DYNAMICS OF DISCRETE–TIME REGULATORY NETWORKS

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Abstract. Genetic regulatory networks are usually modeled by systems of coupled differential equations, and more particularly by systems of piecewise affine differential equations. Finite state models, better known as logical networks, are also used. In this talk we present a class of models of regulatory networks which may be situated in the middle of the spectrum; they present both discrete and continuous aspects. They consist of a network of units, whose states are quantified by a continuous real variable. The state of each unit in the network evolves according to a contractive transformation chosen from a finite collection of possible transformations. The particular transformation chosen at each time step depends on the state of the neighboring units. In this way we obtain a network of coupled contractions. As a first approximation to the complete description of the dynamics we shall focus on a global invariant: the dynamical complexity of the system. This is a well–studied notion in the framework of the theory of dynamical systems, and it is related to the proliferation of distinguishable temporal behaviors. The main motivation of this work is to find explicit relations between the topological structure of the regulatory network and the growth rate of the dynamical complexity. In this work we derive general upper bounds for the dynamical complexity for networks of arbitrary size, and we exhibit specific instances of constraints imposed on the complexity growth by the structure of the underlying network.

Keywords: Regulatory networks, dynamical complexity, symbolic dynamics.