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An SBML-based Metabolic Pathway Reconstruction System

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Biochemical pathways such as metabolic, regulatory, or signal transduction pathways can be viewed as a complicated network of interactions among molecular species in the cell. As the amount of pathway information for various organisms is increasing very rapidly, performing various analyses on the full network of pathways for even multiple organisms can be possible. To do this, developing an integrated database for storing and analyzing pathway information is becoming a critical issue. However, integrating and analyzing these networks are not easy because of the nature of the existing pathway databases, which are often heterogeneous, incomplete, and/or inconsistent. To solve this problem, *SBML(Systems Biology Markup Language)*, a computer-readable format for representing various biochemical pathways, has been adopted by the most of the SW packages in systems biology. We developed an *SBML-based Biochemical Pathway Database System (SPDBS)* that supports (1) efficient integration of the heterogeneous and distributed pathway databases, (2) prediction of the metabolic pathways for a given (non-annotated) genome sequence, (3) dynamic visualization/simulation of the pathways, (4) abstraction of complex pathway networks into a simple one, (5) imports/exports of SBML documents for the simulation and/or exchange of the biochemical pathways in various applications. To evaluate the system, we applied the system to the construction of pathways from its genome sequences. For the *E. coli* genome sequence, SPDBS estimates the same metabolic pathways as the original well-known *E. coli* pathway.