Deductive Calculation Library for KEGG Pathway Simulation

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Abstract

KEGG, Kyoto Encyclopedia of Genes and Genomes, project consists of three types of data, pathways, hierarchies, and binary relations, that are used to represent biological knowledge. We present here a C++ library for efficient calculation of possible pathways from binary relations. In practice, the library is used to calculate metabolic pathways from the substrate-product relations of enzymes stored in the LIGAND chemical database for enzyme reactions. The library consists of three modules, the calculation module that is a core part of the library written as an extension of the relational operations, the reaction agent module that converts real chemical reactions to generalized binary relations, and the interface module that accepts deductive operations.

1 Introduction

With the expansion of genome sequencing data and resulting gene catalogs, it will become necessary to compare and analyze the whole biological systems between various organisms in terms of the interactions amongst molecules and genes. KEGG database[1] has been developed, first, for computerizing current knowledge of metabolic pathways and, second, for correlating the gene catalogs determined by genome sequencing projects with all the enzymes on all known pathways. In addition, KEGG aims at deducing pathways from the gene catalog, namely, calculating reaction pathways from a given set of enzymes. For this purpose all the enzymatic reactions stored in LIGAND[2] database are being converted to binary relations of substrates and products.

In the pathway analysis, deductive searching is important for finding alternative paths. For example, when correlating the gene catalog with the known metabolic pathways, it is often the case that the path is interrupted because of missing enzymes. We have been experimenting this path computation by the CORAL deductive database [3]. However, it is an inefficient system requiring a lot of computation time even for the deduction from a small number of relations. Because we plan to make the path computation capabilities publicly available under KEGG, we have decided to develop a much more efficient and convenient system.

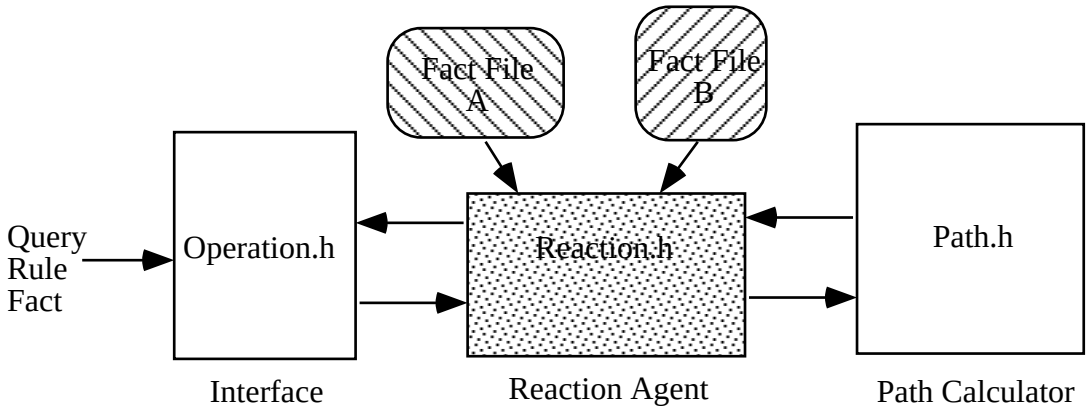

Figure 1: A schematic view of Deductive Pathway Calculation Library system.

2 Method and System

The Deductive Pathway Calculation Library, which works efficiently for deductive calculations from binary relations, has been developed. The library consists of three modules, a calculation module which forms a core part of the library written as an extension of the relational operations, a module for reaction agent which converts actual enzyme reactions to generalized binary relations, and an interface module which accepts deductive operations from the user. Figure 1 shows a schematic view of this library system.

When the user asks a request like the following example:

difference(path(S,P,l,Org1), path(S,P,l,Org2))

which designates that the difference of reaction pathways from substrate S to product P with path length l between two organisms, *Org1* and *Org2*, is to be calculated. The interface module parses the request and passes it to the reaction agent by generating sets of relational operations. The agent module converts reactions into binary relations in order for efficient calculation by, what we call, the partial join operation, which is an extension of the standard join operation.

Acknowledgment

This work was supported in part by a Grant-in-Aid for Scientific Research on Priority Areas from the Ministry of Education, Science, Sports and Culture of Japan. The computation time was provided by the Supercomputer Laboratory, Institute for Chemical Research, Kyoto University.

References

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