

Denis V. Volkov: Usage of ImageJ program for visualization and analysis of microarray experiments data

Abstract

Studying the gene expression profile using microarray experiments lets us explore effect of various factors such as influence of the environment, impact of chemical compound on genetic systems. It can be done, using various approaches, and visualization of differentially expressed genes is one of them. We used information of two genes' expression with two cancer cell lines (one is resistant to the drug studied and the other one is sensitive to it), which were affected by active agent (that stimulated apoptosis), inactive agent (structured analogue of the active one) and control agent (DMSO).

We suggested a method of working with such experiments using visualization. The main feature of this method is that time changes of gene expressions are taken into consideration.

In our work we used data got from microchips Affymetrix. The data was taken from free-for-all data base GEO NCBI, source - Affymetrix U133 Plus 2.0 platform. To realize the first stage we used the environment of statistical programming R, applying libraries of the Bioconductor packet. For visual analysis of gene expression profiles the ImageJ program was used: we downloaded prepared images. Every pixel of such image was matched with expression of one gene. Location of this gene was the same in different experiments. Every layer of the image was matched with profile of expression at one time point of its examination.

We wrote a script for quantative evaluation, which when clicked on a chosen pixel-gene can show the graph of changes of this gene's expression in all time points for every experiment with this gene.

While carrying this investigation out we found out with the help of visualization that out of 54675 initial genes, differential expression with certain criteria was present in 13004 genes. After the procedure of visual choice number of genes which are differentially expressed under conditions of sensitivity/resistance in response to influence studied was 109. They were analyzed and interpreted through KEGG Data Base.

As a result based on visualization we chose differentially expressed genes, most of which, are the genes taking part in the formation of cancer progression, biotransformation of xenobiotics, control of signaling ways of apoptosis.

Keywords

microarrays, differential gene expression, R-project, cell lines, visualization and data analysis

Short CV

bioinformatics and systems biology; microarray researches in biology and medicine; imaging; drug discovery based on bioinformatics approach(results of microarrays experiments); analysis of gene expression of microarray experiments in cancer research;

Administrative data

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