Cluster Growth in a Growing Tree Network

David Lancaster
School of Computer Science, University of Westminster, Harrow, HA1 3TP. UK.
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We analyze a simple model for growing tree networks and find that although it never percolates, there is an anomalously large cluster at finite size. We study the growth of both the maximal cluster and the cluster containing the original vertex and find that they obey power laws. This property is also observed through simulations in a non-linear model with loops and a true percolating phase.

1. INTRODUCTION

Recently there has been interest in the properties of random networks that are constructed by a growing process. These networks appear to model certain observed systems rather better than the random graphs of Erdős and Rényi [4]. Already, two reviews are available [2-3].

At first, interest concentrated on the degree distribution. It has been noticed that networks such as the world wide web, the Internet backbone and scientific collaboration graphs have (at least in some range) a power law degree distribution. This is in contrast to the Poisson distribution found in random graphs. Barabási and Albert [4] noticed that a power law distribution could be obtained in a grown network with preferential attachment.

The grown nature of the network creates correlations that affect more than the degree distribution. More recently, these other aspects of grown networks have been studied: in particular, the phenomenon of percolation, that was of great interest in the study of random graphs. Some grown models are devised to be fully connected and percolation can not be studied, but in a recent paper, Calloway et al. [7] studied percolation in a very simple network growth model. Their model introduces a new vertex at every time step, and also, with probability δ, makes a link between two existing vertices, chosen at random. Percolation in this model displays some interesting features that distinguish it from percolation in a corresponding random graph with the same degree distribution. For example, the location and order of the phase transition are modified by the correlations present in the grown model. A similar treatment of other models has been performed by Dorogovtsev et al. [6], who note that below the percolation transition, the cluster size distribution has a power law dependence in contrast to the exponential dependence typical in non-grown models.

In this paper we pursue the investigation of percolation in grown networks concentrating on models in which the new vertex introduced at each time step, is itself the endpoint of the link possibly created in that time step. Models of this type were in fact the original kind proposed by Barabási and Albert [4]. Only later did Dorogovtsev and Mendes [8] introduce the other type of model in which vertex and link creation are decoupled, and which often happens to be more convenient for calculation. In general there are families of such models in which more than one link is added per time step. When two or more links are added there seems to be little to distinguish the statistical features of the two families of models and they can be used interchangeably. However, for the particular case of single link addition, the models do have a different character because in the case where the vertex is attached, only tree networks can be created. For this reason we call this model, that forms the basis of study in this paper, the “tree growth model”.

Although most of the physical networks motivating the surge of interest in this subject are not treelike, other examples, such as food webs, would appear not to contain, or at least to have a low probability of containing loops. However, a significant reason for studying a tree growth network comes from past experience: tree graphs have provided a fruitful field for investigating percolation in non-grown networks. They have been studied both in the Physics literature and through the mathematical field of branching processes. Tree models provide an infinite dimensional or mean field model that is often tractable in a way that finite dimensional models are not. We shall find that the tree growth model that forms the basis of this paper is indeed a simple tractable model that illuminates more complicated scenarios.

The most interesting feature that we shall use this model to expose is the power law growth of cluster size as the network size increases. In numerical work (and for the size of many practical networks) this feature, and the presence of what appear to be anomalously large clusters, mask the lack of strict percolation in the tree growth model. This is because in random graphs, cluster growth below the percolation threshold is only logarithmic. However, as was pointed out by Dorogovtsev et al. [6], the power law growth based on the underlying power law size distribution, makes the whole phase have scaling characteristics typical of critical behavior.

We study the properties of clusters in depth and besides investigating the distribution of sizes of clusters chosen at random, we also study the size of the cluster containing the initial point. This illuminates the intuition that there is a highly connected “old core” that forms...
the nucleus of the large clusters and turns out to give a useful analytic handle that is not so obvious in non-linear models with loops. To ensure that the phenomena we are studying are not an artifact of the tree model we introduce a non-linear extension and perform some numerical simulations.

