Gene expression analysis of mesothelioma samples

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Motivation

Malignant mesothelioma is a fatal cancer of the pleural and peritoneal surfaces. Tumors can be subdivided into three major histologic subtypes: epithelial, mixed, and sarcomatoid. There is a strong correlation between exposure to asbestos and mesothelioma development. Currently there are limited pretreatment or prognostication strategies mainly based on histologic appearance of the tumors. Gene expression profiling represents a method to identify specific predictive factors or prognostic molecular markers. In order to disclose such markers we analized human mesothelioma samples using one channel arrays.

Methods

The necessity of identify predictor genes cancer-related leads to the development of new accurate analysis tools. In particular most gene expression profiling studies of mesothelioma have been based on relatively small sample numbers limiting their statistical power. Due to the great heterogeneity of mesothelioma samples used in this study, we were not able to retry a gene list with a statistical significance using statistical method validation as SAM. Thus the analysis was performed using a new and more helpful package, OneChannelGui, a graphical interface to Bioconductor libraries for analize data from single channel platforms. OneChannelGUI is based on limma library, which allows differential expression detection by mean of linear model analysis. Limma function was developed to fit a linear model to the expression data for each gene and makes the analysis stable even for experiments with a small number of arrays, like our study. Limma exploits Empirical Bayes and other shrinkage metods to borrow information across genes. OneChannelGui includes limma library and other functions needed to filter the genes.

Results

Our analysis shows that OneChannelGui is an effective method to identify differentially expressed genes from a set of heterogeneous data. In fact a previous statistical analysis performed on this data (i.e. SAM) did not show any differentially expressed gene. According to the reliability of OneChannelGui method, the gene list overlaps with those present in other specific publications Furthermore most of the genes obtained are classified as prognostic in previously published data obtained with larger expression data set. The overlapping between our gene list and the prognostic gene list obtained by other groups confirms the reliability of the method even in respect to eliminate the ``noisy`` derived from the starting heterogeneity of the samples. We are planning to run new analysis using the same method but starting with a large number of samples to confirm the effectiveness of OneChannelGui method.

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