

Identification of Hepatocellular Carcinoma Using Supervised Learning Algorithms

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Abstract : Analysis of diseases integrating multi-factors increases the complexity of the problem and therefore, development of frameworks for the analysis of diseases is an issue that is currently a topic of intense research. Due to the inter-dependence of the various parameters, the use of traditional methodologies has not been very effective. Consequently, newer methodologies are being sought to deal with the problem. Supervised Learning Algorithms are commonly used for performing the prediction on previously unseen data. These algorithms are commonly used for applications in fields ranging from image analysis to protein structure and function prediction and they get trained using a known dataset to come up with a predictor model that generates reasonable predictions for the response to new data. Gene expression profiles generated by DNA analysis experiments can be quite complex since these experiments can involve hypotheses involving entire genomes. The application of well-known machine learning algorithm - Support Vector Machine - to analyze the expression levels of thousands of genes simultaneously in a timely, automated and cost effective way is thus used. The objectives to undertake the presented work are development of a methodology to identify genes relevant to Hepatocellular Carcinoma (HCC) from gene expression dataset utilizing supervised learning algorithms and statistical evaluations along with development of a predictive framework that can perform classification tasks on new, unseen data.

Keywords : artificial intelligence, biomarker, gene expression datasets, hepatocellular carcinoma, machine learning, supervised learning algorithms, support vector machine

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