

# Community Dynamics in Natural and Human Networks

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**ABSTRACT:** One key to the success of organizations lies in the communication between people in communities. Therefore, it is of interest to provide an appropriate organizational and technological infrastructure to establish and foster the interaction of people in communities. These interactions can be represented as networks and a lot of research has been done in the past on the static analysis of such networks in different fields. However, since the interaction of communities are not static but change over time it is necessary to study temporal networks to learn more about the dynamics in communities and the factors that trigger changes. As communities can also be found in nature, we present an overview of research on dynamics in natural communities and discuss whether nature-inspired aspects of community dynamics could be transferred to the analysis of human community dynamics.

**KEYWORDS:** Networks, natural and human communities, community evolution, community dynamics, graph mining

## INTRODUCTION

In the interaction of people in communities lies one key to the success of organizations. Human communities are virtual or real places where people “meet” and communicate e.g. to solve problems. Thriving communities can provide a strategic advantage for organizations and it is thus of interest to support community building. To provide an appropriate organizational and technological infrastructure, it is necessary to develop a deep understanding of how a community works.

Natural communities as well as social communities have been studied widely in the last years and several attempts have focused on properties that different types of networks have in common (see, e.g., [21], [2]). It has been observed for example that the chains in most food webs have no more than four or five links [11] and that the number of links depends, for example, in lakes on the size of the habitat [18]. Furthermore, the majority of species in a habitat are highly connected; they are in average just two links apart. Analogously, the diameter of social networks (the maximal shortest path) is usually very short and people are connected over just a few links, too. The latter observation has been named by Milgram in 1967 as the “small world phenomenon” [16]. Thus, small worlds can be found in animal as well as in human communities.

In the following, examples for natural networks are presented and their characteristics are discussed based on measures to assess structural properties of these networks. Furthermore, factors that influence the evolution of networks are presented with the aim to find commonalities of human and biological networks. Subsequent to this discussion we present our method to detect evolving communities in such networks and to analyze their temporal development. The interaction of members can be represented as a network and a community is traditionally defined as a subgraph of this network consisting of densely connected nodes that are only loosely connected with the rest of the network. However, this definition neglects that participation of members may change over time even though the community is considered to be still there. We address this observation by modeling a community as an evolving structure of similar community instances. Community instances are communities in the traditional sense, i.e. dense subgraphs of interacting members and two community instances are similar if they share a minimum number of active members. This notion of similarity allows for a continuity inside the evolving community, even if the interaction behavior of some participants changes, unless the similarity between community instances over time becomes marginal and the community dies.

## STRUCTURAL PROPERTIES OF NETWORKS

Interdisciplinary research on networks has shown that the structure of a network always affects its function [19]. Since perturbations of network structure are unavoidable due to environmental changes - this holds true for the natural environment of plants or animals as well as for the environment of humans – it is crucial to obtain a better understanding of the properties that sustain the persistence of diverse ecosystems and their functions.

In the following we present some relevant network statistics that are commonly used to describe the essential properties of a network. By observing these network statistics over time we might obtain insights into the evolution of the network and possible hints to explain the changes as well as implications of the changes on the function of the network. For a more detailed description refer to e.g. [5].

### VERTEX DEGREE

The degree of a vertex is an easy to compute measure that provides an indication about the strength of the connection of the vertex to the graph. In contrast to random graphs, the degree distribution in natural networks differs significantly and follows a power law. In [4] examples for networks with a power law degree distribution are given (the WWW, the power grid of the USA, the actor collaboration network) and in [9] we present a student online community that exhibits a power law degree distribution.

### NETWORK DIAMETER

The diameter of a graph  $G$  is the maximal distance of two arbitrary vertices  $u$  and  $v$ , in other words, the maximal shortest path.

$$diam(G) := \max\{d(u,v) \mid u, v \in V\} \quad (1)$$

It is one of several distance measures that are used to characterize the network. By observing the network diameter over time in relation to the number of vertices one gets a rough idea about the connectivity of nodes in the network.

