A Taxonomy Database System for Managing Multimedia Contents

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Abstract

We developed a taxonomy database system for managing multimedia contents . The system is accessible from remote users through World-Wide Web and is implemented in SQL programming and CGI (Common Gateway Interface) scripts of World-Wide Web.

1   Introduction

Recently, many species have been investigated by biologists in advancements such as Human Genome Projects and Bioinformatics. The advancements reflect the topology of the taxonomic trees restructures repeatedly in recognizing topological mismatches between the taxonomic and the phylogenetic trees. The taxonomic trees are appeared in biological dictionaries and are useful in constructing and classifying DNA-sequence data at the international DNA data banks. However, the taxonomy databases have been constructed in loosely-coupled environments; therefore, they are inconsistent with each other. Moreover, the names of the taxonomic and the phylogenetic trees are difficult to understand without contents such as images and documents. In this paper, we will present a taxonomy database system for managing the multimedia contents using both database and WWW servers.
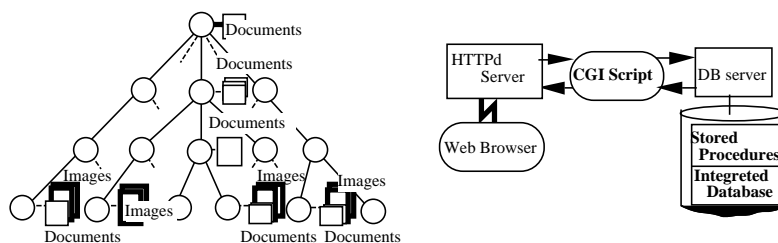
2   System Overview

Figure 1: The taxonomy database.   Figure 2: WWW and database servers.

The taxonomy database system can integrate and manage the continuously enlarging biological taxonomy databases which contain approximately 100,000 tuples. The height of the taxonomic tree stored in the taxonomy databases is about 30 to 40. Each node in the tree structure can be defined as a pair of names which consists of a node name and its parent name. The tree structure shown in Figure 1 is stored as a set of pairs of names in the integrated taxonomy database.

The powerful tree search methods developed by our group can make visible to users a structure which spans both up-and-down and left-and-right for a given node. We can define the neighborhood

area inferred from any node by using the powerful tree search methods. The neighborhood area can cover several nodes made visible using the methods. If we change the given node to one of the other nodes in the area, we can find the new area defined by the change. If we repeatedly apply the methods, we can move to any area of the tree structure shown in Figure 1. Users can also search many documents, 1,500 images and DNA database in the integrated taxonomy database.

3 Accessing the Taxonomy Database

We also developed a tool to interface between the taxonomy database system and World-Wide Web which allows remote access to the integrated database over the computer networks. The tool was implemented in CGI (Common Gateway Interface) script and the program code was about 1,000 lines in size. Figure 2 shows the system framework of the tool we developed. If users access the integrated database using Web Browser , it sends a message which includes the access method to the database server. The method represented by the stored procedure is executed on the database system after the database server has received the message. The tool has an effective window interface in which the query and result windows are the same form so that it provides users with an easy interface for use in repeatedly applying the powerful tree search methods.

Figure 3: Window Interface to repeat the neighborhood searches.

The left window shown in Figure 3 illustrates the initial window to infer a neighborhood area from a given node. We can see the center window after clicking the submit button. It illustrates the execution results of the inference. The search results are shown in the menu of the window. The next query condition can be given by selecting a focused node in the menu. If we select the search button on the center window, the window interface makes us easily move to any area in the tree structure. On the other hand, if we select the contents button, the system displays images and documents as shown in the right window. Access to the taxonomy database system is available from our WWW site (http://www.its.hiroshima-cu.ac.jp/ kitakami/treedb.html). The database service using the system is still in the development stage; therefore, access is free of charge for a trial period.

Acknowledgments