general, tuning the classifiers' parameters can yield notable differences in F-measure values. Therefore, if the computational time is not limited, one may try to improve the classification results by adjusting classifiers' parameters. In combination with other improvements, the overall gain might be very significant.

Classification performance measure

Many measures capturing the classification performance have been proposed and evaluated [42–46]. The most often used measures for binary classification are: accuracy, precision, recall, fscore (F-measure), specificity, and AUC (Area Under the Curve); while for multi-class classification commonly are used: average accuracy, error rate, precision, recall, and fscore (F-measure) [44]. The formulas for all the measures are in Eq. 2-11.

In our study, the F-measure value (which is the harmonic mean of precision and recall) was utilized to indicate the classification performance for the particular class. Additionally, the average of all classes' F-measure values was computed to denote the overall classification quality. The reason for using the plain average F-measure instead of the weighted F-measure, globally averaged F-measure (macro- or micro-averaged [46]), or other measures as the overall score, was to emphasize the lack of classification of some classes better. Furthermore, the plain average F-measure value considers each class to be equally important. Hence, the results of the minority classes are not lost, like in case of the accuracy measure or weighted average F-measure. What is more, the total accuracy might be sometimes misleading, e.g., when one event type suppresses others. In such cases the classifier assigns the dominating type of the event to all observations to increase the accuracy, thus, resulting in a high number of true positive and true negative classifications.

See Tab. K for three samples of classification results and various overall performance measures computed for these samples. The plain average F-measure has the lowest values of all measures for all three samples. Only the macro-averaged F-measure has similar values. Other measures have been impacted too much by the dominating classes and provided much higher overall scores. Sample 1 is a great example of a classifier focusing on the dominating classes. Only the plain average F-measure and the

macro-averaged F-measure are reflecting the poor classification quality of the minor classes. Furthermore, the comparison between Sample 2 and Sample 3 emphasizes why the micro-averaged F-measure, weighted average F-measure, and accuracy are not considered in this paper. Both samples have an identical distribution of events and similar F-measure values, but in the case of Sample 2 the classifier was unable to classify the dissolving event. Yet, the micro-averaged F-measure, weighted average F-measure, and accuracy measures have much higher values in the case of Sample 2 than in the case of Sample 3, ignoring the missing classification. On the other hand, the plain average F-measure and the macro-averaged F-measure values indicate the unsuccessful classification of the dissolving event and have lower values in the case of Sample 2. Since the plain average F-measure value is easier to compute and understand than the macro-averaged F-measure, in this thesis, the plain average F-measure is used to represent the general classification quality.

However, any measure can be used to determine the classification performance, as long as it is appropriate to the problem the one is trying to solve.

Table K. The example values of different classification performance measures showing that the average F-measure and the macro-averaged F-measure best represent the general prediction quality. Other measures have been impacted too much by the dominating classes. Sample 1 was obtained from the Digg data set, while Sample 2 and Sample 3 were obtained from the MIT data set.

		Sample 1	Sample 2	Sample 3
Distribution	Continuing	6391	62	62
	Dissolving	64	9	9
	Growing	5512	78	78
	Merging	504	29	29
	Shrinking	4272	90	90
	Splitting	235	38	38
	Sum	16978	306	306
F-measure	Continuing	0.530	0.359	0.325
	Dissolving	0.029	0.000	0.235
	Growing	0.383	0.390	0.340
	Merging	0.014	0.286	0.277
	Shrinking	0.473	0.491	0.434
	Splitting	0.015	0.725	0.709
Average F-measure		0.2406	0.3752	0.3867
Macro-avg F-measure		0.2420	0.3757	0.3876
Micro-avg F-measure		0.4430	0.4379	0.4020
Weighted avg F-measure		0.4435	0.4339	0.4014
Accuracy		0.4564	0.4379	0.4020

