Conformon P Systems and Topology of Information Flow

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The ten years young field of Membrane Computing saw, in between other things, the definition of a number of formal models of computation all sharing a well defined topological structure, locality of interaction and parallel processing [10, 6, 1]. These models allowed us to broaden our understanding of computation. Now, for instance, we know that the simple passage of symbols from one compartment to another in P systems with symport/antiport is sufficient to compute [9], that conformon P systems with either positive or negative values have similar computational power [4], that dissolution can play an important role in the computing power of P systems with active membranes [8], etc.

All these results told us a lot about *how* to perform computation. One important question that often went unanswered is *why* a certain model of P system could or could not compute a specific set of numbers. The answer to this *why* if from the one hand would be an abstract answer (because it would not immediately link a formal model with the biological reality that inspired it or with possible implementations) from the other hand it would be a deep answer. This answer would allow us to understand more fundamental features that have to be present in a formal system in order to compute, it would allow us to classify different formal systems in a uniform way, it would possibly give us new tools to prove the computational power and other properties of different kinds of systems, etc.

Recently a way to answer this *why*, using the topology of information flow, has been suggested [3, 5, 6, 7] In this paper we survey the links between topology of information flow and conformon P systems. At the same time we show how a similar answer could be given for other formal models of computations (P systems and not). The given directions of research and open problems are meant to inspire further developments in this line of research.

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