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FRACTAL MODELING OF SCALE-FREE NETWORKS IN BIOLOGY

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ABSTRACT

Scale-free networks are copious in nature and are present in diverse systems such as the nervous system of the human body, the World Wide Web and the chemical network of a cell. Developmental models simulate the spatial – temporal development of a complex system. The system described in this paper combines the advantages of a L – systems into a single system with extensive modeling flexibility using fractals. The new system includes the ability to specify dynamic hierarchies as part of the specification. The developmental models used to generate a scale-free topology are stochastic, that is they create networks in which the nodes appear to be randomly connected to each other. Here we propose a simple model that generates scale-free networks in a deterministic fashion.

Keywords*: Fractals, Networks, Scale-free networks, Scaling, L- Systems.*

1. INTRODUCTION

A fractal is an object or quantity that displays self-similarity, in a somewhat technical sense, on all scales. The object need not exhibit exactly the same structure at all scales, but the same "type" of structures must appear on all scales. Benoit Mandelbrot, a French mathematician says that a fractal is "a rough or fragmented geometric shape that can be split into parts, each of which is (at least approximately) a reduced-size copy of the whole."[4] The term "fractal" means "broken" or "fractured" according to the Latin word *fractus.* Fractal objects and processes are said to display 'Self-invariant' (Self-similar or Self-affine) properties [7]. A mathematical fractal is based on an equation that undergoes iteration, a form of feedback based on recursion and they are useful in the field of medicine [5]. Fractal structures do not have a single length scale, while fractal processes (time-series) cannot be characterized by a single-time scale [11].

The emergence of order in natural systems is a constant source of fascination and stimulation for the biological sciences. Many systems around us display rather complex topologies, that often seem random and unpredictable [12]. In particular, many of these systems form complex networks, whose vertices are the elements of the system and edges represent the interactions between them. For example, living systems form a huge genetic network, whose vertices are proteins, the edges representing the chemical interactions between them [8]. Similarly, a large network is formed by the nervous system, whose vertices are the nerve cells, connected by axons [6].

The high interest in understanding the topology of complex networks has resulted in the development of a considerable number of network models. Most of these are based on two mechanisms: incremental growth and preferential attachment [1, 2]. Incremental growth captures the fact that networks are assembled through the addition of new nodes to the system, while preferential attachment encodes the hypothesis that new nodes connect with higher probability to more connected nodes. Both of these mechanisms have been supported by extensive empirical measurements [10], indicating that they are simultaneously present in many systems with scale-free network topology. Stochasticity is a common feature of all network models that generate scale-free topologies. We present such a simple model, generating a deterministic scale-free network using a hierarchical construction and that naturally leads to a power-law distribution, explaining the mechanism responsible for the development of the scale-free state.

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2. L-SYSTEMS

The developmental system described in this paper is strongly influenced by related work in developmental modeling using L-systems in fractals in biology. The original formulation of L-systems by Lindenmayer in 1968 was a conceptually elegant, discrete, symbolic model of development in cellular biology [3]. L-systems are a mathematical formalism proposed by the biologist Aristid Lindenmayer in 1968 as a foundation for an axiomatic theory of biological

development. More recently, L-systems have found several applications in computer graphics (Smith 1984; Prusinkiewicz and Hanan 1989; Prusinkiewicz and Lindenmayer 1991). Two principal areas include generation of fractals and realistic modeling of plants. Central to L-systems, is the notion of rewriting, where the basic idea is to define complex objects by successively replacing parts of a simple object using a set of rewriting rules or productions. The rewriting can be carried out recursively.

Aristid Lindenmayer's work introduced a new type of string rewriting mechanism, subsequently termed L-systems. The essential difference between Chomsky grammars and L-systems lies in the method of applying productions. In Chomsky grammars productions are applied sequentially, whereas in L-systems they are applied in parallel, replacing simultaneously all letters in a given word. This difference reflects the biological motivation of L-systems. Productions are intended to capture cell divisions in multicellular organisms, where many divisions may occur at the same time. Lindenmayer systems is developed as a tool in biology. Certain fractals (Koch curve, Koch islands, Peano curves) can also be expressed using this formalism where as we model it for the cells development. The following diagram depicts the development of an L-System. (Figure 1)

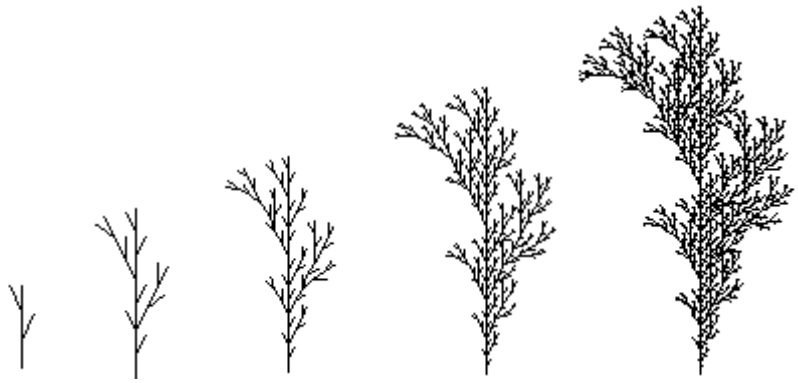

Fig. 1 Development model of the L-System showing the first five steps of the iterative process.