It is useful to contrast the properties of this grown tree model with a non-grown or static analog. In the present case, we argue that the appropriate analog is a branching process rather than a random graph. Calloway et al. in their paper on percolation, ascribe the cause of the differences between percolation on grown networks and random graphs to correlations between the degrees of vertices at each end of connecting links. We demonstrate that the tree growth model does not have any such correlations.

The paper is organized as follows. After defining the tree growth model, the branching process we use as a static analog is introduced. The percolative and other properties of these models are then compared. The main results on the tree growth model are contained in the sections describing the growth of the maximal cluster and the cluster containing the origin. A calculation of the vertex degree correlations in this model is the subject of section IV. The final part of the paper concerns a non-linear extension and perform some numerical simulations.

II. TREE GROWTH MODEL

In each time step a new vertex is introduced. With probability $\delta$, the new vertex is connected to another vertex, chosen at random from amongst the existing vertices. The vertex remains disconnected with probability $1 - \delta$. In numerical simulations we always start with a single vertex at time $t = 1$, but we do not expect this initial condition to affect results at large times.

This model only generates clusters of tree graphs. There is only a single tree cluster for the case $\delta = 1$. These clusters are fragile in the sense that single deletions will always destroy connectivity.

A. Degree Distribution

We commence by investigating the distribution of the vertex degrees, that is, the number of links attached to a given vertex. Following the notation and methods of Calloway et al., we denote the expected number of vertices of degree $k$ at time $t$ by $d_k(t)$. Since the total number of vertices at time $t$ is precisely $t$, the probability of attaching a new link to an existing vertex of degree $k$ is $d_k/t$, leading to the following evolution equations:

\[
\begin{align*}
    d_0(t + 1) &= d_0(t) - \delta \frac{d_0(t)}{t} + (1 - \delta) \\
    d_1(t + 1) &= d_1(t) - \delta \frac{d_1(t)}{t} + \delta \frac{d_0(t)}{t} + \delta \\
    d_k(t + 1) &= d_k(t) - \delta \frac{d_k(t)}{t} + \delta \frac{d_{k-1}(t)}{t}, \quad k \geq 2
\end{align*}
\]

Note that the total number of vertices can be written as $\sum_0^\infty d_k(t) = t$ and that the total expected number of links is given by $1/2 \sum_0^\infty kd_k(t) = \delta t$. Since both quantities grow linearly in time we search for solutions of the form, $d_k(t) = p_k t$, and find:

\[
\begin{align*}
    p_0 &= \frac{1 - \delta}{1 + \delta} \quad (4) \\
    p_k &= \frac{2}{1 + \delta} \left( \frac{\delta}{1 + \delta} \right)^k, \quad k \geq 1 \quad (5)
\end{align*}
\]

This distribution decays exponentially in contrast to random graph models which have a Poisson degree distribution, and the scale free models with power law distribution.

B. Static Analog - Branching Process

Before proceeding to investigate clustering issues we pause to introduce a non-grown or static analog of this model. The static model should have the same vertex degree distribution as the grown model, but should be constructed to avoid any correlation between the degree of linked vertices that might arise from the growing process. Furthermore, the analog should preserve the tree-like character of the model, so it cannot be one of the classic random graphs of Erdős and Rényi. An appropriate model is based on an ensemble of Galton and Watson branching processes.

A branching process may be regarded as a growth process in its own right, but each vertex is treated identically, thus avoiding any potential correlation between vertex degrees. In order to reproduce the vertex degree distribution, we choose the probability of $k$ offspring to be proportional to $p_{k+1}$ in equations (4,5), so:

\[
p_k = \frac{1}{1 + \delta} \left( \frac{\delta}{1 + \delta} \right)^k, \quad k \geq 0 \quad (6)
\]

This choice gives the correct ratios of vertex degrees at all higher levels. However, at the first level, where no link is already present, it is not obvious that the choice correctly weights the vertices with no children at all. We return to this issue when we discuss the ensemble of branching processes.
The properties of the model are then a textbook exercise, but for completeness we summarize the main steps. The main concern is the with the cluster sizes, in particular the question of percolation. This approach based on branching processes is identical to the studies of percolation on trees, for example Bethe lattices, which were popular in the 1980’s and provided a mean field model for the percolation transition.