### CLUSTERING COEFFICIENT

The clustering coefficient – introduced by Watts and Strogatz [21] – is defined for vertices and for the entire graph. The clustering coefficient  $C_i$  for a vertex  $v_i$  is the proportion of edges  $e_{ij}$  between the vertices within its neighborhood  $N_i = \{v_j \mid e_{ij} \in E\}$  (these are all immediately connected neighbors of  $v_i$ ) divided by the number of links that could possibly exist between them. For an undirected Graph  $G$  the clustering coefficient  $C_i$  for vertex  $v_i$  with  $k_i$  neighbors is defined as

$$C_i = \frac{|\{e_{jk}\}|}{(k_i(k_i-1))/2} : v_j, v_k \in N_i, e_{jk} \in E \quad (2)$$

Analogously the clustering coefficient  $C_G$  for the graph  $G$  is defined as the average clustering coefficient over all vertices in  $V$

$$C_G = \frac{\sum_{i=1}^{|V|} C_i}{|V|} \quad (3)$$

### RELATIONSHIP BETWEEN NETWORK STRUCTURE AND FUNCTION

The structure of the network can be described using the above presented measure. However, the question how these network measures relate to biological relevant measures such as robustness or stability is not adequately answered. Only for some networks it is known how the topology of the network and structural changes influence its function (see, e.g., [1], [7]). The main obstacle is that networks in biology do not perform just one distinct function but several different functions. Due to this heterogeneity it is very complicated to infer the function of a network from its structure.

The same holds true for networks that represent interactions of humans. From interactions of humans via e-mail for example we can derive answers to questions such as if a certain topic has been discussed between pairs of actors or inside a group of actors. However, it is not observable whether these interactions have also implications for other discussions or if other relationships between actors have implications on this discussion. Furthermore, it is almost impossible to assess whether a certain structure fulfills a certain function.

At this point, a shortcoming of most network models becomes obvious: Biological systems as well as human systems are complex and representing this system in a network comes along with (over)simplifying relationships. Not all interactions and relationships and their relevant attributes are modeled in the network representation but only a few of them. It is thus important that models are used that reflect the reality of the observed system. A balance between granularity and interpretability must be found to ensure on one hand a realistic model and on the other hand informative analysis results.

## NETWORKS AND COMMUNITIES IN NATURE

A natural community consists of plants or animals in a particular habitat that are bound together by some interaction. The interaction of actors in biological or human systems is usually modeled as networks consisting of nodes that represent actors and edges between actors that represent the interaction. The nodes represent a unit in a system. In biological systems a node can be for example an animal, a gene or a protein. The interaction between these units can be a predator-prey interaction such as in food webs, a message exchange in networks of humans, a physically protein interaction in protein interaction networks, a genetic relation in gene regulatory networks or any other connection between two actors.

In the following we present examples of natural networks and structural properties of these networks that they share with human communities.

### FOOD WEBS

One example for natural communities are food webs. These networks of predator-prey interactions show how an animal satisfies its energy requirements in a particular habitat. Most animals are part of more than one food chain and eat more than one kind of food in order to survive. These interconnected food chains form a food web similar to a web of interacting people in a human community. Dunne et al. [8] have shown that the average shortest path between pairs of species in known empirical food webs is very short. Pairs of species are on average only two links apart from each other. 26.1% of species pairs interact directly, 80.2% and 96.9% of species pairs are within two and three links of each other respectively.

In social sciences, networks with a small diameter comparable with those found in food webs and with a high clustering coefficient are referred to as “small worlds”. Studies have shown that many networks that represent social relationships between people (such as the relation “acquaintance”) show a “small-world effect” meaning, that most actors are only a few links apart from each other (see, e.g., [16], [21]). Some food webs also exhibit this small-world topology but most do not. As mentioned above, most food webs show short paths length but studies by Dunne et al. [8] show that only five out of sixteen food webs that they studied display a much greater cluster coefficient compared to a random network. They suggest that this is mainly caused by the relative small size of food webs. Most nodes only have a limited number of links to other nodes and since the clustering coefficient increases as a linear function of links per node but is independent of the size of the network, high clustering coefficients are not likely for small networks with relatively few links per species.

### MOLECULAR NETWORKS

Molecular networks such as gene-regulatory networks, protein-protein interaction networks and metabolic networks do not only bear similarity with each other but also with non-biological networks: They show for example an approximately power-law degree distribution, meaning that only few nodes are connected with many other nodes while most nodes are only connected with one other node.

