Original Article
ISSN (Online): 2582-7472

ShodhKosh: Journal of Visual and Performing Arts
March 2024 5(3), 1521–1527

BLOOD CANCER DETECTION USING IMAGE PROCESSING

Dr. K. Venkatasalam[1], Mahalakshmi. R[2], Keerthika. E[3], Kavina. S[4]

[1] Associate Professor, Computer Science and Engineering Mahendra Engineering College, Tamil Nadu, India
[2] Ug Students, Computer Science and Engineering Mahendra Engineering College, Tamil Nadu, India

DOI
10.29121/shodhkosh.v5.i3.2024.4883

Funding: This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

ABSTRACT

The conventional technique of diagnosing blood disorders through microscopic visual examination of blood smears is susceptible to error, time-consuming, and based on the physical acuity of the haematologist. Thus, to enable clinical decisions to be made, an optical image processing system has to be automated. One of the features of leukemia is an abnormal growth of immature, faulty white blood cells (WBC), or "blasts." A disease that occurs in blood and/or bone marrow related to white blood cells (WBCs) is referred to as leukemia. Early diagnosis of leukemia that is timely, safe, and accurate is essential for treating and saving patient lives. Typically, WBCs are analyzed using blood smear under microscope. Various machine learning (ML) algorithms have been trained to provide a high misclassification error rate and to detect various diseases, such as leukemia. Therefore, for detecting the microscope images for WBC count study, we can utilize deep learning (DL) approach. Identification module as well as classification module formed 2 modules of WBC differential count system. To differentiate between all the WBCs, red blood cells, colouring impurities, and blood platelets, the identification module first scanned the raw bone marrow smear images. Subsequently, the identified cells were fed into categorization module. Categorization module comprised 2 steps. In initial step, we identified many cells that are not used to diagnose leukemia crushed, degraded, etc. Countable WBCs were forwarded for multi-class differentiation in second step using a convolutional neural network approach.

Keywords: Automation, Classification, CNN, Deep Learning, Leukemia, Microscopy.

1. INTRODUCTION

Cancer is due to abnormal and uncontrollable cell growth and development. Cells are produced, mature, function, and die as natural processes in cell development. The body naturally replaces lost cells with new ones to complete cell functioning properly. Cell growth and reproduction can be disorganized and uncontrollable. It can be that cells develop improperly, which would cause improper cell function. Cells can also die in wrong way. When cells are becoming cancerous, one or more of the above processes occurs. Leukemia is cancer of bone marrow blood-making cells. Blood and body organs become filled with abnormal, immature cells. They cannot do the jobs for which the regular blood cells are responsible. Small variations in the histology and morphology of cells in a blood smear are looked for by hematopathologists to identify the type of leukemia along with its features. There are 2 types of leukemia: acute and chronic. Acute leukemia is a fast-growing disease where the patient's blood becomes more and more loaded with defective leukemic cells at a very fast pace. Leukemic cell counts are high and normal white blood cell levels are low in a routine bone marrow test. Frequent recurring infections, higher chances of bruising, and tiredness are prevalent in people who have acute leukemia. Chronic leukemia takes its time to evolve, though. At the very beginning, leukemic cells are functional and alive. They are severely compromised in the later phase. The initial diagnosis is based on a positive test for an abnormal blood test, and the patient also experiences discomfort and fatigue. Leukaemia cells will ultimately surpass normal blood cells unless therapy is initiated, and this will interfere with systemic function. Acute as well as chronic leukemia types are differentiated into other categories based on cell type involved. The second differentiation

indicates whether myeloid or lymphoid cells are involved in leukemia. Myeloid leukemia cells aggregate to create myeloid "sarcomas," other medullary myeloid tumors, granulocytic sarcomas, or chloromas, whereas lymphoid leukemia cells aggregate to produce lymphadenopathy. The four leukaemias are displayed in Fig.1.

