Analysis and modeling of science collaboration networks

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We analyze a science collaboration network, i.e. a network whose nodes are scientists with edges connecting them for each paper published together. Furthermore we develop a model for the simulation of discontiguous small-world networks that shows good coherence with the empirical data.

Keywords: collaboration network, discontiguous nets, small-world effect, Barabási-Albert model, computer simulation

1 Introduction

Hearing the term network, the first association coming into one’s mind are physically wired networks as telephone or computer nets.

However, network does also denominate the same concept on an universal level: nodes of whatever type connected by links determined by relations of the most different kinds. Mathematically spoken, we often call networks graphs, nodes vertices and links edges.

Thus, there are numerable different kinds of networks, physical ones (e.g. hard wired) as well as logical (e.g. dependencies) or social ones (e.g. contacts, friendships), stretching out to topics far from wired networks [1, 2]. The area is under vigorous research. Good reviews can be found in [3, 4, 5, 6].

As a crucial difference from true random graphs [7, 8], Lots of human created networks show the small world effect [9, 10, 11], i.e. the average path length between two random points is significantly shorter (behaves logarithmically with the system size) than that of random networks (linear with system size).

A model developed by Barabási and Albert [12] describes several small-world networks very well, included e.g. the world wide web [13, 14].

In the context of science the network between scientists as nodes of the graph is of particular interest. This network belongs to the group of social ones, with humans as
nodes. Unlike most other forms of social relationships, that are quite difficult to capture objectively, the field of published papers is very widespread covered by the *Science Citation Index* and so easily available to research.

2 Collaboration networks

2.1 Typology

Apart from linking not the scientists but their papers, there are basically two possible choices in what to consider a link between two authors—both covered equally by the database.

1. We chose to consider citations from one author to another as links. In this case we get a rapidly growing number of papers we have to consider, as each added scientist cites several others and so on. It even is not clear *a priori* that we ever get to an end—except in the case of having all scientists in our set of authors.

2. The only connections in our net are those of co-authorship in one or several papers. Now we have the advantage of being able to choose an arbitrary set of authors as start of our examinations—though we should provide a preferably reasonable one. This choice will be discussed later.

But another problem arises using this method: it is very difficult—if not impossible—to determine all papers a given pair of authors ever published.

2.2 Building the net

As a solution we chose the following proceeding: We start with one paper. As one part of our work will deal with Barabási-Albert networks, we take the corresponding paper as center of our investigation.

To determine the set of authors we want to deal with we select all 185 papers that cite this paper. (Remark: we have to be careful not to mix citation data from different dates as new papers are continuously added to the database. The base of our investigation is October 21st, 2002.)

As a second step we construct a list of unique authors from all these papers. In a first approach we have 559 scientists, whereof some turn out to be identical only appearing in particular papers with typos. We finish with a set of 555 authors to whom we attribute consecutive numbers.

The last step of the network creation consists in establishing links between all these authors. This is done by selecting one paper after the other and introducing a connection between each possible pair of this paper’s authors.

Eventually, this gives us a net which we suppose to be rather typical for scientific collaboration.

The network size is relatively small compared to all data in the *Science Citation Index* (approx. $10^7$ papers). We will study properties of this subnet and compare it to some
classical and recent network models hoping to get an idea of what leads to the structure we observe. Verification with bigger networks is a task for the future.

2.3 Statistics

Now we will analyze a crucial property of the just created net: the cluster size distribution. In our case, clusters of scientists are formed by the links between them, i.e. a single paper of $n$ authors already forms a cluster of size $n$.

Immediately, our eyes are caught by a paper on the Human Genome Project \cite{20} with 274 authors. The giant cluster thus formed is singled out from all others by its hugeness. Regarding it as an anomaly, we chose to remove it from our network. A brief examination yields that this is no harm as the scientists participating in this work did not cooperate with the others of our study and form a big cluster containing only themselves. We will discuss later in section 3.3.1 if this proceeding was justified.

Now, we investigate the frequency of clusters of a given size. Our expectation is to see many clusters with few authors and vice versa.

![Figure 1: frequency distribution of the cluster size]({"figure_path"})
The experimental data (figure 1) shows this behavior but with one surprise: although the most frequent cluster size is 2 due to a big number of publications with two authors, most scientists maintain collaboration with three others.

A probable explanation is this: scientists are often member of research groups involved in different themes, thus connecting different clusters formed by single two-author-papers.

3 Computer simulation

We now describe a model reproducing these results, hoping to understand how this macroscopic behaviour arises by microscopic decisions of the individuals.

A model describing small-world networks quite well is that of Barabási and Albert [12]. Unfortunately, it only deals with networks consisting of one single component. We generalize it to discontiguous networks.

3.1 Standard Barabási-Albert model

The Barabási-Albert network model starts with a set of (mostly) $m_0 = 3$ points, each connected to each other by a link.

In each time step, (usually) $m = 3$ new nodes are added, each with a link to the existing network. The probability of an already existing vertex to be a linking target is proportional to the number of connections already present at this node. “The rich get richer.”

3.2 Modified model

To cope with networks consisting of several components, we have to modify the model. We chose a very simple approach: In each step of adding nodes we start a new network of $m_0 = 3$ nodes with at certain probability $p$.

