Stability of Boolean Multiplex Networks

Emanuele Cozzo, Alex Arenas, Yamir Moreno*
Instituto de Biocompytación y Física de Sistemas Complejos
Universidad de Zaragoza
Zaragoza 50018, Spain

Nearly four decades ago, Random Boolean Networks (RBNs) were introduced as a way to theoretically address several scientific challenges regarding the description and dynamics of biochemical networks[1]. Since then, this framework has been successfully applied to model theoretically and computationally the biochemical and genetic control of cells[2]. RBNs consider that each gene of a genetic regulatory network is a node of a directed graph, the direction corresponding to the effect of one gene on the expression of another. Additionally, the nodes can be in one of two states: they are either *on* (1) or *off* (0) - i.e. in the case of a gene its target protein is expressed or not. The system so composed evolves at discrete time steps. At each time step nodes are updated according to a boolean rule assigned to each node that is a function of its inputs. Notwithstanding the high simplicity of RBNs models, they can capture the behavior of some real regulatory networks[3] allowing for the study of several dynamical features, above all their critical properties. However, although some coupled Boolean networks have been recently investigated[4,5], the vast majority of existent works have considered RBNs as *simplex* networks, in which a single graph is enough to represent all the interactions a given gene is involved in.

The previous description implicitly assumes that all biochemical signals are equivalent and then collapses information from different pathways. Actually, in cellular biochemical networks, many different signaling channels do actually work in parallel, i.e., the same gene or biochemical specie can be involved in a regulatory interaction, in a metabolic reaction or in another signaling pathway. Therefore, a more realistic set up will be obtained by considering the participation in different pathways as different interconnected layers of interaction, something more consistent with a multiplex network[6,7] representation (see Fig. 1). Namely, each level in the multiplex would represent the different signaling pathways or channels the element participates in.

In this work, we study the stability of Boolean networks defined at multiple topological layers. In particular, we inspect a Boolean multiplex network model, in which each gene is a node that participates in one or more layers of interactions. Moreover, we focus on the case of canalizing rules, which has been shown to be relevant to genetic networks. Boolean functions are canalizing if whenever the canalizing variable takes a given value, the canalizing one, the function always yields the same output. Capitalizing on a semi-annealed approximation, we analytically and numerically study the conditions defining the stability of the aforementioned system and show that the interplay between the different layers can be enough to stabilize different levels or the whole system even for parameter values where the sub-systems, if isolated, were unstable.

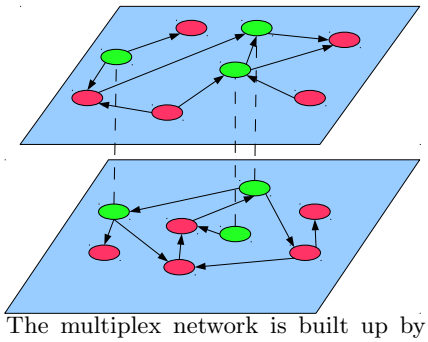

FIG. 1. The multiplex network is built up by randomly connecting N nodes per layer. With probability σ, each of the N nodes can be present in both layers. Therefore, the total number of *different nodes* in the system is $\tilde{N} = (2-\sigma)N$. In the example of the figure, the whole system is made up of $\tilde{N} = 13$ nodes, of which 3 are present in the two layers and there are 5 additional nodes per layer, therefore $N = 8$ and $\sigma = 3/8$.

* yamir.moreno@gmail.com

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