ResRandSVM for Acute Lymphocytic Leukemia Blood Detection

Subjects: Hematology

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Acute Lymphocytic Leukemia is a type of cancer that occurs when abnormal white blood cells are produced in the bone marrow which do not function properly, crowding out healthy cells and weakening the immunity of the body and thus its ability to resist infections. It spreads quickly in children's bodies, and if not treated promptly it may lead to death. The manual detection of this disease is a tedious and slow task. Machine learning and deep learning techniques are faster than manual detection and more accurate.

acute lymphocytic leukemia ResNet152 VGG16 DenseNet121

1. Introduction

Cancer is the most deadly disease and has a negative impact on people all over the world. Among all types of cancer, blood cancer is the most dangerous in its later stages. The disease related to white blood cells (WBC) is known as leukemia. WBCs, also known as leukocytes, are one of the blood constituents and constitute one percent of the total blood volume. Human immunity is dependent on WBCs. The other blood constituents include red blood cells (RBCs) and platelets. Leukocytes, or WBCs, help fight infections and diseases. Leukemia is a cancer that destroys human immunity by affecting the bone marrow.

Leukemia leads to the production of immature leukocytes in large numbers. Leukemia is further divided into two types, chronic and acute. If the disease increases rapidly, it is acute leukemia; when it grows slowly, it is chronic leukemia. The symptoms of acute leukemia are more severe than chronic leukemia. Acute Lymphocytic Leukemia (ALL) [1] is a type of WBC cancer caused by consistent multiplication and unrestrained production of immature leukocytes in the bone marrow. ALL is predominantly found in children, constituting about 25% of all cancers in children. This cancer has similar symptoms to those of the common flu and other symptoms such as weakness, joint pains, fatigue, etc., making diagnosing this disease very difficult. This disease poses a significant risk to one's life. The survival time of ALL patients is 3 months only if treatment is not given on time. Hence, appropriate treatment and therapy are vital for saving the patient's life.

The manual detection of this cancer requires an expert doctor or physician for early and accurate detection. The examination of blood smear images has become common for the detection of ALL. However, manual detection has problems such as noise, blur, weak edges and the complex nature of blood cells, and is also reliant on human interpretation. Machine learning (ML) and deep learning (DL) advancements can help in detecting the disease

more accurately and also help doctors to diagnose and treat the condition properly [2]. The procedure adopted includes pre-processing the images, feature extraction, feature selection, and classification.

ML techniques [3] are also gaining importance in the classification of mitosis in breast cancer. Rehman et al. [4] constructed a novel model that involved neural-network-based [5] concepts and ML classifiers for the classification of mitotic and non-mitotic cells. The cell texture was used for deriving reduced feature vectors through multiple techniques and classification by ML classifiers such as SVM, Random Forest and Naïve Bayes. The ML classifiers performed better than the neural networks for this breast cancer dataset. Neural networks require more time to process the images and the images are also insufficient for optimum training of the neural network.

2. ResRandSVM: Hybrid Approach for Acute Lymphocytic Leukemia Classification in Blood Smear Images

Leukemia is a group of blood cancers affecting bone marrow and blood cells. It is a complex and heterogeneous disease that requires accurate diagnosis, classification, and treatment. ML has shown great potential in enhancing the accuracy and efficiency of leukemia diagnosis and classification and predicting treatment outcomes. Jagadev et al. [6] compared the performance of several machine-learning algorithms for leukemia classification using gene expression data. The results showed that support vector machines (SVM) outperformed other algorithms in terms of accuracy and speed. Ratley et al. [7] put forward a hybrid ML system for the detection and further classification of leukemia images. This approach used a combination of convolutional neural networks (CNN) and an SVM classifier for achievement of high accuracy. Lee et al. [8] proposed a ML model for prediction of the extent of sensitivity of drugs. The model helped in accurate prediction of responses to drugs and also identified potential drug targets. Saeed et al. [9] put forward a DL-based model for the diagnosis of leukemia using blood cell images. The images were classified into normal and leukemia images using a transfer learning CNN model with high accuracy. In the subsequent study, Shaikh et al. [10] developed a machine-learning model to predict the survival of acute myeloid leukemia patients using clinical and genetic data. The model accurately predicted patient outcomes and identified potential prognostic biomarkers.

The SVM classifier is commonly used for leukemia classification as it gives high accuracy and a linearly separable feature space is not required. The SVM classifier works well with both semi-structured as well as unstructured data [11]. It is one of the most efficient ML techniques. It can handle large feature spaces and non-linear feature interactions which do not rely on the entire dataset [12].

Chen et al. [13] proposed a label augmented and weighted majority voting (LAWMV) model for crowdsourcing purposes. This model outperformed other state-of-the-art models by achieving an accuracy of 82.89%. Majority voting is a simple and an effective method for integration [14]. Rehman et al. [4] developed a m6A-Neural Tool for the prediction and identification of m6A sites. This model used majority voting on three sub-architectures. These architectures used a set of convolutional layers to extract the important features from the input. An increased accuracy was obtained by this model as compared to other existing models. It achieved an accuracy of 93.9% for A. thaliana species, 91.5% for M. musculus and 92% accuracy for H. sapiens species. Singh et al. [15] introduced a

hybrid system to classify images of skin affected by lesions. The model was compared with commonly used techniques. The hybrid model utilized majority voting and principal component analysis and factor analysis and achieved an accuracy of 96.80%.

Finally, from the above literature, it can be inferred that ML has great potential to help in the diagnosis and classification of leukemia. This would further help to treat leukemia on a timely basis. However, further research needs to be carried out for the validation of the above models in clinics and hence integrate them in leukemia care on a routine basis.

DL is a subset of artificial intelligence that utilizes neural networks for the analysis and interpretation of data. DL is now gaining increased interest for improvement in leukemia diagnosis, classification, identification and treatment. Boldu et al. [16] proposed a DL system for the classification of acute myeloid leukemia (AML) using blood smear images. This system attained a very good accuracy of 96.4%, thus outperforming other ML techniques. It also exhibited how well DL techniques can help to predict leukemia. Bodzas et al. [17] implemented with a DL model for diagnosing ALL using blood smear images and obtained an accuracy of 94.8%. Boldu et al. [16] created a DL model for classification of leukemia subtypes and achieved an accuracy of 91.7%. Regarding the testing time for a single blood cell image, the BCNet model is proposed. This model outperformed the AI models of DenseNet, ResNet, Inception, and MobileNet by 10.98, 4.26, 2.03, and 0.21 msec. The BCNet model may produce positive results compared to the most recent deep learning algorithms [18]. In a different paper, El Achi et al. [19] put forward a DL model to classify lymphoma subtypes and attained an accuracy of 97.7%. Islam et al. [20] developed a DL model for predicting how well the patient recovers after giving chemotherapy to patients suffering with AML. This model attained an accuracy of 86.3%. So, it can be seen that DL models perform quite well for prediction of leukemia. Hence, both the ML and DL techniques can be integrated to achieve good results in classification of leukemia.

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