

# Random Fuzzy Networks

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## Introduction

No model can be considered effective if fundamentally it is more complicated than what it's trying to represent. However, extreme simplification may potentially overlook important non-primary features, or even neglect the possibility to represent ambiguous or unclear observations. Therefore, achieving a balance between parsimonious and detailed models is of utmost importance for science and engineering.

Over the past few decades, random Boolean networks (RBNs) (Kauffman, 1969) have become popular models for genetic regulatory networks. This popularity is associated with the fact that RBNs are very general models. No functionality or structure is particularly assumed when constructing them. However, the Boolean idealization has been constantly criticized based on the assumption that constraining the variables of the model to have only two possible values (0 and 1) entails a loss of dynamical information in the analysis of real gene expression data.

## Boolean and Continuous Models

To randomly generate a network of dynamically interacting agents is very convenient for modeling systems where the underlying structure or performance is not yet explicitly recognized. The RBN model consists of  $n$  nodes, each of which have  $k$  randomly chosen input links, that determine its value  $\sigma_i(t)$  at time step  $t$  from the set  $\Sigma = \{0, 1\}$  where  $i = 1, \dots, n$ . At time  $t + 1$  the state  $\sigma_i(t + 1)$  is completely determined by a randomly chosen Boolean function  $f_i : \Sigma^k \rightarrow \Sigma$  from its  $k$  inputs at a previous time step, i.e.  $\sigma_i(t + 1) = f_i(\sigma_{i_1}(t), \dots, \sigma_{i_k}(t))$ . These functions can be computed via a lookup table—one for each function.

There have been several critiques for both, the Boolean idealization (Yingjun et al., 2007; Wittmann et al., 2009), and the temporal discretization (Bagley and Glass, 1996; Kappler et al., 2003) of RBNs. On the other hand, methods that justify the Boolean case have been proven effective, e.g., in Shmulevich and Zhang (2002); Karlebach (2013).

Multi-state approaches (Wuensche, 1998; Solé et al., 2000; Wittmann and Theis, 2011) emerged from the consideration that in some natural systems, the discreteness of

the actions performed at individual levels is well defined and thus, the dynamic assumption from a discrete model is fairly plausible; nevertheless, transitions from one state to another may not be sufficiently sharp for being represented by Boolean variables. Multi-valued variables that range over multiple (not only binary) states enhance the capability of the model to accurately portray gradual changes on the dynamic individual behavior of the system.

## Random Fuzzy Networks

We extended the classical Boolean model (Kauffman, 1969; Wuensche, 1998; Aldana et al., 2003; Gershenson, 2004) by using concepts from fuzzy logic (Zadeh, 1965). The number of possible states  $s$  in which a node may be, vary according to the parameter  $\phi \in [0, 1]$ . A random fuzzy network (RFN) is a RBN where the initial state of each node can take values from the set  $\Sigma = \{1, s - 2/s - 1, s - 3/s - 1, \dots, 0\}$  whereas  $s$  depends on  $\phi$ . The *fuzzyness* of the state space—and therefore of the net—can be controlled by ranging  $\phi$  along the interval  $[0, 1]$ . More specifically, when  $\phi = 0$ , we have the Boolean case where  $s = 2$ . Otherwise, if  $\phi = 1$ , then  $s \rightarrow \infty$  and states can take values from all rational numbers between zero and one. We call  $s$  the *base* of the net. Whichever base may be achieved choosing the right  $\phi$ .

Each lookup table in a RBN can be fuzzyfied, representing it in terms of combinations of *AND*, *OR*, and *NOT* and using Zadeh's operators (*MIN*, *MAX*, and  $1 - x$ , respectively). In this way, depending only on the diversity of the initial states, the same RFN can go from Boolean to continuous.

We introduce the concept of a *family of attractors*, to group attractors with the same transition schema. This concept helps us to study the state space dynamics of RFNs, regardless of its base. Specific state values are not taken into account. A family represents in which *direction* the states within an attractor change, i.e., a node state either goes *up* (represented by 1) if  $\sigma_i(t) < \sigma_i(t + 1)$ , *down* (−1) if  $\sigma_i(t) > \sigma_i(t + 1)$  or *stays* (0) if  $\sigma_i(t) = \sigma_i(t + 1)$ . All attractors on a particular family have the same length. Different attractors might belong to the same family. In particular,

steady states (point attractors) are all members of the family, e.g.,  $(0, \dots, 0)$ . Transitions space size  $(3^n)$  is fixed for all  $\phi$ .

## Preliminary Results

The extended RFN model was implemented on Java virtual laboratory RBNLab (Gershenson, 2005). We explore the state space dynamics on ensembles  $\mathbf{F}(n, k, \phi)$  of fuzzy nets with  $n = 10, 20, 100$  and  $k = 1, \dots, 5$ . Five different  $\phi$  values were chosen, giving base numbers  $s$  equals to 2, 4, 8, 16 and  $\infty$ , respectively. The number of initial states explored was arbitrarily bounded because as we let  $\phi \rightarrow 1$ , the size of the state space ( $s^n$ ) increases proportionally to the base –and it rapidly becomes intractable. We do not consider significant the results for  $n = 10$  ensembles. On the other hand, due to the potentially astronomical amount of system states for  $n = 100$  nets, results might be biased because with a high probability one does not explore a representative part of the state space.

