

عنوان مقاله:

Using Classification and K-means Methods to Predict Breast Cancer Recurrence in Gene Expression Data

محل انتشار:

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خلاصه مقاله:

Background: Breast cancer is a type of cancer that starts in the breast tissue and affects about 10% of women at different stages of their lives. In this study, we applied a new method to predict recurrence in biological networks made from gene expression data. Method: The method includes the steps such as data collection, clustering, determining differentiating genes, and classification. The eight techniques consist of random forest, support vector machine and neural network, randomforest + k-means, hidden markov model, joint mutual information, neural network + k-means and suportvector machine + k-means were implemented on 11/11/17 genes and Yoo samples. Results: Thirty genes were considered as differentiating genes which used for the classification. The results showed that random forest + k-means and random forest + k-means performance than other techniques. The two techniques including neural network + k-means and random forest + k-means performed better than other techniques in identifying high risk cases. Conclusion: Thirty of 11/11/17 genes are considered for classification that the use of clustering has improved the classification techniques .performance

کلمات کلیدی:

Classification, gene, K-means

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