

# Visualisation and Analysis of Large and Complex Scale-free Networks<sup>†</sup>

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## Abstract

Scale-free networks appear in many application domains such as social networks and biological networks [BA99, BB03, BO04]. Roughly speaking, scale-free networks have power-law degree distribution and ultra-short average path length and high clustering coefficient [BA99, BB03, BO04].

This paper presents new methods for visualising scale-free networks in three dimensions. To make effective use of the third dimension and minimise occlusion, we use the concepts of layered drawing and concentric spheres, constraining nodes to lie on parallel planes or the surface of spheres.

We implement the algorithms using a variation of the fast force-directed graph layout method [QE00]. Results with real world data sets such as IEEE InfoVis citation and collaboration networks and a protein-protein interaction network show that our method can be useful for visual analysis of large and complex scale-free networks. We further discuss the issue of visualisation of evolution networks and network integration.

## 1. Introduction

The study of connectedness in relational data sources has led to many large and complex network models in a variety of different domains. Examples include webgraphs, social networks (such as telephone call graphs, citation networks and collaboration networks), and biological networks (such as protein-protein interaction networks, metabolic pathways, and gene regulatory networks). In general these networks are very large, from thousands of nodes up to billions of nodes, and their relationships are very complex.

Visualisation can be an effective tool for analysis of such networks. Good visualisation reveals the hidden structure of the networks and amplifies human understanding, thus leading to new insights and new findings. However, there are many domains in which the network models have millions of nodes; visualisation of such networks is very challenging.

Many methods for visualisation of large

graphs have been suggested. For examples, see [GGK00, HK02, KCH02, Wal00, WM04, Duk04, MC03]. Roughly speaking, they use either fast multi-level force directed methods, multi-dimensional embedding, spectral graph drawing, geometric or combinatorial clustering or multidimensional scaling methods. However, current visualisation methods tend to exhibit one or more of the following problems:

- poor scalability;
- poor integration with analysis methods;
- lack of good interaction/navigation methods; or
- lack of good 3D visualisation.

Recently it has been shown that webgraphs, social networks and biological networks all exhibit similar properties, and can be modeled as “scale-free networks” [BA99, BB03, BO04]. Roughly speaking, scale-free networks have power-law degree distribution, ultra-short average path length and high clustering coefficient [BA99, BB03, BO04].

In this paper, we present a new method for visualisation of scale-free networks in three dimensions. To make effective use of the third dimension with minimum occlusion, we use a two-and-a-half dimensional approach [Dwy04, War01].

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Our first approach constrains nodes to lie on parallel planes or the surface of spheres based on the degree of nodes. This approach is designed to highlight hubs in the network. Our second approach constrains nodes to lie on parallel planes based on time. This approach is designed to show network evolution.

We have implemented the algorithm using a variation of the fast force-directed layout method [QE00]. By separating the network into parallel or spherical layers, we reduce the effect of common force-directed issues, such as dense data and occlusion. Results with real world data sets such as IEEE InfoVis citation and collaboration networks and PPI (protein-protein interaction) networks show that our method can be useful for visual analysis and give useful insight into large and complex scale-free networks. We further discuss the issue of visualisation of evolution networks and network integration.

This paper is organized as follows. In Section 2, we review background material. The main results of the paper are detailed in Section 3 where we present a new method for visualising scale-free networks in three dimensions. An implementation of the algorithm and results with real world data sets are described in Section 4. Section 5 concludes.

## 2. Background and Related Work

Recently it was reported that webgraphs, social networks and biological networks all exhibit similar properties, and can be modeled as “scale-free networks” [BA99, BB03, BO04]. In recent years, network researchers have tried to model these networks as *random networks* with Poisson degree distribution. However, the traditional random network model originally defined by Erdos and Renyi [ER59] fails to explain the existence of hubs and cliques in such networks.

The *scale-free network* model proposed by Albert and Barabasi [BA99] explains the existence of hubs and cliques in terms of two features of network evolution: *growth* and *preferential attachment* [BA99, BB03, BO04]. These two mechanisms may explain the existence of hubs and cliques, for example, as new nodes appear, they tend to connect to the hubs, which results in a power-law degree distribution.

