



IJIRCCCE

e-ISSN: 2320-9801 | p-ISSN: 2320-9798



INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN COMPUTER & COMMUNICATION ENGINEERING

Volume 10, Issue 5, May 2022

ISSN INTERNATIONAL
STANDARD
SERIAL
NUMBER
INDIA

Impact Factor: 8.165

 9940 572 462

 6381 907 438

 ijircce@gmail.com

 www.ijircce.com

An analysis of Human Disease-Cancer using Microscopic Images

Belliappa K E¹, Ramesh B², Arun N¹, Anand Sunkad¹, Darshan J G¹

Department of Computer Science and Engineering, MCE Hassan, India¹

Senior Professor, Department of Computer Science and Engineering, MCE Hassan, India²

ABSTRACT: Acute Lymphoblastic Leukemia (ALL) is a cancer of the immature lymphocytes. Lymphocytes are a type of white blood cell involved in the body's immune system. Acute means that the disease begins and gets worse quickly. Cells that comprise the blood are three types: platelets, red blood cells and white blood cells. The normal blood cell growth hampered by the exponential growth of abnormal blood cells is the main cause of blood cancer. Bone marrow is the infected area for a white blood cancer type called ALL.

Deep learning based methods can help in resolving all the enlisted challenges because they derive desirable features from the raw data themselves. Convolution neural networks (CNN) combines various multilayer perceptron and display efficient results with a little pre-processing. The proposed model follows a generic approach to predict the type of cancer on a small dataset.

The automated method of classification is cost-effective and can be deployed quickly in both rural and urban areas. The problems that are invaded through the proposed system include the inconsistencies caused due to labor work of manual classification, the requirement of a skilled professional, the errors due to cells being indistinguishable when observed under a microscope. Deep learning-based methods can help in resolving all the enlisted challenges because they derive desirable features from the raw data themselves. The article consequently evaluates the performance of the proposed deep learning model using accuracy, precision, recall, sensitivity, and specificity as comparison parameters. Data Augmentation is used for Generalization.

KEYWORDS: Acute lymphoblastic leukemia, classification algorithms, deep learning, CNN, image processing, multiple myeloma.

I. INTRODUCTION

Cells that comprise the blood are three types: platelets, red blood cells, and white blood cells. Each of them is made continuously in the bone marrow and released timely in the bloodstream. The normal blood cell growth, hampered by the exponential growth of abnormal blood cells, is the main cause of blood cancer. There are three main types of blood cancers: leukaemia, myeloma, and lymphoma. Bone marrow is the infected area for a white blood cancer type cancer called Acute Lymphocytic Leukaemia (ALL)[1]. "Acute" indicates the fast progress of the disease, and if it does not get treated in the early stages, it might prove to be fatal within a short span.

Deep learning-based methods can help in resolving all the enlisted challenges because they derive desirable features from the raw data themselves. Deep Learning is known to demonstrate better functioning than accustomed Machine Learning for processing a large number of images[2]. Convolution Neural Networks (CNNs) combine various multilayer perceptron and display efficient results with a little pre-processing.

CNN's themselves act as a feature extractor as each convolution layer of the network learns a new feature that is present in the images and hence produces a high activation. In the proposed study, a robust and vigorous automated classification method for the type of white blood cancer, i.e., ALL and MM using Convolution Neural Networks is presented.

In image pre-processing, image data recorded by sensors on a camera related to geometry or brightness values of the pixels may not be very precise, as a lot of noise may interfere with these bit values[3]. These errors are corrected using appropriate mathematical models which are either definite or statistical models. Image enhancement is the modification of images by changing the pixel brightness values to improve its visual impact. Image enhancement involves a collection of techniques to improve the visual appearance of an image- both to machines as well as humans.

Sometimes, images obtained from satellites and digital cameras lack in contrast and brightness because of the limitations of imaging sub-systems and illumination conditions while capturing the image. Images may have different types of noise. In image enhancement, the goal is to accentuate certain image features for the next analysis stages or

display. These may involve contrast or edge enhancement, pseudo-colouring, noise[4] filtering, sharpening and magnifying. Image enhancement is useful in feature extraction, image analysis and display. The enhancement process itself does not increase the inherent information in the data. It simply emphasizes certain special image characteristics. These algorithms are generally interactive and application dependent. Some of these are:

Noise Filtering, Thresholding, Image sharpening

Since we have used noise filtering in our project, we would describe it briefly as a technique used to filter unnecessary information from an image. It is also used to remove various types of noises from the images. Mostly, the feature is interactive. Various filters like low pass, high pass, mean, median, etc. are available. Here, we have used the median filter to effectively filter out noise.