Percolation occurs in this model when the extinction probability of the branching process is less than unity. This extinction probability may be calculated using the generating function for the probabilities (7):

\[ g(x) = \sum_{k=0}^{\infty} p_k x^k = \frac{1}{1 + \delta - \delta x} \]

The extinction probability is given by the smallest root, \( x_0 \), of the equation: \( g(x) = x \). This root is 1 for all values of \( \delta \) so percolation never takes place (though, in the same way as for one dimensional percolation, \( \delta = 1 \) may be regarded as a critical point).

The technique above can be extended to find the distribution \( n_i \), of finite clusters in this model. For a single branching process, the generating function, \( \rho(x) = \sum n_i^0 x^i \), for the quantities \( n_i^0 \), which are the probabilities that the process contains \( i \) nodes, is given by the solution to, \( \rho(x) = xg(\rho(x)) \), and is found to be:

\[ \rho(x) = \frac{(1 + \delta)}{2\delta} - \frac{1}{2\delta} \sqrt{(1 + \delta)^2 - 4\delta x} \]

The quantities \( n_i^0 \) may now be read off, however these are not the cluster numbers \( n_i \), as usually defined. The static model is an ensemble of branching processes, so \( n_i^0 \) corresponds to the number of clusters of size \( i \) per process, but \( n_i \) is the number per node. To relate these quantities we compute the average number of nodes in a branching process as \( \rho(t) = 1/(1 - \delta) \). In the limit of a large ensemble we then find \( n_i = (1 - \delta)n_i^0 \). A proper discussion of the ensemble would allow a number of isolated nodes besides the clusters based on branching processes, in order to adjust the degree distribution. This more careful discussion leads to the same result.

\[ n_1 = \frac{1 - \delta}{1 + \delta} \]
\[ n_2 = \frac{\delta(1 - \delta)}{(1 + \delta)^3} \]
\[ n_3 = \frac{2\delta^2(1 - \delta)}{(1 + \delta)^5} \]

A recursion relation may be obtained for higher order terms. These results are used for comparison with the tree growth model.

**C. Cluster Size Distribution**

The expected number of clusters of size \( i \), \( N_i \), in the tree growth model obey a set of evolution equations that can be obtained by noting that the probability of making a link to a cluster of \( i \) vertices is \( iN_i/t \). In contrast to the situation in more complicated models, these equations are linear, exact and hold for finite \( t \).

\[ N_1(t + 1) = N_1(t) - \delta N_1(t) + (1 - \delta) \]
\[ N_i(t + 1) = N_i(t) - \delta iN_i(t) + \delta (i - 1) N_{i-1}(t) \]

The expected total number of clusters \( \sum N_i(t) \) grows linearly in time and is given by \( (1 - \delta)t \), since a new cluster is created whenever a link is not made in a time step. By summing the equations (weighted by \( i \)), we also find that the first moment is given by the total number of vertices, \( \sum iN_i(t) = t \). These relations also reflect the fact that each cluster is a tree graph, so the number of links is the number of vertices minus one. We search for the cluster size distribution, \( n_i \), of the form, \( N_i(t) = n_i t \) and find the following recursion relations:

\[ n_1 = \frac{1 - \delta}{1 + \delta} \]
\[ n_i = \frac{(i - 1)\delta}{i\delta + 1} n_{i-1} \quad i \geq 2 \]

Although the first term, \( n_1 \), is (by design) the same as for the static model, later terms are different. Figure 1 shows the first few terms of the cluster size distribution for both the static model and the growth model. Notice that while the exact result is similar to the static one for small delta, it is smaller for larger delta.
Indeed, the large cluster behavior of the static and the
growth model are completely different. The large cluster
behavior of (15) is power law:

\[ n_i \rightarrow \infty n_1 \Gamma(2 + 1/\delta) i^{-(1+1/\delta)} \] (16)

That of the branching model is dominated by exponential
decay.

