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Acute Leukemia Detection using Deep Learning Techniques

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Abstract

Leukocytes, which are created in the bone marrow comprise one percent of all blood cells. When these white blood cells grow uncontrollably it gives rise, to the development of blood cancer. The proposed research presents an approach, for categorizing One of the three kinds of Multiple Myeloma (MM) and Acute Lymphoblastic Leukaemia (ALL) are the two diseases that make use of the SN-AM dataset. the malignancy known as acute lymphoblastic leukaemia (ALL), to start with in which an excessively large number of lymphocytes are produced by the bone marrow. Secondly, Multiple myeloma (MM) is a type of cancer that results in the accumulation of malignant cells in bone marrow, rather than their release into the bloodstream. Hence, the growth of blood cells is to be resist and prevent. Beforehand, the procedure was carried out manually evaluated by experienced haematologists. The proposed methodology totally eliminates the chance of human mistake through using deep learning methods, particularly convolutional neural networks. A total of 89 ALL patients 3256 smears of peripheral blood (PBS) pictures were acquired from an online portal. The model undergoes training using modified convolutional neural networks that has been optimized and its ability to predict which type of malignancy is present in the cells is determined. In 96 out of 100 cases, the algorithm strongly replicated every measurement that corresponded to the samples. The accuracy of the system was found to be 97.6%, which is more appropriate than modern techniques like Decision Trees, Random Forests, Naive Bayes, and Support Vector Machines (SVMs), VGG16, VGG19, AlexNet, Google-Net, Mobile-NetV2. The work showcases that Modified CNN performs more accurately.

1. Introduction

The three cell types that make up blood are platelets, red blood cells, & white blood cells. These cells are continuously produced and put into the bloodstream in the bone marrow. Blood cancer usually comes on by the atypical blood cells' rapid proliferation, which inhibits the creation of healthy blood cells. Leukaemia, myeloma, and lymphoma make up the bulk of instances of blood cancer. White blood cell cancer of the acute lymphocytic kind (ALL) affects the bone marrow. In medical treatments, the disease just begun along with its limited duration are indicated by the term "Acute". ALL-classifying approach based on CNN likewise,

first and final layer features are integrated to prevent overfitting, a dropout layer is utilised (Banik, Saha, and Kim). WBCs are divided into the L1, L2, and L3 subtypes of ALL (Shafique and Tehsin). Leukaemia is divided into chronic and acute types. The benefits of transfer learning-based extracting features utilising three modified ResNet models, the best sensitivity (100%) was attained but it takes time and is prone to error to manually detect a haematological disease (Das, Pradhan, and Meher). WBCsNet is a brand-new CNN-based classification system for WBC. The five distinct kinds of white blood cells (WBCs)—monocyte, lymphocyte, basophil, eosinophil, & neutrophil—are categorised using this method using three deep learning algorithms (I Shahin et al.). Using ten cutting-edge architectures, binary cell categorization of healthy versus malignant cells was done in comparison (Gehlot, A. Gupta, and R. Gupta). Due to the synergistic effects of SVM-based classification and MobileNetV2-based feature extraction, it exhibits promising performance. We also note that the proposed hybrid model yields a second-best overall performance with an accuracy of 97.18%. Additionally, among the ALLIDB1 & ALLIDB2 datasets, it obtains the best accuracy, achieving 97.92% and 96.00%, respectively, with 50% trained and 50% testing (Das and Meher). The cytoplasm and nucleus have been segmented, and features have been retrieved based on form and textural signals. On various combinations of set features, different classifiers have been investigated. Trials using normal cells served as the foundation for the findings given here. SVM demonstrated the greatest efficiency: 92% (Laosai and Chamnongthai). The C-NMC dataset is used to validate the proposed technique, which features hard elements that make ALL detection more difficult. The similarity in morphology between ALL and healthy pictures (R. Gupta, Gehlot, and A. Gupta). The automatic approach of classification is economical and could be easily implemented in rural as well as urban places. The suggested method has issues with errors brought by human laborious classification, the need for a qualified professional, and cells that are difficult to differentiate when seen under a microscope. It is made to roughly cope the input, dealing only with input that is similar to the training data. This model is intended to prioritise the copying of the specific input elements. Typically, an automated encoder picks up important data attributes (Goodfellow, Bengio, and Courville). The segmented image is then used to extract form, texture, and tone properties and using an RBF kernel and an SVM (support vector machine), the classification of WBCs is finished. The accuracy and sensitivity of the suggested approach are both 96.00%, which produces encouraging results [10]. CNNs operate as feature extractors as every single layer of convolution of the neural network identifies a new feature that appears in the images and causes a high activation. An aggressive and reliable automatic categorization approach for the kind of ALL blood cancer utilising Convolution Neural Network. Therefore, the article assesses how well the deep learning model that was suggested to perform using as comparison such as recall, sensitivity, specificity, and accuracy. Predicting the kind of cancer in the dataset using the given model is the article's primary concept. The model uses fewer computations and trainable parameters to classify the kind of cancer than present machine learning and learned deep learning models.