II. RELATED WORK

Image processing is a wide area of research field, the literature survey has been carried out to study the projects and researches previously performed on this same topic. We have found many image processing approaches implemented on various datasets which has motivated us to do this project.

1. Hend Mohamed, Rowan Omar, Nermeen Saeed, Ali Essam, Nada Ayman, TaraggyMohiy and Ashraf Abdel Raouf

In the proposed a hybrid methodology to detect white blood cancer cells using deep learning with support to learning system. Gaussian distribution was used for segmentation and random forest as classifier[5]. With a count of 105 images as data set, an accuracy of 93% for L1, L2, M5 and 95% for L3, M2, M3 and Myeloma were achieved.

2. Iterative Thresholding calculation is utilized for division reason particularly from loud pictures by NiranjanChatap, SiniShibu was proposed.

This calculation conquers the issue of cell extraction and division from substantial uproarious pictures. Morphological way to deal with cell picture division is more exact than the established watershed-based calculation. A basic thresholding approach is connected and the calculation is determined about blood smear pictures from priori data.

3. Anitta K Varghese et al., [4] proposed an efficient methodology with the advantage of, its simplicity.

classification of complete blood smear images and helps to segment and detect nucleated cells. Division is finished utilizing K-mean division and layer subtraction division. Hausdorff measurement were utilized for dimensionality decrease[6]. Direct SVMtwo-class classifier is utilized on the grounds that it is modest, and gives a decent execution.

4. Sarrafzadeh et al. [14] proposed another methodology concentrated fundamentally on separate between M2, M3 and M5 sub-sorts to assess their presented strategy.

They utilized a dataset made out of 27 minuscule pictures of three subtypes of AML; 9 AML of M2, 10 AML of M3 and 8 AML of M5. The methodology was connected in the $L^*a^*b^*$ shading space[8]. Division is performed utilizing K-means clustering to isolate leukocytes from other blood segments. Features are extricated with the end goal to be classified using Discriminative Dictionary Learning (DDL)[9]. An accuracy of 97.53% was achieved on Medical Image and Signal Handling Research Centre (MISP) dataset.

The objectives of the project are as follows:

To make the detection of White Blood cancer easier for the doctors and also accurate. To implement the recent advances in technology to make the diagnosis of cancer more digital. To detect and identify white blood cancer in an early stage to avoid the future problems. To reduce the time consumption to detect and classify the stages of white blood cancer.

The scope of the project are as follows:

To develop a system which detects cancer from blood cell images at a level exceeding practicing medical personnel. This technology can improve healthcare delivery and increase access to medical imaging expertise in parts of the world where access to skilled medical personnel is limited. The main scope of the project would be identification and detection White Blood Cancer in an early stage to avoid future problems and disorders. Survival rates

III. PROPOSED METHODOLOGY

A. DATASET DESCRIPTION:

In the proposed study, the dataset is acquired from two different subsets of a dataset collection [13]. The first part of the dataset consists of images of patients having BALL, i.e., B-Lineage Acute Lymphoblastic Leukemia having 90 images

in total. Figure 2 shows the background mask and the nucleus mask of the corresponding ALL image[7]. On the other hand, the second part of the dataset consists of images of patients diagnosed with Multiple Myeloma, i.e., MM having 100 images.

B. DATA AUGMENTATION

The SN-AM dataset is first augmented by rotating the image and extracting edges. The shuffled images are divided into training and testing sets[12]. There should be a considerable amount of data available as the object of interest must be present in varying sizes, poses, and lighting conditions for the model to generalize well during the evaluation (testing) phase.

Data can be manufactured from existing data by manipulating images through various techniques. Figure 4 shows the resulting images after data augmentation. The first technique used is the rotation of images by 90 degrees [10]. All the images are rotated by an angle of 90 degrees as our model should be able to recognize the object present in any orientation