More specifically, a scale-free network has the following properties [AJB00, BA99, BB03, BO04]:

- The whole graph is rather sparse but has locally dense regions.
- It has a “power-law” degree distribution: a few high-degree nodes hold the whole network together. All the remaining nodes have very low degree.
- It is an “ultra-small world” graph with small diameter and ultra-small average path length of  $O(\log n)$ . For example, the average path length of webgraphs with billions of nodes is merely 19 and the Hollywood movie actor collaboration network has average path length 6.

- It has a high “clustering coefficient”
- It is “resilient” (error-tolerant) to random attack, however “vulnerable” to designed attack.

As scale-free networks have few hubs with very high degrees, we will explicitly use this property to design new visualisation methods for scale-free networks.

Recently, some related work for visualisation of scale-free networks has appeared. For example, a method for drawing “power law” graphs was presented in [ACL04]. A method for drawing  $k$ -core graphs of the internet AS graph was presented in [BBGW04]. An interactive visualisation method for small world networks was presented in [vHvW04]. However, our visualisation method is different from those methods in the sense that we make effective use of the third dimension. Independently, a similar method to our parallel plane approach was used in [BBGW04]. In addition we use spherical layering and also constrain nodes based on time. Also, they visualise a different data-set ( $k$ -core graphs) and use a different force directed method.

There has been some debate over when to use 2D or 3D. According to Ware [War01], for applications for managing and interpreting networks “a  $2\frac{1}{2}$ -D design attitude that uses 3-D depth selectively and pays special attention to 2-D layout would seem to provide the best match with the limited 3-D capabilities of the human visual system”. The scale-free networks occurring in many applications fall in this category. The biggest problem with 3-D visualisation is the introduction of occlusion. However, because scale-free networks have the property of few high-degree nodes, there will be a small amount of detail at the top levels and there won’t be too much occlusion.

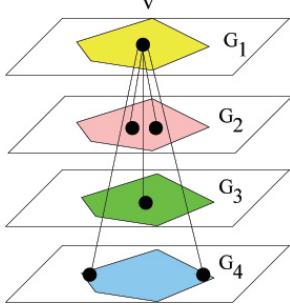
## 3. 3D Layout Methods for Scale-free Networks

In scale-free networks, nodes with high degree have special importance. Some examples are prominent researchers in collaboration networks, highly cited papers in citation networks and proteins closely related to lethality of the cell in protein-protein interaction networks [BA99, BB03, BO04]. Thus, we aim to design a new layout method which highlights these hubs. In particular, we use the third dimension to emphasise the relative importance of nodes.

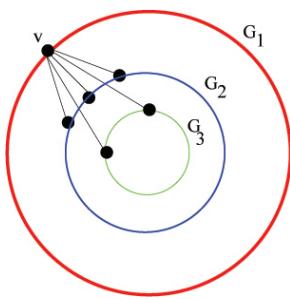
More specifically, we partition a graph  $G$  into  $k$  subgraphs  $G_1, G_2, \dots, G_k$ , based on the degree of the nodes. Then we draw each subgraph  $G_i$  either on parallel planes or concentric spheres. We have two variations in the layout; one uses parallel planes (see Figure 1), the other uses concentric spheres (see Figure 2).

In Figure 1, nodes with high degree are assigned to a subgraph  $G_1$  and placed on the top layer, and nodes with low degree are assigned to a subgraph  $G_4$  and drawn on the bottom layer. In Figure 2, nodes with high degree are assigned to a subgraph  $G_1$  and placed on the outermost sphere, and

nodes with low degrees are assigned to a subgraph  $G_3$  and drawn on the innermost sphere.



**Figure 1:** Parallel plane layout.



**Figure 2:** Concentric sphere layout

Note that in the general case, with  $k$  parallel planes or  $k$  concentric spheres, there may be edges between planes. For example, consider a node  $v$  in Figure 1 and Figure 2. We can classify the inter-plane edges into two types: edges between adjacent layers and edges between non-adjacent layers. Note that the edges between non-adjacent layers can lead to a chaotic, and hence confusing, visualisation. Minimising the length of such edges, by finding a layout with nodes in the upper layer centered with respect to their lower-layer neighbours, helps to mitigate this problem. This can be formulated as an optimization problem.

