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MicroImage as a tool for microarray image artifacts correction

Oligonucleotide single color microarrays are one of the most popular platforms used to characterize transcription profile changes induced by various chemical or physical factors. This method is based on hundreds of thousands unique 25-mer oligonucleotide probes grouped into gene specific sets. Single probes attach labeled transcripts of specific genes which quantity is proportional to the fluorescence intensity of the probe, accessed with a laser scanner. Microarray surface images obtained in such experiment often contain artifacts of various shape and size caused by either defects of the manufacturing process or impurities within target genomic material. Data processing methods often fail to exclude outlying signal values resulting from such defects which leads to artificially increased variation between replicate experiments, decreasing statistical significance of inter sample studies, or to reduced accuracy of sample classification if the experiment aims to search for factor induced genetic response signature.

In this work we present different kinds of artifacts and propose a novel detection and correction method based on signal intensities of other, unaffected replicate probes. The method was implemented as a standalone windows application with a very easy to use graphical interface allowing to process hundreds of microarray images within few minutes and visualize the analysis on various complexity steps. The usefulness of this method was evaluated by the analysis of breast cancer microarray dataset, with marked patients radiosensitivity and technical replicate data with simulated artificial noise objects.

Using common statistical methods inter-group correlation, inter-gene variance and discriminative gene analysis were performed. The overall impact of artifacts processing on sample classification accuracy was also evaluated. The results show that image artifacts correction increases dataset integrity, proving that it is possible to separate image defects from inter sample variations of biological origin and specific features of the microarray chip achieving higher quality of the analyzed data.

ACKNOWLEDGMENT:

The authors would like to thank the teams of Peter O'Neill from the Medical Research Council Radiation & Genome Stability Unit in Harwell, Michael Bonin from University of Tuebingen, Micheline Giphart-Gassler from Leiden University Medical Center and John Yarnold from The Institute of Cancer Research in Sutton for useful comments and for providing the microarray data.

This work was supported by the European Program FP6 - 036452, GENEPIlowRT and Ministry of Science and Higher Education grant no N N519 647840.