2. Related works

The three steps of the affected blood cell analysis approach typically consist of feature extraction, classification, and quantification. Numerous investigations on various cancers, such as leukaemia, lymphoma, and myeloma, have been carried out. Test of ALL affected blood cells are classified by various algorithms CNN, FNN, SVM, and KNN. CNN produces accuracy of 98.33% with 8-layer framework whereas other are less than 95% (Rajpurohit et al.) . CNN faced problems with large hyperparameter tuning and the author used optimised CNN method to achieve high accuracy (Tuba et al.) . The average ML method's leukaemia detection accuracy in PBS imaging analysis was 97% (Ghaderzadeh, Asadi, and Hosseini) . In order to categorise acute myeloid leukaemia, the dataset was initially expanded by making many changes. The final step employs a 7-layer convolutional neural network (Thanh et al.) . A neural networks (NNs) classifier employing the Bayes regularisation (BR) approach was employed to categorise the ALL, and it attained an accuracy of 98.7% (Bhuiyan et al.) . With the aid of image processing techniques, the author uses SVM to analyse the many forms of blood cancer

using blood smear images of normal and cancerous individuals (Elrefaie, Marzouk, and Mohamed) . When MobileNet used for training KNN obtain 95% (Abhishek et al.) . Leukocytes, or white blood cells, are divided into two categories using a two-stage colour segmentation technique such as shape and texture of the nucleus are utilised by SVM for final detection (Mohapatra and Patra) . 90% of the dataset was used for training, and 10% was used for testing (Sakib et al.) . With an overall accuracy of 93.7%, the author was able to classify the cells into normal and blast using the SVM classifier technique on the ALL-IDB-1 dataset (Shafique et al.) . A dual branched architecture is created using this projection loss and the loss of cross-entropy to boost performance and give room for addressing the label noise issue. A symmetrical accuracy of 94.17% is the best that the proposed design can achieved (Shiv, Anubha, and Ritu) . The dual-module deep learning ALL classification framework was put forward by the author. Compact CNN is used in one module to serve as the primary classifier, and kernel SVM is used in another module to serve as an auxiliary classifier (Shiv, A. Gupta, and R. Gupta) . This dataset's annotations were generated automatically during the generation process. Author used the dataset to train a deep neural network, which, when measured compared to the well-known ALL-IDB dataset, obtained an outstanding precision score of 98.72% (Al-Qudah and Suen) . Alert-Net, a deep learning network. It has a softmax, two fully linked layers, and five layers of convolution.2,415 images from 16 datasets were used in the studies, and the accuracy was 97.18% (Claro et al.) . To differentiate between malignant and benign tissue, use the ensemble classifier (the combinations of MLP, KNN, & SVM classifiers). But the price of computation has also gone up (Mohapatra, Patra, and Satpathy) . For a successful ALL classification, significant geometrical, colour, & statistical texture features are extracted and HRC-NNs were applied to categorise WBCs (Su, Cheng, and Wang) . WBC segmentation will be more accurate owing to a semantic segregation method based on learning through transfer. They used DeepLabV3+ and to classify AlexNet with 5 layers (Reena and Ameer) . To efficiently classify ALL using ANN and used the segmentation method based on k-medoids to separate the cytoplasm from the nucleus. Despite being slower than k-means, the k-medoid technique delivers superior segmentation performance and is more stable than k-means (Acharya and Kumar) .