A gene-regulatory network consists of three components: i) the transcription factor ii) the upstream regulatory region on the DNA by which (through another transcription factor) the transcription of the gene is mediated and iii) the downstream binding region to which the transcription finally binds to. These genetic networks can be conceptualized as

directed graphs with nodes representing transcription factors and directed edges that link regulating transcription factors to their regulated target genes. Barabási and Albert [4] studied gene-regulatory networks from the graph analysis perspective and revealed a power law degree topology. This means that only few genes control many other genes and that most genes have only few links. This type of degree distribution is also typical for networks representing social interactions.

Protein-protein interactions are an important aspect of gene function. The nodes of protein-protein interaction networks are proteins and they are connected via directed edges to represent the protein-protein interaction. Two nodes may be connected via two opposing edges and the network may also contain self-loop. Thus, the structure of these networks resembles the structure of food webs. In [12] the protein-protein interaction network of the yeast *S. cerevisiae* containing 1870 nodes and 2240 edges was studied and a power-law degree distribution was revealed. Furthermore, the stability of the network in case of random and chosen nodes was studied, and the authors found that the network is stable in case of a random removal of nodes. However, the removal of most connected vertices poses a threat to the network.

Since many social network exhibit, as mentioned above, a power law degree distribution it is interest to test whether these networks are also vulnerable to the deliberate removal of highly connected nodes. It can be assumed that this is the case but it is furthermore of interest to observe the reaction of the node's neighborhood to the removal and compare it to possible reaction in natural networks.

## CHARACTERISTICS OF BIOLOGICAL NETWORKS

Biological networks represent interactions of actors that take place to fulfill a certain task. Any imbalance in this interaction might lead to severe consequences for a species. A missing actor in a food web might cause other species to leave the habitat or even to extinctions of a species. However, most biological networks are anyway extraordinary robust and stable despite structural disturbances.

Robustness refers to the relative insensitivity of a network function to changes. Some metabolic networks are known to be highly robust to damages meaning that their overall function is not endangered even though one or more enzymes are not active. These networks incorporate a redundancy that ensures the function of the network in case of perturbations which means that a part of the network takes over functions of dropped out actors. This characteristic of biological networks can not be transferred easily to human networks unless a certain performance or task fulfillment can be assessed.

One aspect that is of particular interest especially in food webs is the relationship between the structure of the network and the stability of the community. According to [15], the term stability in ecology is used in two contexts: stability of a system to dynamics and the system's ability to defy change. In the first case, it is measured how variable the system is in general, i.e. how variable the system is in absence of perturbations. The second definition measure if and after how much time a system returns back to its equilibrium state after a disturbance took place.

In human communities, the question of stability has also been discussed, e.g., in the field of group dynamics. Group stability refers to the ability of a group to operate as a system over an extended period [3]. A stable membership structure can benefit the group performance in many aspects: First, group stability fosters the commitment of individuals to their group. As a result, people are more willing to invest in the group [17]. Second, it is easier to build shared mental models (the basis for reaching agreements, resolving conflicts and facilitating cooperation) in stable groups [6] which is important to foster cooperative work. Third, membership stability is crucial when the performance of the group requires a certain amount of participants [20]. Instability is primarily caused by changes in the membership structure while membership stability is affected by two separate forces: i) the entry of new members into the group and ii) the exit of current group members ([3], [17]). Since both cases pose as threats to the group stability it is important to determine when and to what extent changes in the membership structure occur and how they influence the group's stability.

In large interaction networks of humans (e.g. in online communities), we often encounter heterogeneous community structures where a community consists of subgroups of densely connected members that are rather loosely connected to the rest of the network. A subgroup is a circle in which "one knows each other". Especially in online communities, subgroups gain in importance as they stabilize the community by providing for a familiarity between their members. This is especially important for fast growing communities as old users still have a tight bond to other members with whom they are comfortable. Furthermore, established subgroups are important for new users too, as it is easier for them

to find a group of people with similar interests (see, e.g., [13]). Thus, facilitating the emergence of subgroups in social networks as well as observing and analyzing them are of particular interest for organizations and community providers.

## OBSERVING AND ANALYZING COMMUNITY DYNAMICS

Biological networks as well as networks representing human interactions are not static but evolve over time. Networks can gain or lose nodes and properties of nodes can change. In biology these changes may be caused by natural selection or evolution or by external forces such as intrusions by other species or humans that cause e.g. a decreasing biodiversity. Luscombe et al. [14] found by applying a statistical analysis on a transcriptional regulatory network that the underlying network structure changes surprisingly over time. In response to diverse stimuli, the transcription factors alter their interactions to varying degrees. The same can be observed in networks of interaction people. The changes may have internal causes such as changing interests of one or more members or external influences such as a report in mass media which has a strong impact on the network structure because it has attracted a large number of new members.

