Branching process for network growth with geometric restrictions

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Abstract.

We study an evolving tree with interacting nodes embedded into a Euclidean space. The growth of the network is generated by a branching process in which up to two new nodes are attached to a previous generations node at each time step. The new nodes are born if their positions are sufficiently far from one of the previous generations nodes, where the minimum allowed distance between two nodes is a. This results in an explosive (exponential) growth in the initial period, and, after some crossover time $t_x \sim \ln(1/a)$ for small a, in a slow (power-law) growth. This special point is also a transition from "small" to "large words" in terms of network science. We show that if the space is restricted and for small enough values of a, the evolution may end by extinction.

1.   Introduction

Evolutionary process can be schematically depicted as a tree ("the tree of life" [1]), where branches, are, for example, different species. Importantly, the growth of this tree is complicated by interaction and competition between species. In this work we discuss one of the simplest models of growing trees which can mimic this process. Growing trees naturally represent a wide range of real-life processes and phenomena [2, 3, 4, 5, 6, 7].

We study a model of an evolving tree network with interacting nodes, representing a competition of species for resources in a limited Euclidean space. When the network has no spatial restrictions the number of nodes always grows in time. On the other hand, when a spatial restriction limits the total size of the network, the number of new nodes reaches a constant value, and in some cases the population can disappear. We show that the competition between the nodes combined with spatial restrictions can lead the network to extinction.

2.   The Model

Starting from a single root, each node in the network can branch to produce up to two new daughter nodes of the next generation, at each time step. The network is embedded in a D-dimensional Euclidean space. The root node have zero coordinates. At each time step, each of the nodes of the tree attempts to emit two leaves (leaf is a link with a new node), so at each time step a new generation of nodes is born. At each time step, make the following:

1. Choose uniformly at random a node i (coordinates $\mathbf{x}_i$) from the previous generation and make an attempt to create its leaf with a new node at the point $\mathbf{x}_i + \mathbf{\Delta}_i$. Here the random vector $\mathbf{\Delta}_i$ is uniformly distributed within $-1 \leq \Delta_{x,i} \leq 1, -1 \leq \Delta_{y,i} \leq 1, \ldots$. If among the nodes of the previous generation (excluding the parent node i) and among the nodes already created at this time step, no nodes are closer than at distance a from the point, $\mathbf{x}_i + \mathbf{\Delta}_i$, then create the leaf. If such nodes exist, abandon this attempt. Make the next attempt to create the second leaf from this node using the same rules.

2. From the rest nodes of the previous generation, choose uniformly at random nodes one by one and repeat (1) again and again until all the nodes of the previous generation will be updated.

3.   Interaction among nodes and spatial restriction

The number of new nodes N (or the total number of nodes, without any loss of generality) initially grows exponentially at initial times, i.e., $N \sim 2^t$, where time is actually generation number. After certain crossover time, t_x, the network reaches a new regime of a much slower growth. For a D-dimensional space, the number of new nodes in the second growth regime is $N(t) \sim t^D/a$. Figure 1(a) shows N versus t in a log-linear scale in the case of $D = 1$.

   If we take into account the crowding effect of all nodes in the network, the number of new nodes reaches a limit. Figure 1(b) show that, accounting for all generation the number of new nodes finally reaches a limiting value. One can estimate, $N_{tot} \sim C(t/a)^D$, where N_{tot} is the total number of nodes in the network, and we have $N_t = dN_{tot}(t)/dt \sim Dt^{D-1}/a^D$, and, in particular, $N_t \sim 1/a$ at $D = 1$. Here N_t is the number of t-generation nodes. The results of simulations for this model, which give $\overline{N}_{max} \approx 0.4/a$, for this plateau see Figure 2(a), agree with this estimate.

   If the model takes into account only the previous generation, then, $N_t = 2^t$ for $t \le t_x$. For $t \gg t_x$ we have roughly $N_t \sim (\frac{t}{a})^D$. If $t = t_x$, then $2^{t_x} \sim (\frac{t_x}{a})^D$ which leads to

$$t_x \sim \frac{D}{\ln 2} \ln(1/a) \ . \tag{1}$$

Figure 1(c) show that our results are consistent with this estimate. Note that the result, $t_x(a) = -0.34 + 1.46 \ln(1/a)$, agrees well with Eq. (1), $t_x \approx (D/\ln 2) \ln(1/a)$, since $1/\ln 2 = 1.44....$ Clearly, the time t is of the order of the diameter d of this tree (the maximum separation between two nodes in a network). So we have the logarithmic dependence of the diameter d on the total number N_{tot} of nodes in these trees for $t \ll t_x$, and the power-law dependence $d(N_{tot})$ for $t \gg t_x$, which corresponds, respectively, to the small-world and large-world network architectures.

