

# CNN-Assisted Automatic White Blood Cancer Type Detection from Bone Marrow

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## ABSTRACT

Leukocytes, which are made in the bone marrow, account for about 1% of all blood cells. These white blood cells multiply out of control, which leads to the development of blood cancer. Acute lymphoblastic leukemia (ALL) and multiple myeloma are two cell-based cancers that are identified by the proposed study's precise categorization approach (MM). The suggested methodology uses deep learning methods, particularly convolution neural networks, to completely eliminate the possibility of human error. The model pre-processes the photos after being trained on cell images, then it extracts the best features. The sort of cancer that is present in the cells is also predicted.

## I. INTRODUCTION

Platelets, red blood cells, and white blood cells are the three different types of blood cells. Each one is produced continually in the bone marrow and delivered into the bloodstream at the appropriate times. The fundamental cause of blood cancer is the aberrant blood cells' exponential growth, which inhibits the growth of regular blood cells. The three primary blood malignancies are leukemia, myeloma, and lymphoma. The bone marrow is where Acute Lymphocytic Leukemia, a kind of white blood cell malignancy, is infected (ALL). "Acute" denotes the rapid progression of the illness, and if it is not treated in the beginning, it could quickly prove fatal [1], [2]. Everything is divided into L1, L2, and L3 categories. [3] In order to remove the infection, Multiple Myeloma (MM) is an immature teratoma of cells termed plasma [4]. It is three times more frequent as ALL. In contrast to leukaemia, the blood count in this situation remains normal, but the infected person is found to have anaemia (low red blood count) because the healthy cells are taking up the area that would otherwise be occupied by RBCs.

Thrombocytopenia, often known as a low platelet count in the blood, is brought on by multiple myeloma. [5].

Moreover, it leads to bone erosion that is identified as bone lesions on CT scans. [6] Around 1500 persons died from this illness in 2019, accounting for 0.2% of all cancer-related deaths [7]. In the US, myeloma is diagnosed in close to 20,000 people annually. The course of treatment for blood cancer is determined by the patient's age, cancer kind, rate of progression, contaminated areas, etc. [8]. One of the main determinants for classifying the various types of blood cancer is the blood count. Both manual and automated counting methods are available. If performed by a skilled individual, the manual method yields a 100% recognition rate but is also a time-consuming procedure [9]. On the other side, automatic counting is quicker but has a greater chance of inaccurate results. As a result, each approach has benefits and drawbacks. This study provides a summary of the automatic method for classifying the kind of white blood cancer. In both urban and rural locations, the automated method of classification is rapid and affordable to implement. The proposed system has a number of flaws, such as the inconsistent results of manual categorization work, the need for a qualified professional, mistakes brought on by cells' indistinguishability under a microscope, etc. Deep learning-based approaches can assist in fixing all of the listed issues since they extract useful features directly from the raw data [10].

For processing a huge number of photos, Deep Learning has been shown to perform better than conventional machine learning [11]. Convolution Neural Networks (CNNs) mix different multilayer perceptrons and, with a little preprocessing, display effective results. [12] As each convolution layer of the network learns a new feature that is present in the images and results in a high activation, CNNs themselves operate as a feature extractor. In the suggested study, a strong

and robust automated classification approach for ALL and MM, two types of white blood malignancy, is described. As a result, the article compares accuracy, precision recall, sensitivity, and specificity to evaluate the performance of the suggested deep learning model.

## II. LITERATURE REVIEW

The analysis of images of infected blood cells normally consists of three steps: preprocessing of the images, extraction, selection of features, and classification. Many studies have been conducted on various cancers, including leukemia, lymphoma, and myeloma. Without first segmenting them, Zhang et al. suggested a convolutional neural network model for the direct categorization of cervical cells into infected and uninfected cells [13]. For categorizing the numerous types of white blood cells (WBCs) present in the body, Zhao et al. presented machine learning techniques including CNN, SVM, Random Forests, etc. [12]. For identifying both cancerous and healthy cells, the Stain DE convolution Layer (SD Layer) was proposed, in which the classifier learned from images in the Optical Density (OD) space rather than from images trained in RGB space [14].

