Development of a Microarray Data Analysis Software (MicroArrayWare) with a Calibration Step for Automatic Selection of Optimal Analysis Methods and Parameters

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Summary:
MicroArrayWare is a tool that we developed to analyze microarray data using a set of optimal methods. There are a number of analysis methods and even more microarray analysis tools available commercially and publicly. However, those tools cannot automatically select the optimal analysis methods and parameters and thus, require users to select the analysis methods which they may not understand. In our approach, the microarray analysis workflow, which consists of preprocessing, normalization and identification of differentially expressed genes, is integrated with an additional process called calibration to select a set of optimal methods. Using this calibration process prior to data analysis, MicroArrayWare ensures high-quality data analysis at each step.

Software description:
MicroArrayWare is built as a stand alone application using Java technology. It is able to handle many projects where each project can consist of many experimental comparisons and each comparison in turn comprises of many hybridization replicates. It takes two-channel-arrays files as input and processes them to produce analysis results. The results of each analysis step are presented in graph and text formats for convenient visualization and comparison. As well known to biologists, prior to measurements, calibration or standardization should be performed. However, microarray data analysis is currently performed without incorporation of any validation data. With our microarray data analysis tool, validation data are required and calibration is performed prior to microarray data analysis. At the calibration step, validation data are required as input files. Validation data are microarray data obtained from validation experiments. The validation experiments are e.g. deficient media culture versus enriched media culture or mRNA spike-in experiments. The former experiments are designed for validation of different normalization methods and the latter experiments are suitable for differentiation of gene identification methods.

Software specification:
• Microarray data analysis with automatic selection of optimal analysis methods and parameters
• PC version (Windows), Java platform
• Email contact to obtain the software