Networks are thus not stable structures but change over time and to analyze the temporal development of communities we propose a method that detects persistent structures by linking similar community instances over time.

### ANALYZING SINGLE SUBGROUPS

In the following we briefly present our three-step approach to detect, visualize and analyze subgraphs and their dynamics to assess whether a community shows stable subgroups.

In the first step the time axis is partitioned into time windows to allow for a temporal analysis of the network (overlapping sliding window approach). In the second step a weighted graph of interactions between members for each time window is built (the weight represents the strength of the interaction). In the third step a hierarchical edge betweenness clustering of the graph is applied to find subgroups of highly connected nodes in each time window. The detected subgroup in each time window can be observed over a chosen time interval to determine group dynamics. To observe transitions we track a detected subgroup over time by measuring the structural equivalence. The development



Figure 1: Temporal Development of Subgroups

of one subgroup can be described and assessed by measuring and interpreting different measures which are: Stability, density and cohesion, Euclidean distance, correlation coefficient and group activity. The measures are computed for each time window and the results are compared in two ways (i) a chosen time window is compared with all other time windows and (ii) each time window is compared to the previous time window to assess the development in consecutive periods. In Figure 1: a screenshot of the statistical analysis is shown. On the left side, the user can mark a subgroup that has been detected in a certain time window and the resulting structural equivalence calculations are shown on the right side in several curves. (For a more detailed description of the process and the implemented measures please refer to [9].)

## ANALYZING LINKED SIMILAR SUBGROUPS (COMMUNITIES) OVER TIME

Since members in online communities are not necessarily constantly active or not always active in the same subgroup of a community we propose a method that links subgroups - we call them “community instances” - that are observed over time by means of similarity. A “match” of a community instance  $C$  is an instance  $C'$  that overlaps with  $C$  for more than a given threshold. For the comparison of community instances, the overlap of two clusters is the number of users found in both of them.

### Similarity of Community Instances

We define similarity among community instances that have been discovered at different times as the overlap of members between the two community instances. Thus, two instances are similar if their overlap exceeds a given threshold. In particular, let  $t_i, t_j$  be two distinct time periods, let  $G_i, G_j$  denote the corresponding graphs of interactions and let  $C^{G_i}, C^{G_j}$  be the corresponding clusterings. Further, let  $x \in C^{G_i}$  and  $y \in C^{G_j}$  be two community instances. We define the overlap between two community instances as:

$$overlap(x, y) = \frac{|x \cap y|}{\min(|x|, |y|)} \quad (4)$$

where  $|x|$  is the number of vertices in a community instance or intersection. Using this notion of overlap, we define a function  $sim(x, y)$  as follows:

$$sim(x, y) = \begin{cases} 1 & overlap(x, y) \geq \tau_{overlap} \\ 0 & otherwise \end{cases} \quad (5)$$

The overlap threshold  $\tau_{overlap}$  captures the tolerance to member fluctuation: In some communities, the number of interactions of any member is low and the number of time periods where this member is active is also small; nonetheless, the community is there for many more timeslots than any of its members. To identify community instances that constitute such a community, we need a low overlap threshold.

The definitions of overlap and similarity allow for comparisons between community instances in arbitrarily remote time periods. It is of course possible to compute the similarity of a community instance to any past community instance. However, this is computationally expensive. Moreover, it may lead to noisy results in environments where individuals participate in several communities but are active in different communities at different times. Therefore, we introduce an upper boundary  $\tau_{periods}$  to the number of periods that may separate two potentially similar community instances; instances that are more than  $\tau_{periods}$  apart have zero similarity by default. Thus, we extend the similarity definition of Eq. (2) into the following:

*DEFINITION 1.* Let  $t_i, t_j$  be two time periods, such that  $t_i < t_j$  let  $G_i, G_j$  be the graphs of interactions in those periods and let  $x^{G_i} \in C^{G_i}, y^{G_j} \in C^{G_j}$  be two community instances in the corresponding clusterings. The similarity of the community instances is defined as

$$similarity(x^{G_i}, y^{G_j}) = \begin{cases} 1 & t_j - t_i < \tau_{periods} \wedge \\ & overlap(x, y) \geq \tau_{overlap} \\ 0 & otherwise \end{cases} \quad (6)$$

## *Graph of Similar Community Instances*

Using the notion of similarity in Eq. (6) we build a graph  $G(V, E)$  of community instances: The set of vertices consists of all community instances detected during the periods of observation. An edge between two vertices  $x, y$  exists if and only if  $\text{similarity}(x, y) = 1$ .

