

Modelling the Dynamic Structure of Biological State-Based Systems

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Abstract

The paper discusses the modelling aspects of systems with dynamic processes and dynamic structure. A combination of models bringing together the benefits of two paradigms, Population P Systems and Communicating X-machines, is introduced. A simple case study is used in order to illustrate the potential of the combined use of the two methods.

1 Introduction

Biological systems exhibit highly dynamic processes within a very dynamic environment. The individual components which they consist of demand modelling of evolving data structures and modelling of the control over their internal changing states. In addition, the systems overall imply modelling of their configuration, including the ability to exchange messages between individual components as well as the ability to re-structure their formation over time. Examples of such systems include colonies of ants or bees, flocks of birds, cell tissues etc (Dorigo et al., 1996), (Gheorghe et al., 2001), (Stamatopoulou et al., 2005).

The complexity of such systems is due to substantial differences in attributes between their components, high computational power required for the processes within these components, non-trivial type or volume of data manipulated by these processes and finally considerable amount of communication in order to achieve coordination and collaboration. The use of a computational framework that is capable of modelling both the dynamic aspect (change) and the static aspect (data), will facilitate modelling and simulation of such complex systems.

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