The formulas for individual quality measures are as follows:

$$precision = \frac{tp}{tp + fp} \quad (2)$$

where tp is the number of true positive classifications and fp is the number of false positive classifications;

$$recall = \frac{tp}{tp + fn} \quad (3)$$

where fn is the number of false negative classifications;

$$accuracy = \frac{tp + tn}{tp + tn + fp + fn} \quad (4)$$

where tn is the number of true negative classifications;

$$F\text{-measure} = 2 \cdot \frac{\text{precision} \cdot \text{recall}}{\text{precision} + \text{recall}} \quad (5)$$

$$\text{precision}_{\text{micro}} = \frac{tp_1 + \dots + tp_n}{tp_1 + fp_1 + \dots + tp_n + fp_n} \quad (6)$$

$$\text{recall}_{\text{micro}} = \frac{tp_1 + \dots + tp_n}{tp_1 + fn_1 + \dots + tp_n + fn_n} \quad (7)$$

$$F\text{-measure}_{\text{micro}} = 2 \cdot \frac{\text{precision}_{\text{micro}} \cdot \text{recall}_{\text{micro}}}{\text{precision}_{\text{micro}} + \text{recall}_{\text{micro}}} \quad (8)$$

$$\text{precision}_{\text{macro}} = \frac{\text{precision}_1 + \dots + \text{precision}_n}{n} \quad (9)$$

$$\text{recall}_{\text{macro}} = \frac{\text{recall}_1 + \dots + \text{recall}_n}{n} \quad (10)$$

$$F\text{-measure}_{\text{macro}} = 2 \cdot \frac{\text{precision}_{\text{macro}} \cdot \text{recall}_{\text{macro}}}{\text{precision}_{\text{macro}} + \text{recall}_{\text{macro}}} \quad (11)$$

Predictive features

The list of all features considered in the paper is provided in Tab. L. The new features proposed and analyzed in this paper are highlighted in bold.

Group	Name	Description
Nodes - microscopic local	sum_group_degree_in	The sum of indegree [47] of nodes belonging to the community calculated within the community. Indegree is a node measure defining the number of connections directed to the node.
	avg_group_degree_in	The average value of indegree of nodes belonging to the community calculated within the community.
	min_group_degree_in	The minimum value of indegree of nodes belonging to the community calculated within the community.
	max_group_degree_in	The maximum value of indegree of nodes belonging to the community calculated within the community.
	sum_group_degree_out	The sum of outdegree [47] of nodes belonging to the community calculated within the community. Outdegree is a node measure determining the number of connections outgoing from the node.
	avg_group_degree_out	The average value of outdegree of nodes belonging to the community calculated within the community.
	min_group_degree_out	The minimum value of outdegree of nodes belonging to the community calculated within the community.
	max_group_degree_out	The maximum value of outdegree of nodes belonging to the community calculated within the community.
	sum_group_degree_total	The sum of total degree of nodes belonging to the community calculated within the community. Total degree is the sum of indegree and outdegree.
	avg_group_degree_total	The average value of total degree of nodes belonging to the community calculated within the community.
	min_group_degree_total	The minimum value of total degree of nodes belonging to the community calculated within the community.
	max_group_degree_total	The maximum value of total degree of nodes belonging to the community calculated within the community.

