

Visualizing Evolving Networks: Minimum Spanning Trees versus Pathfinder Networks

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Abstract

Network evolution is a ubiquitous phenomenon in a wide variety of complex systems. In fields such as statistical mechanics, there has been increasingly widespread interest in modeling the growth of complex networks. In this article, we compare two network visualization techniques, minimum spanning trees (MSTs) and Pathfinder networks (PFNETs), and their visualizations of co-citation networks of scientific publications. Our primary goal is to identify the strengths and weaknesses of the two methods in fulfilling the need for visualizing evolving networks. Two criteria are derived for assessing visualizations of evolving networks. We examine the animated visualization models of the evolution of botulinum toxin research in terms of its co-citation structure across a 58-year span (1945-2002). The results suggest that although high-degree nodes dominate the structure of MST models, such structures can be inadequate in depicting the essence of how the network evolves because MST removes potentially significant links from high-order shortest paths. In contrast, PFNET models clearly demonstrate their superiority in maintaining the cohesiveness of some of the most pivotal paths, which in turn make the growth animation more predictable and interpretable. We suggest that the design of visualization and modeling tools for network evolution should take the cohesiveness of critical paths into account.

CR Categories: I.3.6 [Methodology and Techniques]; I.3.7 [Computer Graphics]: Three-Dimensional Graphics and Realism – Virtual Reality; E.1 [DATA STRUCTURES] -- Graphs and networks.

Keywords: Network evolution, network visualization, co-citation networks, Pathfinder networks, minimum spanning trees.

1 Introduction

The significance of tracking the evolution of a complex system is widely recognized. For example, research in complex network theory has focused on modeling the growth mechanisms of small-world networks [41] and scale-free networks [4]. Scale-free networks are characterized by a power law degree distribution. A major concern is how to simulate the evolution of a network that demonstrates such special topological properties so that one can improve the understanding of real-world networks. Few empirical studies have examined changes in the topological properties of a network over time. According to [28], the principal reason has been the lack of good time-resolved data on how networks grow.

Visualizing fundamental changes in scientific networks is one of the toughest challenges for research in information technology. The shortage of comprehensive examinations of the evolution of citation networks is largely due to the lack of widely accessible longitudinal citation network data, the lack of integrated network

analysis and visualization tools, and the lack of tools that specifically facilitate the analysis of network evolution.

Network visualization has a long history in information visualization, such as, SemNet [19], ConeTree [33], NicheWorks [43], and Hyperbolic Browser [25]. Researchers are increasingly interested in visualizing emerging patterns in association with evolving information structures, using tools such as Disk Trees and Time Tubes [17] and Botanical trees [26].

Pathfinder network scaling is a procedural modeling algorithm originally developed by cognitive psychologists to capture salient relationships between concepts [36]. The strengths of such relationships are typically measured by human experts' subjective ratings of how similar those concepts are. Prior studies exclusively used Pathfinder networks to represent interrelations between concepts or keywords. One of our contributions is the extension of Pathfinder networks to a much richer range of applications, especially co-citation networks [11, 16].

Pathfinder networks have demonstrated various useful features in co-citation studies [12, 42]. On the other hand, the Pathfinder network scaling algorithm has its limitations. In order to achieve a network of high clarity and legibility, it is necessary to impose the so-called triangular inequality throughout the network. While this requirement leads to the simplest representation of the essence of an underlying proximity network, this is at a considerable computational cost. Additionally, as the size of the original network increases, the algorithm requires a considerable amount of memory to run. Therefore, it would be desirable if either an equivalent but more efficient algorithm can be developed, or a hybrid approach can be used to achieve cost-effectiveness.

A minimum spanning tree (MST) is widely known and commonly used in information visualization. MST algorithms such as Kruskal's algorithm and Prim's algorithm can be efficiently implemented. Despite its popularity, few empirical studies have investigated the relationships between MSTs and PFNETs. Even fewer studies have addressed the strengths and weaknesses of using MSTs versus using PFNETs.

In this article, we aim to address a number of issues concerning visualizing the evolution of a network with special reference to the use of MST and PFNET. In particular, we intend to address the following questions: 1) What should be a preferable topological structure of a visualized network? 2) What are the additional criteria for visualizing the evolution of a network? 3) To what extent can MST and PFNET be expected to meet such criteria? 4) What are the implications of our finding on visualizing the evolution of a network in general? The rest of the article is organized as follows. Related work is outlined first. Criteria are derived in terms topological properties and dynamical properties. Then we examine these criteria in MST and PFNET versions of animated visualizations of co-citation networks in botulinum toxin

research between 1945 and 2002. The results are analyzed and their implications for further research are discussed.

2 Network Visualization

Graphically representing nodes and links is the most commonly used approach to network visualization. Much of the attention in graph drawing has been given to the efficiency of algorithms and the clarity of end results.

