ELSEVIER

BioSystems 2217 (2003) 1–14

Bio Systems

www.elsevier.com/locate/biosystems

Simulation and verification of P systems through communicating X-machines

P. Kefalas [a,*], G. Eleftherakis [a], M. Holcombe [b], M. Gheorghe [b]

[a] Department of Computer Science, CITY College, 13 Tsimiski Street, Thessaloniki 546 24, Greece

[b] Department of Computer Science, University of Sheffield, Regent Court, 211 Portobello Street, Sheffield S1 4DP, UK

Abstract

The aim of this paper is to prove the suitability of a parallel distributed computational model, communicating X-machines, to simulate in a natural way a well established model of molecular computation, P systems, and to present some further benefits of the approach allowing us to check for some formal properties. A set of rules to transform any P system with symbol-objects into a communicating X-machine model is presented and a variation of temporal logic for X-machines is briefly discussed, which facilitates model checking of desired properties of the system. Finally, the benefits resulting from the transformation are discussed.

Keywords: X-machines; P systems; Cell modelling

1. Introduction

In the last years attempts have been made to devise computational models in the form of generative devices like P systems (Paun, 2000, 2002), inspired by bio-chemical mechanisms occurring in live cells, splicing systems (Paun et al., 1998), expressing transformations defined upon DNA strands (more information on these subjects may be found at http://psystems.disco.unimib.it/ and http://www.wi.leidenuniv.nl/~pier/dna.html, respectively). New computational paradigms of modelling concurrent systems' behaviour such as Gamma (Banatre and Le Metayer, 1990) or Cham (Berry and Boudol, 1992), inspired by chemical reactions developing in parallel, were introduced in the field of concurrent programming. Experiments have been made in order to show how DNA strands may be used as a massive parallel computer to solving well-known hard problems (Adleman, 1994). All these models, paradigms or experiments rely on some bio-chemical facts in approaching new ways of computing either at some abstract level or in a more practical manner. There are, on the other hand, computational models like random grammars, Boolean networks (Kauffman, 1993), developed to express bio-chemical reactions occurring at the cell level, or X-machines, utilised to model metabolic pathways (Holcombe, 2001), or the behaviour of bee colonies (Gheorghe et al., 2001). The important role of generative models has been emphasised in the context of analysis of the emergence of functional adaptive systems (Kauffman, 1993).

The need for developing complementary models (Clark and Paton, 1998) as well as for the use of general universal models, such as Turing machines

* Corresponding author. Tel.: +30-310-275575; fax: +30-310-287564.

E-mail addresses: kefalas@city.academic.gr (P. Kefalas), eleftherakis@city.academic.gr (G. Eleftherakis), m.holcombe@dcs.shef.ac.uk (M. Holcombe), m.gheorghe@dcs.shef.ac.uk (M. Gheorghe).

0303-2647/03/$ – see front matter © 2003 Published by Elsevier Science Ireland Ltd.
doi:10.1016/S0303-2647(03)00036-4