sum_group_betweenness	The sum of betweenness [47] of nodes belonging to the community calculated within the community. Betweenness is a node measure describing the number of the shortest paths from all nodes to all others that pass through that node.
avg_group_betweenness	The average value of betweenness of nodes belonging to the community calculated within the community.
min_group_betweenness	The minimum value of betweenness of nodes belonging to the community calculated within the community.
max_group_betweenness	The maximum value of betweenness of nodes belonging to the community calculated within the community.
sum_group_closeness	The sum of closeness [47] of nodes belonging to the community calculated within the community. Closeness is a node measure defined as the inverse of the farness, which in turn, is the sum of distances to all other nodes.
avg_group_closeness	The average value of closeness of nodes belonging to the community calculated within the community.
min_group_closeness	The minimum value of closeness of nodes belonging to the community calculated within the community.
max_group_closeness	The maximum value of closeness of nodes belonging to the community calculated within the community.
sum_group_eigenvector	The sum of eigenvector [48] of nodes belonging to the community calculated within the community. Eigenvector is a node measure indicating the influence of a node in the network.
avg_group_eigenvector	The average value of eigenvector of nodes belonging to the community calculated within the community.
min_group_eigenvector	The minimum value of eigenvector of nodes belonging to the community calculated within the community.
max_group_eigenvector	The maximum value of eigenvector of nodes belonging to the community calculated within the community.
avg_group_eccentricity	The average value of eccentricity [49] of nodes belonging to the community calculated within the community. Eccentricity of a node is its shortest path distance from the farthest other node in the graph.
min_group_eccentricity	The minimum value of eccentricity of nodes belonging to the community calculated within the community. Also called the groups diameter.
max_group_eccentricity	The maximum value of eccentricity of nodes belonging to the community calculated within the community.
avg_group_clustering_coefficient	The average local clustering coefficients of all the nodes in the community [50].
sum_network_degree_in	The sum of indegree of nodes belonging to the community calculated within the network.
avg_network_degree_in	The average value of indegree of nodes belonging to the community calculated within the network.
min_network_degree_in	The minimum value of indegree of nodes belonging to the community calculated within the network.
max_network_degree_in	The maximum value of indegree of nodes belonging to the community calculated within the network.
sum_network_degree_out	The sum of outdegree of nodes belonging to the community calculated within the network.
avg_network_degree_out	The average value of outdegree of nodes belonging to the community calculated within the network.
min_network_degree_out	The minimum value of outdegree of nodes belonging to the community calculated within the network.

	max_network_degree_out	The maximum value of outdegree of nodes belonging to the community calculated within the network.
	sum_network_degree_total	The sum of total degree of nodes belonging to the community calculated within the network.
	avg_network_degree_total	The average value of total degree of nodes belonging to the community calculated within the network.
	min_network_degree_total	The minimum value of total degree of nodes belonging to the community calculated within the network.
	max_network_degree_total	The maximum value of total degree of nodes belonging to the community calculated within the network.
	sum_network_betweenness	The sum of betweenness of nodes belonging to the community calculated within the network.
	avg_network_betweenness	The average value of betweenness of nodes belonging to the community calculated within the network.
	min_network_betweenness	The minimum value of betweenness of nodes belonging to the community calculated within the network.
	max_network_betweenness	The maximum value of betweenness of nodes belonging to the community calculated within the network.
	sum_network_closeness	The sum of closeness of nodes belonging to the community calculated within the network.
	avg_network_closeness	The average value of closeness of nodes belonging to the community calculated within the network.
	min_network_closeness	The minimum value of closeness of nodes belonging to the community calculated within the network.
	max_network_closeness	The maximum value of closeness of nodes belonging to the community calculated within the network.
	sum_network_eigenvector	The sum of eigenvector of nodes belonging to the community calculated within the network.
	avg_network_eigenvector	The average value of eigenvector of nodes belonging to the community calculated within the network.
	min_network_eigenvector	The minimum value of eigenvector of nodes belonging to the community calculated within the network.
	max_network_eigenvector	The maximum value of eigenvector of nodes belonging to the community calculated within the network.
	avg_network_clustering_coefficient	The average of the local clustering coefficients of all the nodes in the network [50].
Group - mesoscopic	group_size	The number of nodes in the group.
	group_density	The number of connections between nodes in the group in relation to all possible connections between them [50].
	group_cohesion	The vertex connectivity of the community [51].
	group_coefficient_global	The ratio of the triangles and the connected triples in the community [50].
	group_reciprocity	A fraction of edges that are reciprocated within the community [52].
	group_leadership	A measure describing centralization in the community (the largest value is for a star network) [47].
	neighborhood_out	The number of nodes outside the community that have incoming connection from the nodes inside the community divided by the number of nodes in the community.
	neighborhood_in	The number of nodes outside the community that have outgoing connection to the nodes inside the community divided by the number of nodes in the community.

