MicroGen, a Web based system for microarray experiment management

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Motivation

Improvements of bio-nano-technologies and biomolecular techniques have led to increasing production of high-throughput experimental data. Spotted cDNA microarray is one of the most diffuse technologies, used in single research laboratories and in biotechnology service facilities. Although they are routinely performed, spotted microarray experiments are complex procedures entailing several experimental steps and actors with different technical skills and roles. During an experiment, involved actors, who can also be located in a distance, need to access and share specific experiment information according to their roles. Furthermore, complete information describing all experimental steps must be orderly collected to allow subsequent correct interpretation of experimental results. To satisfy such requirements, we developed MicroGen, a Web based system for managing information and workflow in the production pipeline of spotted microarray experiments. Our aim was to realize a multi-database system able to store all data completely characterizing different spotted microarray experiments according to the Minimum Information About Microarray Experiments (MIAME) standard, and to support the collaborative work required among multidisciplinary actors and roles involved in microarray experiment production.

Methods

MicroGen architecture is based on a multi-database structure with intuitive and user-friendly Web interface for managing microarray experiment information and workflow. The system uses MS-Access as relational database management system. The central database collecting information of each performed experiment has been designed according to the MIAME standard. Different sets of tables, closely reflecting experimental workflow, are used to store descriptions of experiment design, used samples, preparation extraction and labeling, array design, hybridization procedures and parameters, measurement information and specifications. All data regarding microarrays and clones available for spotting (i.e. type, name, identification code, and characteristics) are orderly stored in other databases, customizable according to the types of microarrays used. MicroGen core system is constituted of Active Server Page scripts, and uses Microsoft ActiveX Data Object technology and Standard Query Language to connect the database management system. It manages user requests and runs all system processing, including management of MIAME data, generation of microarray labeling files, upload and download of processed microarray images and worksheets containing quantitative image analysis data. Worksheet and image files are stored in dedicated directories of MicroGen file system, protected with opportune access privileges. MicroGen graphic user interface, implemented as Web pages using Hyper Text Markup Language and Javascripts, enables connecting distributed user Web browsers to the central Web server core system through an intranet or Internet communication network.

Results

MicroGen enables managing the workflow of spotted microarray experiments by supporting six types of user roles: the researcher who designs and requests the experiment, the spotting operator, the hybridization operator, the image processing operator, the system administrator, and the generic public user who can access the unrestricted part of the system to get information about MicroGen services. A researcher can request a specific microarray experiment by compiling the corresponding initial required MIAME information, view the progress status of requested experiments, and access all information and data results of performed experiments. During experiment definition, the system shows to the researcher clone libraries available according to the data stored in system databases. Information about the clones chosen to be spotted on experiment microarrays is saved in a MS-Excel file called "labeling file" and automatically generated by the system. Technical operators receive new experiment requests, perform the required tasks, and insert the corresponding MIAME information in MicroGen system. Produced microarray labeling files, images and quantitative experimental results are uploaded in the system and centrally orderly stored. At any time, all users involved in an experiment can verify its processing status and read all compiled MIAME information completely describing all experimental steps. Therfore, MicroGen represents a MIAME compliant information system supporting the collaborative work required to perform molecular biology microarray experiments. Through its Web interface, it enables managing workflow of spotted microarray experiments, easily collecting in a central repository results and complete MIAME information of all experimental steps and different involved actors. Collected information is easily available to all people, biologists and technicians, who take part in the experiment, even when they are located in different and geographically distributed centers.

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