Modeling of Human Red Blood Cell Using the E-CELL Simulation System

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In this work, we try to model and simulate human red blood cell using E-CELL system, a generic software for simulation of cellular processes [1]. Human red blood cell has been well-studied in last three decades, and extensive biochemical data on its enzymes and metabolites have been accumulated [2].

The cell uptakes glucose from the environment and processes it through the glycolysis pathway, generating ATP molecules for other cellular metabolism. The ATP molecules are consumed mostly for cations transport in order to keep the cell's electroneutrality and osmotic balance. The cell also has several other pathways such as nucleotide metabolism and pentose phosphate pathway (Fig. 1).

The model we have constructed using E-CELL contains 44 reactions and 43 intermediates. Kinetics of the most enzymatic reactions are modeled using various types of Michealis-Menten equations (Phosphoglucoisomerase, Triose phosphate isomerase, Adenine phosphoribosyl transferase, etc.).

Kinetics of other enzymatic reactions such as 6-Phosphogluconate dehydrogenase Glutathione reductase and Transaldolase is modeled as Ordered Bi-Ter system and Ping-Pong Bi-Bi system, respectively.

Other reactions use kinetic equations specific to the reaction (ex, Hexokinase, Pyruvate kinase, etc.), nine of which are membrane transportation.

Kinetic parameters of all the reactions are based on experimental data in the literature [2, 4]. We then compare behavior of the simulated model cell with that of the real red blood cell observed in laboratory experiments. We also compare our model with other computer models [3, 4, 5, 6, 7].

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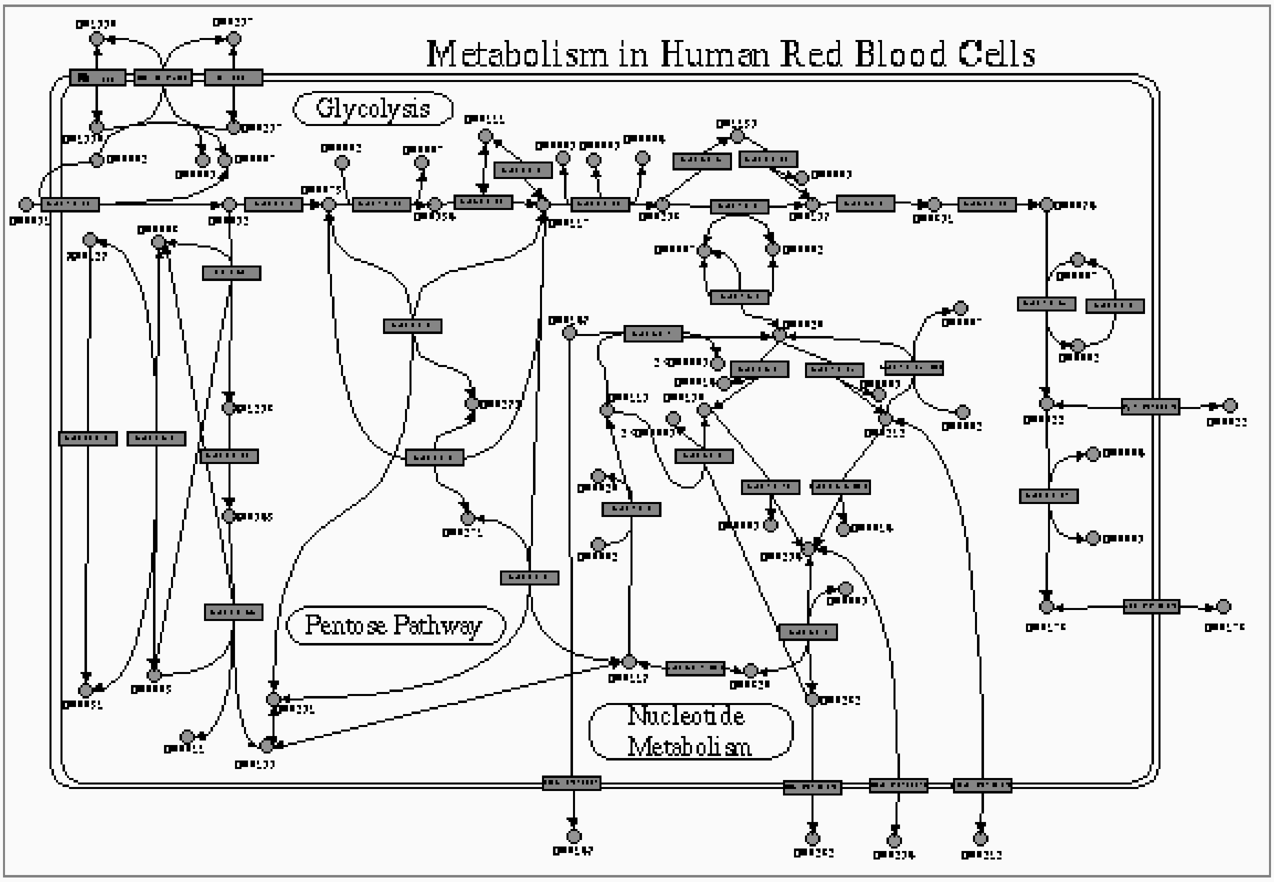

Figure 1: Metabolim in Human Red Blood Cell.

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