The most widely known graph drawing techniques include force-directed graph drawing algorithms and spring-embedder algorithms [18]. The primary goal of these algorithms is to optimize the arrangement of nodes of a network algorithmically, such that strongly connected nodes in a graph-theoretical model appear close to each other in the final geometric representation, and weakly connected nodes appear far apart. Force-directed algorithms often lead to node placements that are aesthetically appealing. These algorithms, however, face some challenges in terms of efficiency, especially in terms of scalability, which is closely related to the clarity of a visualized network.

Cluttered network visualizations should be avoided whenever possible. An excessive number of links in a display may severely obscure the discovery of essential patterns. A commonly used strategy to reduce clutter is to reduce the number of links. There are several ways to achieve this goal:

1. Impose a link weight threshold and only include links with weights above the threshold [44];
2. Extract a minimum spanning tree (MST) from a network of N vertices and reduce the number of links to $N - 1$;
3. Impose constraints on paths and exclude links that do not satisfy the constraints, for instance, as in Pathfinder network scaling [36].

Option 1 is straightforward and easy to implement. However, it does not take the intrinsic structure of the underlying network into account, so the transformed network may not preserve the essence of the original network.

Option 2 guarantees the number of links in the transformed network is always $N - 1$, whereas option 3 may not have such upper bounds. For instance, we know that a Pathfinder network is the set union of all possible MSTs of the original network, but the number of distinct MSTs depends on the weight distribution of individual links. Therefore, the number of extra links varies not only from network to network, but also from measurement to measurement. For instance, Noel, Chu, and Raghavan [30] showed that using document co-citation counts normalized as cosine coefficients or Pearson correlation coefficients can lead to MSTs of different topological properties, and that the former resulted in more favorable structures, i.e. the presence of highly connected nodes with a fixed number of links. In [30], the size of the MST is relatively small, less than 200 nodes. For PFNETs, Chen has established that the most concise PFNET for visualization is PFNET ($q = N - 1$, $r = \infty$). In an author co-citation analysis (ACA), White [42] demonstrated that a 120-node PFNET derived from author co-citation counts was predominated by a number of high-degree nodes. In contrast, if author co-citation links were weighted by Pearson correlation coefficients, the resultant PFNET did not have this pattern. He concluded that using raw counts in ACA would be a preferred method [42]. As a side note, the use of Pearson correlation coefficients is studied in [1], where an example is constructed to show that Pearson correlation coefficients could lead to counter-intuitive results in author co-citation analysis.

3 Criteria on Preferable Network Visualization

3.1 Criterion I: Topological Properties

The above analysis leads to our first criterion for selecting a preferable topological structure of a visualized network – the presence of highly connected nodes in derived networks. The most recognizable patterns in a network are stars, rings, and spikes. The notion of reference points is proposed in [24], referring to conceptually or visually salient or distinctive points in a geometric model. Such reference points play the role of a reference context to which other points are seen “in relation to.” For instance, a star in a network is a node which is the only node many nodes connect to. The “starkness” of a pattern is also studied by Rosch et al. [34]. A star pattern indicates the star node carries the most information, processes the highest cue validity and the most differentiated from one another. It has been demonstrated in [14] that star patterns emerged in a hybrid PFNET of documents and users’ profiles and profiles are in the center, connecting to documents. The preference of star-like patterns is also implicit in Salton’s model of an effective indexing space for information retrieval [35]. In such indexing spaces, similar documents should be easily separable from the rest of documents so that as one is retrieving a relevant document, it is possible to scoop many other relevant ones in its vicinity and to reject documents located remotely.

Existing studies appear to suggest that co-citation counts are likely to form such star patterns in both MST and PFNET. In terms of small-world networks, star-rich networks have relatively high clustering coefficients; we will return to this subject later in the article. The first part of our study is to identify the boundary conditions of this claim so that one can select the most appropriate method for a given network.

Our second criterion is specifically related to the need for visualizing the growth of a network. What is necessary in visualizing the evolution of a network?

3.2 Criterion II: Dynamical Properties

The latest advances in statistical mechanics of complex networks have attracted much attention [2]. Small-world network properties as well as power-law degree distributions are found in scientific collaboration networks [29]. The growth of scale-free networks has increasingly become the focus of the attention. Most network growth models draw upon the rich-get-richer notion and cumulative advantage. As a result, if the degree of a node indicates its “richness,” a node with a higher degree will have a better chance to receive the next new link than a node with lower degree. In a citation network, this means that a highly cited article is more likely to be cited again than a less frequently cited article. This type of growing mechanism is known as *preferential attachment*.

