Networks of splicing processors with evaluation sets as optimization problems solvers

Sandra Gómez-Canaval [a], Victor Mitrana [a,b,*], José Ramón Sánchez-Couso [a]

[a] Department of Information Systems, University College of Computer Science Polytechnic University of Madrid, Crta. de Valencia km. 7 - 28031 Madrid, Spain
[b] Faculty of Mathematics and Computer Science, University of Bucharest, Str. Academiei 14, 010014, Bucharest, Romania

A R T I C L E   I N F O

A B S T R A C T

In this paper we consider a new highly parallel and distributed bio-inspired computational model having its underlying structure an undirected graph whose nodes are processors that use the splicing operation on the data they are processing. They communicate with each other via a protocol based on the compatibility between their accepting values with respect to some predefined evaluation sets and the values of the data computed by a valuation mapping. Here we use the valuation mapping from a quantitative perspective, hence this model might be more suitable to solve some specific hard optimization problems in a more efficient and succinct way. In the aim of supporting this possibility, we propose an algorithm based on these networks able to efficiently solve an **NP**-hard combinatorial problem, namely the 0/1 knapsack problem. We prove that the computation time of the network solving an instance of the problem is linear. Surprisingly enough, the size of the network is very small, only four nodes are sufficient and the topology of the network may be chosen as chain, ring or complete graph. Furthermore, the evaluation sets and the sets of compatible values associated with the nodes as well as the valuation mapping remain unchanged for all instances of the same size. This result suggests that this model is suitable to address optimization problems where quantitative conditions have a relevant role.

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1. Introduction

Bio-inspired computational models are theoretically able to solve hard problems in an efficient manner by abstracting, from a computational point of view, the way in which nature evolves. Networks of bio-inspired processors is one of the well known bio-inspired family of highly parallel and distributed computational models based on the string processing. Networks of bio-inspired processors resemble other models of computation with different origins: *evolutionary systems* inspired by the evolution of cell populations [10], *tissue-like P systems* in the membrane computing area [21], *networks of parallel language processors* as a formal languages generating device [8], *flow-based programming* a well-known programming paradigm, distributed computing using mobile programs, etc.

Informally speaking, such a network can be defined as a graph whose nodes host processors performing bio-inspired operations on the strings contained in the corresponding node. Every node has filters that block some strings from being sent out and/or receiving in. A network of bio-inspired processors alternates processing and communication steps, until a

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* Corresponding authors.
  E-mail addresses: sgomez@etsisi.upm.es (S. Gómez-Canaval), victor.mitrana@upm.es (V. Mitrana), jcouso@etsisi.upm.es (J.R. Sánchez-Couso).

predefined halting condition is fulfilled. In each processing step, all processors change simultaneously the contents of their nodes according to their associated sets of rules. In the communication step, all the strings that pass the corresponding filters are interchanged between the connected nodes.

Two main type of processors have been considered so far: evolutionary processors and splicing processors. An evolutionary processor can perform very simple operations on strings. These operations, which might be viewed as formal operations of the gene mutations in DNA molecules, consist in: delete a symbol, insert a symbol, and substitute one symbol by another. The networks with such processors, which are called networks of evolutionary processors (NEP), have been introduced in [7]. NEP has been widely investigated from a theoretical point of view: NEPs as language generating, accepting devices and problem solvers [5,7,16], characterization of the complexity classes **NP**, **P**, and **PSPACE** based on accepting NEPs [17], universal NEPs and descriptional complexity results in [18,19], etc. An early survey may be found in [20]. On the other hand, a splicing processor can perform an operation inspired from one of the basic mechanism by which genetic material is merged, namely recombination. DNA sequences are recombined under the effect of enzymatic activities. Formalizing this process as a string rewriting operation, it can be used to define computing systems. In 1987, T. Head introduced the *splicing* operation as a language theoretical approach of the recombinant behavior of DNA under the influence of restriction enzymes and ligases [12]. Roughly speaking, the main idea of the splicing operation is that two sequences are cut at specific sites, and the first substring of one sequence is pasted to the second segment of the other and vice versa. The networks with such processors, which are called networks of splicing processors (NSP), have been introduced in [15]. In [16] it was proved that NSP of constant size accept (decide) all recursively enumerable (recursive) languages, and can solve all problems from **NP** in polynomial time; also an universality result for NSP was proposed. In both cases the number of nodes (the size of the network) needed was 7. In [13], the size of NSP that can decide all languages from **NP** in polynomial time has been reduced to only 3, while the size 2 is sufficient for accepting all recursively enumerable languages.

However, quantitative aspects are essential when considering some properties of the biological phenomena. Therefore, it is necessary to consider a more flexible and general model able to take into account quantitative features. To this aim, this work introduces a new model named Network of Splicing Processors With Evaluation Sets (NSPES) in which the valuation mapping gives the exact value of a string. The new model refines the communication protocol based on polarization introduced in [2] to a new one that resembles the biological concept of the concentration gradient in a solution. Thus, the communication between two nodes is regulated by the compatibility between their accepting values with respect to some predefined evaluation sets and the values of the data computed by a valuation mapping. This new communication protocol might be interpreted as the movement of molecules or particles along a concentration gradient between two areas. We prove that NSPES are able to solve **NP**-hard optimization problems in an efficient and succinct way. This result suggests that the NSPES model is more suitable for such problems.

This work is organized as follows. In the next section we recall some previous works related to the model considered here and place our contribution in this context. In Section 3, we introduce the NSPES model. Section 4 discusses the potential of NSPES model to solve computationally hard optimization problems. In particular, we design an NSPES algorithm to solve the well-known 0/1 knapsack problem. An analysis of the time complexity of this algorithm as well as a descriptional complexity of the network is done. The paper ends with some final remarks and possible directions for further research.

2. Related work

We consider here a variant of NSP where the protocol regulating the communication steps is not based on context-conditions anymore, but on a generalization of the strategy of cooperation in the networks of polarized evolutionary processors (NPEP) introduced in [2], as the most recent model of the NEP family. More precisely, in an NPEP, all nodes are "polarized" in the sense that a sign in the set $\{-, 0, +\}$ is associated with each node of the network. We say that a node can be negative, neutral or positive. The strings that become mobile agents can navigate through the network following a protocol defined by a filtering strategy based on polarization. This strategy is an analogy to the electrical charge of particles (positive, negative or neutral) which is applied to both strings and nodes. While the polarization of a node is previously defined and fixed for the whole computation process, the polarization of every string is dynamically computed by a valuation mapping which computes the polarity of that string depending on the values assigned to its symbols. Actually, the valuation mapping does not give the exact value, but just the sign of this value. Strings migration from one node to another depends both on their polarization and the node polarization which by simplicity reasons have to be the same. Thus, the strings migration from one node to another might simulate the communication channel between the two cells. As far as the computational power of this model is concerned, NPEP has been proved to be computationally complete in two recent works [3,4]. In the model proposed here, the strategy of communication is based on the compatibility between the accepting values of the nodes with respect to some predefined evaluation sets (which replaces the node polarization) and the values of the data (which replace the data polarization) computed by a valuation mapping .

The computing model considered in this work, namely the NSPES model, is similar to some extent to the test tube distributed systems based on splicing introduced in [9]. However, there are several differences: first, the model proposed in [9] is a language generating mechanism while our model is an accepting one which can be used as a problem solver; second, NSPES uses a single splicing step, while every splicing step in [9] is actually an infinite process consisting of iterated splicing steps; third, each splicing step in an NSPES is reflexive, which means that both strings obtained in a splicing step are considered; fourth, the filters of an NSPES are based on the compatibility between the accepting values of the processors