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Yves Demazeau · Juan Pavón · Juan M. Corchado · Javier Bajo (Eds.)
7th International Conference on Practical Applications of Agents and Multi-Agent Systems (PAAMS 2009)

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Multiagent Systems in Expression Analysis

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Abstract. This paper presents a multiagent system for decision support in the diagnosis of leukemia patients. The core of the system is a type of agent that integrates a novel strategy based on a case-based reasoning mechanism to classify leukemia patients. This agent is a variation of the CBP agents and proposes a new model of reasoning agent, where the complex processes are modeled as external services. The agents act as coordinators of Web services that implement the four stages of the case-based reasoning cycle. The multiagent system has been implemented in a real scenario, and the classification strategy includes a novel ESOINN neuronal network and statistics methods to analyze the patient's data. The results obtained are presented within this paper and demonstrate the effectiveness of the proposed agent model, as well as the appropriateness of using multiagent systems to resolve medical problems in a distributed way.

Keywords: Multiagent Systems, Case-Based Reasoning, microarray, neuronal network, ESOINN, Case-based planning.

1 Introduction

Currently, there exist many different systems aimed to provide decision support in medical environments [11] [12]. Cancer diagnosis is a field requiring novel automated solutions and tools, able to facilitate the early detection, even prediction, of cancerous patterns. The continuous growth of techniques for obtaining cancerous samples, specifically those using microarray technologies, provides a great amount of data. Microarray has become an essential tool in genomic research, making it possible to investigate global gene in all aspects of human disease [13]. Currently, there are several kinds of microarrays such as CGH arrays [16], expression arrays [17]. Expression arrays contain information about certain genes in patient's samples. Specifically, the HG U133 plus 2.0 [17] are chips used for this kind of analysis of expression. These chips analyze the expression level of over 47.000 transcripts and variants, including 38.500 well-characterized human genes. It is comprised of more than 54.000 probe sets and 1.300.000 distinct oligonucleotide feature. The great amount of data requiring analysis makes it necessary the use of data mining techniques in order to reduce the processing time. These data have a high dimensionality and require new powerful tools. Usually, the existing systems are focused on working with very concrete problems or diseases, with low dimensionality for the data, and it is very difficult to adapt them to new contexts for diagnosis of different diseases. Nowadays, there are

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