Our simple solution to this problem is to use a force-directed layout method. More specifically, we modified the FADE algorithm [QE00], a fast force-directed method which reduces the time complexity of the traditional spring algorithm from  $O(n^2)$  to  $O(n \log n)$ . The algorithm is based on the Barnes-Hutt method to approximate computation of repulsive forces between nodes using spatial partitioning (or geometric clustering) [QE00].

We design and implement an interactive version of the FADE algorithm with modification, in particular, adding constraints to ensure the nodes remain in either parallel planes or concentric spheres. Also, in cases where the network has weighted edges, the forces are similarly weighted

so that there is a greater attraction force between nodes connected by a highly weighted edge.

#### 4. Implementation and Experimental Results

We implement our visualisation methods for scale-free networks as a plug-in to WilmaScope [Wil], an interactive 3D graph visualisation tool. For data sets, we use real world scale-free networks. These include an IEEE InfoVis citation network, an IEEE InfoVis collaboration network and a protein-protein interaction network. We now describe the results in detail.

##### 4.1. PPI Network

PPI networks are scale-free [BO04]. Of particular importance is the observation that roughly 60 percent of high degree nodes are closely related to the lethality of the cell [JMBO01].

We use the same data set from [JMBO01]. The details of the data set are:  $|V| = 1846, |E| = 2203$ . Some parts of the network are disconnected. Note that in [JMBO01], the largest component was drawn in 2D using Pajek [Paj].

Figure 3 shows the parallel plane layout of the PPI network. Proteins with high degree are placed on the top layer and proteins with low degrees are placed on the bottom layer. More precisely, we have three layers numbered 1 (the bottom-most layer) through 3 (the top-most layer). Initially, we assign each node  $v \in V$  to a layer based on the degree  $d(v)$ , as follows:

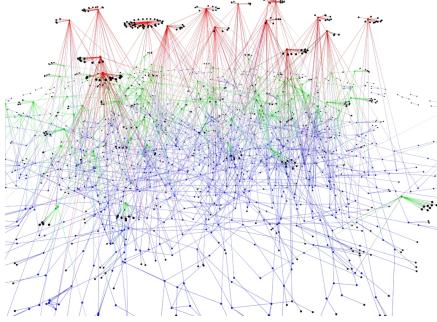
- $d(v) \geq 15 \Rightarrow \text{layer}(v) = 3$ ;
- $7 \leq d(v) < 15 \Rightarrow \text{layer}(v) = 2$ ;
- $d(v) < 7 \Rightarrow \text{layer}(v) = 1$ ;

A node on the top-most layer is called a hub. A feature specific to the PPI network is that many nodes of degree 1 are connected directly to a hub. As a result many edges pass through the middle layer. To reduce visual complexity, we move each degree 1 node to the same layer as their neighbour. It remains clear which nodes are hubs and which nodes are degree 1 and edge lengths, occlusions and visual complexity of edges which go through the middle are reduced. It is easy to identify "lethal" proteins drawn on the top layer.

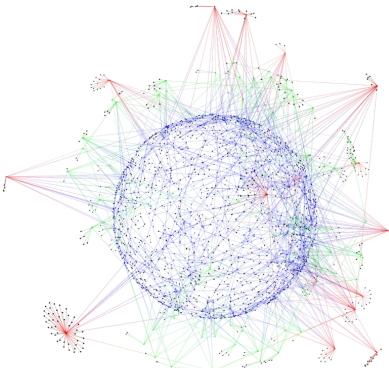
Figure 4 shows the concentric sphere layout of the PPI network. Proteins with high degree are placed on the outermost sphere and proteins with low degrees are placed on the innermost sphere. Single degree nodes are placed on their neighbours sphere. It is easy to identify "lethal" proteins as they are each drawn as an "apex".

