Abstract

The identification and functional annotation of genes involved in the development and progression of complex diseases is a difficult and non trivial task. DNA microarrays allow generating a composite picture of the expression profile of the cell and are widely used in basic research as well as in clinical medicine and pharmacogenomics. However, to the best of our knowledge there is no freely available bioinformatics platform for multi color microarray experiments allowing an efficient storage and platform and application independent analysis.

We have developed a bioinformatics platform based on the Java 2 Enterprise Edition platform called MARS (Microarray Analysis and Retrieval System) that is MIAME (Minimum Information About a Microarray Experiment) compliant and fully integratable into the microarray workflow. The web based user interfaces allow to store information regarding the sample preparation, RNA extraction, labeling and hybridization procedure, to upload array designs, hybridization images, raw and normalized datasets, and to define experiments where the experimental design of a set of hybridizations can be annotated. The SOAP web service and the External Application Connector Interface (EACI) provide mighty interfaces for the integration of external or third party applications. An additional web application MARS-QM which is connected to MARS using the EACI was initiated. MARS-QM integrates several quality measurements performed during the microarray production as well as during the sample preparation, extraction, and hybridization process to assure high-quality data, to understand or optimize lower value data and to prove the concept of the EACI. Finally, the ability to export all the gained data into MAGE-ML allows to share the valuable results with other researchers.

Additionally to understand the function of the cell and to gain knowledge about biological pathways, their components, and the interaction between the components we have developed an interactive drawing tool called PathwayMapper that allows to model pathways, to import them from other pathway databased and map gene expression data form microarray experiments onto available pathways.

Finally, in order to avoid unauthorized access in a multi-user environment and to control user access we have developed an Authentication and Authorization System (AAS) which provides one username-password combination for all applications and allows single sign-on to increase usability. The developed AAS affords to manage authorization and authentication for any number of applications.

Summarizing, the MARS database design, state-of-the-art software technology, well designed user interface, and its powerful application interfaces provide a capable tool for storing, retrieving and analyzing multi color microarray data. The unique affiliation of using web-based and standalone applications connected to the latest powerful application server technology facilitate MARS users to transform microarray data into valuable knowledge.

Keywords: microarray database, multi color microarray experiments, MIAME, MAGE-ML, J2EE