Newman [28] studied the evolution of scientific collaboration networks in physics and biology and found that how often scientists publish jointly has something to do with the number of collaborators they have in common. If a scientist already has many collaborators, it is more likely that he or she will have even more collaborators down the line than a scientist who has relatively fewer collaborators. Barabási and his colleagues [5] found that preferential attachment mechanisms could statistically reproduce the topological properties of the co-authorship networks of mathematicians and neuroscientists.

One of the underlying assumptions is that the study of networks scientific papers can reveal insights into the dynamics of scientific frontiers. Price suggested that it is possible to identify objectively defined subjects in citation networks and particularly emphasized the significance of understanding such moving frontiers in depicting the topography of current scientific literature [32].

In the 1970s, Small and Griffith pioneered the method of mapping the structure of scientific literatures, especially through analyses of co-citation networks [40]. Small subsequently demonstrated the occurrence of rapid changes of research focus using the example of collagen research [39]. Documents clustered by their co-citation links can represent leading specialties. The abrupt disappearance and emergence of such document clusters indicate rapid shifts in research focus. By tracing key events through a citation network, Hummon and Doreian [20] successfully reconstructed the most significant citation chain in the development of DNA theory. Their study has great impact on subsequent studies of citation networks in the graph drawing community [6, 8].

An interesting study [31] analyzed the evolution of the biotechnology industry through a study of a network of contractual collaborations in the field between 1988 and 1999. The nodes in the networks are organizations and the links are collaborative ties. Various stages of the network were visualized. No link reduction or pruning was made. It appears to be particularly problematic to identify significant topological and dynamical patterns in such visualization models because of the high density of the underlying network.

An et al. [3] suggested that the evolution of citation networks could be useful in predicting research trends and in studying a scientific community's life span. Few studies in the literature visualized the growth of an evolving network. Chen and Carr [13] represent the evolution of the field of hypertext by visualizing its author co-citation networks over consecutive periods of time. The evolution of discourse is visualized in a recent example [7].

The second criterion is specifically related to the visualization of network evolution. Criterion I emphasizes the topological properties of preferable network visualization. Criterion II requires that the changes of topological properties over time must convey emergent trends or patterns beyond isolated nodes and links. Visualizing network evolution should not merely inform users of changes of individual nodes and links; rather, it is essential to inform users how an intrinsically cohesive structure changes locally and globally. For instance, Branigan and Cheswick [9] use their Internet Mapping techniques to show how the Internet in Yugoslavia was affected by the war. The focus is no longer on an individual connection; instead, it is now on the connectivity of a subset of nodes. Criterion II implies that a good visualization should be predictable in that the visualization should give the user various clues of where the next new node is likely to appear and where the next new link is likely to emerge.

4 MSTs versus PFNETs

Based on the available evidence in recent studies reviewed in earlier sections, both MST and PFNET appear to be capable of meeting the first criterion when conditions on the proximity measurements are satisfied. For instance, MSTs of similarity measures normalized by cosine coefficients are likely to have relatively high clustering coefficients, whereas PFNETs of author co-citation counts with no normalization at all were found to have similar clustering patterns. MST is a common choice in

information visualization. Clusters in MST appear to reflect the concepts of hubs and authorities. We also know that MST algorithms are more efficient than PFNET algorithms. Therefore, a number of theoretically and practically important questions now need to be addressed. Will MSTs be a generally better choice? As far as co-citation networks are concerned, will MSTs in general meet the second criterion? To what extent will the topological properties of highly clustered PFNETs be preserved by the use of raw author co-citation counts? Will PFNETs stand up the second criterion for visualizing the evolution of document co-citation networks?

In this study, we construct animated visualization models of the evolution of a research field from 1945 through 2002 in both MST and PFNET. This is essentially an empirical study. We compare the resultant models against the two criteria derived earlier in this article. The goal is to identify examples that can identify the boundary conditions in association with the selection of MST or PFNET. The evolution of the underlying research field is represented by the evolution of its co-citation network over its 58-year span. The nature of components of the co-citation network is identified in both MST and PFNET models using an independent method – accumulative co-citation clustering.

4.1 Botulinum Toxin Research (1945-2002)

The chosen research field for our empirical study is botulinum toxin research between 1945 and 2002. Botulinum toxin is a poison produced by the anaerobic bacteria *Clostridium botulinum* [22]. The toxin is one of the most potent poisons known, as little as .1 to 1 µg of toxin can be fatal to humans. It attacks the synapses used by the nervous system to activate muscle movement, preventing the production of the neurotransmitters, thereby causing muscle paralysis. Death can occur if the toxin paralyzes the respiratory muscles. There are seven forms of the neurotoxin, designated A through G. Additionally, *C. botulinum* produces a two-part cytotoxin designated C2 and an exoenzyme, designated C3.