According to Eq. (6), the community instances that may be compared and found similar need not belong to adjacent time periods. This means that there may be edges connecting community instances that are two, three or as many as periods as  $\tau_{\text{periods}}$  apart from each other. Those edges bring temporarily remote community instances close to each other. This ensures (a) that similar community instances are connected to each other independently of their temporal proximity; subject only to  $\tau_{\text{periods}}$  and (b) that communities that experience little change over time correspond to highly connected groups of community instances, i.e. to tight clusters. The mining algorithm presented in the next subsection discovers such clusters that correspond to stable, persistent communities.

## *Clustering the Graph of Similar Community Instances*

We perform clustering upon the graph to detect groups of similar community instances. As for the discovery of community instances in each time period, we weight the edges of the graph on edge betweenness and then we progressively remove edges as part of a hierarchical divisive clustering algorithm. The connected subgraphs retained after  $k$  iterations correspond to the communities found thus far.

The algorithm takes as input the number of iterations  $k$  to be performed, or equivalently the maximum number of edges to be removed from the graph.  $k$  is determined empirically and thus chosen by the user. The value of  $k$  depends on the size and the structure of the network. In each round, the edge betweenness of the remaining edges is (re-) computed. A connected subgraph returned at the end of the iterative process is a community, comprised of similar community instances.

## *Visualizing the Temporal Development of the Community Instances*

The proposed method to find communities in a changing environment and to detect structural changes in evolving communities has been implemented in a software tool. The outcome of the analysis process is represented in different visualizations as shown in Figure 2:. For a detailed description of the visualizations and analysis modes please refer to [10].

To visualize the similarity between community instances we use a graphical representation that positions more similar vertices closer to each other than less similar. For this we implemented a Kamada-Kawai graph layout which positions the vertices in a way that the Euclidean distance between them is as close as possible to their graph-theoretic (path) distance. This layout is displayed in Figure 2: in the upper part on the left side. Each community instance is represented by a circle and the diameter of the circle represents the size of the community instance (= number of participants). Instances that are detected as similar according to  $\tau_{\text{overlap}}$  are connected with an edge. The whole graph can be rotated and single community instances can be moved to obtain a different view. After moving or rotating, the layout is renewed and all nodes are repositioned. Note, that in this visualization, the temporal development can not be observed, as the communities are only displayed according to their similarity.

The clustering result is visualized by different colors of the nodes. That is, at first all community instances have the same color. Groups of similar community instances that are detected during the clustering process are visualized by a different color. The example in Figure 2: shows three communities that have been detected after 38 clustering iterations. One community is shown in red, another in blue and one in green.

In a next step, the filtered and clustered data is copied to a community history view (see Figure 2:, right side). For this, the y-coordinates for each community instance are taken from the graph representation in Figure 2: left side. This is important to note, because a rotation or repositioning of vertices in the graph results in a different layout in the history view which displays the temporal development. The x-coordinate of the vertex is determined according to the period it appears in. Thus, community instances displayed on the left side are detected in earlier periods. To the right, more recent community instances are displayed. Each community instance is now represented as a rectangle and the height of