##### 4.2. InfoVis Citation Network

Our second scale-free network is IEEE InfoVis citation network. In the citation network, each node represents a paper.



**Figure 3:** Parallel plane layout of PPI network.



**Figure 4:** Concentric sphere layout of PPI network.

It is a directed graph where an edge  $(u, v)$  indicates that the paper represented by  $u$  cites the paper represented by  $v$ . The details of the data set are:  $|V| = 535$ ,  $|E| = 1562$ .

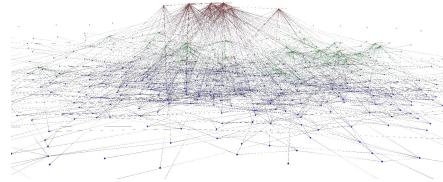
Figure 5 shows the parallel plane layout of the citation network. We assign each node  $v \in V$  to a layer based on the degree  $d(v)$ , as follows:

- $d(v) \geq 20 \Rightarrow \text{layer}(v) = 3$ ;
- $10 \leq d(v) < 20 \Rightarrow \text{layer}(v) = 2$ ;
- $d(v) < 10 \Rightarrow \text{layer}(v) = 1$ ;

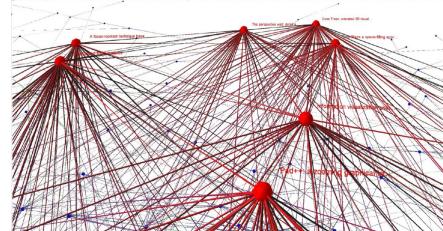
Due to the force directed layout, highly connected nodes are reasonably well centered with respect to their neighbours and appear as an "apex". In particular, the zoomed image (see Figure 6) identifies 7 of the most highly cited papers.

#### 4.3. InfoVis Collaboration Network

Our third scale-free network is the IEEE InfoVis collaboration network. In the collaboration network, nodes represent researchers (that is authors of a paper) and there is an edge between  $u$  and  $v$  if the researcher corresponding to node  $u$  has a joint paper with the researcher corresponding to node  $v$ . The network is a weighted graph, that is each edge has a weight which represents the number of joint papers between



**Figure 5:** Parallel plane layout of citation network



**Figure 6:** Zoomed view showing the most highly cited papers

two researchers. The size of the data set is:  $|V| = 982$  and  $|E| = 2012$ ; after the edges were filtered based on a threshold.

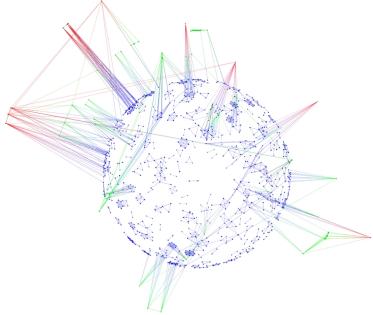
Figure 7 shows the concentric sphere layout of the collaboration network. Researchers with many collaborators are assigned to the outermost sphere and researchers with few collaborators are assigned to the innermost sphere. The same degree values are used for the partitions as for the citation network.

Note that it is easy to identify "prominent" researchers as they are drawn as an "apex". Further, research groups or clusters (cliques) of researchers can be identified easily as they tend to lie on the innermost sphere, with possibly some of the larger clusters spread across several spheres. It seems that students and younger researchers, with fewer collaborators tend to occupy the inner sphere, while supervisors and more senior researchers rise to the outer sphere, showing the hierarchy of the research clusters.

#### 4.4. Evolution Network of InfoVis Research Areas

We also visualise an evolution network of IEEE InfoVis research areas. We use two methods for visualisation of the evolution network: using parallel planes and animation [BC03, CM03, EHK\*03]. In this section, we use parallel planes to show the overview of the evolution network.