The power law decay of the cluster distribution for
the growing model has been noticed by Dorogovtsev et al. [7] in the non-percolating phase of non-linear growth
models. They have termed it a self organized critical
state because the preferential attachment to larger clusters
which causes the power law decay occurs automatically.
For non-grown networks, exponential decay of the
cluster numbers is a common feature (as in the static
example). This difference has consequences for the way
clusters grow.

III. PERCOLATION

Direct numerical simulations of the growing network
indicate that for values of \( \delta \) larger than about 1/2, there
is a cluster of size considerably larger than the others.
This cluster often contains the original vertex and sug-
sists that there may be a percolating cluster based on
the “old core” of vertices that are created early in the
growth. These numerical simulations are in fact mis-
leading, but expose anomalous finite size effects that are
studied below.

An analytic approach to percolation does not take the
usual route because the equations (12,13) are exact and
hold for any incipient percolating cluster besides the fi-
nite clusters. Ordinarily, the sum, \( \sum_i^{\infty} n_i \) only accounts
for finite clusters and the infinite cluster must be added
separately. However, according to the equations, this
sum equals \( t \) and contains all the vertices, thereby leav-
ing no room for an infinite cluster. The generating func-
tion approach used in [3], although pleasantly tractable,
merely reproduces this information.

Percolation does not occur in this model, except in the
trivial limiting case \( \delta = 1 \) where the network just consists
of a single tree graph. This phase diagram resembles that
of ordinary one dimensional percolation. To understand
the reasons why percolation does not take place, yet large
clusters do appear at finite size, it is helpful to study the
numerical data for the maximum sized cluster. This will
then lead us to an investigation of the cluster containing
the original site.

A. Numerical Study

On closer inspection of the numerical data it is found
that the fraction of sites contained in the largest cluster
suffers from an anomalously slow finite size effect, becom-
ing smaller as the growth process is continued to larger
times. For example, at \( \delta = 0.8 \), the fraction drops from
about 0.29 at \( t = 10^3 \), to 0.17 for a network 10 times
larger. In figure 2 we show the largest cluster fraction
against log(\( t \)) for various \( \delta \). The straight lines clearly
indicate a power law dependence. The exponent can be
determined by fitting, or by noticing that another plot of
the same quantity (log) against \( \delta \) displays linear de-
pendence. In any event, the lack of any transition is clear.
The fit suggests the form:

\[ \bar{i}(t+1) = \bar{i}(t) + \frac{\delta}{t} \] (18)

There is no solution linear in \( t \), but a form \( \bar{i} \sim t^\delta \) solves
the equation in the large time limit. The fraction of sites
in this largest cluster, \( \bar{i}/t \), therefore follows the scaling be-
behavior observed numerically in [3]. As the system grows
very large, the relative size of even the largest cluster de-
creases and it is apparent that the tree growth model
never experiences true percolation.

In most static models with percolation, for example
random graph models, the finite size scaling of the maxi-
mum cluster size is given by log(\( t \)). This is related to the
usual exponential decay of the cluster size distribution,
and the power law behavior we see here follows from the
distinctive decay [10] in growth models.

B. Cluster Containing the Initial Point

The overall distribution of the sizes of randomly chosen
clusters [14,15] does not give any hint of the presence of

FIG. 2. Scaling of largest cluster size fraction against \( t \) for
\( \delta = 0.1, 0.5, 0.8 \)
the large cluster seen in the numerical work above. It is hard to investigate the maximal cluster analytically, but if we rely on the observation that the maximal cluster is likely to be based on one of the oldest vertices, we may approach the problem from a different perspective. The distribution of the size of clusters that contain the original point is amenable to analytic methods and does shed some light on the presence of a large cluster. The possibility of studying this quantity is of course only available in grown networks that have distinguished vertices.

