

Natural Computing, Informatics, and Models of the Functioning of Living Cells

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Natural Computing is an interdisciplinary research field that investigates human-designed computing inspired by nature as well as computation taking place in nature, i.e., it investigates models, computational techniques, and computational technologies inspired by nature as well as it investigates phenomena/processes taking place in nature in terms of information processing.

We are now witnessing exciting interactions between Informatics and the Natural Sciences. While the Natural Sciences are rapidly absorbing notions, techniques, and methodologies intrinsic to information processing, Informatics is adapting and extending its traditional notion of computation, and computational techniques, to account for computation taking place in nature around us. Natural Computing is an important catalyst for this two-way interaction.

One of research areas of Natural Computing is a computational understanding of the functioning of the living cell. We view this functioning in terms of formal processes resulting from interactions between (a huge number of) individual reactions. These interactions are driven by two mechanisms, facilitation and inhibition: reactions may (through their products) facilitate or inhibit each other.

In our lectures we present a formal framework for the investigation of these interactions. We motivate this framework by explicitly stating a number of assumptions that hold for processes resulting from these interactions, and we point out that these assumptions are very different from the ones underlying traditional models of computation. We discuss some basic properties of these processes, and demonstrate how to capture and analyse, in our formal framework, some notions related to cell biology and biochemistry.

The main (first) lecture gives an overview of this research area while the following lectures discuss specific research topics which are motivated by biological considerations as well as by the need to understand the underlying computations. The models we discuss turned out to be novel and attractive from the theory of computation point of view - this is extensively discussed throughout the lectures.

The lectures are of a tutorial style and self-contained. In particular, no prior knowledge of biochemistry or cell biology is required.

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