Firstly, we use a self organizing map (SOM) [Koh01] to classify (or cluster) papers into research areas. More specifically, the vector data using to train the SOM is calculated based on the term histogram. Each paper is transformed to a vector based on the frequency of words in its title, abstract and keywords. We use a stemmer to change the words into



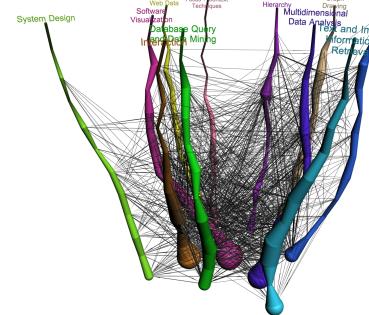
**Figure 7:** Concentric sphere layout of collaboration network.

their morphological root and use a stop word list to eliminate the meaningless words such as "the", "some", etc. After this process, the most popular words ("information", "visualization", "data", etc.) and the words which appear less than 5 times in total are eliminated. 827 words remain so that each vector is 827 dimensional. Some papers are also removed because none of their words remained after the above preprocessing. In order to increase the accuracy, we weighted each word according to the term frequency/inverse document frequency. The clustering is then done by a 42 neuron spherical self organizing map [WT05].

As a result, the following 11 research areas were identified: "Database Query and Data Mining", "System Design", "Web Data", "Interaction", "Graph Drawing", "Focus + Context Techniques", "Software Visualization", "Hierarchy", "Multidimensional Data Analysis", "Trees", "Text and Image Information Retrieval".

Based on the result, we created an evolution network of research areas, where each node represents a research area and year, and edges between nodes represent citations between research areas in different years. Before visualising this network we add edges between pairs of nodes representing sequential years in the same research area, so that all the nodes of the same research area can form a "column", ordered by year of publication.

For visualisation, we use a similar method as the parallel plane layout, constraining research area nodes to layers defined by year. More specifically, we use a force-directed method, with edges in each column having much stiffer springs than the springs representing citation edges. The positions of the nodes are constrained, such that all nodes for a given year must lie in the same plane. The planes corresponding to each year are arranged parallel to one another, and perpendicular to the  $z$ -axis, such that the top most plane (when viewed from the side) corresponds to the most recent year (2004) and the bottom most corresponds to the earliest (1993 and earlier). Figure 8 shows the parallel plane layout of the research area evolution network with citations.



**Figure 8:** Visualisation of InfoVis research area evolution

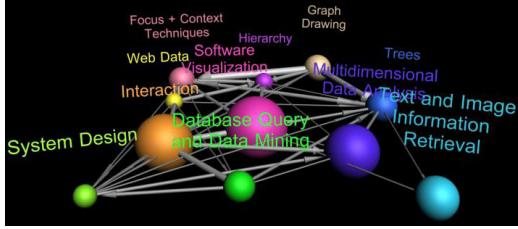
Each column in Figure 8 clearly shows the evolution of a different research area. The "thickness" of each column indicates the number of papers published in the corresponding year in that research area. Note that the columns lean and bend towards each other when they are strongly coupled (there are many citations between them), otherwise they bend apart. Roughly speaking, the "twistedness" of each column represents the evolution of relationships between each research area. The research area columns are given distinctive hues, uniform within each column, except where no paper was published in a particular year. Citation edges between columns were represented with a 3D arrow of radius and colour intensity is proportional to the number of citations represented. One feature of the visualisation is that all columns are very thin at the top. This is because the data-set did not contain many entries from the more recent years.

#### 4.5. Animation of Evolution Network

Another method for visualising an evolving network is to use animation [CM03, EHK\*03]. In this section, we use a cross-sectional viewer to study citations from individual years in details. Using this, we can show an animation, stepping through the citation edges emanating from a particular year. We now describe each step in detail.

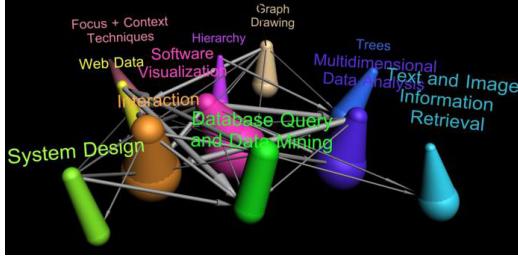
Firstly, see Figure 9. This first layer in our column visualisation shows citations from papers in each of the 11 research areas, to papers in other research areas published in 1993 and before. The relative size of the nodes indicates that "Database Query and Data Mining" and "System Design" are the most popular research areas at that time. A small distance between nodes, determined by the force directed algorithm attempting to minimise the edge lengths of citation edges, tends to indicate research areas that are more frequently referenced by other research areas. For example, the fat edge from "Software Visualization" to "Graph Drawing" indicates a strong tie between these two research fields. Papers in "Multidimensional Data Analysis" seem to be cited by many different fields. In contrast "Text and Image Information Retrieval" seems to be a relative outlier, only occa-

sionally cited by papers in the "Multidimensional Data Analysis" and "Database Query and Data Mining" research areas.



