

عنوان مقاله:

Diagnosis and Classifying Cancer Subtypes Based On Gene Expression Data Using Cost-Sensitive Hybrid Deep Learning

محل انتشار:

اولین کنگره بین المللی هوش مصنوعی در علوم پزشکی (سال: 1402)

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خلاصه مقاله:

Accurately identifying cancer subgroups is crucial for effective diagnosis and prediction of cancer outcomes. Deep-learning methods have gained popularity in recent years for this purpose. However, the optimal performance of a deep neural network relies heavily on its architecture, which makes it challenging to determine the best structure. Moreover, the large number of genes in gene expression datasets and the imbalanced data distribution among different classes pose significant obstacles to achieving high accuracy in cancer subgroup classification models. To address these issues, we propose a novel convolutional neural network model that uses a cost-sensitive learning approach to improve the accuracy of minority class identification. We also utilized three techniques, namely, the Fisher ratio, anomaly sets, and a combination of both, to reduce the number of genes in the preprocessing stage. Our cost-sensitive approach involves creating a cost matrix based on class distribution and utilizing it in the loss function of the convolutional neural network to calculate the error rate. We evaluated our proposed method using two cancer datasets, and compared the results with those of a convolutional model without feature selection and cost-sensitive learning. We used four standard metrics, namely, accuracy, recall, precision, and F1-score, to measure performance. Our results demonstrate that selecting appropriate genes and using a cost-sensitive learning approach significantly improves the performance of our proposed method, achieving increases of 11%, 10%, 18%, and 21% in accuracy, recall, precision, and F1-score, respectively. Overall, our approach demonstrated the effectiveness of combining cost-sensitive learning and feature selection techniques to address the challenges of imbalanced data and a large number of genes in cancer subgroup classification. This study has important implications for improving the accuracy and efficiency of cancer diagnosis and prediction using deep learning methods.

کلمات کلیدی:

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