Botulism, the medical condition caused by botulinum toxin, was first systematically studied by J. Kerner, a German medical officer, in the 1820's. The bacteria *C. botulinum* itself was first isolated and its toxin identified by Ermengem in 1897. Most of the different toxin types were identified in the first half of the twentieth century. Modern toxin research started with a seminal paper by Burgen, et al, in 1949, which revealed that the toxin attacked the neuromuscular junction.

4.2 Co-Citation Networks of Botulinum Toxin

Co-citation networks of botulinum toxin research were derived from a citation dataset, containing citation records from 1945 to 2002. Figure 1 shows a power law model of the relationship between the number of nodes and the number of links in co-citation networks at various citation thresholds. For instance, at the thresholds of 5, 10, and 25 citations, the size and the density of the co-citation networks are: 1,250 nodes and 91,483 links, 516 nodes and 19,631 links, and 104 nodes and 2,677 links.

In the rest of the article, we primarily focus on the 516-node co-citation network. In addition, we briefly discuss two PFNETs without any normalization on the co-citation counts: one is a 407-node author co-citation network for authors who have more than 15 citations; the other is a 380-node document co-citation network for articles with more than 12 citations. These two networks are

analyzed in order to identify the extent to which a PFNET can keep the number of links close to N .

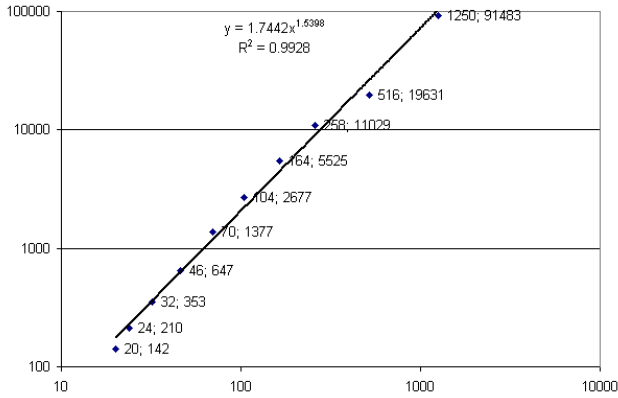


Figure 1. Log-log plot of the size of co-citation network at various citation thresholds, from 5 through 50 increased by 5. X axis is the logarithm of the number of nodes. Y axis is logarithm of the number of links.

The weight of a link in the network was calculated in two ways: first, weight links by direct co-citation counts; secondly, weight links by normalized co-citation coefficients. The following normalization (I) is used in this study :

$$sim(d_i, d_j) = \frac{cc(d_i, d_j)}{\sqrt{c(d_i) \cdot c(d_j)}} \quad (I)$$

where $cc(d_i, d_j)$ is the number of times document i and document j are cited together, and $c(d_i)$ and $c(d_j)$ are the number of times document i and document j are cited respectively. Alternatively, one may choose to use the following normalization (II), but a detailed comparison between the two is beyond the scope of this article:

$$sim(d_i, d_j) = \frac{cc(d_i, d_j)}{c(d_i) + c(d_j) - cc(d_i, d_j)} \quad (II)$$

MSTs were extracted using Prim's algorithm. PFNETs were extracted using the algorithm described in [36]. Both types of network models were examined against the first criterion given in Section 3 In order to examine the compliance to the second criterion, animated visualizations were generated as a sequence of annual snapshots of the evolving network throughout the 58-year period. The animated visualization revealed two types of state transitions as originally specified in [15]. The connectivity of the underlying co-citation network was represented by three node states and three link states. The three node states of an article are:

1. Before the publication date of the article.
2. Between the publication date and the earliest citation date.
3. After the earliest citation date.

Similarly, a co-citation link connecting two articles has three states as well. Suppose article A_i was published earlier than article A_j .

1. Before the publication date of A_j .
2. Between A_j 's publication date and the year of the first co-citation of the pair.
3. After the year of first co-citation of the pair.

Animated visualizations allow us to examine closely the growth of the underlying co-citation networks.

The following two paragraphs outline the method used to label and explore research topics in the network models. For this purpose, research fronts are considered as collections of papers on specific research problems in a field [27]. Base reference clusters are groups of references that represent the foundational knowledge used by workers when investigating research problems. Research fronts can be found by clustering documents that tend to cite the same references, using bibliographic coupling [23] as the basis for measuring similarity between pairs of papers. Base reference clusters can be formed by clustering references that tend to be cited together, using co-citation [38] as the basis for measuring similarity between pairs of references.