	neighborhood_all	The number of nodes outside the community that are connected to the nodes inside the community divided by the number of nodes in the community.
	group_adhesion	The minimum number of edges needed to be removed to obtain a community which is not strongly connected [51].
	alpha	The GED inclusion measure of group G_i from time window T_n in group G_j from T_{n+1} [53].
	beta	The GED inclusion measure of group G_j from time window T_{n+1} in group G_i from T_n [53].
	network_ratio_size	The ratio of group_size to network_size.
	network_ratio_density	The ratio of group_density to network_density.
	network_ratio_cohesion	The ratio of group_cohesion to network_cohesion.
	network_ratio_coefficient_global	The ratio of group_coefficient_global to network_coefficient_global.
	network_ratio_coefficient_average	The ratio of group_clustering_coefficient to network_clustering_coefficient.
	network_ratio_reciprocity	The ratio of group_reciprocity to network_reciprocity.
	network_ratio_leadership	The ratio of group_leadership to network_leadership.
	network_ratio_eccentricity	The ratio of avg_group_eccentricity to network_avg_eccentricity.
	network_ratio_adhesion	The ratio of group_adhesion to network_adhesion.
Network - macroscopic	network_size	The number of nodes in the network.
	network_density	The number of connections between nodes in the network in relation to all possible connections between them.
	network_cohesion	The vertex connectivity of the network.
	network_coefficient_global	The ratio of the triangles and the connected triples in the network.
	network_coefficient_average	The average of the local clustering coefficients of all the nodes in the network.
	network_reciprocity	A fraction of edges that are reciprocated within the network.
	network_leadership	A measure describing centralization in the network (the largest value is for a star network).
	network_avg_eccentricity	The average value of eccentricity of nodes within the network.
	network_adhesion	The minimum number of edges needed to be removed to obtain a graph which is not strongly connected.

Table L. Predictive features - newly proposed features (bolded) and features known from the literature.

GED

The GED method uses the sizes and inclusion measures of two groups in the consecutive time frames to identify the event type. The alpha and beta parameters can be adjusted according to the needs. For example, to keep only evolutions between very similar groups the values of alpha and beta should be kept high, e.g., at the level of 80%). On the other hand, sometimes the network evolves very rapidly, and the only way to track some evolutions is to lower the alpha and beta parameters e.g. to 30%. Tab. M demonstrates the influence of the alpha and beta values on the number of identified events of the particular type for the IrvinaMessages data set.

alpha	beta	forming	dissolving	shrinking	growing	continuing	splitting	merging	total
10	10	362	350	424	351	97	217	164	1965
10	20	362	350	403	291	97	82	222	1807
10	30	362	350	378	280	93	66	233	1762
10	40	362	350	370	269	93	42	244	1730
10	50	362	350	347	260	94	35	253	1701
10	60	362	350	334	259	94	35	254	1688

10	70	362	350	322	258	94	38	255	1679
10	80	362	350	319	257	94	37	256	1675
10	90	362	350	319	257	94	37	256	1675
10	100	362	350	319	257	94	37	256	1675
20	10	362	350	360	323	91	280	70	1836
20	20	362	350	349	280	87	120	89	1637
20	30	362	350	327	272	84	60	97	1552
20	40	362	350	300	267	84	37	102	1502
20	50	362	350	273	262	86	17	107	1457
20	60	362	350	249	261	86	7	108	1423
20	70	362	350	231	260	86	6	109	1404
20	80	362	350	229	260	86	2	109	1398
20	90	362	350	229	260	86	2	109	1398
20	100	362	350	229	260	86	2	109	1398
30	10	362	350	349	297	88	294	60	1800
30	20	362	350	342	261	78	129	40	1562
30	30	362	350	318	253	72	58	35	1448
30	40	362	350	278	251	71	40	37	1389
30	50	362	350	242	247	73	14	41	1329
30	60	362	350	205	247	73	7	41	1285
30	70	362	350	181	246	73	6	42	1260
30	80	362	350	175	246	73	2	42	1250
30	90	362	350	175	246	73	2	42	1250
30	100	362	350	175	246	73	2	42	1250
40	10	362	350	339	289	84	308	48	1780
40	20	362	350	337	248	75	137	22	1531
40	30	362	350	315	228	69	61	16	1401
40	40	362	350	270	221	64	39	18	1324
40	50	362	350	229	218	64	13	21	1257
40	60	362	350	185	218	64	5	21	1205
40	70	362	350	151	218	64	4	21	1170
40	80	362	350	143	218	64	0	21	1158
40	90	362	350	140	218	64	0	21	1155
40	100	362	350	140	218	64	0	21	1155
50	10	362	350	345	280	83	303	52	1775
50	20	362	350	339	224	74	136	19	1504
50	30	362	350	315	191	67	62	16	1363
50	40	362	350	270	179	61	38	15	1275
50	50	362	350	223	175	52	13	16	1191
50	60	362	350	172	175	52	5	16	1132
50	70	362	350	131	175	52	4	16	1090
50	80	362	350	116	175	52	0	16	1071
50	90	362	350	110	175	52	0	16	1065
50	100	362	350	110	175	52	0	16	1065
60	10	362	350	343	272	83	305	43	1758
60	20	362	350	337	208	74	138	13	1482
60	30	362	350	314	166	67	63	8	1330
60	40	362	350	269	142	60	39	9	1231
60	50	362	350	222	134	50	14	11	1143
60	60	362	350	169	136	47	6	8	1078
60	70	362	350	129	136	46	2	8	1033
60	80	362	350	108	136	46	0	8	1010

