Construction of Molecular Interaction Database and Searching for Similar Pathways

Shuichi Kawashima shuichi@kuicr.kyoto-u.ac.jp
Toshiaki Katayama katayama@kuicr.kyoto-u.ac.jp
Minoru Kanehisa kanehisa@kuicr.kyoto-u.ac.jp

Institute for Chemical Research, Kyoto University
Gokasho, Uji, Kyoto 611, Japan

Abstract

We have developed a database named BRITE, which contains knowledge of interacting molecules and/or genes concerning cell cycle and early development. Here, we report an overview of the database and the method of automatic search for functionally common sub-pathways between two biological pathways in BRITE.

1 Introduction

While the majority of existing molecular biology databases focus on representing the information about DNA, RNA or protein sequence and/or structure, there are few cases that are suitable for the representation of regulatory networks in various biological processes. We have constructed a knowledge base BRITE (Biomolecular Relations in Information Transmission and Expression) concerning molecular interactions that form regulatory networks in living organisms [2]. In BRITE, each entry consists of one molecular interaction in the form of a binary relation, associated reference information and cross references to other molecular databases.

We consider that this type of knowledge base would lead to a new research area for analysis of biological networks. As a first step , we report here an automatic search for functionally common sub-pathways between two biological pathways which consist of data in BRITE.

2 System and Method

Originally, molecular interaction data concerning only cell cycle controls were accumulated in BRITE. We are going to collect data on various biological processes. Now BRITE contains data about cell cycle of *S.cerevisiae*, *S.pombe* and *H.sapiens* and on early development of *D.melanogaster*. The core section of each entry in BRITE is RELATION, which describes about a molecular interaction in style of binary relation. RELATION section consists of three lines; FROM for regulating molecule, TO for regulated molecule and MESSAGE for relation such as activate or suppress. Since these data are maintained as a flat-file and organized in the DBGET system, the user can easily retrieve entries in BRITE through clickable maps implemented on WWW server (Figure 1).

In order to find functionally similar sub-pathways in maps of BRITE automatically, we employed a method similar to the one utilized for recognizing common structural fragments among chemical compounds [1]. By regarding each molecule and relation in a map as a vertex and edge, respectively, pathway in BRITE is represented as a graph. Because the method introduces relations among all molecules whether they exist or not in the database, the graph representing pathway is defined as an

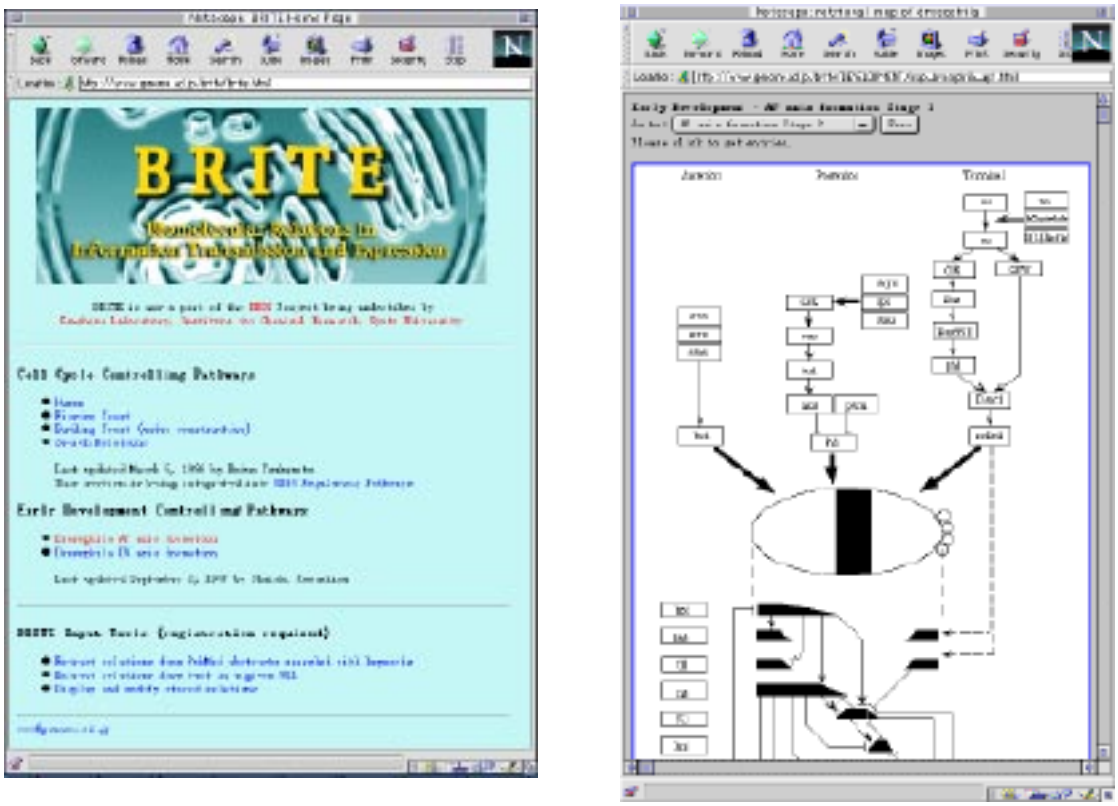

Figure 1: BRITE home page and map example

edge-weighted complete graph. Then we construct a docking graph from two edge-weighted complete graphs. Searching for an edge-weighted maximal common subgraph for the two complete graphs is equivalent to searching for a clique (complete subgraph of graph) in this docking graph.

3 Accessing the Database

The BRITE database is available through the GenomeNet WWW service at the following address: http://www.genome.ad.jp/brite/brite.html

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