



The Advances in Cancer Survival Prediction by Gene Expression Data; Using Machine Learning Approaches

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ABSTRACT

Introduction: Cancer is one of the main diseases, and accurate diagnosis of various types of malignancy is a major challenge in the world. Despite the many advances in early detection of diseases, cancer patients have a poor prognosis, and their survival rates are typically low. According to the cancer priority as an important health issue in the world that imposes mortality and costs, there is an urgent need for survival prediction strategies. This study presents the advantages of machine learning for survival prediction of cancer based on gene expression data.

Methods: This review article conducted by searching articles in scientific databases (SCOPUS & Google Scholar & Pub Med & IEEE) and e-Journal (science direct) and by using keywords such as cancer, machine learning, and gene expression data and cancer.

Results: Research in biology and medicine domain can confirm new achievements in cancer. Recently, microarray technologies have been used for gathering thousands histopathological data about the gene expression level of cells. Studies have shown the high accuracy and effectiveness of gene expression data in comparison with clinical data in survival prediction. Because of bewildering and high volume of such a data, new analytical methods must be developed to discover the distinctive signatures of gene expression in cancer tissue. Machine learning algorithms such as artificial neural networks (ANN) and support vector machine (SVM) are suitable for genomic usages. These algorithms improve the efficiency of probing and analyzing biological data in gene expression of cancer profiles and so result in accuracy of detection, diagnosis, classification, and survival prediction of cancer.

Conclusion: Accurate cancer survival prediction in delivering optimal health care for patients is important. By paying attention to capabilities of machine learning techniques in proteomics and genomics applications, developing clinical decision support systems based on these methods for analyzing gene expression data can prevent potential errors, which have caused fatigue and impatience of oncology experts in cancer survival estimation. This has resulted in providing appropriate and individualized treatments to patients according to their survival rate, thus improving the prognosis of cancers and preventing unnecessary surgical and treatment procedures, which can reduce cost.

KEYWORDS: Survival, Cancer, Gene expression, Machine learning techniques, Clinical decision support system

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