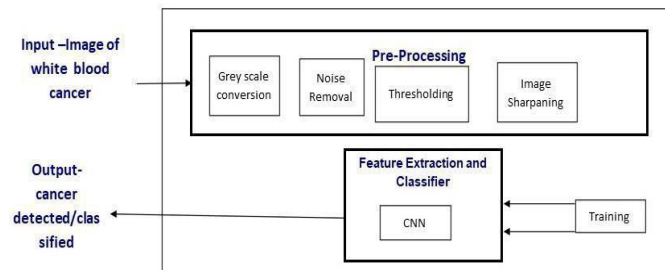


Figure: Architectural Diagram of the Proposed System using CNN

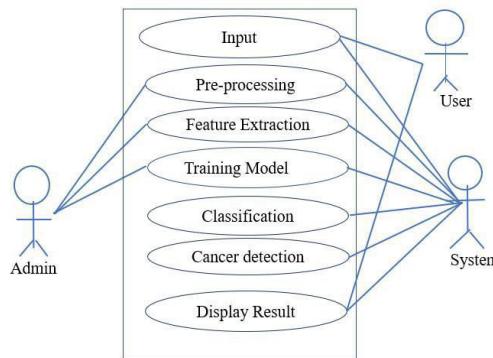


Figure: Use Case Diagram for white blood cancer detection model

C. PROPOSED CONVOLUTION NEURAL NETWORK AND ARCHITECTURE

In the proposed research, an optimized CNN model for classification of the type of cancer, i.e., ALL or MM, has been deployed. The network used for our deep learning model. Convolution Neural Networks (CNNs) are majorly used for analyzing visual imagery. CNN's are the heart of image classification algorithms. They work fast and efficient for image classification. In comparison to other image classification algorithms, they use a little pre-processing. A CNN model is comprised of an input layer, an output layer, and multiple hidden layers. In this article, the proposed model takes an image as input and returns the type of cancer as output i.e. standard neural networks to classify images based on the features extracted by the convolutions.

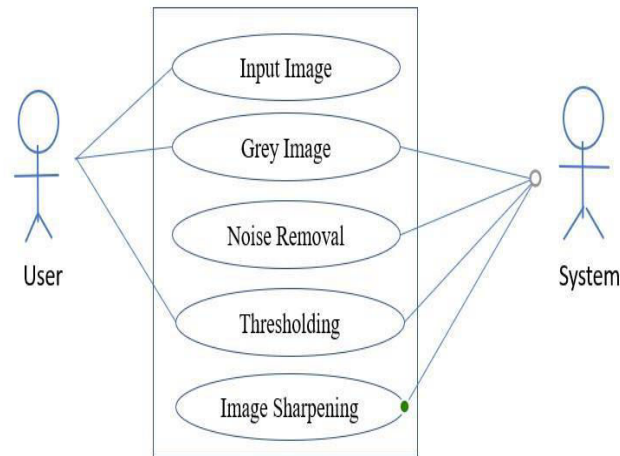
At this step, the error is calculated and then back-propagated. The proposed model consists of five fully connected layers, including the final output layer. The softmax activation function is used in all the four fully connected layers. The output layer contains the sigmoid activation function, which, for each of the classification labels that the model is trying to predict, outputs a probability value of 0 to 1. The sigmoid function is defined by equation.

$$Sig(z) = \frac{1}{(1+e^{-z})} = \frac{e^z}{e^z+1}$$

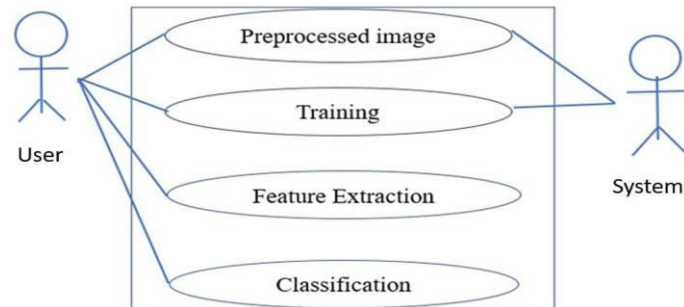
Here, z is the input vector.

The algorithm used to classify the images using the deep learning approach is shown in pseudo-code Algorithm 1.

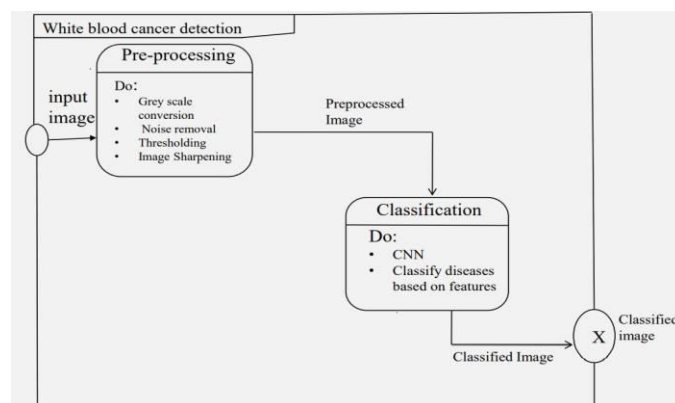
IV. IMPLEMENTATION



Use Case Diagram of pre-processing module



Use Case Diagram of Feature Extraction and Classification using CNN.



