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Classifying Microarray Gene Expression Cancer Data Using Statistical Feature Selection and Machine Learning Methods

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Abstract

Objective: A breast microarray data is a repository of thousands of gene expressions with different strengths of each cancer cell. It is necessary to detect the genes which are responsible for cancer growth. The proposed work aims to identify a statistical test for extracting the differentially expressed genes from a microarray gene expression and a suitable classifier for classifying the gene as diseased and control genes. Method: Cancerous genes are identified by six statistical tests, namely Welch test, analysis of variance (ANOVA) test, Wilcoxon signed rank sum test, Kruskal–Wallis, linear model for microarray (LIMMA), and F-test using their p-values. The identified cancer genes are used to classify cancer patients using seven classifiers, namely linear discriminant analysis (LDA), K-nearest neighbor, Naïve Bayesian, linear support vector machine, support vector machine with radial basis function, C5.0, and C5.0 with boosting technique. Performance is evaluated using accuracy, sensitivity, and specificity. Result: The microarray breast cancer dataset of 32 cancer patients and 28 non-cancer patients is considered in the experiment. Microarray contains 25,575 numbers of genes for each patient. When LIMMA test is used to extract differentially expressed cancer genes and KNN is used for classification, the maximum classification accuracy 100% is obtained.



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