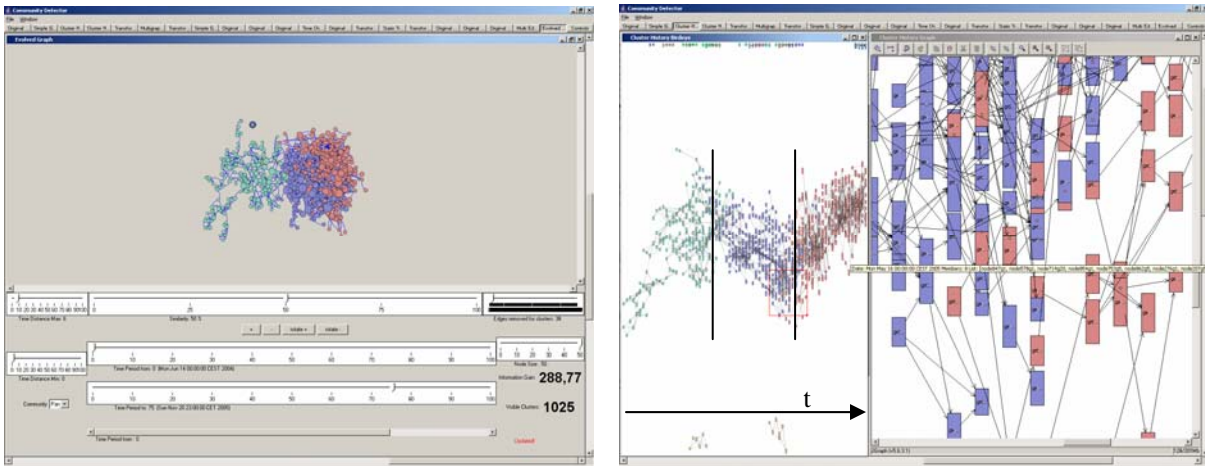


Figure 2: Left side: Graph visualization of similar community instances and control panel; After the removal of 38 edges three clusters of similar community instances are obtained as shown by different colors (green, blue and red circles); Right side: Graph visualization of temporal development of similar community instances; colors show cluster membership (to enhance visibility, vertical bars are added to indicate the cluster borders)

the rectangle corresponds to the size of the community instance. All communities that are considered as similar according to the actual setting of  $\tau_{overlap}$  are connected by edges. Clusters of similar community instances are displayed in the same color.

By moving a rectangle (see red rectangle on left side in Figure 2:) a cutout view of the graph (zoom in) is displayed which shows the structure of the community instances in more detail. The edges between rectangles represent similar community instances. If for example a community instance has edges to more than one rectangle in a later period it shows that members have separated. The horizontal box in Figure 2: on the right provides further information about a marked community instance. It shows the time period when the instance was detected and the list of participating members. This information is shown when the user marks a community instance.

The transformation of the graph in Figure 2: on the left side to the temporal view in Figure 2: on the right side, allows observing the development along the time axis because each community instance is displayed according to the period when it was observed. Now, the colors of the community instances indicate the borders of the clusters. The break between two differently colored clusters may show a period when a change in the community structure occurred. In our example we see two breaks that separate three communities. The changes in the structure can have different reasons, e.g. the set of participants strongly fluctuated, the interaction behavior of the participants changed, or both. This visualization reveals periods that exhibit structural changes and thus offers a starting point for users to analyze the triggers for such developments.

## CONCLUSION AND OUTLOOK

We discussed natural networks and their characteristics using measures from network analysis to find commonalities between natural and human networks. Furthermore, we presented our approach to detect and analyze the temporal evolution of communities in networks to learn more about the triggers that cause changes in the network structure and eventually in the function of the network.

Currently we study whether these factors that influence community dynamics are transferable to the dynamics of human communities. In natural communities it can be observed that, for example, monocultures can only survive with high costs whereas a diversity of species often leads to a more stable and productive and thus cheaper to maintain environment. Is it possible that similar to natural communities the diversity of human community members determines the stability and success of the group? Furthermore, it is known that plants can have positive effects on each other. For example, the accumulation of nutrients, provision of shade, amelioration of disturbance, or protection from herbivores by some species can enhance the performance of neighboring species. Thus, the distribution of plants is not independent of other species. In online communities we assume that people interact because they share a common interest. But people may play different roles in the community. Based on these results, we assess possible implications for the

research on how insights into the evolution of natural communities might foster the research on human community dynamics.

Note: Adapting methods and insights from biological system is not a one-way track. Since network analysis and especially the analysis of complex networks is of interest in fields such as engineering and computer science, many computational tools have been developed that are also be of high interest to study biological networks. These methods are especially helpful in fields that deal with complex networks such as gene or protein networks to develop realistic models of network formation and evolution.

General limitations: Modeling interactions in biological or human networks enables us the calculation networks measures and the compare networks but it should be kept in mind that interactions in real biological systems as well as in human networks are actually much more complex. Enzymes can be represented as nodes that are connected by the substrates that they metabolize, however the activity of enzymes depends on many factors that are can only be represented in networks to some extend.

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