

Dynamical models of genetic regulatory networks

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It is nowadays generally acknowledged that the static information embedded in DNA sequences is not sufficient to understand biological complexity, and that a major challenge is that of understanding the mechanisms whereby gene expression is regulated. In this respect it is interesting to observe that an old model, that of Random Boolean Networks (RBNs for short) which is more than 40 years old, has recently proven able to describe experimental data made available by DNA microarray techniques.

The studies related to the perturbations due to gene knock-out will be reviewed, showing that they not only indicate the effectiveness of RBNs in simulating the phenomena, but that they also allow one to address a very important conceptual issue, namely that of understanding whether real cells are found in a critical state (the "edge of chaos").

In the second part of the talk it will be shown how a modification of RBNs, namely noisy random Boolean networks, allows one to describe in a unified framework the phenomena involved in cell differentiation, i.e. the process whereby stem cells, which can develop into different types, become progressively more specialized. In this work cell differentiation is described as an emergent property of a generic model of the underlying gene regulatory network, without the need to introduce ad hoc assumptions concerning the role of particular genes or of particular genetic circuits. The model helps in identifying special groups of attractors, whose composition determines the differentiation level of the system, and points to a peculiar role of cellular noise in differentiation, leading to non trivial predictions which could be subject to experimental testing.