A number of cellular models of development have been proposed. The cellular model of Fleischer and Barr [9] modeled developing cells that exchanged chemicals by diffusion with simple 'cell programs'. More recent work combines related cellular development models with evolution to create structures that grow into target shapes [13]. One area that these systems have difficulty in addressing is in the design of a hierarchy – a mechanism often observed in natural systems. Additionally, they are typically designed for some specific simulation or application and are not necessarily applicable to generalized development. The system described in this paper addresses these issues. The following sections describe the model in detail.

3. MODELING THE DEVELOPMENT SYSTEM

Modeling biological systems is a significant task of systems biology and mathematical biology. Computational systems biology aims to develop and use efficient algorithms, data structures, visualization and communication tools with the goal of computer modeling of biological systems. It involves the use of computer simulations of biological systems, like cellular subsystems (such as the networks of metabolites and enzymes which comprise metabolism, signal transduction pathways and gene regulatory networks) to both analyze and visualize the complex connections of these cellular processes.

Biological systems manifest many important examples of emergent properties in the complex interplay of components. Traditional study of biological systems requires reductive methods in which quantities of data are gathered by category, such as concentration over time in response to a certain stimulus. Computers are critical to analysis and modeling of these data. The goal is to create accurate real-time models of a system's response to environmental and internal stimuli, such as modeling of the cells.

3.1 Cellular model

Creating a cellular model has been a particularly challenging task of systems biology and mathematical biology. It involves the use of computer simulations of the many cellular subsystems. This paper describes a new developmental system for the dynamic simulation of biological processes.

3.2 Model Description

The construction of the proposed model follows a hierarchical rule commonly used in deterministic fractals [4, 14], is shown in Figure 2. The network is built in an iterative fashion and is repetitive and reusable.

Step 0: We start from a single node that designates the root of the graph.

Step 1: We add two more nodes, and connect each of them to the root.

Step 2: We add two units of four nodes, each unit identical to the network created in the previous iteration (step 1), and we connect each of the bottom nodes (see Figure 2) of these two units to the root. That is, the root will gain four more new links.

Step 3: We add two units of sixteen nodes each, identical to the units generated in the previous iteration, and connect all eight bottom nodes of the two new units to the root.

Step n*:* Add two units of 4^{n-1} nodes each, identical to the network created in the previous iteration (step $n-1$), and connect each of the 2^n bottom nodes of these two units to the root of the network.

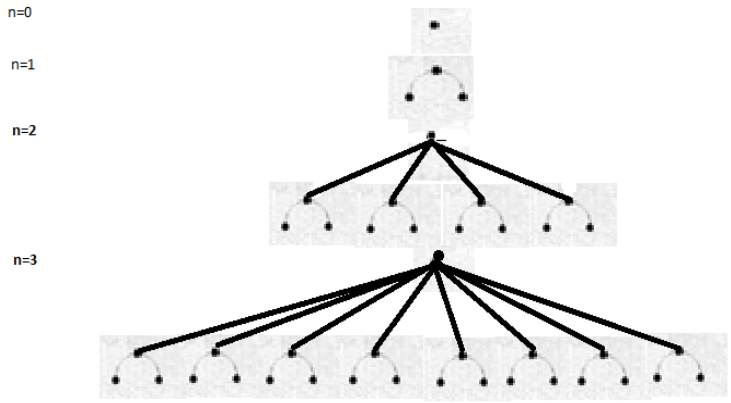

Fig. 2. Cell Development model of the deterministic scale-free network, showing the first four steps of the iterative process.

IV. CONCLUSION

The proposed system introduces a simple model that allows us to construct a deterministic scale-free network and an important feature of the model is its hierarchical representation where as at its each iteration it combines identical elements to generate a larger network. This method leads to the construction of the network naturally lends itself to immediate generalizations, leading to structures that are self – similar and allows to generate networks with different scaling exponents and connectivity. The developmental system described here unifies a number of previous L-system and cellular models based on both discrete cellular changes and continuous state development. The model successfully integrates these two modes of development, and permits complex temporal sequences not achievable using previous techniques. The hierarchical nature of the cellular developmental system allows management of complexity from the point of view of the user specifying a system model. Hierarchical ordering increases the control over structure at variety of levels. This permits a more intuitive control over creation of modeled systems.

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