# Membrane Kauffman Networks

**Giuditta FRANCO**

University of Verona
Department of Computer Science
strada Le Grazie, 14
37134 Verona, Italy
E-mail: `franco@sci.univr.it`

**Abstract.** A formalization of Kauffman Boolean Networks in terms of P systems is suggested along two lines: by means of register machines and directly by means of membranes with receptors.

## 1 Introduction

Membrane systems are a discrete computational model inspired by the biological structure of living cells [8]. In [3] a simulation of Petri Nets is studied in order to 'use', by means of a suitable translation in P systems, the powerful theorems known in Petri Nets theory. In particular, a compositional encoding of PB systems [1] into Petri nets is proposed and the properties of boundedness, reachability and cyclicity are proved to be decidable.

In the same perspective it could be interesting to simulate with membranes other important computational models such as $\lambda$-calculus, von Neumann machine, cellular automata, Kauffman networks.

In this work we focus on Kauffman Boolean Networks (briefly KBN). Since they are deterministic systems with different chaotic behaviors, we think that the expressive power of P systems could help in formulating an interesting discrete characterization of chaos [7]. Moreover, KBN are an idealization of the complex genetic regulatory network that guides cell differentiation in embryonic development, where attractors are associated to alternative cell types in an organism, and the size of an attractor represents the basic cycle time of a cell type.

## 2 Some Remarks on KBN

A KBN can be seen as a dynamical system acting on the space $A^N$, with $N \in \mathbf{N}$ and $A = \{0, 1\}$, of the finite strings $s = (s_1, s_2, \ldots, s_N)$ with $s_i \in A$ for all $i = 1, \ldots, N$. The *transition map* $f : A^N \to A^N$ from one string to another is specified in terms of *block maps* $F_i : A^k \to A$, where for all $i = 1, \ldots, N$, $F_i$ is one among the possible $2^{2^k}$ boolean functions, and $k$ is the *connectivity*, that is, the maximum number of arguments for the $F_i$ functions. Formally, if $s_i^{(t)}$ is the state of the $i$-th spatial cell at time $t$, then $s_i^{(t+1)} = F_i(s_{i_1}^{(t)}, s_{i_2}^{(t)}, \ldots, s_{i_k}^{(t)})$.

Cellular automata are a special case of KBN, where $F_i$ is a unique function for all $i = 1, \ldots, N$, and its $k$ arguments are neighbors of the $i$-th spatial cell. In the particular case that $k = 1$, we find the Lindenmayer systems OL.

As a biological model KBN has the following interpretation [2]. A string $s$ represents the N genes of a cell, and each state $s_i$ indicates whether the $i$-th gene is active ($s_i = 1$) or not ($s_i = 1$) — of course, it is a simplification because a gene can be differently regulated between 0 and 1.

The action of a gene is the transcription into RNA to encode proteins, and the dynamics of a string under block maps $F_i$ models the interaction between genes in the following sense. The protein made by a gene can diffuse in the cell and bind to a DNA site near a second gene: this binding can turn the second gene on or off; in a simple example, if we have $k = 1$ and $s_j^{(t+1)} = F_j(s_i^{(t)}) = s_i^{(t)}$, then it means that a protein made by gene $i$ activates gene $j$, but in general this activation is realized among groups of (maximum $k$) genes.

From a dynamical point of view, since configurations space $A^N$ is finite, the orbits $s^{(0)} \to s^{(1)} \to \ldots$ have to be eventually periodic, therefore any string is in the basin of a periodic attractor. If we call *chaotic* a Kauffman system which has an (intuitively) unpredictable behavior, and this is connected with the exponentially growing of the size of attractors with the number $N$ of spacial-cells [9, 10], regardless the choice of the block maps only three different regimes have been identified: $k = 1$ (ordered), $k = 2$ (edge of chaos), $k = N$ (chaos). The first one is the case of Lindenmayer systems, and the last one is the case of random maps. 'Edge of chaos' means that these networks are in the ordered regime, but (experiments showed that) to increase the connectivity to $k > 2$ breaks the order in the network.

This interpretation of the behavior of networks with connectivity has been confirmed by analytical results. Nevertheless, it seems that the order found in KBN with low connectivity does not depend only on the connectivity, but also on other interesting parameters: formation of *homogeneity clusters* and *canalyzation* related to the form of the block maps [5].

## 3    Membrane Systems for KBN

In [6] several improved universality results on P systems with catalysts and evolution-communication P systems are proved by simulating computations of a register machine with a membrane system.

Therefore, here it is sufficient to note that any boolean function, in this case $F_i(s_{i_1}^{(t)}, s_{i_2}^{(t)}, \ldots, s_{i_k}^{(t)})$, is the combination of three logic operators $\wedge$, $\vee$, $\neg$ (on $k$ arguments) that can be simulated in a register machine, for example, by the following routine (we use a different notation from [6]) related to the $i$-th boolean function.

Let $R_1, \ldots, R_k, R_{k+1}$ be registers, where $R_{k+1}$ contains 1, and $R_j$ contains the value of $s_{i_j}$, with $j = 1, \ldots, k$.

$$\text{Routine } \wedge \begin{cases} 1. & test_{1,k+1} & 2, k+2 \\ 2. & test_{2,k+1} & 3, k+2 \\ \vdots & & \\ i. & test_{i,k+1} & i+1, k+2 \\ \vdots & & \\ k. & test_{k,k+1} & k+1, k+2 \\ k+1. & stop & \\ k+2. & test_{i,k+1} & k+3, k+1 \\ k+3 & dec_i & k+1 \end{cases}$$

A more biological approach to model KBN taking account of the specificity of cellular receptors (see [4]) is the following one.

In order to study the configurations (constituted by a string of 0s and 1s) of a KBN we can take trace only of its positive values in each time, that means observing the variation only of active genes. We indicate the activation of gene $i$ as the presence of symbol $s_i$ in a membrane labeled with $G$, and we represent each block map $F_i$ with a membrane which contains many copies of $s_i$ and has $k$ receptors which are specific of each argument of $F_i$.

In this system we are interested to study the evolution of the membrane $G$ by means of its configurations. The initial configuration is

$$[_s \, \{[_{F_1} \, s_1 \, ]\}_{F_1} \, \ldots \, \{[_{F_N} \, s_N \, ]\}_{F_N} \, [_G \, s_i, s_j, s_k \, ]_G]_s,$$

where $[_s \, ]_s$ is the skin membrane, $\{[\,]\}$ are membranes with specific receptors, and $s_i, s_j, s_k$ are the active genes.

The system works in such a way that all membranes $F_i$ enter the membrane $G$, there they find the active genes and their receptors recognize them, if the sound arguments are 'active' (that is have positive value) then they expel copies of $s_i$ in $G$ region, otherwise they bring the present copies of $s_i$, and go back to the skin region.

In this way we relax the constraint of sequentiality of KBN, so obtaining a more realistic model for gene activation networks. A more accurate formalization of this system will be the object of our future work.

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