3. Proposed Methodology

The model, which has five layers and includes three convolutional layers and hidden layers, is trained on the training set before being used to generate predictions on the testing set.

3.1. Dataset Descriptions

The dataset includes 3256 pictures of peripheral blood smears (PBS) taken from 89 patients with ALL. The categories of benign and malignant data were spilt from this data collection. The former is made up of haematogones, while the latter is made up of the ALL group, which contains all four cancerous lymphoid subgroups Early Pre-B, Benign, Pre-B, & Pro-B ALL as shown in fig.1. A Zeiss microscope with a 100x magnification was used to capture each image, which was then stored as a ZIP file, these files are converted into folders for the process. The technique of flow cytometry was used to determine the precise types and subtypes of these cells. Following segmentation using colour thresholding in the HSV colour space, segmented images are provided. This dataset was already augmented.

3.2. Pre-processing and Feature Extraction

In pre-processing, training data and img_size=50, are in following as an array, variable is declared respectively. Image values are stored as an array by using numpy and matplotlib libraries. The dataset consist of images, hence comes under opencv2. Firstly, the image has converted into grayscale. Afterward, reduction of noise was done by using medianblur and the images in dataset are in different size, to make it common resize was used as mention above as 50. The values are converted into matrices and append to the training data for all the images presented in the dataset. In addition to, that data has been stored randomly for better efficiency. X, y variable has declared for feature extracting. The captured values from image such as shape, size, colour, texture, etc... are known as features that are stored in X as an array. Whereas, the dataset consists of 4 categories like benign, early, pre, and pro. For classifying these categories, the values are stored as labels in y variable. Pickling is a little language that

