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Machine Learning-Based Liver Cancer Classification Using Gene Expression Microarray Data

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Mahmoud, Amena [a] ; Meraj, Syeda [b] ; Saini, Shilpa [c] ; Juneja, Sapna [c] ; Talpur, Kazim Raza [d] ; +2 authors

[a] Sophia University, Faculty of Science and Technology, Dept. of Information and Communication Sciences, Japan

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Abstract

Detecting a liver tumor early and accurately can save lives because the liver is an important and multifunctional human organ. Machine learning algorithms have recently emerged as effective tools for enhancing liver cancer categorization using gene expression microarray data. This study proposes a supervised machine learning-based approach for liver cancer diagnosis that influences gene expression profiles to achieve an accurate diagnosis. A large sample size is crucial to be obtained and leads to a precise and reliable outcome. In this research, we combine multiple datasets from the Curated Microarray (CuMiDa) Database with the same features and use machine-learning models. Random forest (RF) model, SVM model, Xgboost model, K-nearest neighbor (KNN) model, and Decision tree (DT) model, and are used as classification models for classifying liver cancer using gene expressions. The results indicate that effect size and classification accuracies increase, while variances in effect size shrink with the increase in sample size. The results reveal that the RF model has better accuracy of 96.55%. © 2024 IEEE.

Author keywords

Gene Expression Microarray Bioinformatics; Liver Cancer Classification; Machine learning

Indexed keywords

Engineering controlled terms

Bioinformatics; Classification (of information); Diagnosis; Diseases; Gene expression; Learning systems; Liver; Nearest neighbor search; Random forests; Supervised learning

Engineering uncontrolled terms

Cancer classification; Effect size; Gene expression (microarray) data; Gene expression microarray; Gene expression microarray bioinformatic; Liver cancer classification; Liver cancers; Machine-learning; Random forest modeling; Sample sizes

Engineering main heading

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