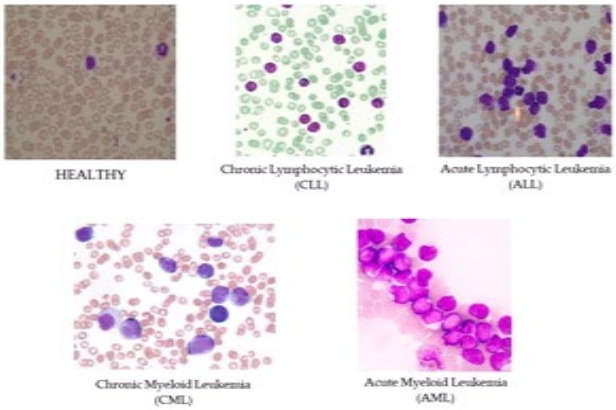

Fig 1: Leukemia Types

2. LITERATURE SURVEY

M. Abdeldaim et al,…[1] pay attention to the lymphocyte cells targeted by lymphoblastic carcinoma. Research objective is to identify lymphocytes from microscopic images by segmenting them and marking each segmented cell as normal or not. This chapter evaluated the viability of the suggested diagnosis methodology on the publicly available ALL-IDB2 dataset. 260 images of cells in total in the database; the ALL are half, and the normal ones are the other half. The segmentation phase in the new method's technique includes color change from RGB space to CMYK color space. To add contrast stretching, histogram equalization comes next. Thereafter, follows the noise removal, i.e., background removal, thresholding, and removal of noise. Then features from every cell were eliminated. They can be categorized based on their shape, color, and textural feature. In an attempt to enhance the performance of the classification, three normalization methods were used for each extracted feature: min-max, grey-scaling, and z-score. Lastly, various classifiers were employed for evaluating performance of proposed system, encompassing Naive Bayes (NB), K-Nearest Neighbors, Decision Trees (DT), and Support Vector Machines (SVM).

M. Nassar et al,…[2] introduced technique based on ML and image flow cytometer for examining, classifying, and producing WBC differential counts that can be utilized by doctors to monitor and diagnose patients. GB plus random under sampling was the best approach found for classifying WBCs into the primary types with an average F1-score of 97% after six machine-learning classifiers were compared. Moreover, we demonstrated that lymphocytes can be morphologically separated for the first time by Gradient Boosting with random under sampling, having mean cross validation F1-score of 78%. The method being introduced is a step above the existing state-of-the-art flow cytometer technique by enabling cell identification without fluorescent markers. This could minimize the mechanical load on cells and enhance sample preparation process.

R. B. Hegde et al.,…[3] showed how WBC classification can be performed by employing both conventional image processing and DL techniques. Both methods yielded similar results with 99% overall accuracy and sensitivity. Segmentation and feature extraction accuracy control the classifying accuracy of a common image processing method. To rule out this, deep learning techniques are used. It is a long process needing abundant tagged data and robust infrastructure facilities, but it learns the feature automatically irrespective of image variations. Because of its data availability, CNN can classify WBCs and resize cell images as per network requirements. The future concern of the current study will be to develop a robust segmentation approach to deal with variability in peripheral blood smear images. With the simpler and low-resource classical image processing method, we were able to produce results as good.

Pau Rodr´ıguez, et.al,…[4] introduced a quick, SGD-trained, modular feed forward attention technique that doesn't change base CNN architecture. As it is to be run parallel to core architecture without incorporating additional computing time, proposed model can thereby be employed for enhancing any pretrained architecture, i.e., "residual neural networks (ResNets)" or VGG. With attention modules positioned at various CNN depths, local input-based class predictions are made from fine-grained features of core CNN feature map activations at multiple levels of abstraction. Local predictions are then scaled by attention gates to fix original network output class distribution. For example, when blue sirens are involved, the new model alters the prediction from "sedan" to "police-car." Yet this model involves extra computation

steps, enhancing the load. Conversely, our method can run in parallel with the enhanced structure, which would significantly reduce its computational expense.

Jianpeng Zhang, et.al,…[5] propose classifying skin lesions in ceroscopy images with the ARL-CNN model. The method improves DCNNs' discriminative representation learning ability by combining special attention learning methods with residual learning. Generating attention maps for lower levels from the feature maps learned by higher levels is objective of new attention learning method. Our model was evaluated with ISIC-skin 2017 dataset. As per experiments, introduced ARL-CNN model is capable of automatically focusing on discriminative regions of lesions and delivering advanced classification accuracy for skin lesions. For each ARL block, a novel combination of residual learning and attention learning is utilized for enhancing its capability in discriminative representation. The learning process of the proposed attention leverages feature maps learned by high layer for building attention maps for low layer, rather than relying on other learnable layers. This relies on the inherent self-attentional ability of DCNNs.