**Figure 9:** The first layer of research area evolution network.

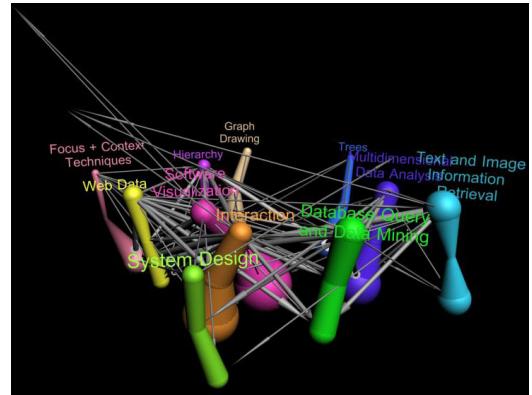
Next, see Figure 10. We now add another layer of nodes showing papers published by research area in 1994. We also add edges for citations made in 1994 and remove the edges associated with earlier citations. One can see in general that there are fewer papers published in this category. This is to be expected since the previous layer included papers not only from 1993 but also all earlier papers back to the 1980s. "Interaction" is still the most popular research area, and the small dimmed node for "Web Data" (at the left rear) indicates that there were no papers in the data-set for this research area in 1994.



**Figure 10:** Addition of the second layer to evolution network.

Finally, consider Figure 11. In 1995, "Text and Image Retrieval" has increased significantly in popularity and "Database Query and Data Mining" somewhat less so. Citations from "Software Visualization" papers seem to be leaning (literally the column is leaning over) towards "System Design" and "Focus and Context Techniques".

Note that in Figure 11, one can easily find a number of upward edges, which represent citations of future papers. Closer investigation revealed that many of these were due to older papers being reprinted in compilations. For example: "S. G. Eick and G. J. Wills, Navigating large networks with hierarchies, Proceedings Visualization'93, IEEE, October 1993" was reprinted in "Readings in information visualization using vision to think" in 1999. In the data set, the year for the entry representing both versions of the paper was set to 1999. Because it was first printed in 1993 it is cited by papers from as early as 1994. This case is a good example



**Figure 11:** Reference to future publication.

of the power of visualisation as an analysis tool for finding abnormal patterns.

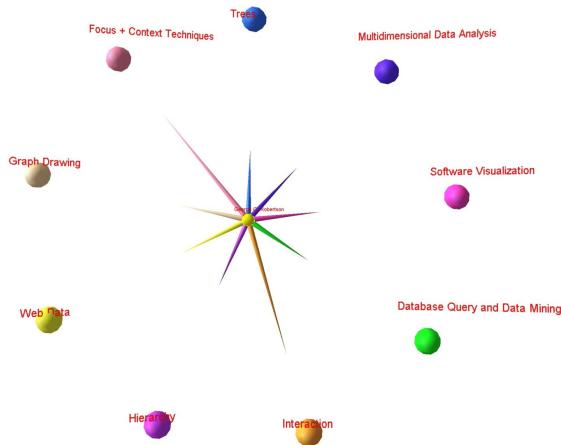
#### 4.6. Network Integration and Visualisation

Finally, we further address the issue of network integration and visualisation: that is, integrating several related networks into one visualisation. The aim for network integration and visualisation is to analyse how two different networks are closely related to each other visually. For example, suppose that we want to know whether there is a close relationship or some interesting pattern between the authors in the collaboration network and the research areas while still showing the relationship between authors. It may be useful to visualise these networks simultaneously in a single visualisation to get a general overview of their relation.