As shown in figure 1, the average number of attractors  $\langle att \rangle$  found for  $n = 20$  RFNs, increases exponentially for  $s > 2$ . The average number of families  $\langle fam \rangle$  also increases but the growth-rate seems to be linear. For  $\langle att \rangle$ , standard deviations were maximal on continuous ( $\phi = 1$ ) ensembles, and for  $\langle fam \rangle$  they were when  $k = 5$ . We did not observe a significant increase on  $\langle fam \rangle$  when data representation goes from Boolean to continuous. This result suggests that in the process of discretization there is few loss of information (families), and hence we can assert that fuzzy networks are capable to achieve a significant degree of complexity reduction –via its  $\phi$  parameter. Therefore, we conclude by saying that the use of Boolean models for coarsely studying the discrete dynamics of real-valued observations is further supported.

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## References

Aldana, M., Coppersmith, S., and Kadanoff, L. P. (2003). Boolean dynamics with random couplings. In Kaplan, E. e. a., editor, *Perspectives and Problems in Nonlinear Science*, pages 23–89.

Bagley, R. J. and Glass, L. (1996). Counting and classifying attractors in high dimensional dynamical systems. *Journal of Theoretical Biology*, 183:269–284.

Gershenson, C. (2004). Introduction to random boolean networks. In Bedau, M. e. a., editor, *ALife IX Workshop and Tutorial Proceedings*, pages 160–173.

Gershenson, C. (2005). *RBNLab*. <http://rbn.sourceforge.net>.

Kappler, K., Edwards, R., and Glass, L. (2003). Dynamics in high-dimensional model gene networks. *Signal Processing*, 83:789–798.

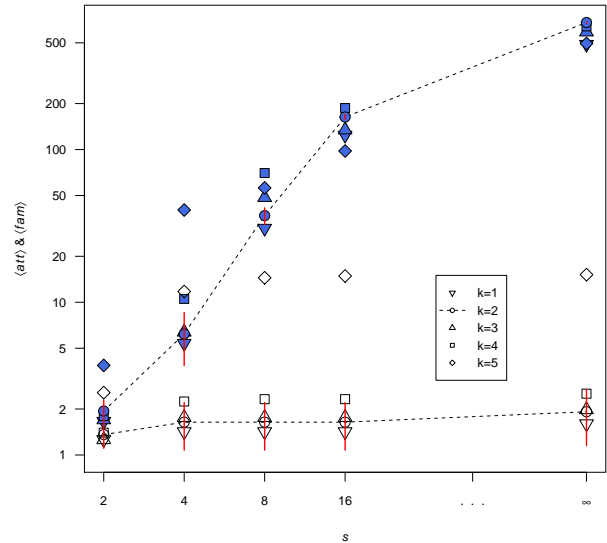


Figure 1: Average numbers of attractors  $\langle att \rangle$  and average number of families  $\langle fam \rangle$  found in ensembles with  $n = 20$ ,  $k = 1, \dots, 5$  and  $0 \leq \phi \leq 1$ . Shaded symbols represent  $\langle att \rangle$  and empty symbols represent  $\langle fam \rangle$ . Standard deviations shown only for  $k = 2$ . Note the logarithmic scales.

Karlebach, G. (2013). Inferring boolean network states from partial information. *EURASIP Journal on Bioinformatics and Systems Biology*, 2013 (11).

Kauffman, S. A. (1969). Metabolic stability and epigenesis in randomly constructed genetic nets. *Journal of Theoretical Biology*, 22:437–467.

Shmulevich, I. and Zhang, W. (2002). Binary analysis and optimization-based normalization of gene expression data. *Bioinformatics*, 18 (4):555–565.

Solé, R. V., Luque, B., and Kauffman, S. (2000). *Phase transition in random networks with multiple states*. Technical Report 00-02-011, Santa Fe Institute.

Wittmann, D. M., Krumsiek, J., Saez-Rodriguez, J., Lauffenburger, D. A., Klamt, S., and Theis, F. J. (2009). Transforming boolean models to continuous models. *BMC Syst Biol*, 3.

Wittmann, D. M. and Theis, F. J. (2011). Dynamic regimes of random fuzzy logic networks. *New Journal of Physics*, 13.

Wuensche, A. (1998). Discrete dynamical networks and their attractor basins. In Standish, R. e. a., editor, *Complex Systems '98*, pages 3–21.

Yingjun, C., Wang, P. P., and Resconi, G. (2007). Reverse engineering of the nk boolean network and its extension – fuzzy logic network. *New Mathematics and Natural Computation*, 3 (1):69–87.

Zadeh, L. A. (1965). Fuzzy sets. *Information and Control*, 8:338–353.