60	90	362	350	101	136	46	0	8	1003
60	100	362	350	101	136	46	0	8	1003
70	10	362	350	343	265	83	305	38	1746
70	20	362	350	337	193	74	138	7	1461
70	30	362	350	314	146	67	63	4	1306
70	40	362	350	269	113	60	39	6	1199
70	50	362	350	222	100	50	14	6	1104
70	60	362	350	169	101	47	6	4	1039
70	70	362	350	128	101	44	2	4	991
70	80	362	350	106	101	43	0	4	966
70	90	362	350	99	101	43	0	4	959
70	100	362	350	99	101	43	0	4	959
80	10	362	350	341	262	83	307	39	1744
80	20	362	350	337	188	74	138	7	1456
80	30	362	350	314	138	67	63	5	1299
80	40	362	350	269	105	60	39	4	1189
80	50	362	350	222	90	50	14	4	1092
80	60	362	350	169	88	47	6	2	1024
80	70	362	350	128	87	42	2	2	973
80	80	362	350	106	87	35	0	2	942
80	90	362	350	99	87	35	0	2	935
80	100	362	350	99	87	35	0	2	935
90	10	362	350	341	261	83	307	40	1744
90	20	362	350	337	187	74	138	8	1456
90	30	362	350	314	137	67	63	6	1299
90	40	362	350	269	103	60	39	2	1185
90	50	362	350	222	86	50	14	2	1086
90	60	362	350	169	83	47	6	0	1017
90	70	362	350	128	81	42	2	0	965
90	80	362	350	106	79	35	0	0	932
90	90	362	350	99	79	35	0	0	925
90	100	362	350	99	79	35	0	0	925
100	10	362	350	341	261	83	307	40	1744
100	20	362	350	337	187	74	138	8	1456
100	30	362	350	314	137	67	63	6	1299
100	40	362	350	269	103	60	39	2	1185
100	50	362	350	222	86	50	14	2	1086
100	60	362	350	169	83	47	6	0	1017
100	70	362	350	128	80	42	2	0	964
100	80	362	350	106	78	35	0	0	931
100	90	362	350	99	78	35	0	0	924
100	100	362	350	99	78	35	0	0	924

Table M. The number of events of the particular type tracked with the GED method for different values of the alpha and beta parameters for the IrvinaMessages data set.

