

A Web Approach for Maintaining Medical Services

Kush Sehgal¹, Mr. Lokesh²

¹M. Tech Student, RIEM, Rohtak, Haryana ²HOD, CSE Dept. RIEM, Rohtak, Haryana

ABSTRACT

We want to describe the approach which automatically compose integration plans to create new information providing web services from existing web services. When framework receives a request to create a new web service, it generates a parameterized integration plan that accepts the values of the input parameters, retrieves and integrates information from relevant web services, and returns the results to the user. The emergence of large number of bioinformatics datasets on the Internet has resulted in the need for flexible and efficient approaches to integrate information from multiple bioinformatics data sources and services. Data access over the Web has made some major advances in recent years. It's moved from accessing simple text files for small guest books to moving large corporation's entire data systems online some consisting of several terabytes of data. Here we will mainly focus on reducing the response time of the generated integrate informatics Data sets and collect it in efficient matter, An interface to use data efficiently, Fast Retrieval & Collection of Data, Easy Querying, Robust and Data consistency.

I. INTRODUCTION

In the past few years the World Wide Web has experienced phenomenal growth. Not only are millions browsing the Web, but hundreds of new Web sites are added each day. Yet, despite the increasing number of Web (i.e., HTTP) servers in use. Server hardware, Web server software, and a connection to the Internet are required elements of any Web site, and they are all expensive. To generate the best possible performance for any Web site an understanding of the interrelated effects of these elements on Web server performance is vital. This thesis presents an analytical performance model of Web servers, in which the Web server and the Internet are collectively modeled as an open queuing network. Analysis of this model yields several interesting results. The emergence of large number of bioinformatics datasets on the Internet has resulted in the need for flexible and efficient approaches to integrate information from multiple bioinformatics data sources and services. Data access over the Web has made some major advances in recent years. It's moved from accessing simple text files for small guest books to moving large corporation's entire data systems online some consisting of several terabytes of data.

II. OBJECTIVE

We are describing approach to automatically compose integration plans to create new information providing web services from existing web services. When framework receives a request to create a new web service, it generates a parameterized integration plan that accepts the values of the input parameters, retrieves and integrates information from relevant web services, and returns the results to the user. The emergence of large number of bioinformatics datasets on the Internet has resulted in the need for flexible and efficient approaches to integrate information from multiple bioinformatics data sources and services. Data access over the Web has made some major advances in recent years. It's moved from accessing simple text files for small guest books to moving large corporation's entire data systems online some consisting of several terabytes of data.



We will mainly focus on:

- Reducing the response time of the generated integration plans.
- Automatic composition techniques can efficiently generate parameterized plans that integrate data from large numbers of Bioinformatics Data sets and collect it in efficient matter

Main objective of Registrar Service Model:

- **1.** Easy Accessing to Data from various datasets
- 2. Not a Baffling situation for user.
- **3.** An interface to use data efficiently.
- 4. Fast Retrieval & Collection of Data.
- **5.** Easy Querying.
- 6. Robust
- 7. Data consistency

III. PROBLEMS OF DATA MANAGEMENT IN BIOINFORMATICS

Today a bioinformatics information system typically deals with large data sets reaching a total volume of about one terabyte. The problem of managing this information is not solved satisfactorily. The difficulties in dealing with the bioinformatics data come from some of its idiosyncrasies than from its quantity:

- Data are complex to model. There are many different types of data presenting numerous relationships.
- New types of data emerge regularly: complete sequences of genomes, microarrays, interaction maps of proteins, proteomics.
- Data analysis generates new data that also have to be modeled and integrated.
- Raw data must be archived, because scientists often need to return to them to confirm computer-generated results.
- Granularity of data is rather fine, and the terabyte of bioinformatics data consists of a large number of objects.
- Data are updated very frequently, accessed intensively and exchanged very often by researchers on the internet.
- All kinds of users of users need to issue complex queries.

In addition he mention some technical issues when handling data in bioinformatics

- The volume of data grows exponentially, doubling in less than two years for the EMBL/GenBank/DDBJ database for instance.
- Data are disseminated in a myriad of different databases that are duplicated in several repositories.
- These databases have heterogeneous formats.

IV. FACTORS IN CONSIDERATION

We have considered following factors while enhancement:

- Large Regularly increasing Size of Bioinformatics Databases
- Increasing Information fields regarding bioinformatics molecules.
- Problems of Mediocre Web Services
- Complexity
- Regular Maintenance of Bioinformatics Mediocre Web Services

While designing the model I was taken the factors as follows:

Large Regular Increasing Size of Bioinformatics Databases determines the problem of Large Databases. As Bioinformatics database are regularly increasing at a high speed. So handling and processing such a large amount of information is very difficult task.



Increase in Information Fields determines that bioinformatics data sources are expanding at a huge speed as information about various different molecules are being added so fields in database are also increasing at a huge speed.

Problems of Mediocre Web Services determines the problems faced by mediocre web services. i.e. regular changes in parent web services or source web services causes the mediocre service to be changed regularly. As the mediocre service are dependent on Parent Web Services.

Complexity determines the complexity of code, i.e. how much complex the code is.

Regular Maintenance of Bioinformatics Mediocre Web Service determines the problems faced by mediocre web Services.

At the design state of this new Web Service we have tried to overcome all problems of previous Web Services.

V. RESULT AND ANALYSIS

To be able to evaluate the implementation of the enhanced web service, a sample mediocre web service was built that displays information about viruses according to their sequence number. The enhance web service uses the data from two Existing Web Services. It collects data in the form of XML and displays the information in consolidated form to the user from the both data sources.

We have described approach to automatically compose integration plans to create new information providing web services from existing web services. When framework receives a request to create a new web service, it generates a parameterized integration plan that accepts the values of the input parameters, retrieves and integrates information from relevant web services, and returns the results to the user.

The emergence of large number of bioinformatics datasets on the Internet has resulted in the need for flexible and efficient approaches to integrate information from multiple bioinformatics data sources and services. Data access over the Web has made some major advances in recent years. It's moved from accessing simple text files for small guest books to moving large corporation's entire data systems online some consisting of several terabytes of data.

REFERENCES

- [1] William M. Shui Utilizing Multiple Bioinformatics Information Sources: An XML Database Approach , Sydney, NSW 2052, Australia.
- [2] Sandeepan Banerjee A Database Platform for Bioinformatics Redwood Shores, CA, USA.
- [3] K.K.Aggarwal, Software Engineering, New Age International Publisher.
- [4] Zoe Lacroix, Terence Critchlow -Bioinformatics Managing Scientific Data 2003.
- [5] Eckman, B.A., lacroix Z. Raschid L: Optimized seamless integration of biomelocular data. In: Proceedings of 2nd IEEE International Symposium on Bioinformatics and Bioengineering (2001).
- [6] Ullman, J.: Principles of Data and Knowledge-Base Systems. Computer Sciences Press, New York (1988).
- [7] Bultan, T. Fu, X. Hull, R. Su, J.: Conversation specification: a new approach to design and analysis of e-service composition. In: Proceedings of 12th International World Wide Web Conferences (www) 2003.