A virtual laboratory for simulating metabolic pathways

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Introduction

Generally, a biological system consists of interconnected processes cooperating to carry out the global behaviour of the system, by defining functional rules and relationships between the subunits. This kind of processes organization leads to a dynamic system model based on the temporal evolution of its parameters. The difficulty to establish a priori the response to new stimulus from the environment increases the complexity of this kind of systems. Among the great number of biological systems, that we can find in nature, we consider metabolic pathways, that are a collection of enzymatic processes involved in the transformation of several substances. Visiting the KEGG web site[1] it's possible to view the available pathways; we choose to study the *citric acid cyclic process* drawn in Figure 1 and we propose a virtual laboratory for simulating the behaviour of the selected pathway. In the Figure 1, we have highlighted the main activities involved in this process, by drawing black boxes labelled with a capital letter.

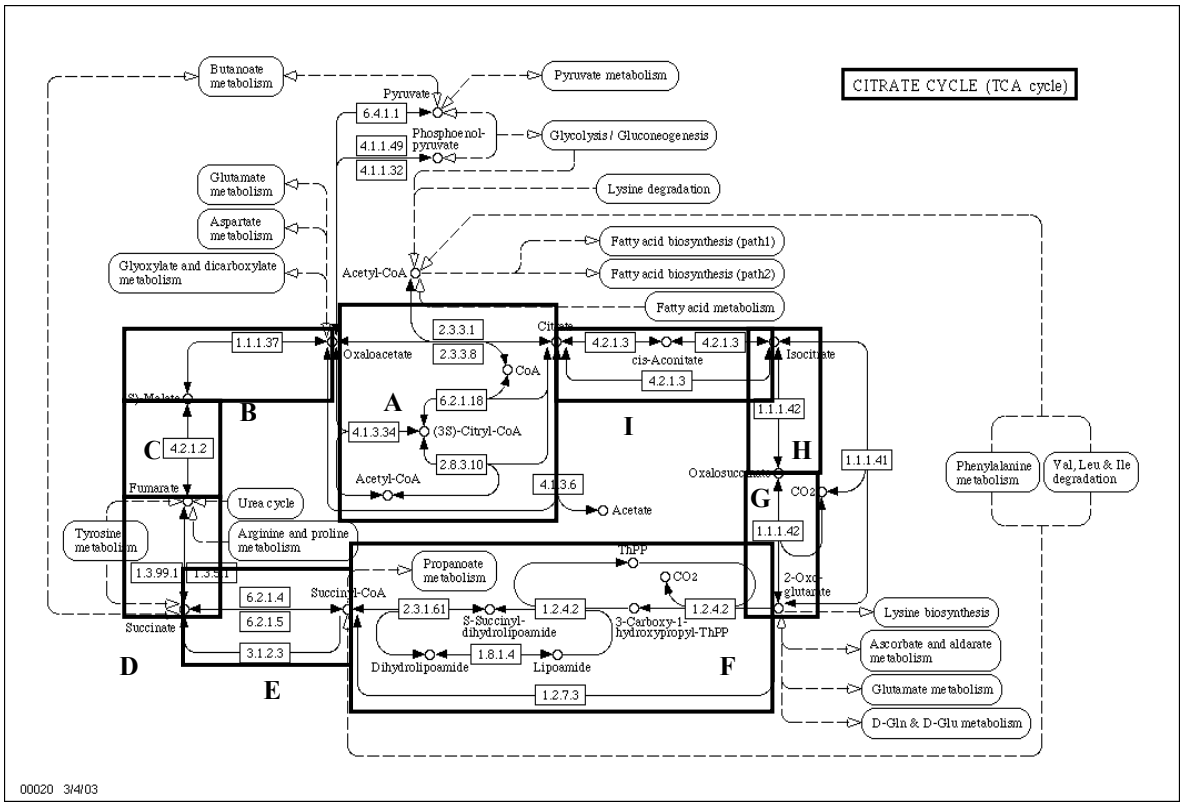

Fig. 1: Citric acid cyclic process

By simulating the behaviour of metabolic pathways, in particular the *citric acid cyclic processes*, we aim to study and analyse: 1) the global behaviour of the system; 2) the response of the system to variation of any substrate concentration; 3) the response of the system to the introduction of enzymatic inhibitors.