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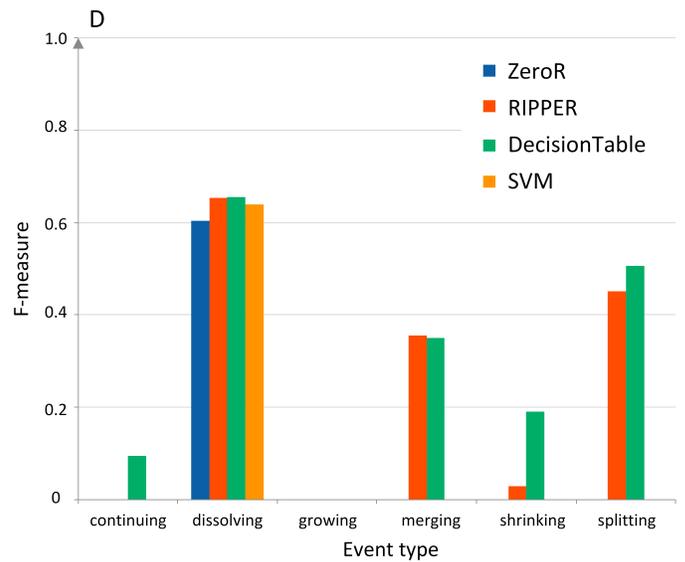
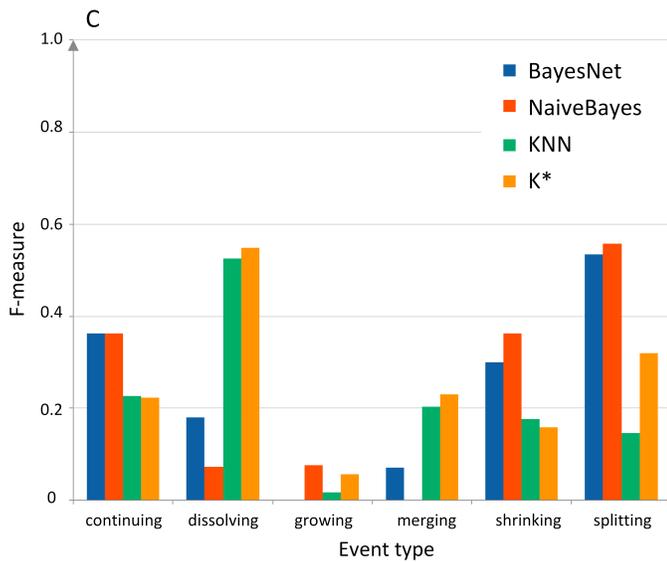
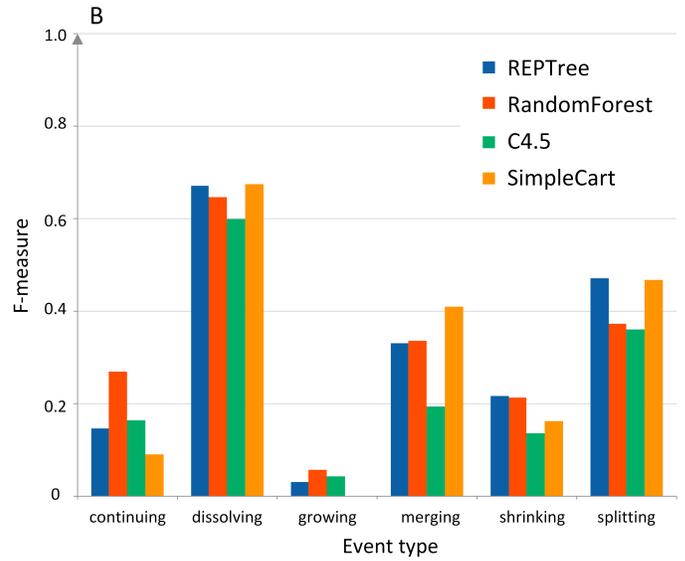
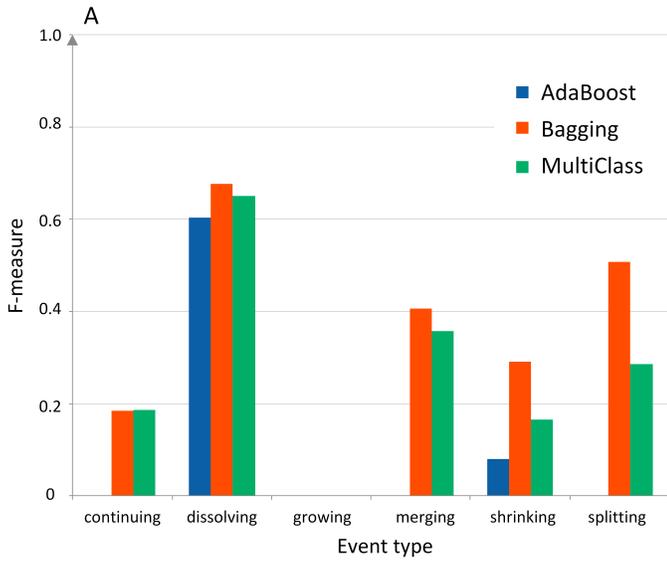


