A Knowledge Base for Searching and Browsing Metabolic Pathways

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Abstract

We developed a knowledge base for searching and browsing metabolic pathways. Using this system, we can retrieve various pathways related to genetic diseases, chemical compounds, and enzymes.

1 Introduction

Metabolism is a complex system of the chemical reactions that take place in living cells. These reactions are catalyzed by hundreds of enzymes working in reaction chains, which we call metabolic pathways, so that the product of one reaction is the substrate for the next.

Although a large amount of knowledge about metabolism has been obtained by biological experiments, it cannot be accessed via computers and used for simulating metabolic pathways. It is necessary to check several databases, such as LIGAND, PIR and PDB, and even read many papers to simulate metabolic pathways.

The main purpose of this work is to develop a knowledge base system with graphical interface for simulating interaction between proteins. Therefore we considered enzymes (proteins), instead of ligands, as elements of pathways. With this system, biologists can ask the information about metabolism, such as

- whether there is an alternative pathway in case that the given enzyme is deficient or altered, and
- which enzyme or pathway relates to the given disease.

2 System and Methods

We exploited LIGAND database[1] as data for the system. LIGAND is an enzyme database based on "Enzyme Nomenclature." It has many cross references to PIR, PDB and OMIM. It also contains various information about ligands. As well as keyword search by enzyme, chemical and disease names, the system constructs metabolic pathways or enzyme network based on the chemical reactions described in LIGAND by making the product of one reaction to be the substrate for the next.

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System: First, we designed the ASN.1 specification for LIGAND and converted the database into the specification, which allows portability among various platforms. Next, we built a system for searching metabolic pathways of the enzymes in the database. We also developed a graphical interface for keyword search and browsing pathways using Vibrant library, which also provides portability. All the system are written in C and built on a Sun workstation with X window environment. Fig. 1 shows a query window of the system.

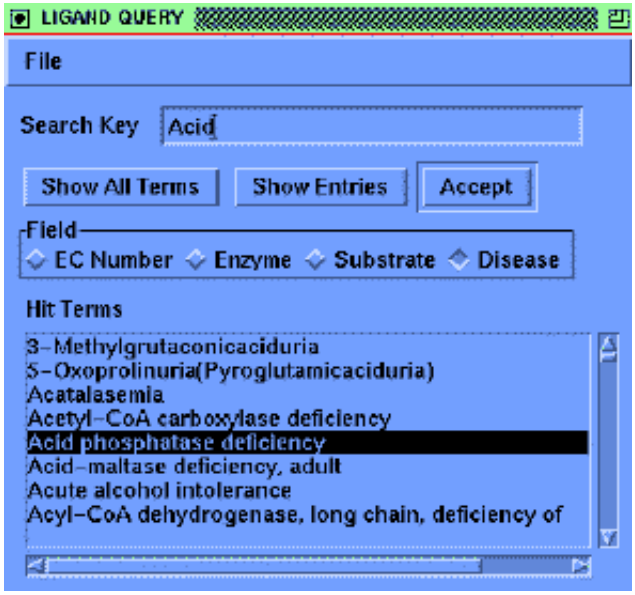

Figure 1: A query window of the system

3 Conclusions and Future Works

We developed a tool for searching and browsing metabolic pathways from the enzyme database LIGAND. This system can be adapted to not only metabolic pathways but also other pathways such as signal transduction, because the elements of all those pathways are proteins.

Since this is a first step for building a knowledge base for metabolic pathways, there are many future works that include:

- adopting deductive database techniques to search metabolic pathways with various conditions, for instance, existence of inhibitors, cofactors and effectors,
- searching an alternative pathway using a deductive database technique such as query relaxation.

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References

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