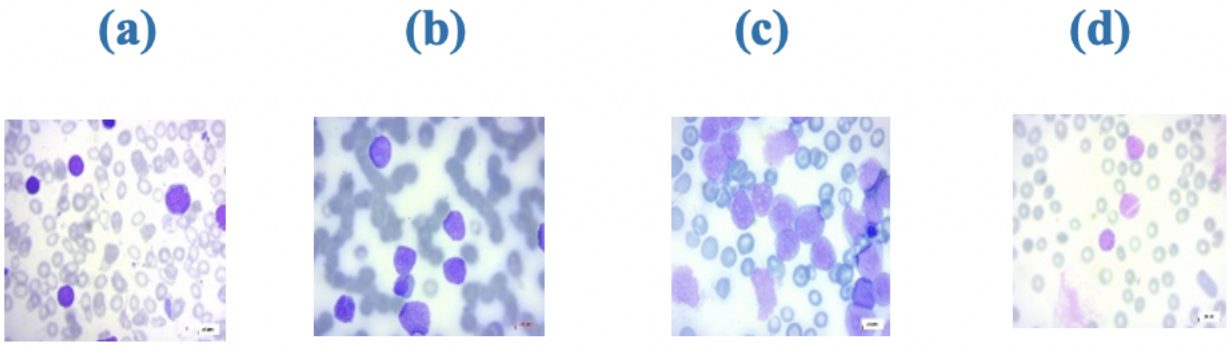

FIGURE 1. (a) Benign (b) Early (c) Pre-B (d) Pro-B

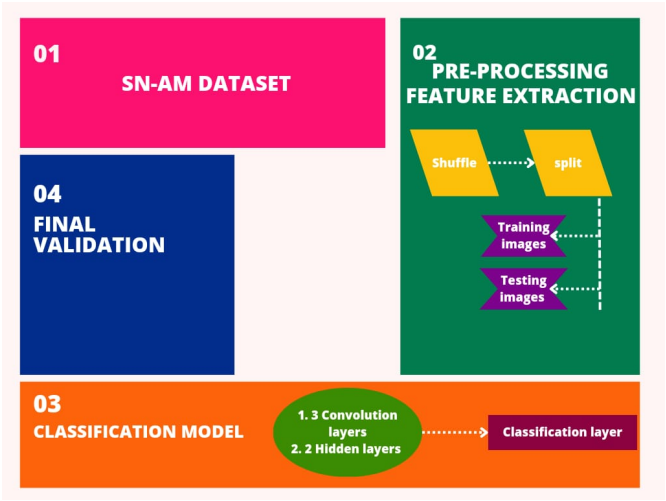

FIGURE 2. Process of the dataset

may be used to translate a Python object's important state into a string that specifically identifies the object. In this case, X.pickle was created to dump X(features) that use mb to hold picture values .similarly, Y.pickle was created to write y(labels) uses kb. Hence, the values store only 0,1... Pre-processing along with feature extraction were completed in the proposed investigation, and the data were then randomly separated into sets for training and testing. The dataset is split into 20% for model testing and 80% for training as shown in Fig.2 and 3.

3.3. Model Development

A modified CNN model has been used in the planned study to classify ALL cancers into benign, early, pre, and advanced stages. CNNs are the computational units of image classification algorithms. They classify photos quickly and accurately. Compared to other picture categorization techniques, they use less pre-processing. A modified CNN model has two hidden layers and three convolutional layers. The model presented in this article accepts a picture as input and predict the type of cancer as shown in fig.5.

3.3.1. Convolution layer

A layer of convolution, that is the first layer into which the image is fed, is made up of neurons that serve as extraction of features units. An activation map is created by convolving an input image with a k by k (3x3) matrix filter. The amount by which a filter shifts the image is referred to as a "stride." A convolution process with a kernel of size k, padding p, & stride s yields an output of size for an input image of size, a x b.

$$(a-k+2p)/s+1 \times (b-k+2p)/s+1.$$

Three convolution layers are present as input layer in the suggested model, with ReLU serving as their activation function and Maxpooling coming after. Every first layer has 32 features map whereas, other two layer are 64. The standard function of ReLU Equation (2) defines, while Equation (3) provides the Maxpooling2D. Equation (4) provides the activation map that was created after applying the kernel function's convolution operation to the input image.

$$f(x) = max(0, x)$$

where x is the input of neuron, if a negative value is supplied, the function returns 0, and if a positive value is input, The function will give the same positive result back. ReLu involves addressing the vanishing gradient issue

$$(a-k)/(s+1) \times (b-k)/(s+1)$$

Where the maximum value in a certain area on an image of size a x b is specified using a kernel of size k & a stride of size s as shown fig.4.

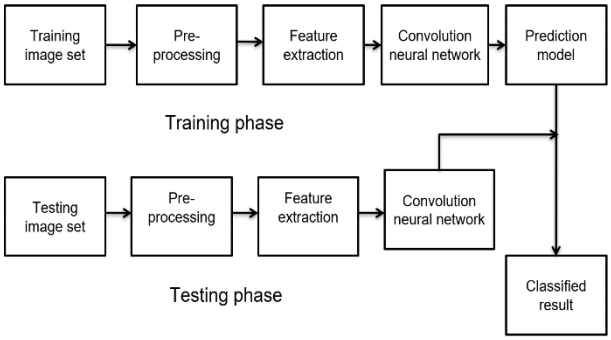

FIGURE 3. Block diagram

$$A\,(x,y] = (I * f)\;\;(x,y]$$

$$= \sum_i \sum_j I\;\;(i,j]\, f[x-i, y-i]$$

where i and j are both the rows and columns of an input image matrix, I is the image being input, f is the kernel's function, x and y are the rows & columns of the resultant matrix, respectively.

3.3.2. Hidden layer

The network's inputs are subjected to nonlinear changes by the hidden layers. The goal of every layer and the function performed by each neuron in it varies based on the function of a neural network, which is similar to how hidden layers do. These are utilised to perform the necessary activation function, add the bias, and compute the weighted average of the inputs and weights. There are two hidden layers and one output layer in this model. By using, flatten the matrix is converted into single dimensional array by training top 128 values and ReLU activation function is used in two hidden layers in equation (2). The function that activates softmax is present in the output layer. the default softmax feature $s\;:\;R^n \to R^n$ is defined in equation (5).

$$s\,(x_i) = \frac{e^{x_i}}{\sum_{j=1}^{n} e^{x_j}}$$

for i = 1..., n and $x = (x_1, \ldots, x_n) \in R^n$, where n is the total number of elements of the input vector x and x_i represents each element of the input vector x.