3. FEATURES EXTRACTION

To determine microscopic characteristics of leukemia and reach diagnosis on basis of these characteristics, the process of feature extraction is extracting picture parameters. Medicine professionals rely on leukaemia's characteristics. Chosen diagnosis technique plays essential part in choosing features. For example, for contour rule in addition to pattern analysis, features are asymmetry and cultured network, respectively. Visual inspection of leukemia diagnosis is particularly challenging due to the intricate information provided by images, which needs inspection by skilled medical experts. Feature selection is a significant step prior to classification. Its purpose is to minimize the number of derived feature descriptors so as to lower the computational cost of the classification. This illness is not minor as duplication was ruled out. This may have an adverse impact on discriminating power.

A. FEATURE EXTRACTION (COLOR BASED)

Color of an image is the most prominent thing noticed and most important by people. Color is considered first while extracting features because color information is more perceptible to the human eye than black and white. A widely used method for displaying color contents is the color histogram. The algorithms work in the same manner, selecting a color space, determining color features, and designing related algorithms.

The technique most often used to remove a picture's color feature is the color histogram. It represents the image through different perspective. It displays frequency distribution of the colour bins within image. It stores it once it counts the respective pixels. There are 2 types of colour histograms: local and global. A colour histogram is global colour descriptor which evaluates each statistical colour frequency in image. It is employed for solving problems of rotation, translation, as well as angle of view variation. Local colour histogram is concerned with an image's composition. Global color histograms disregard the spatial locality of the pixel; local color histograms take this into consideration. Because it is simple to compute and unaffected by even the smallest change UN the image, the color histogram plays essential role in indexing and retrieval of image databases. It possesses two significant drawbacks apart from these benefits. In the first place, the entire geographical information isn't considered. The second drawback is that histogram isn't robust as well as unique; 2 different images possessing the same color distribution will contain identical histograms, yet the same view photos captured using different light exposures will contain different histograms. A set of bins demonstrating the chance that a given pixel in the image is of a certain color is referred to as "color histogram. For a particular image, a colour histogram is a vector:

H = {[0, H, H1, H2,... H[i] H[N]}

N is number of bins in the color histogram, H[i] is the number of pixels in color i in the picture, and I is a color in the color histogram representing a sub cube in the RGB color space"

Number of colors in selected color model is indicated by the histogram.

Value of each bin of image's color histogram that contains same corresponding color is referred to as the value of the bin. Pixels in an image are frequently grouped into bins. Color histograms need to be normalized in order to enable comparison of photographs of different sizes. Normalized color histogram H' is described "as:

H′ ={H′[0], H′[1], H′[2],…, H′[i],…, H′[N]}

Where P is the number of pixels in an image and H ′[i] = H[i]/P (all other variables unchanged)."

The assumption of ideal color space quantization is that homologous and different colors will be in different sub-cubes and not in the same one. The information richness of the images will be reduced further when there are fewer colors since it is more probable that unlike colors will be placed in the same bins rather than similar colors in different bins. On

contrary, color histograms having large number of bins will provide more information about content of an image and lower the chances that various colors are grouped in the same bins. Conversely, they increase the computation time to obtain the color histogram separation and enhance chances that similar colors will be grouped in distinct bins. Hence, how many bins should be included in color histograms is a trade-off.

B. SHAPE-BASED EXTRACTION OF FEATURES

One of the intrinsic characteristics employed to define the content of an image is shape. Shapes are often distorted due to noise, occlusion, and random distortion, which complicate the object detection problem. Shape features are the primitive building block of shape representation and can be obtained from boundary plus inside content or from boundary content. A group of feature types for form of an object are generated for recognition; the measure of how useful they are is how much they can retrieve similar forms from the database. Shape descriptors should be capable of retrieving similar forms in database rapidly even after having gone through huge transformations like rotation, translation, flipping, scaling, etc., so that high retrieval accuracy is ensured. For comparison and retrieval, the shape descriptor should also be able to recognize effectively the noisy and inaccurate shapes that can be tolerated by humans. This requirement of resilience is known as. It must be possible for an application-independent shape descriptor to retrieve images for any shape, not only specific ones.