Vertices added in consecutive time steps can connect to any node in any component respecting the same probability rule as in the standard model.

In the case $m = 1$, components can only grow (isolated clusters), whereas in the case $m > 1$, new nodes are able to connect two or more existing components of the network (merging clusters).

3.3 Results

To compare the results with the data collected in section 2.2 we let the network grow up to the same size of 555 nodes. This is repeated $10^4$ times for statistical reasons.

3.3.1 Isolated clusters

In the case $m = 1$, i.e. the case isolated clusters, we can be sure to get scale-free behavior within the distinct clusters, as the probabilities for attachment of a new node to an ex-
isting one are the same as in a single Barabási-Albert network (modulo a proportionality factor due to a new node having a “choice” between different clusters to connect to).

However, the complete network does not necessarily have to be scale-free, as the total statistics is a sum of multiple scale-free sub-networks or clusters.

![Figure 2: Frequency of clusters vs. cluster size at different probabilities for a new net. Simulation was run $10^4$ times with a network growing up to 555 nodes. The curve for $p = 0.01$ is the one with the rightmost peak; to the left follow the other $p$-values in ascending order.](image)

First, we examine the number of clusters of different sizes (figure 2).

Obviously, a high probability of starting a new net leads to many smaller networks, whereas a low one privileges bigger networks. Yet, we make an interesting observation: low probabilities lead to a cluster-size distribution that is not monotonic any more, but favors big networks.

The explanation is straight-forward: For $p = 0$ we will see a graph $\propto \delta(555)$, as there is only one giant cluster, for $p = 1$ a graph $\propto \delta(m_0 = 3)$, because there are only embryonic sub-nets. What we observe for $0 < p < 1$ is the transition between both extremes.

For all $p$ we start with a power law region regarding the distribution for small and medium cluster sizes. The exponent varies with the network-birth probability $p$. In figure 3 we analyze this correlation in a semi-logarithmic plot.
Figure 3: Negative exponent of the power law part of the curves in figure 2 vs. probability $p$ for a new net. The line corresponds to $\text{exponent} = -e^{2.25p}$.

We find that $-e^{2.25p}$ describes our data rather well. Of course, this formula cannot be true for general $p$ as for $p \to 1$ we expect $m \to -\infty$!

Finally, we compare the cluster distribution from computer simulation with real-world data (figure 4) and are surprised. The data fits well—including the giant cluster we thought to be an anomaly whilst building the network. The plot gives strong evidence that indeed it was an organic part of the network. Its hugeness is simply due to the graph forming rules.

3.3.2 Merging clusters

Now, we modify the model by examining $m > 1$. In this case, newly added vertices develop several links to existing nodes (and thus existing clusters), being able to connect hitherto separated networks. In this paper, we limit our considerations to the standard Barabási-Albert case $m = m_0 = 3$.

Using different $p$, we quickly recognize that low and medium probabilities make the simulation nearly always end up with a single giant cluster containing all vertices. Points of interest are higher $p$ in the region of 60–90%.
What about scale-free behavior in this case? In figure 5 we can see that there is no pure scale-free behavior. There seems to be power-law behavior for small degrees and an exponential cutoff at higher values as has been verified by a semi-logarithmic plot of figure 5. Similar results have been observed by Newman [18] for collaboration networks.

One could argue that this effect is due to the fact that we do not plot the degree distribution for single clusters but for the whole set of them. This demur only counts at first sight, though. At $p = 80\%$ we have several small clusters but virtually only one giant cluster dominating the degree distribution for high degrees. So, the fact of averaging of many different sized clusters should manifest mainly in the area of small degrees opposite to our observations.

For small cluster sizes, we observe a non-uniform behavior regarding the frequency of clusters of a given size. There is no monotony of the sort that larger clusters are less probable than small ones.

The explanation is as follows: newly born clusters have a size of $m_0 = 3$ and thus appear very often. Also, cluster of sizes 4 or 7 are very probable, whereas a cluster of
size 5 is very rare, because it can only be formed by a new cluster to which two new ones have connected without glueing it to a second cluster.

In a semi-logarithmic plot, we find a parabolic dependence for high cluster sizes (i.e. a Gaussian distribution around a mean depending on $p$).

4 Conclusion

We constructed a network of coauthorship with 555 authors. Only scientists were chosen that cite a specific paper [12]. We find a cluster size distribution showing an exponential decay for small cluster sizes and a giant cluster that cannot be explained by common network models.

A change of the model of Barabási and Albert [12] by allowing a certain probability to start new clusters, enables us to simulate networks consisting of distinct clusters, e.g. friendship or collaborational networks.

The modification provides two different models. In the isolated clusters variant, newly born clusters stay distinct forever and show up scale-free behavior on their own.
This model is able to explain facts formerly regarded as statistical anomalies as the observation of a giant cluster of a size exceeding largely all others in the network. Following the simulation this observation fits very well (figure 4).

*Merging clusters* is the second variant, i.e. new nodes are able to merge existing clusters. This model shows an exponential fall-off for higher degrees in the degree distribution and thus no pure scale-free behavior. Furthermore, it results mainly in a Gaussian distribution of cluster sizes for bigger clusters and thus cannot cope with reality.

More results will be given in [21].

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