In order to distinguish between distinct hematologic malignancies using image processing, FORAN et al. created an administered clinical decision support prototype. Based on the "gold standard" dataset, the system enabled picture analysis and provided treatment recommendations based on the plurality justification of the instances gathered [15]. By first enhancing, then enriching, and ultimately processing the training data and then putting it into a convolutional neural network (CNN) framework for image classification, the paper demonstrates a structure for classifying Human Epithelial Type 2 cell IIF images [16]. The ALL-IDB dataset is originally enhanced for classification of acute myeloid leukaemia by applying various adjustments such as histogram equalisation, reflection, translation, rotation, blurring, etc. The 7-layer convolutional neural network is then employed [17]. In order to distinguish Acute Lymphocytic Leukemia (ALL) by microscopic blood sample images, ShrutikaMahajan et al. developed an SVM-based system using changes in texture, geometry, and histograms as the classifier's inputs [18].

One of the research considered preprocessing a picture to extract the green planes, followed by a reinforcement algorithm to extract the features. The most effective method for classifying leukaemia was reached by using SVM

and Nearest Neighbor Network[19]. Using pictures of the bone marrow, Markiewicz, Tomasz, et al. proposed a technique for the classification of 17 different types of blood cells in myelogenousleukaemia. The Gaussian Kernel Support Vector Machine (SVM) was utilised by this system for final grouping after it first classified and retrieved only the best features from all the available features [20].

In a leukaemia image slide, N.H.A. Halim et al. suggested an automated method for counting the infected cells of acute lymphoblastic leukaemia (ALL) and acute myelogenousleukaemia (AML). Their method involved HSV-based segmentation (Hue, Saturation, and Value) to remove background white blood cells, followed by morphological erosion to remove overlapping cells [21]. Given that the H component of the HSI (Hue, Saturation, Intensity) colour space contains information on white blood cells, the authors have talked about segmenting colour smear microscopic images. In addition, the iterative Otsu's technique is used in the S component to store data about the nuclei of these cells [22].

By utilising image processing methods, the paper's authors offered a solution to the manual counting issues. The ratio of white blood cells to red blood cells is calculated using the image that has been preprocessed to reduce the possibility of error, and it is used to determine whether the image is normal or abnormal for the purpose of detecting leukaemia [23]. For esophageal cancer, including squamous cell carcinoma and adenocarcinoma, Horie et al. [24] shown the diagnostic capabilities of deep learning techniques like CNN with a sensitivity of 98%. [25] Saba, Tanzila, et al. developed an automated cascaded architecture for skin lesion detection that included contrast stretching and border extraction using CNN and depth feature extraction utilising transferred learning as the final two significant steps. Sekaran, Kaushik, and colleagues [26] created a technique that uses a convolutional neural network to distinguish between infected and healthy photos. Furthermore, statistics on the percentage of cancer spread to date are obtained using the Gaussian Mixture Model with EM method.