In this study, research fronts were identified by agglomerative clustering using only papers that had at least five bibliographic coupling counts with some other paper in the dataset. Similarity calculation was based on Salton's cosine coefficient [35] applied to bibliographic coupling counts. The titles for each research front were derived manually by exploring titles of papers within each research front for common themes. Base reference clusters were formed by agglomerative clustering using only references that had been cited 10 or more times. Similarity calculation was based on Salton's cosine coefficient applied to co-citation counts. For each base reference cluster, labels were found by using the label of the research front that contained the most citations to references in the cluster. A map of the references in the pathfinder network was produced identifying each reference by its base reference cluster membership, which allowed labeling of sections of the pathfinder network based on base cluster labels.

5 Results

The MST model indeed contained many clusters. Many articles did not connect to any other articles in their cluster apart from the cluster center. Figure 2 shows the 516-node MST based on the normalized co-citation counts. A three-dimensional visualization with the citation counts depicted in the third dimension also confirms that the cluster centers tend to have higher citation counts than non-center members of clusters. The MST model in this particular case evidently met the first criterion and it would be reasonable to hypothesize that MSTs can meet the criterion in a broader range of networks.

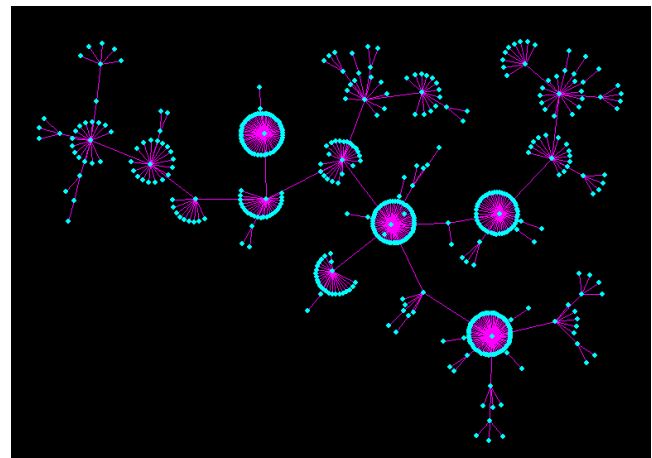


Figure 2. The MST extracted from the 516-node co-citation network on botulinum toxin (1945-2002). Co-citation counts are normalized (I).

However, an examination of the animated visualization over the 58-year span indicates that the MST model did not meet the

second criterion, which requires the visualized network to convey the evolution of globally and locally cohesive structures. A key question is how the relationship between the center of a cluster and other non-center members in the cluster was depicted over the course of evolution. In general, due to the arbitrary choice inherited from the MST algorithms, one cannot guarantee the uniqueness of an MST. As a result, an MST may not preserve all the necessary links for representing the growth of a co-citation network. If this is the case, then important diffusion patterns may be distorted or inadequately represented by the extracted MST model. Users will probably find it hard to understand the way new nodes and new links emerge. The nature of the problem will become clear shortly when we contrast the growth animation of the PFNET and MST models.

The 516-node PFNET ($q = N - 1, r = \infty$) is shown in Figure 3. The two parameters q and r were chosen to ensure that the extracted PFNET has the least number of links. The network in this case contains 525 links, which gives the node-link ratio of 0.98. We have developed a number of visualization methods to identify the nature of local structures of a PFNET, including node color mapping based on principle component analysis (PCA) on co-citations normalized as cosine coefficients, chronologically synchronized animated visualizations of state transitions for both nodes and links, and base reference cluster memberships based on the clustering algorithm outlined at the end of Section 4, where clusters are formed independently from algorithms used in modeling the network. In Figure 3, each node is depicted as its cluster number. The PFNET and the clustering methods appear to have a nearly perfect match between each other.

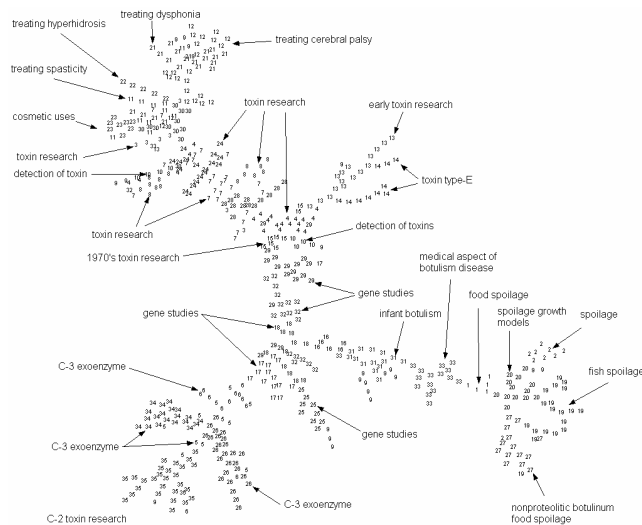


Figure 3. The 516-node PFNET ($q = N - 1, r = \infty$) containing 525 links.