The minimal processing complexity of the shape descriptor is one of its major advantages. By decreasing the number of image features utilized in computing process, the calculation complexity is decreased and form descriptor is enhanced. Stability and clarity are obtained here through low computational complexity. For applications in shape retrieval, numerous form representations and description methods have been established. The form representation and description techniques are classified into two classes based on whether shape features are extracted through whole shape region or just contour.

i. Methods based Contour.
ii. Methods based Region.

Each technique further divides the two approaches: the global approach and the structural approach. What distinguishes structural approaches from global procedures is whether the form is represented in its whole or portions.

C. TEXTURE BASED FEATURES

Texture is an important aspect of photos that can be used as a powerful geographic cue to assist in retrieval. While texture by itself cannot pick out related photos, it can be employed for differentiating between textured photos and non-textured photos. To enhance retrieval, other visual cues, including color, can be added to the set.

"Textural features are: Statistical measures

- Contrast
- Entropy
- Homogeneity"

Utilized for extracting texture characteristics such as Contrast: Measurements On the contrary, P (i,j) on diagonal, i.e., i=j, will be affected by local intensity changes. Formula below can be employed for measuring contrast of pixels to their neighbors.

1. CONVOLUTIONAL NEURAL
2. n=0
3. i=1
4. j=1
5. NETWORK ALGORITHM
6. Various Neural network approaches are
7. Correlation: The extent of the gray level inter-pixel linear dependence on the relative positions of each pixel is known as correlation (correlation). Correlation can be estimated as follows:
8. Correlation = $\sum G-1 \sum G-1 \{ i*j\} XP(i,j)-(\mu x-\mu y)$
9. Used to categorize leukemia cell images. Currently used neural networks for illness prediction are convolutional neural networks.
10. i=0
11. j=0
12. $\sigma x X \sigma y$

13. The picture below shows how a typical CNN is constructed using a combination of four primary layers.
"Contrast = ∑G−1 n2{∑G ∑G
P(i, j)}, |i − j| = n
Where μx, μy, σx, σy is mean and P(i,j) is standard deviation values"
Homogeneity: It is abbreviated as HOM. Value is shifted to the GLCM diagonal, which determines the extent of dispersion of the elements within the GLCM. Its range is [0,1] and its value is 1 for diagonal GLCM. Homogeneity weight values are reverse of contrast weight, having weight drops exponentially loose through "diagonal.

Homogeneity = ∑N−1 P(i, j)/R
Energy: Orderliness is" paired with energy consumption in work. It utilizes the texture to identify the photo order. It offers the sum of square components of the GLCM. It is very different from entropy. An optimally placed window is one that consumes less energy. The character ASM for the texture (Angular Second Moment) can be represented with the square root of energy. Its range is [0 1]. The value of the image is 1 since it is constant. Energy equation has been computed "as follows:

Energy = ∑N−1 P(i, j)^2"
Among the other normalization methods, this worked best. It normalized the color by dividing every color component by average of same component in healthy blood cells of patient. Texture information is derived with the help of generalized co-occurrence matrices, which are extensions of co-occurrence matrices to cell images.
Rectified Linear Unit

- ReLU for short
- Fully linked layers
- Pooling layers; convolutional layers

LAYERS OF CONVOLUTION

This is the first element of CNN. Primary mathematical operation done here is convolution, which is simply as the term implies; it involves employing sliding window function to matrix of pixels which forms image. Both "filter" and "kernel," which are names for the sliding function used with the matrix, can be synonymous.
In convolution layer, multiple filters of the same size are used, and each filter is utilized for identifying particular pattern from image,

A) ACTIVATION FUNCTION

After each convolution operation, a ReLU activation function is applied. This function trains network non-linear relationships among image's features, reinforcing network for identifying many different patterns. It also reduces the impact of vanishing gradient problems.

Pooling layer
To draw out most essential features from intricate matrix is the goal of the pooling layer. This is achieved by applying a couple of aggregation processes, which reduce feature map's (convoluted matrix) size and, consequently, memory required for network training. Pooling is also essential in preventing overfitting.
Most frequently employed and available aggregating functions for use are:
• Max pooling, or feature map's maximum value
• Sum pooling is equivalent to adding together all of the feature map's values.
• Average of all values is used in average pooling.

