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Beyond Boolean networks, a multi-valued approach

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Boolean networks can be viewed as functions on the set of binary strings of a given length, described via logical rules. They were introduced as dynamic models into biology, in particular as logical models of intracellular regulatory networks involving genes, proteins, and metabolites. Since genes can have several modes of action, depending on their expression levels, binary variables are often not sufficiently rich, requiring the use of multi-valued networks instead. The steady state analysis of Boolean networks is computationally complex, and increasing the number of variable values beyond 2 adds substantially to this complexity. I will report on joint work with Juliana García Galofre, Ayelén García Rial, Reinhard Laubenbacher and Mercedes Pérez Millán. We propose a representation of multi-valued networks using multi-valued logic functions (which are tropical operations), providing a biologically intuitive representation of the network. We give an algorithm to compute the steady states of a multi-valued network that has a complexity that, in many cases, is essentially the same as that for the case of binary values. We provide a basic implementation of the algorithm, that uses tools to compute lattice points in rational polytopes.

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