Intelligent Comprehensive Web Service Portal for microRNA Information System

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Abstract. In view of the rapid development of biotechnology, as well as miRNA in the biological sciences have attracted more and more attention, inquiries on miRNA information will have good prospects. The system came into being in this environment, adapt to market demands. On the other hand, Web Service is a wildly used technology. It is with the simple page, simple operation and combined with new technologies such as Web Service technology in biotechnology can be more convenient, faster, and much more about the genetic information to enhance biological productivity in information technology, to speed up the development of biotechnology, so it has good value. In this work, we propose an integrated intelligent comprehensive Web Service portal for microRNA Information System which incorporates multiple existing microRNA information systems.

Introduction

microRNAis also known as miRNA. Due tothe important role microRNA taking in human diseases, particularly in the field of cancer and tumors , it is popular to study microRNA in biological research. However, there are more or less shortcomings and deficiencies in existing systems about microRNA on the market, as most of the system data is not complete and does not contain all of the microRNA; and most systems provide only partial information of microRNA. Meanwhile , query efficiency of most systems is very low and slow.

Therefore, the development of an integrated system of information about the microRNA meets the market demand, and has high practical value. System described in this paper will integrate existing microRNA system resources to overcome their shortcomings, improve query mechanism, speed up queries, reduce information redundancy, be combined with Web Service technology to provide a secondary development platform . So that the workers of biological field can be more convenient, faster and more comprehensive understanding of microRNA information.

Related work

Now there are many information systems about microRNA on the market, as shown in Table 1.

Table 1 available microRNA information systems

Tool Name	Internet Site
miRanda	http://www.microrna.org/
DIANA-microT	http://www.diana.pcbi.upenn.edu/
RNAhybrid	http://bibiserv.techfak.uni-bielefeld.de/rnahybrid/
PicTar	http://pictar.bio.nyu.edu/
NCBI	http://www.ncbi.nlm.nih.gov/
Flybase	http://flybase.org/
Wormbase	http://www.wormbase.org/

Although these systems are powerful, there are following shortages overall:

The information is not complete, not only the kinds of microRNA, but also the description of the nature of microRNA;

As in the area of field: PicTar only provides Species, DataSet, mRNAid and other fields; and although NCBI provides ORIGIN, GI and other fields that PicTar WEB INTERFACE lacks of, it lacks of PicTar WEB INTERFACE field;

Also in species: miRanda and TargetScan are mainly for vertebrates; Target Boost mainly is about nematodes and fruit flies; microTar mainly is used in nematodes, fruit flies and mice.

(2) Information is redundant. As PicTar WEB INTERFACE queries for the same content will be hundreds of records, of which there are just a lot of different names, and other information are the same; in the same, NCBI and other systems also hava more or less same existence issue;

(3) Information of result inquired is incomplete. Comprehensive information can not be displayed, only one piece of information, piece of a jigsaw, saw evident.

(4) Despite their huge databases storaging vast amounts of information, the user can only query part of the information, and can not obtain comprehensive information;

(5) Information inquiry inefficient ,primarily caused by query interface provided by the system . Most of systems only provide several options for users to choose, but not to enter the user's key word according to their own demands, so the results checked out are often different with that the user really needs;

(6) The system is slow. When the user submits a query, it takes a period of time to wait the system displaying the results.

For these reasons, there are feasibility and practical value to develop a microRNA portal system what is complete, efficient, fast, the least information redundant.

System Design

3.1 Data Acquisition. First, we integrate the existing systems related MicroRNA , extract their respective proprietary information based on the expertise of each system, remove duplicate information, optimize the structure of the database on the maximum extent, and ultimately get our data as following:

(1)Identify all types of microRNA: Through the investigation and analysis of the existing system, we finally summarized in the microRNA of four types, namely: "mouse" rodent specie, "vertebrate" vertebrate specie, "fly" Drosophilaspecie, "nematode" nematode specie.

(2)Obtain various types of all of the microRNA id: Through the comparison of each system, Pictar system provides the most comprehensive microRNA's id, so system mentioned in this paper is mainly to obtain data from PictarmicroRNA id system. We will gradually record the data contained in other systems but not provided by Pictar with the depth of investigation in the future.

(3) Obtain RefSeq Id, Gene ID and origin information of microRNA of "mouse", "vertebrate" specie.

In this regard , quite a good system is NCBI,US National Center for Biotechnology Information , at http://www.ncbi.nlm.nih.gov/.

4) Obtain RefSeq Id, Gene ID information of microRNA of "fly" species: Flybase (at http://flybase.org/.bin/fbidq.html) system does better in this regard, so we acquired most of the information from it.

3.2 Functional Design. The system functions include two respects:

(1) Information inquiry

This function is part of the system functional entities, as well as the interface between the system and user interaction. This function is designed primarily to draw up the ways of search and strategies. In the query, we provide two patterns: one is simple query, the user simply enter a microRNA id, and system will capture each website to search and organize information by the way of data acquisition mentioned in previous step, then present user the results in the form of table. Another is the exact queries, the user needs to enter a variety of information types, microRNA id, Gene id, etc. (of course they can be empty), then the system returns detailed information on all the

information that exactly matches the microRNA. The interface can be as similar to the search engine interface. Meanwhile, in order to improve the performance of the system, we can use some of Cache to cache data frequently accessed, and technologies such as AJAX to operate asynchronously.

(2) Combined with Web Service technology to provide a secondary development platform

Because this system basically calls to services provided by the other online system, we want to make the results of the work done by the system available to other people, so that more people involve to improve the completeness of microRNA information systems jointly and do something for the development of biological science. This system ,making the search function Web Service, will package the code that query the entered keyword into the Web Service methods, constitute a remote Web Service method to provide to external. The initial decision is to use C # language to develop Web Service components.

Conclusion

In view of the booming development of biotechnology ,and more and more attention on microRNA in the field of biological sciences, information about the query microRNA there will be a good prospect. This system comes into being in this case , complying with the demand of the market. Its simple page, simple operation processes and new technologies combined with Web Service enable workers in the field of biotechnology to understand of the genetic information more conveniently, more quickly and more comprehensively. It improves the efficiency of biological information technology workers, accelerates the development of biotechnology, so it has high practical value.

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