

Interactive Transcription Maps Over Microarray Data

Petr Krontorád, Irena Koutná, Michal Strehovský

Centre for Biomedical Image Analysis, Faculty of informatics, Masaryk University, Brno, Czech Republic

ABSTRACT

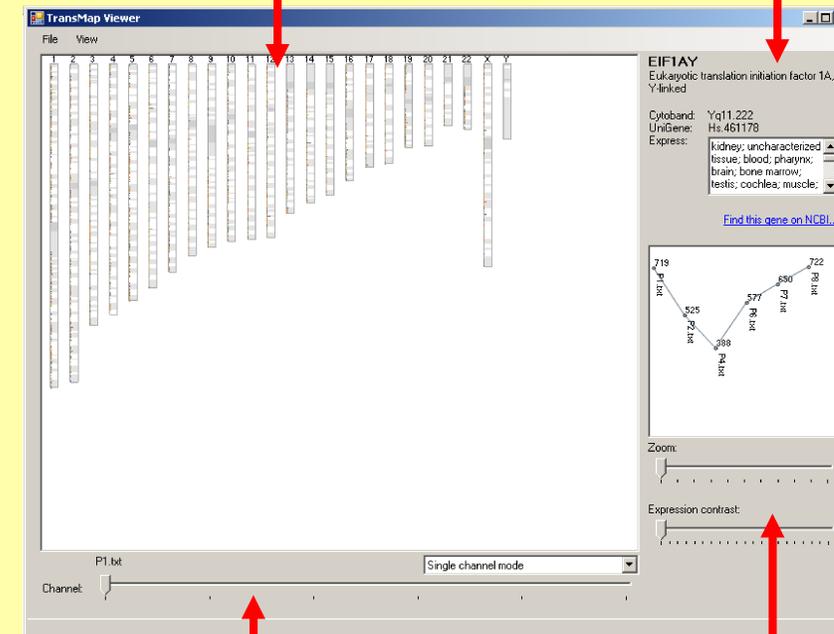
Sophisticated microarray data analysis is in general very complex problem. High level of statistical education is often needed and the results are sometimes very unclear (even if the data seems to be clear). It is very common that various statistical methods provide different results over the same data and then it is very hard problem to determine which method is correct and why. For final description of microarray experiment results it is necessary to use some statistically robust method especially when the results deal with big number of samples. But final results should come from data observations. And observations can be performed using intuitive data visualisation. Transcription maps (TM) are used to map results of gene expression analysis into individual chromosomes. Expression of each gene involved in analysis is visualised by rectangle of appropriate size (related to expression level). There are two types of TMs according to ordering of genes. The first type maps genes sequentially. Sequential ordering causes problems with spaces between genes. The second type maps genes according to their position in basepairs. TMs can be successfully used to study spatial distribution of various expression levels, groups of similarly expressed genes etc. We have enhanced TMs by adding display of various information about observed genes. This allows monitoring of spatial distribution of many features that can be found on widely used databases.

We have implemented graphical tool for interactive display of TMs. This tool allows displaying of arbitrary information for each gene. We have also implemented tool for retrieving information from internet databases to enable displaying of fresh knowledge. Every one who works with these databases knows that their content changes in time and this was one of the main reasons why we have started to implement this tool. It provides a capability to refresh custom information about genes. Together with interactive TMs tool it is possible to work with fresh data.

The target of our research is to enhance data mining features of our tool and to increase the informative capabilities of our visualization tool. Together with research in this area we are performing biological research. We are using interactive TMs for displaying of data and for observations from which possible biological findings can be estimated.

Interactive display of chromosomes

Interactive display of annotations



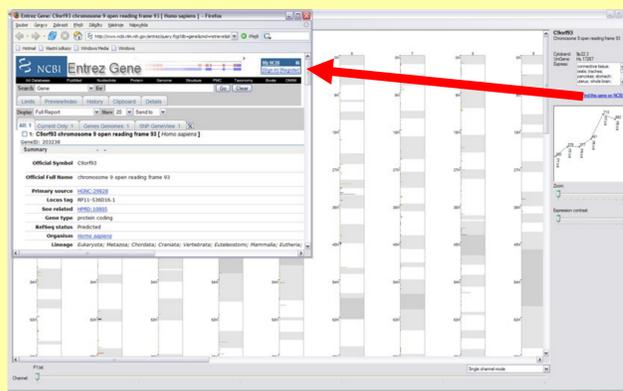
Link to NCBI database

Multiexperiment view of expression levels

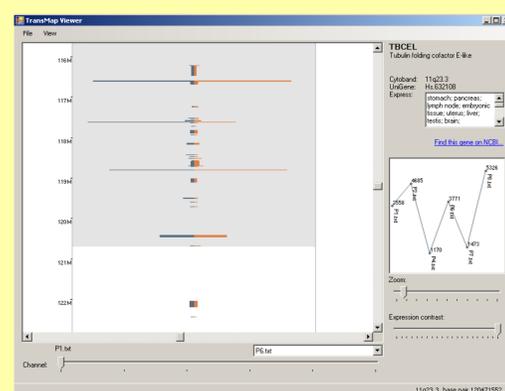
Experiment browsing

Easy to use zooming and scaling

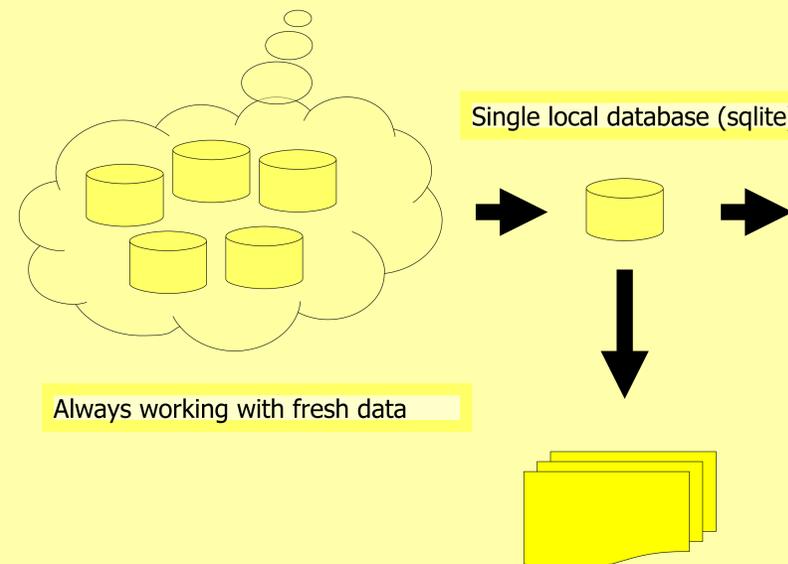
Various online databases (Gene, ...)



Very handy for gene browsing

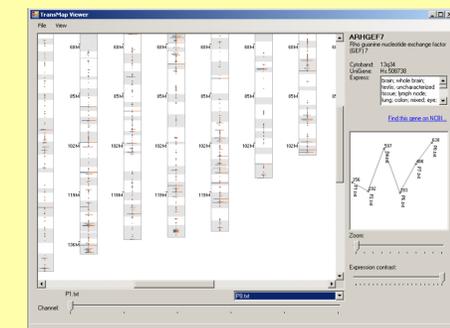


Allows detailed visual analysis (also of multiple experiments)



Always working with fresh data

Annotation files containing custom information



Information and download page
<http://genomics.migeel.sk>