To classify the categories softmax activation function is used. while processing 0 and 1. sometimes, decimal number may arise therefore, this activation will round-off the values.

3.4. Performance Analysis

Actually, the model carried out CPU and the categorization model is created with Keras and TensorFlow. 30 training epochs of a binary classification model were trained on 2604 images. similarly, 652 images were also taken for the testing phase. Hyperparameter tuning was done to increase batch size of 64. The loss function is optimised for each epoch using the Adam Optimizer, producing the lowest loss at the final epoch. The type of cancer in images was then predicted using the training model. The outcomes of the suggested model are described first. It is also described how the proposed approach compares and contrasts with cutting-edge deep learning and state of art methods.

3.5. Desired Output

The network in the modified CNN is trained using Adam Optimizer. Decrease function a sparse categorical cross-entropy loss equation is utilised, which uses a single integer for each class rather than a whole vector that is optimised by the Adam optimizer. This reduces computation and memory requirements. The model's sensitivity is in the percentage of 96.9%. The following criteria have been used for comparison: The following equations determine accuracy, precision, recall, specificity, and F1-score:

$$AC = (TP + TN)/(TP + TN + FP + FN)$$

$$P = TP/(TP + FP)$$

$$R = TP/(TP + FN)$$

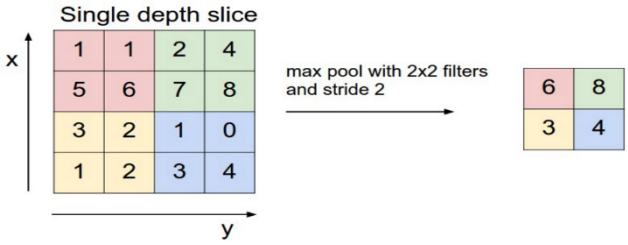

FIGURE 4. Maxpooling Function

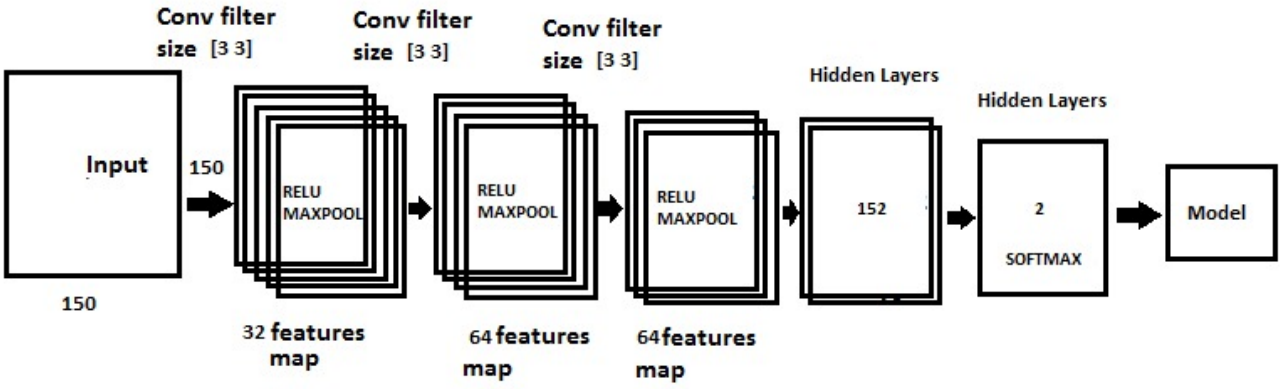

FIGURE 5. Modified CNN Architecture

$$S = TN/(TN + FP)$$

$$F = (2 * P * R)/(P + R)$$

The proposed model's accuracy, precision, recall, specificity and F1-score are in the percent of 97.6%, 0.98, 0.98, 95.3% and 0.98 respectively.

