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Modeling complex biological events by MAS

Alfredo Colosimo - Dept. SAIMLAL - Sapienza University of Rome

The Galileo's dream of using a mathematical language for simple, complete and deterministic descriptions of physical phenomena, after an impressive success in the XVIII and XIX centuries was somehow downsized, in the first half of the XX century, by the uncertainty principle and the occurrence of unpredictable atmospheric events. Moreover, any quantitative study of living objects had to face the even more intriguing problems due to their complex interactions among each other and with the environment. As a matter of fact, it was soon realized that the uncertainty levels of mathematical models based on differential equations rapidly increase with: A) the spatial resolution of the structural, descriptive information, and B) the width of the time window spanned by functional, dynamic predictions.

Since its introduction in 1970 by the British mathematician John Conway, the cellular automaton named *game of life* paved the way to an original simulation strategy of collective biological phenomena like evolution, competition, adaptation, etc. The seminal idea of the underlying algorithm was the simplified representation of the physical space through a n-dimensional grid (matrix) where the living objects (cellular automata) move and interact among each other and with the environment. In the last quarter of the XX century, the idea provided significant contributions to Bioinformatics and Biocomputing. In this frame, the present contribution deals with the heuristic power of Multi Agents Systems (M.A.S.), some non trivial members of the cellular automata class of models, and illustrates their efficiency and flexibility in the simulation of:

- the influence of environmental force fields (e.g. electromagnetic or gravitational) on the morphofunctional phenotypic changes occurring in cellular populations;
- the mechanisms of information processing in artificial neural networks and their dependence upon the (a)symmetric arrangement of links among the network's nodes.

In the former case, changes in the relative abundance of different cellular populations can be made sensitive to aggregation phenomena induced by external force fields; in the latter, the role of (randomic) rearrangements of connections between the networks nodes was investigated in model systems of minimal size.