General research on botulinum toxin proceeded until the mid-1980's when several distinct research fronts emerged. While investigations continued into the operation of the toxin itself, gene sequencing research on *C. botulinum* started in the early 1990's. Toxin research base references are located in the areas slightly above the center of the map. Furthermore, research fronts have opened up on C2 cytotoxin and C3 exoenzyme recently. C2 cytotoxin is a two-part pore forming toxin, similar in operation to anthrax toxin, where one part of the toxin, C2II, attaches to host cell membranes and forms a hole into the cell, which allows the second part, C2I, to enter cells to do damage inside them. The C2 toxin is being investigated as a delivery system for inserting

foreign proteins into cells for research. This is similar to research being performed with anthrax toxins, where anthrax protective antigen, the pore-forming part of the anthrax three-part toxin, is being studied a means to insert substances into cells to induce immunity to HIV. Additional research in botulinum toxin is using the C3 exoenzyme to study Rho proteins. C3 exoenzyme is also being studied as a possible neurotrophic drug, used for encouraging nerve growth. Base references related to C-2 and C-3 toxins are located in the South-Western region of the map in Figure 3.

Other research fronts in botulinum toxin research have focused on the mechanisms of food spoilage (located in the South-Eastern region of the PFNET in Figure 3), the medical aspects of botulism (along the branch stretching towards East in Figure 3), and infant botulism (also in the same branch), which is often attributed to cases of sudden infant death syndrome. There is also research being performed to develop methods of detecting and assaying the botulinum toxin in the environment. Current assay methods are time-consuming and involve injecting mice with the toxin and measuring time to death. Botulinum toxin can be used as a chemical/biological warfare agent and possible bioterror weapon, making the search for a cheap and efficient detection method an important area for research. There does not appear to be a consistent set of base references for botulinum toxin bioterrorism and biological warfare as there is for the case of anthrax [27].

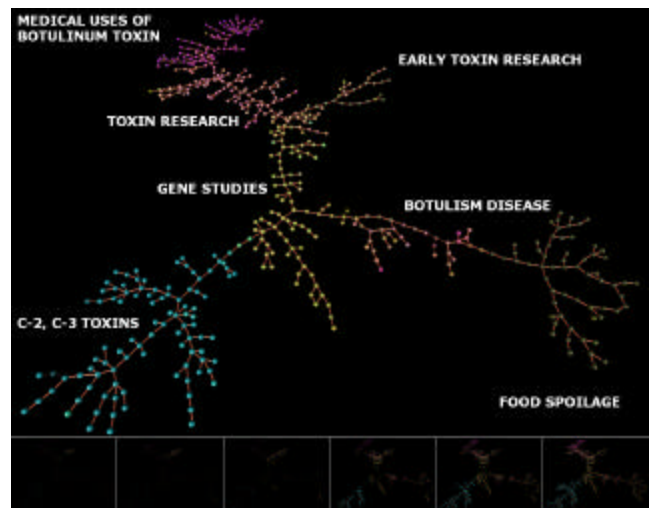


Figure 4. The 516-node PFNET consistently partitioned by base reference clusters and PCA factors.

The medical uses of botulinum toxin have received a great deal of public attention in the last year or two. In a seminal paper in 1973, Scott [37] described experiments on monkeys to treat eye alignment disorders. This was followed by an equally important paper describing results on human patients to treat strabismus ("cross-eyes"). In the 1990's botulinum toxin has been studied for the treatment of, spasticity, dysphonia (clamping muscles), achalasia (a disorder of clamping throat muscles that interferes with swallowing and food ingestion), cerebral palsy, hyperhidrosis (excessive sweating), anal fissures, and more. An important review paper on medical uses of botulinum toxin was published by Jankovic in 1991 [21]. Most medical uses of botulinum toxin are based on toxin type A, which is manufactured under the commercial name of Botox.

In the 1980's it was noticed that many patients being treated for blepharospasm (a disorder of clamping of eyelids) using

botulinum toxin exhibited reduced facial wrinkles and improved cosmetic appearance. Based on this effect, a seminal study by Carruthers in 1992 [10] reported the use of botulinum toxin for cosmetic purposes. The toxin has gained wide use for this purpose and as a result, the toxin is the current focus of much public attention.

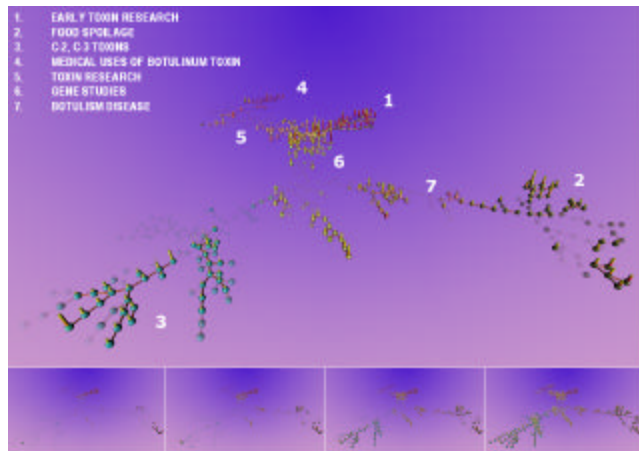


Figure 4. The growth of the field as shown in an animation sequence of how the PFNET network becomes populated.

