

(54) Title of the invention : DETECTION AND CLASSIFYING OF GENE EXPRESSION CANCER DATA USING DEEP LEARNING APPROACH

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(57) Abstract :
ABSTRACT DETECTION AND CLASSIFYING OF GENE EXPRESSION CANCER DATA USING DEEP LEARNING APPROACH The detection and classification of gene expression cancer data using deep learning approaches is a promising area of research. Deep learning networks are increasingly being used to model the complexity of gene expression data in order to accurately detect and classify cancer types. In order to do so, deep learning networks leverage large datasets and a range of feature selection techniques to identify the relevant gene expression relationships, which can then be used to generate a model capable of accurately classifying gene expression information. Additionally, deep learning networks are able to identify patterns and trends in gene expression data that traditional classification methods may have missed, providing more accurate results. Deep learning has demonstrated strong performance in the detection and classification of gene expression cancer data, and its potential benefits have been increasingly explored. Deep learning-based models have been developed to assess the presence of cancer in medical imaging and to determine the efficacy of drugs used in cancer treatment. Deep learning-based approaches are also being considered for the predictability of the survival rate and risk of radiation-induced trismus in cancer patients. Taken together, these advances indicate the potential of deep learning to facilitate improved detection and classification of gene expression cancer data. Recent advances in deep learning approaches have enabled the development and evaluation of highly accurate models for both detection and classification of gene expression cancer data. In particular, convolutional neural networks (CNNs) have been the basis for developing novel detection approaches for gene expression cancer datasets. In addition, artificial neural networks (ANNs) such as Deep Belief Networks (DBNs), Multilayer Perceptrons (MLPs) and Recurrent Neural Networks (RNNs) have been used to improve classification performance for gene expression cancer datasets. Various data pre-processing and feature engineering techniques have also been developed for deep learning models used for the detection and classification of gene expression cancer data. These include feature selection, feature extraction, and data normalization strategies, which help to improve the accuracy of the deep learning models. Deep learning methods for the detection and classification of gene expression cancer data have demonstrated improved performance in comparison to traditional machine learning methods. Furthermore, by combining deep learning models with data pre-processing and feature engineering approaches, high accuracy results can be achieved. With the advancement of deep learning techniques and continued improvements in pre-processing strategies, these methods can be used to more effectively diagnose and predict cancer progression in patients.

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