By comparing, with state of art methods, deep learning performs better. The two characteristics, Discrete Fourier Transform (DFT) and histogram, are taken from the images by the machine learning methods. Then, these features are used to train all classifiers. The classification model was created using the 'RBF' kernel and the supervised learning algorithm SVM (Suykens and Vandewalle). A probabilistic classifier called Naive Bayes employs the Gaussian method to distinguish between the two forms of cancer (Rish). Predicting the value of a parameter from the input sequence of the generated feature vector is the objective of the choice tree classifier system (Ben-Haim and Tom-Tov). An ensemble learning approach called random forests outputs the mean forecast of each individual decision tree that was created at the back end, providing the final difference (Liaw and Wiener). Only three layers are present in the VGG-16 convolutional neural network (CNN) model, and they are stacked on top of one another. The model used with Softmax for classification consists of two layers that are completely linked with 4096 nodes (Yu et al.). Due to the advantages of MobileNetV2 and ResNet18 combined, this new hybrid ALL detection model performs admirably [10]. Ensemble1 (an ensemble of KNN, decision tree, SVM, and and Naive Bayes classifiers), Ensemble2 (an ensemble of linear, Gaussian radial basis, multi-layer perceptron, as well as quadratic SVM kernels), and Ensemble3 were created (a classifier constructed using the quadratic SVM kernel)—are two ensemble classifiers (Moshavash, Danyali, and Helfroush). The table.1 shows the comparisons

4. Results and Discussion

652 photographs are taken for testing or validation, while 2604 images are taken for training. The findings will appear in a graph when 30 epochs of training are complete, increasing both simultaneously. As a result, the blue line displays the training picture accuracy, while the orange line displays the testing image accuracy. The training loss compared. validation loss across the number of epochs plot is similar in that the erroneous prediction is reduced to 0.2 as shown in Fig.6. Applying the modified CNN model, the confusion matrix for malignant white blood cancer's binary classification. The matrix approach is a reliable and popular method for evaluating the efficacy of a model of classification since it shows where the approach has failed and offers guidance on how to turn things around. Confusion matrix values are returned by the Sklearn.confusion_matrix() function. The results, however, deviate slightly from previously researched. It uses the columns as Predicted Label and the rows as True Label. The remainder of the idea is unchanged as shown in fig.7.