As before, we start by writing evolution equations, this time for the probability $P_i(t)$ that a distinguished cluster has size $i$ at time $t$ $(1 \leq i \leq t)$.

\begin{align}
P_1(t + 1) &= P_1(t) - \delta P_1(t) \\
\frac{P_1(t + 1)}{t} &= \frac{P_1(t)}{t} - \frac{\delta P_1(t)}{t} + \frac{\delta (i - 1) P_{i-1}(t)}{t} \\
P_{i+1}(t + 1) &= \delta P_i(t)
\end{align}

These equations are very similar to the ones for the overall cluster size distribution $N_i(t)$ in (24), however, the difference in the first equation prevents any solution $P_i(t) \propto t$. The equations actually hold for any distinguished cluster, with the initial condition determining which cluster is selected. Simplest is to choose the cluster distinguished as containing the original point, in which case $P_1(1) = 1$. Other possibilities, for example the cluster containing the second point would be determined by the values at $t = 2$, $P_1(2) = 1 - \delta$ and $P_2(2) = \delta$. This in fact leads to the same distribution as for the first point, but a difference is obtained for the third point which is specified by: $P_1(3) = 1 - \delta$, $P_2(3) = \delta(1 - \delta)$ and $P_3(3) = \delta^2$. In the following, we shall only consider the cluster containing the original point.

The sum $\sum_i P_i(t)$ is preserved by these equations, and can be set to 1, as expected for a probability, by the initial condition. The average size of the distinguished cluster, $k(t) = \sum_i kP_i(t)$, obeys $k(t + 1) = (1 + \delta/t)k(t)$. So at large times we expect that $k(t) \sim t^\delta$. This is essentially the same argument as in (18) of the last section and indeed the evolution equation has the same intuitive origin. In this form the prefactor can be determined from the initial condition. Evolution equations for all the higher moments of the distribution will be considered below.

For large $t$ and $k$, the continuum version of the evolution equation becomes:

$$
\frac{t}{\delta} \frac{\partial P}{\partial t} = -\delta \frac{\partial (kP)}{\partial k}
$$

which has a scaling solution,

$$
P(t, k) = t^{-\delta} f(kt^{-\delta})
$$

where $f(u)$ is any function.

This result is confirmed, and the form of the scaling function $f(u)$ determined, by numerically solving the difference equations (19, 20, 21), up to $t = 10^4$.

The scaled cluster distribution shows a clear change in form around $\delta = 1/2$. Although the mean of the distribution varies smoothly with $\delta$, and is close to 1 on the scaled plot (corresponding to $\delta = t^{\delta}$ before scaling), the mode moves away from zero (cluster size, $k = 1$, before rescaling) as $\delta$ becomes greater than about $1/2$. Eventually, as $\delta \to 1$ the scaling function becomes progressively more peaked around $u = 1$. This provides an argument for the likely presence of a large maximal cluster for $\delta \gtrsim 1/2$.

The form of the scaling function is not easy to determine analytically. Only in the limit of large or small $\delta$, can $f(u)$ be determined using the solutions for $P_1(t)$ and $P_0(t)$ obtained from (13) and (24).

For comparison with simulations it is better to compare the moments of the distribution rather than the full form. The moments, defined as,

$$
S_n(t) = \sum_k k^n P_k(t)
$$

obey simple equations obtained from weighted sums of (19, 20, 21).

$$
S_0(t + 1) = S_0(t)
$$

$$
S_1(t + 1) = (1 + \frac{\delta}{t})S_1(t)
$$

$$
S_2(t + 1) = (1 + \frac{2\delta}{t})S_2(t) + \frac{\delta}{t}S_1(t)
$$

And similar equations for higher order moments. By
FIG. 4. First two moments of the size of cluster containing the origin. The upper curve is for the second moment, and the lower curve is for the mean. Each moment is scaled according to $t^{-n\delta}S_n(t)$ and based on simulations of 4000 samples of networks containing $10^4$ vertices. The lines are the theoretical results including the sub-leading finite size terms.

