

4.48 Gene Expression Warehousing in Leipzig

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Microarray-based gene expression profiling is an important issue of genome research in biomedical and basic science. The Interdisciplinary Centre for Clinical Research (IZKF) in Leipzig therefore runs a core facility for microarray analysis to support multiple research groups. As a consequence of up to 500 experiments per year which produce a huge amount of valuable information data handling becomes a major problem and will limit efficient data analysis. In particular, it is often very difficult to compare and analyse data from different sets of experiments. Furthermore, linking measured gene expression with information of the experimental setup and with publicly available data, such as sequences, pathways or other complex biological information will be very helpful.

To address these problems we have started to develop a *gene expression data warehouse* for microarray data at the Interdisciplinary Centre for Bioinformatics (IZBI) Leipzig. At its core it uses a central database to uniformly collect and store microarray measurement data from many experiments. Moreover, it aims at a semantic integration of annotations,

taxonomies from public resources such as UniGene (NCBI), sequences from dbEST (NCBI) and pathways. In addition the database can be used as a platform to integrate published data from other experiments and to validate and use their result sets. Although the process of setting up and organizing a gene expression warehouse is time and effort-intensive it allows a variety of flexible analysis approaches (e.g. interactive queries, comprehensive reports, data mining, visualization of results). We will focus this project to achieve a new quality of data accessibility, analysis and cross comparison that will help to answer important questions in biomedical research.

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