Processes Inspired by the Functioning of Living Cells: Natural Computing Approach

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Natural Computing (cf., e.g., [12,13]) is concerned with human-designed computing inspired by nature as well as with computation taking place in nature, i.e., it investigates models, computational techniques, and computational technologies inspired by nature as well as it investigates, in terms of information processing, phenomena/processes taking place in nature.

Examples of the first strand are evolutionary, neural, molecular, and quantum computation, while examples of the second strand are investigations into the computational nature of self-assembly, the computational nature of developmental processes and the computational nature of biochemical reactions. Obviously, the two research strands are not disjoint.

A computational understanding of the functioning of the living cell is one of the research topics from the second strand. A motivation for this research is nicely formulated by Richard Dawkins, a world leading expert in evolutionary biology: "If you want to understand life, don't think about vibrant throbbing gels and oozes, think about information technology", cf. [4].

We view this functioning in terms of formal processes resulting from interactions between individual reactions, where these interactions are driven by two mechanisms, facilitation and inhibition: reactions may (through their products) facilitate or inhibit each other.

We present a formal framework for the investigation of processes resulting from these interactions. We provide the motivation by explicitly stating a number of assumptions that hold for these interactive processes, and we point out that these assumptions are very different from assumptions underlying traditional models of computation.

The central formal model of our framework, reaction systems (cf. [1,5,10]), follows the philosophy of processes outlined above, and moreover:

(1) it takes into account the basic bioenergetics (flow of energy) of the living cell,
(2) it abstracts from various technicalities of biochemical reactions to the extent that it becomes a qualitative rather than a quantitative model, and

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(3) it takes into account the fact that the living cell is an open system and so its behavior (expressed by formal processes) is influenced by its environment.

Our full formal framework (cf. [1,5]) contains also models that are extensions of the basic model of reaction systems. The research themes investigated within this framework are motivated either by biological considerations or by the need to understand the underlying computations. Some examples of these themes are:

– the notion of time in reaction systems, cf. [11],
– formation of modules in biological systems, cf. [9,16],
– understanding decay and its influence on interactive processes, cf. [3],
– how to include in our framework quantitative aspects of processes in living cells, cf. [1,5,9,11],
– static and dynamic causalities, cf. [2],
– the nature of state transitions in reaction systems, cf. [6,14,8,15].

We (hope to) demonstrate that the framework of reaction systems is:

(i) well motivated by and relevant for biological considerations, and
(ii) novel and attractive from the theory of computation point of view.

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