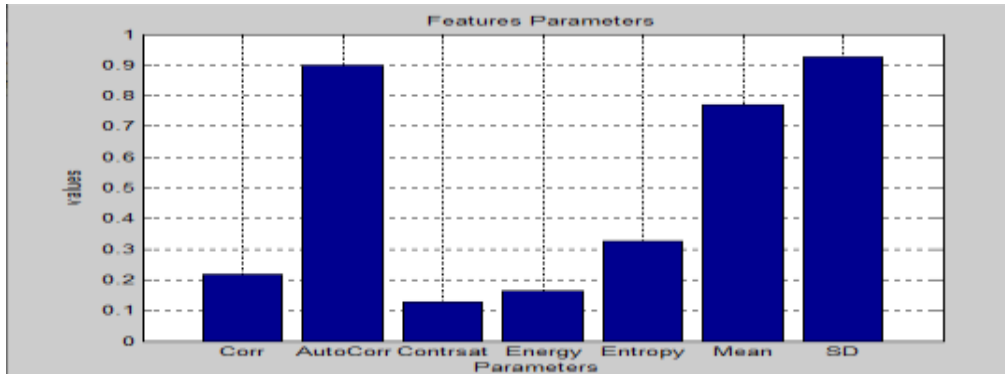
## III. PROPOSED METHOD WITH RESULTS

### IMPLEMENTATION STEPS

- Step1: Take image the from the data set
- Step2: perform the pre-processing steps for the further processing .
- Step 3: Classify the images based on the k means algorithm

- Step 4: apply the clustered mages to the convolution layer input.
- Step 5: The output of the Convolution layer is feature map image.
- Step 6: Apply the feature map image to the pooling layer it reduces the image less size by applying the max pooling function

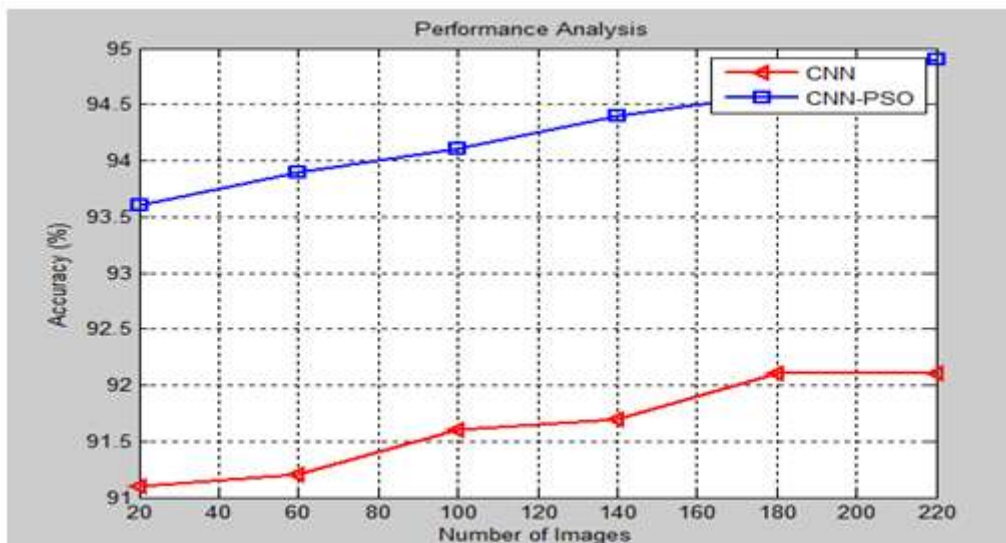
- Step 7: The output of the pooling layer applied as input to the fully connected layer.
- Step 8: The fully connected layer converts the input into column format .
- Step 9: The classifier sum the total value and compares with the existing data value.
- Step 10: If the values matches with acceptable range it classifies the same image



#### IV. CONCLUSION

By employing an extensive learning technique, specifically convolutional neural systems, the suggested model eliminates the possibility of errors in the human process. Preparing the model with a modified convolutional neural network structure comes after the model first pre-forms the samples and concentrates the greatest highlights from them. The model's accuracy was assessed at 97.2%, and in the end, it correctly

predicted the type of cancer in the image. A clear comparison between the model and some existing proposed models is also shown over three discrete datasets where the former performed better in terms of accuracy. However, we have to admit that a broader experimental study considering the dependence on the size of the databases has not been performed and presented here. This work has been implemented in MATLAB 2013a.



#### V. FUTURE SCOPE

Instead of using k-means algorithm we use Fuzzy means algorithm for getting best results for overlapped dataset, and data point belong to more

than one cluster center and having more number of convolutional neural layers will increase the performance of the model and decreases the number of parameters required.

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