Abstract

The objective of this thesis was to develop a bioinformatics platform for cancer immunogenomics which enables the classification of patients suffering from cancer based on molecular markers and gene expression profiles into clinically useful categories. Furthermore, the discovery as well as the evaluation of markers applied in cancer research should be facilitated.

Therefore we have developed a comprehensive and versatile platform consisting of the Microarray Analysis and Retrieval System (MARS) and the Tumoral MicroEnvironment Database (TME.db), which are Web based databases built on a 3-tier architecture implemented in Java 2 Enterprise Edition (J2EE). This unique combination brings about a complex data management system, which integrates public and proprietary databases, clinical data sets, and results from high-throughput screening technologies.

MARS is a MIAME compliant microarray database that enables the storage, retrieval, and analysis of multi-color microarray experiment data produced by multiple users and institutions. It covers the complete microarray workflow starting from microarray production to the concluding data analysis. By providing a Web service interface and Application Programming Interfaces (API), third party applications can connect to MARS to query data, perform high-level analysis, and finally write back the transformed data sets. The intention of TME.db is to provide researchers access to means and data particularly relevant in tumor biology and immunology, diagnosis management and the treatment of cancer patients. TME.db integrates clinical data sets and results from high-troughput screening technologies with special emphasis on phenotypical and functional data gathered using flow cytometry analysis. Furthermore, due to the integration of TME.db and MARS it is possible to directly link gene expression data stored in MARS to patients in TME.db. Since TME.db is handling sensitive patient related data, special attention has been payed on security and in this context on arising ethical, legal, and social implications to avoid that specific patients could be traced back by unauthorized people.

As it has been shown in preliminary studies, this unique combination of Web based applications and the resulting integration of microarray and flow cytometry data, clinical data sets, and proposed analysis methods provides powerful means to successfully accomplish immunogenomic studies that may ultimately help to decipher cancer related immunological questions and improve cancer diagnosis and treatment.

Keywords: microarray, tumoral microenvironment, database, cancer, immunogenomics, MIAME, J2EE