Accepting Hybrid Networks of Evolutionary Processors

Maurice Margenstern[1] Victor Mitrana[2] Mario J. Pérez-Jiménez[3]

[1]LITA, UFR MIM, University of Metz,
Ile du Saulcy, 57045 Metz-Cedex, France,
`margens@lita.univ-metz.fr`

[2]Faculty of Mathematics and Computer Science, University of Bucharest,
Str. Academiei 14, 70109, Bucharest, Romania
and
Research Group in Mathematical Linguistics, Rovira i Virgili University,
Pça. Imperial Tarraco 1, 43005, Tarragona, Spain
`vmi@fll.urv.es`

[3]Department of Computer Science and Artificial Intelligence,
University of Seville,
`Mario.Perez@cs.us.es`

Abstract. We consider time complexity classes defined on accepting hybrid networks of evolutionary processors (AHNEP) similarly to the classical time complexity classes defined on the standard computing model of Turing machine. By definition, AHNEPs are deterministic. We prove that **NP** equals the class of languages accepted by AHNEPs in polynomial time.

1 Introduction

The origin of networks of evolutionary processors (NEPs for short) is twofold. In [5] we consider a computing model inspired by the evolution of cell populations, which might model some properties of evolving cell communities at the syntactical level. Cells are represented by words which describe their DNA sequences. Informally, at any moment of time, the evolutionary system is described by a collection of words, where each word represents one cell. Cells belong to species and their community evolves according to mutations and division which are defined by operations on words. Only those cells are accepted as surviving (correct) ones which are represented by a word in a given set of words, called the genotype space of the species. This feature parallels with the natural process of evolution.

On the other hand, a basic architecture for parallel and distributed symbolic processing, related to the Connection Machine [10] as well as the Logic Flow paradigm [6], consists of several processors, each of them being placed in a node of a virtual complete graph, which are able to handle data associated with the respective node. Each node processor acts on the local data in accordance with some predefined rules, and then local data becomes a mobile agent which can navigate in the network following a given protocol. Only such data can be communicated which can pass a filtering process. This filtering process may require to satisfy some conditions imposed by the sending processor, by the receiving processor or by both of them. All the nodes send simultaneously their data and the receiving nodes handle also simultaneously all the arriving messages, according to some strategies, see, e.g., [7, 10].

In [1](further developed in [2, 11, 3]), we modify this concept (considered in [4] from a formal language theory point of view) in the following way inspired from cell biology. Each processor placed in a node is a very simple processor, an evolutionary processor. By an evolutionary processor we mean a processor which is able to perform very simple operations, namely point mutations in a DNA sequence (insertion, deletion or substitution of a pair of nucleotides). More generally, each node may be viewed as a cell having genetic information encoded in DNA sequences which may evolve by local evolutionary events, that is point mutations. Each node is specialized just for one of these evolutionary operations. Furthermore, the data in each node is organized in the form of multisets of words (each word appears in an arbitrarily large number of copies), and all copies are processed in parallel such that all the possible events that can take place do actually take place. Obviously, the computational process described here is not exactly an evolutionary process in the Darwinian sense. But the rewriting operations we have considered might be interpreted as mutations and the filtering process might be viewed as a selection process. Recombination is missing but it was asserted that evolutionary and functional relationships between genes can be captured by taking only local mutations into consideration [12]. Furthermore, we are not concerned here with a possible biological implementation, though a matter of great importance.

In this paper, we consider time complexity classes defined on accepting hybrid networks of evolutionary processors (AHNEP) similarly to the classical time complexity classes defined on the standard computing model of Turing machine. By definition, AHNEPs are deterministic. We prove that **NP** equals the class of languages accepted by AHNEPs in polynomial time.

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