Fig B. The classification results of different classifiers for the 1-state evolution chains obtained from the imbalanced Twitter data set. (A) Meta-classifiers. (B) Tree classifiers. (C) Bayes and lazy classifiers. (D) Rule and function classifiers.

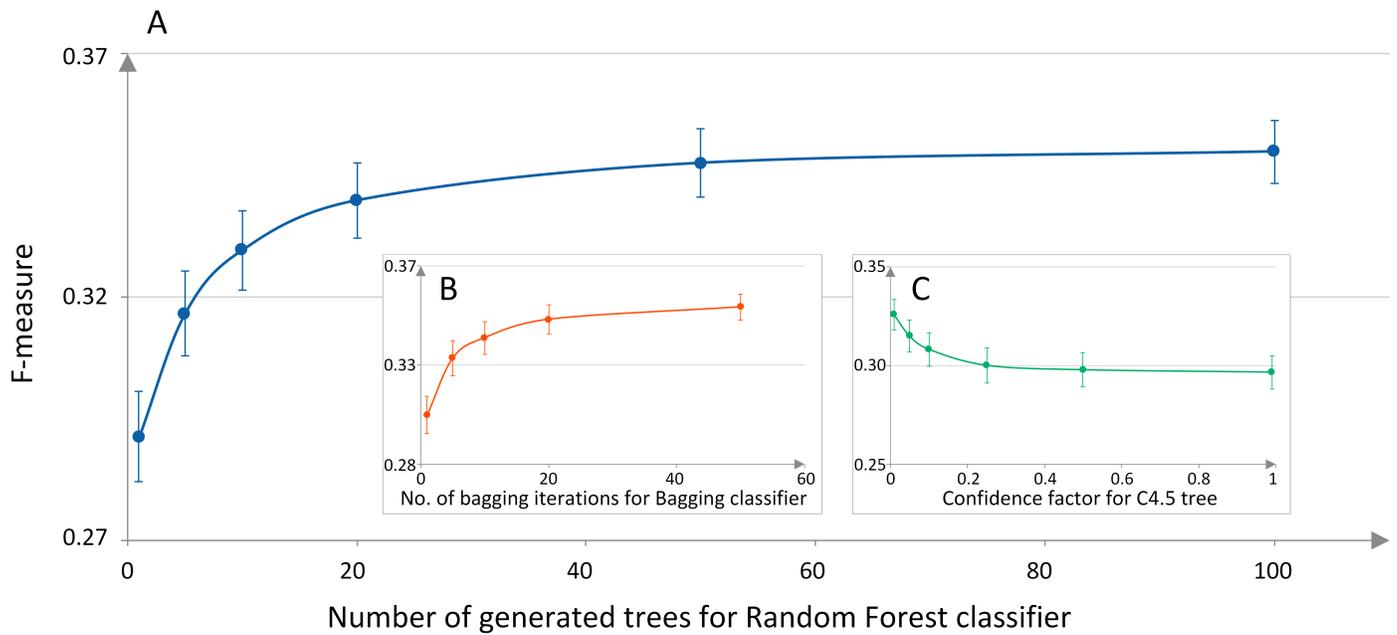


Fig C. The influence of classifiers' parameters adjustment on the F-measure value for the Facebook data set. **(A)** Tuning the number of generated trees in the Random Forest classifier. **(B)** Adjusting the number of bagging iterations in the Bagging classifier. **(C)** Fixing the confidence factor in the C4.5 tree.