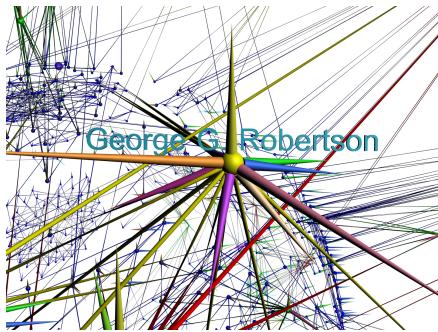
As an example, we use IEEE InfoVis collaboration network and create a new network including research areas. More specifically, we take the same node set as the collaboration network, that is the same set of researchers, plus 11 nodes, each representing a research area. In this new network, there is an edge between a researcher node and a research area node if the researcher published a paper in that research area. Note that the graph is weighted such that the weight of each edge indicates the number of papers in that research area.

We visualise these edges as "spikes" coming from the researcher node, pointing towards the research area node. The colour of each spike matches the colour of the research area node and the length of each spike indicates the weight, that is the number of papers of the researcher in that particular research area. For example, Figure 12 shows the case for George G. Robertson. Clearly, "interaction" and "focus + context techniques" are his speciality areas.

The advantage of this representation is that the spikes can be simultaneously displayed on nodes, thus the two networks are well-integrated into one visualisation. See Figure 13.



**Figure 12:** Research area of G. Robertson.

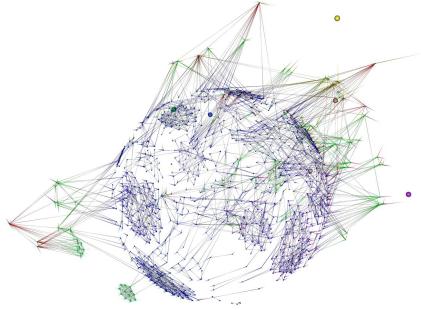


**Figure 13:** Integration with collaboration network.

Thus, a researcher's contribution to a specific research area can be visualised locally by the spikes, and globally by the position of the researcher node relative to the research area node (see Figure 14). Note that one may visualise this edge as a line between the researcher and research area, but we observe that that the spikes show the same information with less clutter.

#### 4.7. Navigation

We generated animations to navigate the user through the networks. The animations were carefully constructed using NavAssist [AE05], a simple technique for constrained navigation of graphs having pre-computed 3D layout. This technique demonstrates effective navigation through the network structure. The user view is transformed from one location, along a pre-computed path, to another location keeping important graph elements in the view throughout the process. NavAssist reveals as many graph elements as possible in the background to build and preserve the viewer's mental map of the graph during view point trans-



**Figure 14:** A global view of integration with collaboration network.

formation. For the resulting animations see the WilmaScope video at: <http://www.cs.umd.edu/hcil/InfovisRepository/contest-2004/> [ADM\*04].

#### 5. Conclusion

We have presented new visualisation methods for scale-free networks in three dimensions. Our methods use the concept of constraining nodes to lie on planes or the surface of spheres. This allows us to highlight hubs or show the evolution of a network.

We implement the algorithms using a variation of the fast force-directed graph layout method and results with real world data sets show that our method can be useful for visual analysis of large and complex scale-free networks.

Note that “degree” is just one centrality measure from social network analysis [WFG94]. We chose this measure as it has particular importance in the specific networks we used. It would also be possible to use our 3D layout methods in conjunction with other centrality measures such as betweenness centrality or closeness centrality (see [WFG94]) for visual analysis of other network models.

We are currently developing a visual analysis tool, GEOMI (GEOMETRY for Maximum Insight), which combines network analysis methods with graph visualisation. Our first step was to combine WilmaScope [Wil] (for graph visualisation) and JUNG [JUN] (for centrality measures) with a number of new 3D graph layout methods. We plan to include more extensive network analysis methods (such as group analysis measures) as well as new visualisation methods.

Another area for future work is a thorough evaluation of the proposed methods. There is a need to show how much performance improvement each method achieves. This could be achieved with a user-based evaluation with domain experts comparing the new methods with existing techniques.

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