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Analysis and modeling of septic shock microarray data using Singular Value Decomposition

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Abstract

Being a high throughput technique, enormous amounts of microarray data has been generated and there arises a need for more efficient techniques of analysis, in terms of speed and accuracy. Finding the differentially expressed genes based on just fold change and p-value might not extract all the vital biological signals that occur at a lower gene expression level. Besides this, numerous mathematical models have been generated to predict the clinical outcome from microarray data, while very few, if not none, aim at predicting the vital genes that are important in a disease progression. Such models help a basic researcher narrow down and concentrate on a promising set of genes which leads to the discovery of gene-based therapies. In this article, as a first objective, we have used the lesser known and used Singular Value Decomposition (SVD) technique to build a microarray data analysis tool that works with gene expression patterns and intrinsic structure of the data in an unsupervised manner. We have re-analysed a microarray data over the clinical course of Septic shock from Cazalis *et al.*, 2014 and have shown that our proposed analysis provides additional information compared to the conventional method. As a second objective, we developed a novel mathematical model that predicts a set of vital genes in the disease progression that works by generating samples in the continuum between health and disease, using a simple normal-distribution-based random number generator. We also verify that most of the predicted genes are indeed related to septic shock.

Keywords: septic shock; microarray; singular value decomposition; microarray modelling; predictive modelling

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