As Figure 1 shows, the *citric acid cyclic process* can be represented as a dynamic complex system consisting of 9 macro-activities (labelled from A to I) cooperate during the process execution. The interactions which can exist among these activities are regulated by a well-known biological protocol which represents the coordination component of the simulated dynamic system. We proposed to use workflow to model the biological process as suggested in [1] and to

[1] http\\www.genome.ad.jp/kegg/pathway.html

support the workflow execution by a MAS (Multi Agent Systems) technology [2]. The workflow model applied to the proposed example gives rise to a graphical representation as shown in Figure 2, where main activities are represented by ovals and the input/output data by rectangles. Any activity associated to specific enzyme is represented in the dynamic system by a software agent which is specialized to behaviour like the corresponding enzyme and to respect the "*social*" coordination model given by the metabolic pathway.
We highlight that the main features of MAS allow: 1) to control the system, considering several classes of constrains; 2) to establish the kind of cooperation between the agents, each one with an own goal and 3) to work in an environment where the agent society itself changes over time. The resulting virtual laboratory specialized to simulate the *citric acid cyclic processes*, in the future will be extend to other metabolic pathways. We aim to compare our work to other virtual laboratories proposed in literature, especially to Cellulat: a virtual laboratory for the modelling of the signalling pathway [3].

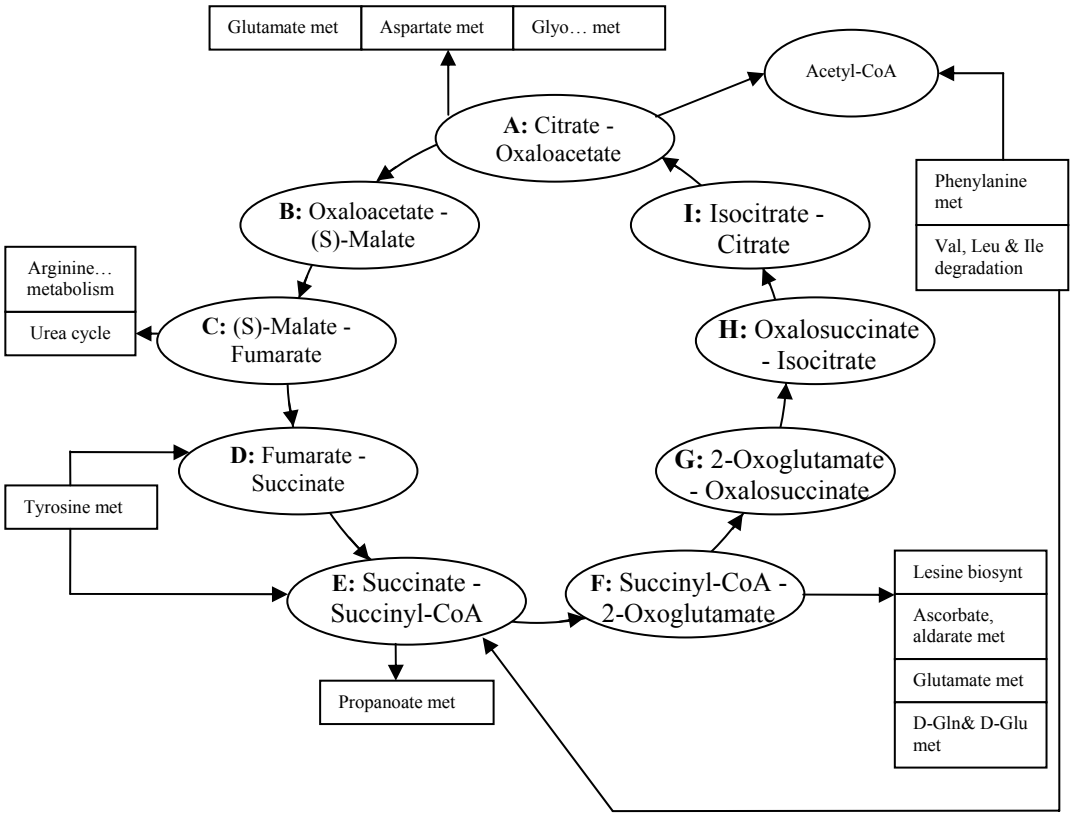

Fig. 2: Workflow model of citric acid cycle

References

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