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Feature selections in microarray survival data analysis using Boruta algorithm

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With the existence of microarray data in the bioinformatics and clinical areas, the following questions frequently arise for both computer and biological scientists that which genes among the thousands of genes are significantly involved in classifying cancer classes and which genes are statistically significant with respect to specific cancer pathology. This study focuses on microarray survival data where the number of covariates is greatly exceeding the number of observations. Series of analytical methodological models have been developed to identify and classify informative genes from the gene expression and microarray survival data; however, the integrity of the reported genes is still uncertain. In this regard, this study is motivated to propose a hybridized model with respect to Boruta Algorithms (BAs) and Cox Proportional Hazard model (Cox-PH), to extract and identify the highly differentially expressed genes for specific cancer pathology. A real-life data on blood cancer (lymphoma) was considered and the proposed method together with Iterative Bayesian Model Averaging (IBMA) was used to select highly expressed genes from the data. The performance of the two algorithms was tested based on the number of genes selected and the system time and it was observed that the proposed algorithm perform better than the IBMA algorithm irrespective of the criteria.

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