The PFNET in Figure 4 was colored by factor loading from PCA based on cosine coefficients of co-citation frequencies. It is clear from Figure 3 and Figure 4 that base reference clusters and PCA factors are consistent with each other. For instance, C-2 and C-3 toxins base references identified by timeline visualization correspond to the area in light blue, which is consistently identified by PFNET and PCA.

Unlike the MST model, the PFNET model was not predominated by high-degree nodes. If we use the first criterion alone, MSTs would be a more preferable choice than PFNETs. In addition, PFNETs derived from raw co-citation counts appear to form more interpretable structures than normalized versions, cf. [42]. However, our further study of the second criterion indicates that this may not be the case if we take the temporal factor into account.

The examination of the second criterion was based on animated visualizations of the 58-year growth history of the field. Figure 4 shows some of the frames in the animation sequence. The enlarged frame shows the diffusion process of how several base reference clusters emerge and spread. State transitions were shown by changing the transparency level of nodes and links in question. The four smaller frames in the figure were selected from the animation sequence to show the emergence of early toxin research in late 1940s and the research front of gene studies formed at the center more recently.

The animated PFNET visualization model demonstrated that nodes with similar colors often emerged simultaneously and formed local structures. And these local structures were reinforced by the timely emergence of salient co-citation links. The growth process can be represented by the dynamics shown in such local structures. Features such as continuity, predictability, and local cohesiveness in the PFNET indicated that the second criterion was met. More significantly, it was found that these properties were missing from the MST model (See Figure 5). In PFNET, five pioneering toxin research articles formed a distinct thread, or a pathway. One can follow the development of the thread visually

as new nodes and new links extend the pathway. In contrast, in the MST model, four of the five articles were in the same cluster and one article was found in a different cluster.

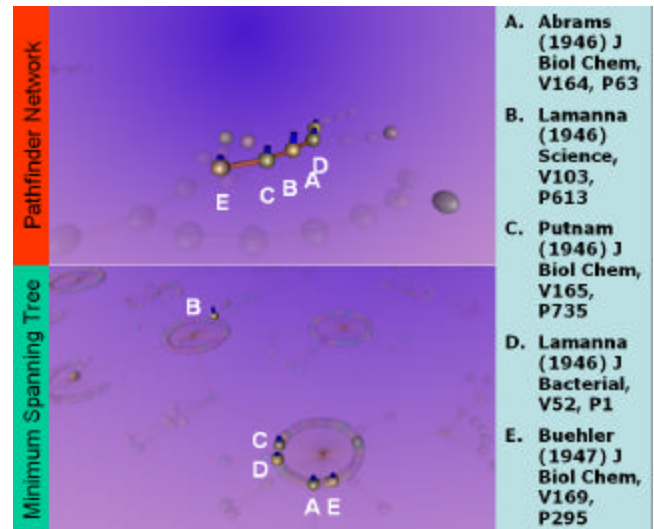


Figure 5. The growth process is better preserved in PFNET than in MST. PFNET successfully captured a co-citation pathway linking the five early toxin research articles, whereas MST failed to capture the pathway.

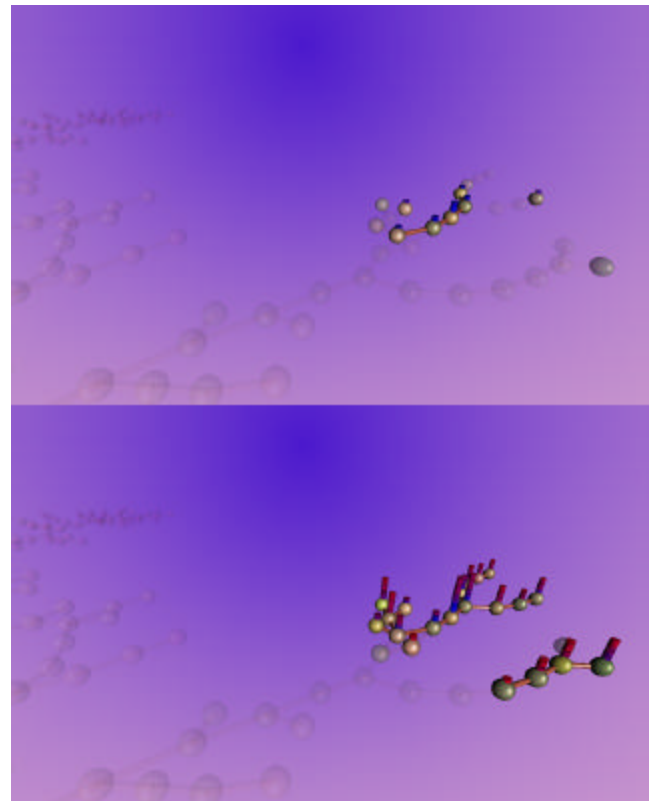


Figure 6. PFNET clearly tracked the growth of the underlying co-citation network. No such pathways were found in MST.