forming suitable linear combinations, these equations can be solved in terms of the following function:

$$R(z, t) = \prod_{i=1}^{t-1} (1 + z/i) = \frac{\Gamma(z + t)}{\Gamma(z + 1)}$$

$$\lim_{t \to \infty} \frac{t^2}{\Gamma(z + 1)} (28)$$

For example:

$$S_0(t) = R(0, t) = 1$$

$$S_1(t) = R(\delta, t)$$

$$S_2(t) = 2R(2\delta, t) - R(\delta, t)$$

The general case is not difficult to work out, and it is also possible to treat clusters containing other than the original point. As $t$ becomes large, $R(n\delta, t) \sim t^{n\delta}$, so the leading term dominates and $S_n(t) \to n! R(n\delta, t)$. However, for finite $t$, the sub-leading terms are large in the region $\delta \lesssim 1/\log(t)$ and must be kept in numerical work.

In figure 4 we show comparisons of these formulae against simulation results for the mean and the second moment. Bearing in mind the scaling behavior, we plot each moment divided by a power of $t^\delta$. These first moments show excellent agreement.

IV. VERTEX DEGREE CORRELATIONS

To conclude our study of the tree growth model we follow the same argument used by Calloway et al. to determine the correlations between the vertex degree at each end of a randomly chosen link. The number of edges that join vertices of degrees $j$ and $k$ is denoted $E_{jk}$. This matrix is symmetric. For links that join vertices of the same degree, $E_{kk}$ is defined to be twice the number of such links. In this case exact evolution equations can be derived by treating the vertices with a single link specially:

$$E_{11}(t + 1) = E_{11}(t) + 2\delta d_0 \frac{d_0}{t} - 2\delta p_1 \frac{E_{11}}{d_1}$$

$$E_{1k}(t + 1) = E_{1k}(t) + \delta \frac{d_{k-1}}{t} \frac{d_k}{t} - \delta \left( p_1 \frac{E_{1k}}{d_1} + p_k \frac{E_{1k}}{d_k} \right)$$

$$E_{jk}(t + 1) = E_{jk}(t) + \delta \left( p_{k-1} \frac{E_{jk-1}}{d_k} + p_{j-1} \frac{E_{j-1k}}{d_j} \right) - \delta \left( p_j \frac{E_{jk}}{d_j} + p_k \frac{E_{jk}}{d_k} \right)$$

(33)  

(34)  

(35)

Where the $d_k(t)$ and $p_k$ are the vertex degree numbers and their probabilities as determined earlier in section III.

The total expected number of links is given by $\frac{1}{2} \sum_{jk} E_{jk}(t)$ and the evolution equations show that it is given by $\delta t$ as anticipated. We therefore write the probabilities as $E_{jk}(t) = 2\delta t e_{jk}$, and derive the following equations.

$$(1 + 2\delta)e_{11} = p_0$$  

$$(1 + 2\delta)e_{1k} = \frac{p_{k-1}}{2} + \delta e_{1k-1}$$  

$$(1 + 2\delta)e_{jk} = \delta (e_{jk-1} + e_{j-1k})$$

(36)  

(37)  

(38)

By appropriately multiplying these equations and adding, we can find the following relations between the moments:

$$M_0 = \sum_{jk} e_{jk} = 1$$

$$M_1 = \sum_{jk} je_{jk} = 1 + \delta + \frac{1}{2} \sum_{j=0} p_j$$

$$M_2 = \sum_{jk} jke_{jk} = 1 + 2\delta M_1 + \sum_{j=0} p_j$$

(39)  

(40)  

(41)

Using the results of section III on the vertex degrees, we find the average degree $\sum_k k p_k = k = 2\delta$. The sum above includes vertices with no links, and the average degree on the end of a randomly chosen link is, $\mu = k^2 p_k / \sum_k k p_k = 1 + 2\delta$.

The covariance between vertex degrees at each end of a randomly chosen link is defined as:

$$C = \sum_{jk} (j - \mu)(k - \mu)e_{jk}$$

$$= M_2 - 2\mu M_1 + \mu^2 M_0$$

(42)  

(43)

Combining these results we find that $C$ vanishes identically and that there is no correlation between the degrees at the end of randomly chosen links in this model. This result is supported by simulations.

