Development of an Integrated System for Genetic Network Analysis and Microarray Data Management

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1 Introduction

As the DNA microarray technology advances, experiment researchers need software systems for supporting and managing lots of microarray data. Moreover, they also need to construct the genetic network from those microarray data sets. For microarray data management purposes, a few LIMSS (Laboratory Information Management Systems) such as BASE [3], ARGUS [1], GeNet [6], have been announced. And only for the purpose of genetic network analysis, GNA [5] was introduced. Here we propose an integrated software system, ISMIG, for the integrated managing of microarray database and genetic network constructor. Our system can generate some feasible genetic networks with the given experimental microarray data. In this system, the microarray data set given and its corresponding genetic network can be stored in a single data entry and users can easily retrieve the genetic network from microarray data attributes and vise versa. And these data entry can be exported in XML.

2 Software Architecture

Our system consists of two parts, microarray LIMS and genetic network analyzer. LIMS module is responsible for the management of microarray data (image files and signal/noise sheet), data import, export and visualization. Also it supports various types of query processing with gene name, experiment condition and the level of data unit(project, experiment, work, shot) et al. with a backup facility.

Our genetic network module accepts the XML format metafile. After preprocessing the metafile for genetic network analysis, the network analysis module generates Boolean network model [4], Bayesian network model and Differential equation model.

Figure 1: Snapshots of ISMIG system: (a) Main window (b) Metafile viewer (c) Genetic network analyzer.
3 Discussion

Main features of this system are follows. First, this system is implemented in pure JAVA (JDK 1.4.1), so this can be easily ported on MS window system and LINUX based system. Second, metafile processing is possible. The metafile is a file composed of user-selected columns from the microarray analysis data sets. This file enables users to compare gene expressions between genes with similar gene expression patterns in different condition. Third, this system supports data backup and restoration in XML environments for the easy exchange and sharing of data among users. Finally, an integrated processing microarray data and its corresponding genetic network is possible.

This system is available via http://164.125.164.72:8080/ismig/index.html upon request by emailing. We welcome advices and comments about this system, which could be left on the Bulletin board of the above web.

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References