State Chart Diagram of model using CNN

V. CONCLUSION

The outcome of adults with ALL remains suboptimal with cure rates of less than 60% in most subtypes. However, a better understanding of the disease biology has generated important knowledge on the prognostic and predictive value of MRD, which has helped guide our treatment strategies, such as intensification or referral to HSCT, the use of MRD-directed novel agents or even treatment de-escalation.

With the development of novel, effective therapies such as InO, blinatumomab, and CAR T cells, our treatment options have not only expanded, but our focus is shifting toward strategies that minimize cytotoxic chemotherapy and HSCT. However, until the best combination and sequence of these novel agents are fully defined, enrollment in clinical trials, and referral to tertiary centers remains crucial. With continued efforts to optimize the available therapies with novel combinations, there is reason for optimism that the treatment of adult ALL may eventually become another oncological success story.

REFERENCES

- [1] Kai Kessenbrock, Vicki Plaks, and Zena Werb. Matrix metalloproteinase regulators of the tumor microenvironment. *Cell*, 141(1):52–67, 2010.
- [2] Amjad Rehman, Naveed Abbas, Tanzila Saba, Syed Ijazur Rahman, Zahid Mehmood, and Hoshang Kolivand. Classification of acute lymphoblastic Leukemia using deep learning. *Microscopy Research and Technique*, 81(11):1310–1317, 2018.
- [3] Sarmad Shafique and Samabia Tehsin. Acute lymphoblastic leukemia Detection and classification of its subtypes using pretrained deep convolutional neural networks. *Technology in cancer research & treatment*, 17:1533033818802789, 2018.
- [4] Michael Hallek, P Leif Bergsagel, and Kenneth C Anderson. Multiple myeloma: increasing evidence for a multistep transformation process. *Blood*, The Journal of the American Society of Hematology, 91(1):3–21, 1998.
- [5] John G Kelton, Alan R Giles, Peter B Neame, Peter Powers, Nina Hageman, and J Hirsch. Comparison of two direct assays for platelet-associated igg (paigg) in assessment of immune and nonimmune thrombocytopenia. 1980.
- [6] Matthias Perkonig, Johannes Hofmanninger, Björn Menze, Marc-André Weber, and Georg Langs. Detecting bone lesions in multiple myeloma patients using transfer learning. In *Data Driven Treatment Response Assessment and Preterm, Perinatal, and Paediatric Image Analysis*, pages 22–30. Springer, 2018.
- [7] Ahmedin Jemal, Rebecca Siegel, Elizabeth Ward, Yongping Hao, Jiaquan Xu, and Michael J Thun. Cancer statistics, 2009. *CA: a cancer journal for clinicians*, 59(4):225–249, 2009.
- [8] Ying Liu and Feixiao Long. Acute lymphoblastic leukemia cells image analysis with deep bagging ensemble learning. In *ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging*, pages 113–121. Springer, 2019.
- [9] S. Kant, "Leukonet: Dct-based cnn architecture for the classification of normal versus leukemic blasts in b-all cancer," 2018, arXiv:1810.07961. [Online]. Available: <https://arxiv.org/abs/1810.07961>
- [10] I. Arel, D. C. Rose, and T. P. Karnowski, "Deep machine learning. A new frontier in artificial intelligence research," *IEEE Computing Intell. Mag.*, vol. 5, no. 4, pp. 13–18, Nov. 2010.
- [11] J. Zhao, M. Zhang, Z. Zhou, J. Chu, and F. Cao, "Automatic detection and classification of leukocytes using convolutional neural networks," *Medical. Biol. Eng. Computing.*, vol. 55, no. 8, pp. 1287–1301, Aug. 2017.
- [12] L. Zhang, L. Lu, I. Nogueira, R. M. Summers, S. Liu, and J. Yao, "Deep-Pap: Deep convolutional networks for cervical cell classification," *IEEE J. Biomed. Health Information* vol. 21, no. 6, pp. 1633–1643, Nov. 2017.
- [13] R. Duggal, A. Gupta, R. Gupta, and P. Mallick, "Sd-layer: Stain deconvolutional layer for CNNs in medical microscopic imaging," in *Proc. Int. Conf. Med. Image Computer. Computer Assist. Intervention*. Cham, Switzerland:



INNO  SPACE
SJIF Scientific Journal Impact Factor

Impact Factor: 8.165

 **doi**[®]
CROSS **ref**

ISSN INTERNATIONAL
STANDARD
SERIAL
NUMBER
INDIA



INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN COMPUTER & COMMUNICATION ENGINEERING

 9940 572 462  6381 907 438  ijircce@gmail.com



www.ijircce.com

Scan to save the contact details