In view of this result, it is slightly surprising that the analog static model which was specifically designed to
avoid these correlations, is not identical to the tree graph model. There is still a distinction as was apparent from the cluster numbers.

V. TWO LINK GROWTH MODEL

The preceding study of cluster growth in the tree growth network has been reasonably tractable, fundamentally due to the tree property of the network. The question arises as to which features are preserved in more general models.

The most obvious difference in more complicated models is the presence of a percolating phase. The tree growth model has no percolating phase except the trivial one at $\delta = 1$. The physical reason for this deficiency is not directly the tree nature of the network. The cause should rather be sought in the growth itself. There is no mechanism to attach existing clusters to each other. A mechanism of this type was responsible for the percolating mechanism to attach existing clusters to each other. A mechanism of this type was responsible for the percolating phase. The tree growth network has been reasonably tractable, fundamentally due to the tree property of the network. The cause should rather be sought in the growth itself. There is no mechanism to attach existing clusters to each other.

A. Two Link Growth Model - Degree Distribution

The equations leading to the degree distribution that are obtained by the same means as for the tree growth model.

\[ d_0(t+1) = d_0(t) - 2\delta \frac{d_0(t)}{t} + (1 - \delta) \]
\[ d_1(t+1) = d_1(t) - 2\delta \frac{d_1(t)}{t} + 2\delta \frac{d_0(t)}{t} \] (45)
\[ d_2(t+1) = d_2(t) - 2\delta \frac{d_2(t)}{t} + 2\delta \frac{d_1(t)}{t} + \delta \] (46)

\[ d_k(t+1) = d_k(t) - 2\delta \frac{d_k(t)}{t} + 2\delta \frac{d_{k-1}(t)}{t} \] (47)

Note that the total number of vertices, $t$, can be written as \( \sum_{0}^{\infty} d_k(t) \) and that the expected number of links, $2\delta t$, is given by \( \frac{1}{2} \sum_{0}^{\infty} kd_k(t) \). Searching for solutions of the form, $d_k(t) = P_k t$, we find:

\[ p_0 = \frac{1 - \delta}{1 + 2\delta} \] (48)
\[ p_1 = \frac{2\delta(1 - \delta)}{(1 + 2\delta)^2} \] (49)
\[ p_k = (1 + 8\delta) \frac{2^{k-2}\delta^{k-1}}{(1 + 2\delta)^{k+1}} \] (for $k \geq 2$) (50)

Again, this distribution decays exponentially after the first couple of terms.

B. Two Link Growth Model - Cluster Size Distribution

The cluster sizes $N_i$ in the two link growth model obey a set of evolution equations which are now approximate and only valid for finite clusters at large $t$ since processes in which both links end in the same cluster are ignored. This is the same approximation that is made in the Calloway et al. analysis.

\[ N_1(t+1) = N_1(t) - 2\delta \frac{N_1(t)}{t} + (1 - \delta) \] (51)
\[ N_2(t+1) = N_2(t) - 2\delta \frac{N_2(t)}{t} \] (52)
\[ N_i(t+1) = N_i(t) - 2\delta \frac{iN_i(t)}{t} \]
\[ + \delta \sum_{j=1}^{i-2} jN_j(t) \frac{(i-j-1)N_{i-j-1}(t)}{t} \] (53)

Solutions of the form $N_i(t) = n_i t$ are considered and a recursion relation obtained:

\[ n_1 = \frac{\delta}{1 + 2\delta} \] (54)
\[ n_2 = 0 \] (55)
\[ n_i = \frac{\delta}{1 + 2\delta} \sum_{j=1}^{i-2} jn_j(i-j-1)n_{i-j-1} \] (56)

Analysis of these cluster numbers is best carried out using the generating function for the cluster sizes, $g(x) = \sum_{1}^{\infty} in_{i}x^{i}$, which obeys a non-linear equation:

\[ g' = \frac{1}{2\delta} \left( 1 - \delta - g/x + \delta g^2 \right) \] (57)
We compute $g(1)$ by numerically integrating the equation \[ (57) \] starting from an initial condition $g(\epsilon) = n_1 \epsilon$. Figure 5 shows the results, and we recall that $g(1)$ is the expected fraction of vertices contained in the finite clusters, so when it differs from 1, percolation occurs.