B) FULLY CONNECTED LAYERS

The inputs of these levels, last layers of "convolutional neural network (CNN)", correspond to one-dimensional matrix that last pooling layer flattened. They are applied to ReLU activations functions to check for non-linearity.
The last predicted label is the one with the largest probability score. Softmax prediction layer is utilized to produce probability values for all of the possible output labels.

C) DROPOUT

The regularization method dropout is employed in order to add more capacity to the generalization of the neural networks when they possess large numbers of parameters. Random neurons are dropped during training, and the remaining neurons are required to learn fresh features from the input data.

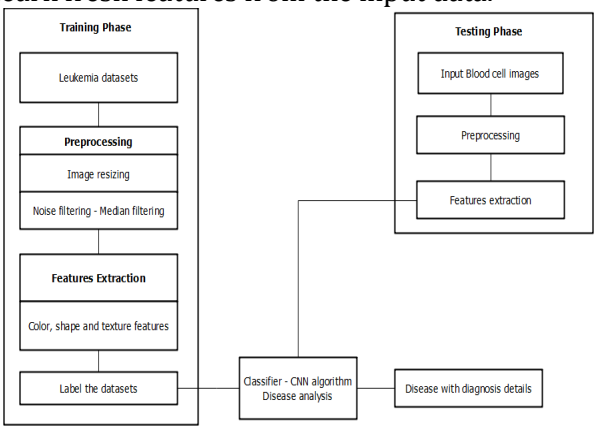

Fig 2: Proposed Architecture Diagram

4. EXPERIMENTAL RESULTS

KAGGLE Blood cell records can be employed for examining how well system works. Various performance metrics can be evaluated for assessing system's effectiveness, encompassing accuracy, specificity, sensitivity, error rate, as well as precision.

"True positive (TP): quantity of precise positive predictions true positives
False positive (FP): number of false positives - imperfect positive prediction
True negative: Number of true negatives (TN) or perfect negative prediction
False negative (FN): number of true negatives - imperfect negative prediction"

ACCURACY

Ratio of overall number of perfect predictions to whole amount of test data is referred to as "accuracy (ACC)". It can also be represented as 1-ERR. Accuracy has a range of 00-10, where 10 denotes highest possible accuracy

"ACC = TP+TN
TP+TN+FN+FP
x 100

Algorithm	Accuracy
Naives Bayes algorithm	50%
Support Vector Machine	65%"
CNN	80%

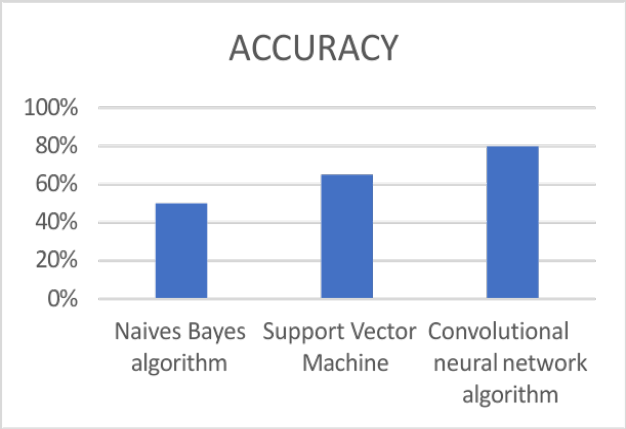

Figure 3: Evaluation comparison chart

From the figure 3, the CNN model performed in the current machine learning methods in terms of accuracy rate.

5. CONCLUSION

This research applied Back Propagation Neural Network methods to rapidly help hematologists in categorizing WBCs into subgroups based on microscopic cell images. This configuration facilitates cell recognition and a correct diagnosis of a patient's specific disease. The experiment output enhances photo identification over ML algorithms. Over 80% of the exam set questions were correctly answered. Thus, an optimal model can be developed and used in medicine diagnosis and medicine applications based on the number and kinds of WBCs if model is well-trained by good computational powers available.

CONFLICT OF INTERESTS

None.

ACKNOWLEDGMENTS

None.

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