Abstract

Uncovering the functional relationship of proteins is the major challenge of the post-genomic area after the human genome has been successfully deciphered. To this end, high-throughput technologies in the form of biomolecular arrays have been developed, which are generating a wealth of data which is neither comprehensible nor useful without proper bioinformatic data management and analysis tools.

In the course of this thesis we have developed an application for the analysis of protein microarrays (PMAs), a database solution for data from tissue microarrays (TMAs) and a validation pipeline for the comparison of DNA microarray and qPCR results.

The PMA analysis application covers capture as well as reverse phase arrays and allows relative and absolute quantification of protein abundance coupled with extensive visualization of the results. It was successfully applied in an expression profiling study of apoptosis related proteins in colorectal cancer.

TAMEE, the tissue microarray management and evaluation environment covers the complete TMA workflow from production to molecular analysis and processing and evaluation of the generated images. A plug-in framework for evaluation algorithms facilitates integration of additional algorithms without any adaptations of the system.

Finally, the validation pipeline supports the confirmation of probe-assay pairs utilized in the comparison of DNA microarray and qPCR results. Application of the pipeline to mRNA expression data from cancer cell lines identified one fifth of the pairs as invalid and therefore not appropriate for comparison.

The bioinformatic solutions developed here allow researchers to extract valuable knowledge from the data produced in experiments using high-throughput technologies.

Key words: DNA microarrays, protein microarrays, tissue microarrays, qPCR, bioinformatic applications, J2EE