The model percolates for most of the range of $\delta$, but for a range of small $\delta$ there is no percolation. It is possible to obtain the critical value $\delta_c$ by studying $g'(1)$. In the percolating region $g(1) < 1$, so it is simple to take the $x \to 1$ limit of the right hand side of equation \[ (54) \] to obtain,

\[
g'(1) = \frac{1}{2\delta} (1 - \delta (1 + g(1))) \tag{58}
\]

In the case $\delta < \delta_c$, $g(1) = 1$, and this limit must be taken more carefully with the help of L'Hopital's rule. The resulting quadratic equation can be solved to give:

\[
g'(1) = \frac{1 - 4\delta \pm \sqrt{1 - 16\delta + 16\delta^2}}{4\delta} \tag{59}
\]

We omit regions where the root is not real, and further require that it be positive. Finally, recognizing that $g(1) \to 1$ as $\delta \to 0$ since in this limit all clusters have size one, we are able to pick the negative sign as being the only correct branch. 

In summary: $\delta_c = 1/2 - \sqrt{3}/4 \approx 0.06699$. With $g'(1)$ taking different values on each side:

\[
g'(1) = \begin{cases} 
1 - 4\delta - \sqrt{1 - 16\delta + 16\delta^2} & \text{for } \delta < \delta_c \\
\frac{4\delta}{2\delta} (1 - \delta (1 + g(1))) & \text{for } \delta > \delta_c
\end{cases} \tag{60}
\]

The critical behavior we have described is very similar to that observed in the model studied by Calloway et al. By performing a similar investigation near the critical point, we find the same signals of an infinite order transition with $1 - g'(1) \sim e^{a/\sqrt{\delta - \delta_c}}$.

C. Two Link Growth Model - Percolation

VI. CLUSTER GROWTH IN THE TWO LINK GROWTH MODEL

In this section we describe the results of numerical simulations to find how large clusters grow in this model. We track both the maximal cluster and the cluster containing the original vertex.

In the region above the percolation threshold the maximal cluster naturally grows with $t$. It is interesting to see how finite size effects influence this and how the cluster containing the original point grows. This is shown in figure 6 which indicates that there is a region where the original cluster is smaller than the maximal one, but as the size of the network increases, this cluster approaches the size of the maximal one. This result supports the intuition that the “old core” of vertices act as a seed for the percolating cluster. Indeed, the probability that the maximal cluster contains the original vertex appears to grow to 1 for any $\delta$ in the percolating phase. Unfortunately, the statistics for this analysis are not good for the sizes we have considered and this result should only be taken as suggestive.

The finite size effects are most apparent for $\delta = 0.1$ which is quite close to the critical point. In this case the fraction of sites in the either maximal or original cluster decrease with $t$ in a way reminiscent of the behavior in the tree growth model. Estimates of a correlation size can be made on the basis of logarithmic plots which show a clear change in slope as the network size exceeds the correlation size at that value of $\delta$.

It is the situation below the percolation threshold that holds more interest for comparison with the tree growth model. In figure 5 we show evidence that the maximal cluster scales with a power law decay in this region. The original cluster behaves in the same way. This is exactly
as in the tree growth model, and as emphasized before, quite distinct from the log($t$) behavior in random graph models.

Having demonstrated that scaling occurs in the same way as in the tree growth model, we postpone any further study of the exponent of the growth. This is because of the difficulty of getting far from the critical point in this particular model.

VII. CONCLUSION

The study of grown networks was originally motivated by real networks which are by nature finite. We have shown in a simple tree growth model, that although an infinite size system does not display percolation, finite systems of sizes that may have relevance to observations, often contain large clusters. These clusters grow with a power law dependence on the system size and provide another manifestation of the critical nature of the whole phase. The power law growth can be analysed carefully in this model, especially by studying clusters with distinguished points, but the pattern of power law growth appears to be general as found in numerical simulations in a non-linear model.

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