

Poster presentation

Gene classification for microarray data with multiple time measurements

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Background

In microarray data analysis, we considered the problem of classifying genes based on ratio of the mean gene expression levels between the control and the treatment factors measured at t fixed times. In this setting, we assume that the control and treatment responses come from two independent normal populations, and the two treatment groups are significantly different only if the ratio of the two population means is less than r_1 or greater than r_2 . We propose an approach based on the mapping of the T scores into $C = \{+1, 0, -1\}$, where $+1$ is the value when the t -score is greater than the upper critical point, -1 if it is less than the lower critical point, and 0 otherwise. Misclassification probability under small replications is given and the method is demonstrated using a microarray data.