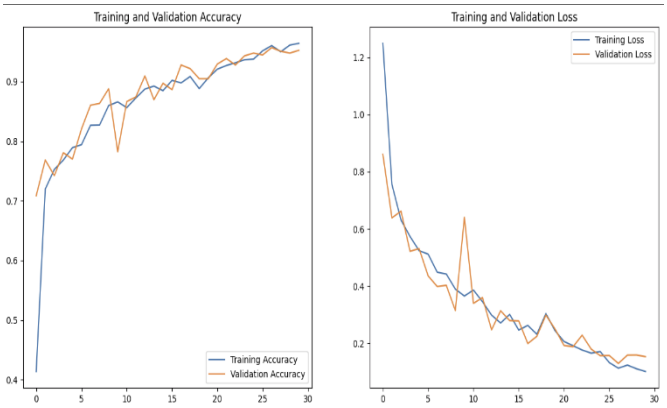

FIGURE 6. Accuracy and loss graph of training and validation

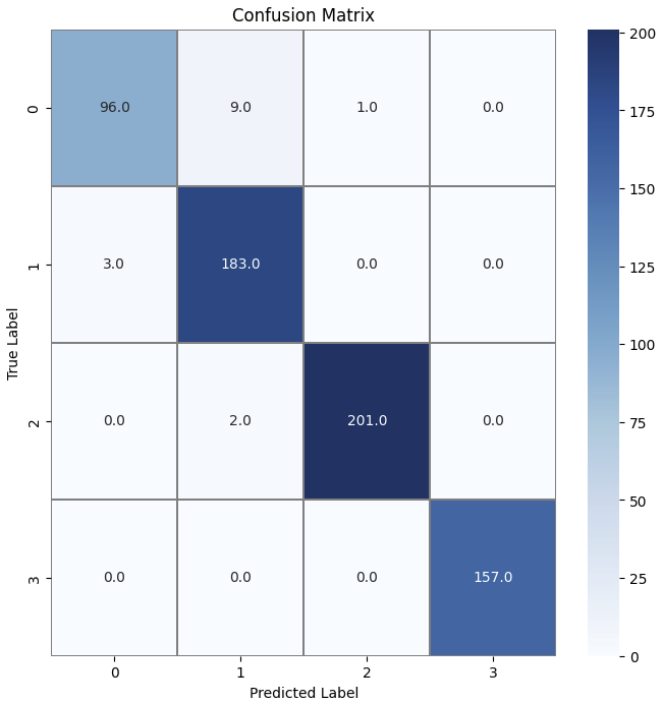

FIGURE 7. Confusion Matrix

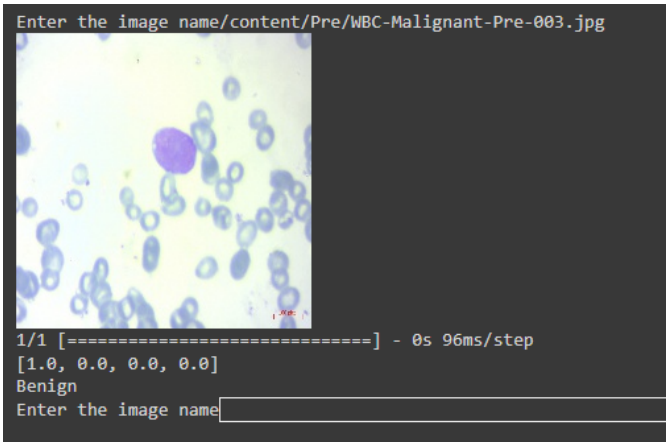

FIGURE 8. Test image

5. Conclusion

Before being built with a modified Convolutional neural network (CNN) structure, the model first pre-forms the images and separates their best features. Finally, it identifies the kind of malignant tumour in the provided image. 97.6% was the model accuracy evaluation. Additionally, a comparison of a number of cutting-edge methods, such as Support Vector Machines (SVMs), Decision Trees, Random Forests, Naive Bayes, VGG-16, Hybrid - MobileNetV2 & ResNet18, E1 E2, etc., was conducted and presented. The suggested model outperformed these approaches. A direct comparison of the model to some already-proposed models. The model's accuracy increased. As a result, to accurately determine the type of cancerous tumour present in the bone marrow, the model can be utilised as a tool. However, we must acknowledge that a more extensive experimental investigation taking into account the dependence on database size has not been carried out and provided here.

TABLE 1. Comparison between state ofart algorithms and Modified CNN

S.NO	ALGORITHM	ACCU-RACY	PRECI-SION	RECALL	SPECI-FICITY	F1-SCORE
1.	SVM	73.02	89.47	53.12	65.9	66.66
2.	VGG-16	90.1	84.88	93.58	87.5	89.01
3.	NAÏVE BAYES	74.6	69.05	90.65	85.71	78.37
4.	DECISION TREES	96.77	94.11	100	100	96.96
5.	RANDOM FOREST	96.83	100	93.75	93.93	96.77
6.	HYBRID - MOBILENETV2 & RESNET18	97.18	98.52	-	98.46	0.97
7.	E1	75.00	64.47	-	54.24	0.78
8.	E2	89.81	81.67	-	81.36	0.89
9.	MODIFIED CNN	97.69	0.98	0.98	95.3	0.98

TABLE 2. Classification Report

	PRECISION	RECALL	F1-SCORE	SUPPORT
CLASS 1	0.97	0.91	0.94	106
CLASS 2	0.94	0.98	0.96	186
CLASS 3	1.00	0.99	0.99	203
CLASS 4	1.00	1.00	1.00	157
ACCURACY			0.98	652
MACRO AVG	0.98	0.97	0.97	652
WEIGHTED AVG	0.98	0.98	0.98	652

Authors' Note:

I want to sincerely thank my guide for supporting me as I worked on this project. Without the assistance of medical reports of patients, it would not have been feasible to detect acute leukaemia using deep learning algorithms. Firstly, the medical information and insights have advanced our knowledge of acute leukaemia identification greatly. The creation of the deep learning models as well as the utilisation of the required computational resources were both greatly aided by this concept and the project's support. The project's direction has been heavily shaped by the guide input, which has greatly enhanced this work's success. The result of uncountable hours of laborious labour is this research report. My research is intended to further the early diagnosis and better management of acute leukaemia, ultimately improving the quality of life for people around the world.

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