A Knowledge Base of Biological Cascades

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Knowledge of both genes and proteins are essential to understand biological phenomena such as the signal transduction system (kinase cascades) which we are interested in. However, such information are scattered over several sources: textbooks, papers and databases. Papers and biological data will be available sufficiently at database services. We should consider the way to get knowledge from textbooks. Visualization is important as well. It helps understanding biological phenomena through showing relationships of proteins and genes. It inspires us with new ideas and researches.

We have developed a prototype knowledge base to study representation of biological/ biochemical knowledge. It covers cooperations of signal transductions and gene transcriptions in a cell. It is written in micro-Quixote [Yokota et al. 1993], which is a DOOD language, developed at ICOT and available in UNIX environment. The prototype system as well as micro-Quixote are available at IFS (ICOT Free Software service). Quixote proved suitable to biological knowledge representation in [Hirosawa et al. 1993] and [Tanaka 1993]. Micro-Quixote is a reduced set. Whereas, metabolic pathways are well represented in Lisp [Karp 1994].

An image of the query window and the answering window are shown in the figure 1. The behavior of the prototype system is regarded as a qualitative simulation. It shows how the cascaded protein activations and gene transcriptions are proceeded when a certain signaling ligand arrives to the surface of the cell. The system is explained in detail at [Hirosawa et al. 1994]

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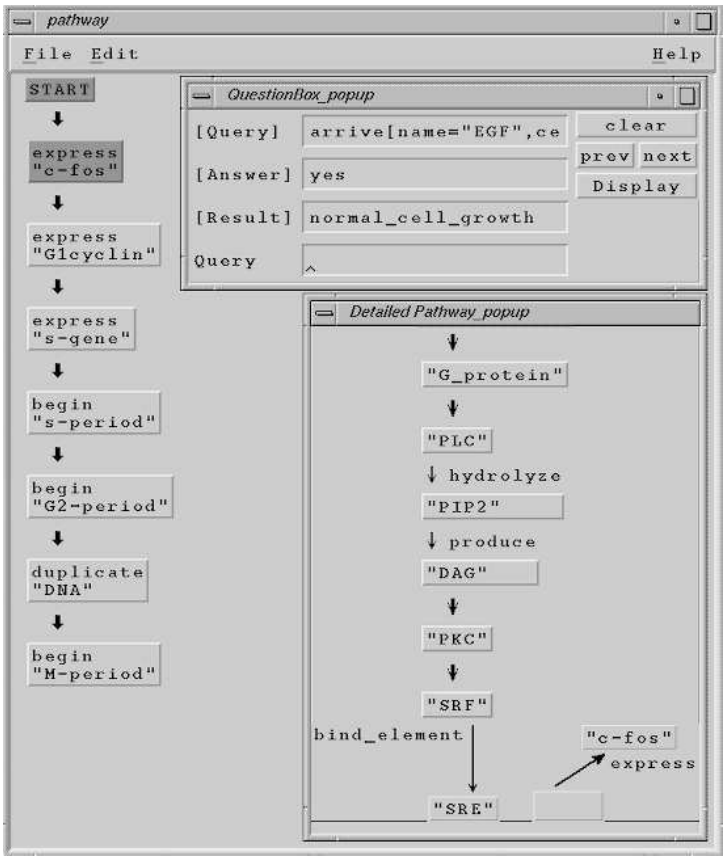

Figure 1: Window images of the prototype system

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