

Reconstruction of Kauffman networks applying trees

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Abstract

According to Kauffman's theory the enzymes have two possible behavior in living organisms: they may be active and passive. Behaviors of enzymes at a given moment together form the actual state of the organism. The states change step by step following prescribed rules dictated by a system called Kauffman network. After a possible initial phase one previous state returns and then the whole process is systematically repeated. The repeated states together form an attractor of the organism. In microarray measurements the activity of clones is measured. In the present investigation we reduce the experimental results to two possible outputs: one clone may be active or passive likewise the enzymes themselves. The problem what we are discussing here is the reconstruction of the structure of enzymatic interactions of the living organism from microarray data. The task resembles recapitulating the whole story of a film from unordered and perhaps not complete collections of its pieces. We shall use two basic ingredients in tackling the problem. In our earlier works we used an evolutionary strategy called Tierra which was proposed by Tom Ray for investigating complex systems. Here we apply the method together with the tree-structure of clones found in our earlier statistical analysis of microarray measurements.

Keywords

Regulatory networks, Kauffman's theory, Microarrays, Tierra.

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