The animation showed that the pathway clearly captured by PFNET was simply not in the MST model. None of the four articles was the center of the cluster. Each article in the cluster connected to the center through a single co-citation link.

However, such links in MST were not necessarily the earliest or the most salient co-citation links. MST may have excluded some vital links in the crucial pathways in the course of evolution.

A distinct advantage of the PFNET is evident in Figure 6, which clearly shows the evolution of the co-citation network, starting with the short pathway at first, and then continuing the growth by the emergence of the second pathway alongside. The two frames were separated by a few years. Users can easily recognize the nature of the newly added nodes.

Finally, we briefly discuss the potential weakness of using un-normalized link weights. Figure 7 is a 407-node PFNET of author co-citation network, containing 428 Pathfinder links. The node/link ratio is 0.95. Figure 8 is a 380-node PFNET of document co-citation network, containing 523 links. The node/link ratio is as low as 0.73. Instead of normalizing link weights, the two PFNETs used direct co-citation counts as link weights. A low node/link ratio means that the PFNET has too many links and it can quickly lose the advantage of a Pathfinder network as the PFNET drifts too far from a tree structure.

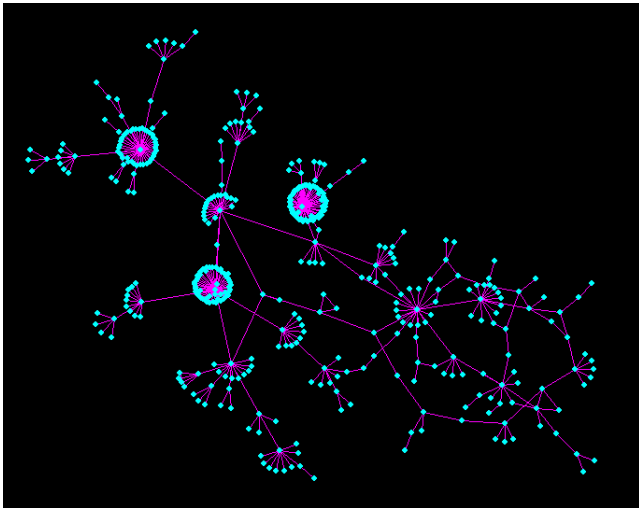


Figure 7. ACA PFNET of 407 authors who have more than 15 citations, containing 428 links (node/link ratio 0.95).

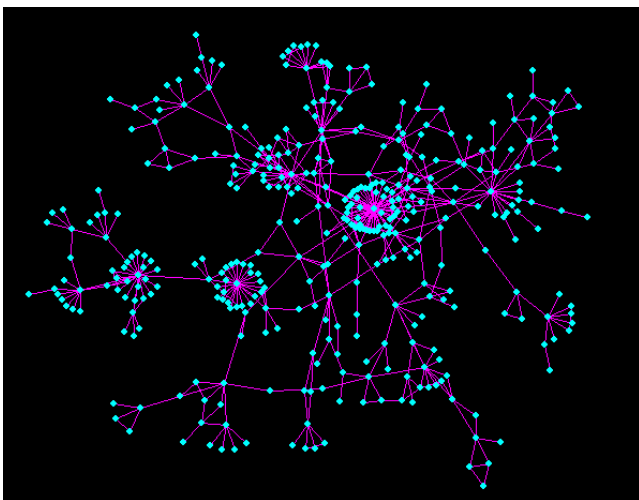


Figure 8. DCA PFNET of 380 articles with more than 12 citations, containing 523 links (node/link ratio 0.73).

6 Conclusion

In conclusion, the examples in this article have highlighted the importance of two criteria that designers should take into account in visualizing evolving networks. The most distinctive advantage of PFNETs is its ability to preserve critical pathways in the course of evolution. PFNETs have more accurate local structures than MSTs. On the other hand, MST algorithms can be implemented more efficiently. It is recommended that integrative strategies should be developed so as to match the strengths of the two methods to temporal as well as topological properties of networks.

Future studies are needed to improve our understanding of theoretical, methodological, and empirical implications. The development of a set of assessment criteria is crucial for improving the practice of network visualization.

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