

Preprocessing and Differential Analysis of a Microarray Data Set with Application in Oncology

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Abstract

Microarray technology nowadays is one of the best methods which provide us a huge data set useful in studying the genes expression. Once we have this data set we can use an automated work-flow to extract from it only the genes relevant in a molecular study and the output of this system will be a short data set containing top ranked genes. The whole work-flow has two important parts, first the preprocessing block where using an algorithm we transformed our raw data in a uniform set more relevant in a study and second the differential analysis block which extract from the preprocessed data-set only the most expressed genes. The application gives the opportunity to diagnosis faster and easier a cancer and also using statistical research it can be a good solution in treating the cancer.