E-CELL Project: Towards Whole Cell Simulation

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E-CELL Project (http://www.e-cell.org) was launched in 1996 at Keio University in order to model and simulate various cellular processes with the ultimate goal of simulating the cell as a whole. E-CELL System, a generic software package we have developed, enables us to model not only metabolic pathways but also other higher-order cellular processes such as protein synthesis and signal transduction.

Using the system, we have successfully constructed a virtual cell with 127 genes sufficient for ``self-support'' (ref. Science 284:5411 p80-81). The gene set was selected from the genome of Mycoplasma genitalium, and the metabolisms include transcription, translation, membrane transport, the glycolysis pathway for energy production, and the phospholipid biosynthesis pathway for membrane structure.

We are presently constructing the following cell models: (1) human erythrocyte, (2) E. coli signal transduction for chemotaxis, (3) gene expression network in E. coli lactose operon, and (4) human mitochondria.

The basic model of a human erythrocyte has been completed. All of the parameters, such as the kinetic constants, are based on experimental data available in published literature. With ample nutrition, this "virtual" erythrocyte reaches a steady state, and its metabolite concentrations in the steady state are comparable with those in real mammalian erythrocytes reported by laboratory experiments. We are currently conducting in silico experiments on our erythrocyte model by artificially hindering its enzymatic activities. Hereditary anemia is known to be largely due to deficiency of enzymes such as hexokinase, G6PDH, phosphofructokinase, and pyruvate kinase. E-CELL offers a convenient and utile means for studying the cellular metabolism of anemic patients.