   Populations are usually restricted by geographical boundaries, so it is natural introduce a spatial restriction into our model. If the area of the space in which the network is embedded is restricted, then the model has an extra parameter, namely the linear size of the area, L. Let the Euclidean coordinates $\mathbf{x}_i$ of all nodes in the network be within the area $-L \le x_i \le L$. If L is finite, then one may expect that the size of the tree will finally approach some limiting value. The network has even a chance to extinct if at some moment all its nodes occur in one small area. In, e.g., population biology, it is known that the smaller a population, the more susceptible it is to extinction by various causes [8]. In our simulations we use periodical boundary conditions and observe the system during 10^5 generations. Figure 2(b) demonstrates an example of the
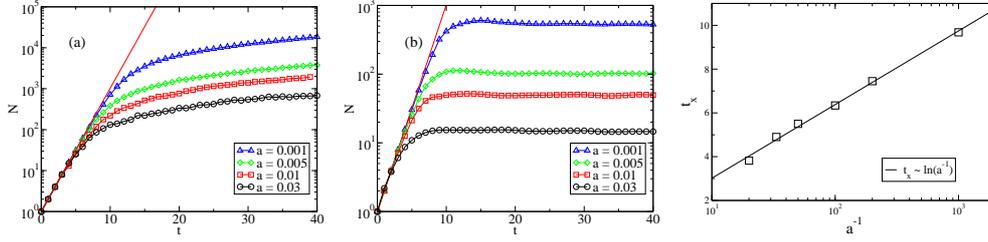
Figure 1: (Color online) Time evolution of the number of new nodes for different values of the parameter a averaged over 100 samples, taking into account only the previous generation (a) and all generations (b) for $D = 1$. Crossover time versus a^{-1} (c). Fitting gives $t_x(a) = 0.34 + 1.46ln(a^{-1})$, consistent with Eq.(1).

evolution of the network, which in this case has $a = 0.1$, $D = 1$, and $L = 1$. The network rapidly enters the fluctuation regime, in which N_t fluctuates around a mean value $\overline{N}_{max}$, and extincts before 900 time steps. After that we again introduced a root and restarted the process.

We analysed the extinction for L in the range $1 \leq L \leq 80$ and investigated the minimum values of the parameter a where extinction events happen. One can see that the extinction event only occurs for some small values of the ratio L/a, for high values of nodes' density. On the $(a/2, L/2)$ diagram, Figure 2(c), the boundary separating the extinction and non-extinction regions is a monotonously growing curve $L(a)$. Here 2 is the maximum distance between two nodes branched from the same "old" node.

4.   Conclusions

The cooperative branching model accounts for the effect of overcrowding of nodes in which the branching process is determined by the relative position of nodes in space. The number of nodes in the network grows exponentially in the initial period, and, after some crossover time $t_x \sim \ln(1/a)$ for small a, in a slow (power-law) growth. We have demonstrated that the embedding of the network in a restricted area sets limits to growth and can result in complete extinction. This simple model schematically describe real evolution processes in biology and demonstrate the transition from an explosive to gradual evolution accompanied by a dramatic change of the network structure.
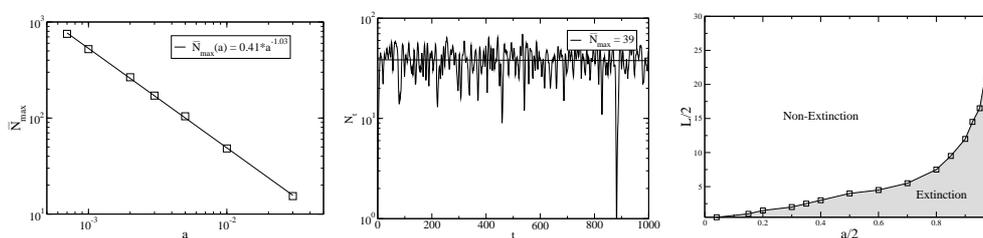
Figure 2: (a) Log-log plot of $\overline{N}_{max}$ versus a in which newborn nodes cannot be closer than at distance a from any of existing nodes. The straight line has slope -1. (b) Evolution of the number of new nodes for a single realization in one-dimension, $L = 1$ and $a = 0.1$. (c) The extinction and non-extinction regions for the network embedded in the $(-L, L)$ interval during 10^5 generations.

Acknowledgements

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