Dynamics of Random Fuzzy Networks

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Genes are the fundamental unit of inheritable information. A gene is a part of the genomic sequence that encodes how to produce (synthesise) either a protein or some RNA (a gene product). Gene product synthesis is called gene expression. Not all genes are expressed at the same time. The expression of each gene is affected by the expression of other genes in a process called gene regulation. This gives rise to a network-like structure called genetic regulatory network.

Random Boolean networks were proposed by Kauffman in [] as models of genetic regulatory networks. The expression of each gene is represented using one bit: 1 represents the gene is expressed, and 0 the gene is not expressed. Let $\{0,1\}^n$ be the set of all binary words of length n. A point $x = (x_1, \ldots, x_n) \in \{0,1\}^n$ is called a *state* and $\{0,1\}^n$ is called the *state-space*. Each index $i \in I := \{1, \ldots, n\}$ is identified with a gene.

A *Boolean network* with parameters n and k, $1 \le k \le n$, consists of a family $y = \{y(i) : i \in I\}$ of subsets $y(i) = \{i_1, \ldots, i_k\} \subseteq I$, and a family $f = \{f_i : i \in I\}$ of functions $f_i : \{0,1\}^k \to \{0,1\}$. The k genes in $y(i)$ are called the *regulators* of i. Notice that the number k of regulators is the same for all genes. A *random Boolean network* is a Boolean network (y, f), where $y(i)$ and f_i are chosen randomly and independently of each other.

A *directed graph* (or *digraph*) G consists of a finite set of elements $V(G)$ called vertices (or nodes), and a set of pairs of elements $E(G) \subseteq V(G) \times V(G)$ called directed edges (or arcs). For any arc $(x, x') \in E(G)$, we say that x' is a *successor* of x. The *out-degree* of a node x is the number of successors of x. A *directed pseudoforests* is a disjoint union of digraphs where each node has out-degree one. Given a set X, every function $F : X \to X$ defines a directed pseudoforest with elements of X as vertices, and for all $x, x' \in X$, a directed edge from x to x' if $F(x) = x'$.

Similarly, every Boolean network (y, f) defines a directed pseudoforests on the state-space $\{0,1\}^n$. For each state $x = (x_1, \ldots, x_n) \in \{0,1\}^n$ and each gene $i \in I$, let $x_{y(i)} := (x_{i_1}, \ldots, x_{i_k})$. Given a fuzzy network (y, f), we define $F : \{0,1\}^n \to \{0,1\}^n$ by

$$F(x) := (f_1(x_{y(1)}), \ldots, f_n(x_{y(n)})), \quad x \in \{0,1\}^n.$$

We can identify a Boolean network (y, f) with the mapping F, and so with the directed pseudoforest on $\{0,1\}^n$.

Fuzzy networks are directed pseudoforests on the state-space of a gene regulatory network, where the expression of each gene is represented by one of $q \ge 2$ different values. A fuzzy network where $q = 2$ is precisely a Boolean network. Fuzzy networks have been recently used to study some aspects related to the differentiation of cells from the immune system [], and also to explain the importance of certain gene products associated with the development of metabolic syndrome and type 2 diabetes [].

A *fuzzy network* is a Boolean network (y, f) with $f_i : \{0, 1, \ldots, q-1\}^k \to \{0, 1, \ldots, q-1\}$, $q \ge 2$, $i \in I$, such that

$$f_i(x_{i_1}, \ldots, x_{i_k}) = (x_{i_1} \wedge f_i(x_{i_1}, \ldots, x_{i_k})) \\ \vee (\neg x_{i_1} \wedge f_i(\neg x_{i_1}, x_{i_2}, \ldots, x_{i_k})),$$

where $x \vee y := \max\{x, y\}$, $x \wedge y := \min\{x, y\}$, and $\neg x := q - 1 - x$. The number q is called the *base* of the network. Notice that in this model, the base is the same for all genes. Every fuzzy network with base q is a directed pseudoforest on $\{0, 1, \ldots, q-1\}^n$.

A random fuzzy network is a fuzzy network (y, f), where $y(i) \subseteq I$ and $f_i : \{0, 1, \ldots, q-1\}^n \to \{0, 1, \ldots, q-1\}$ are chosen randomly and independently of each other, for all $i \in I$. Random fuzzy networks are a particular class of the random networks with multiple states of Solé et. al. [].