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Classification of Leukemia Using Convolution Neural Network

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Abstract: The death caused by Leukemia has been ranked in the top ten most dangerous mortality cause for the human being. There are numerous reasons and causes, in spite of the causes and reasons the profound problem is the slow decision-making process which delays the time required to proceed with medical treatment for the patients. That's why the enhanced medical support process has become necessary for the classification of leukemia. The four different types of Leukemia are as follows Myeloid Leukemia where we have acute and chronic subcategories and in the same way, it goes for the myeloid type as well, these affect various cells and systems such as the blood cells, bone marrow, lymphatic system and which causes the death of patients. The proposed method improves the CML, CLL, AML and ALL characteristic accuracy by scanning color and textural features from the blood image using image processing and to aid in the grouping of CML, CLL, AML and ALL. The following technique proposes a quantitative microscopic approach toward the grouping of blood sample images. A model using Modified Convolution Neural Network (CNN) architecture is used to optimize the classification process. Based on optimized feature space, a CNN model with various kernel functions (filters) used to abstract the features from the pixel values. The proposed method is tested using nearly 10000 microscopic blood images. The outcome confirmed that the accuracy of the classification using blood sampled images which was up to 98%.

Keywords: Convolution Neural Network, Leukemia, Lymphocytes, Myeloid, Max pooling

1. Introduction

Leukemia (blood cancer) is a type of cancer that affects various blood cells and many agents that can be a cause for it. The most common ones are by radiation exposure in industries or other areas where the radiation is severe, inherited from the family tree, exposure to some kind of chemicals. Generally, leukemia was clustered based on the speed of progression and the type of cells that are been affected. Based on the researches of the past, leukemia is categorized into two main sets: acute and chronic. In acute leukemia, there is an unusual functioning of blood cells (immature blood cells predominately) which are unable to carry out their regular functions increases rapidly. On the other side chronic leukemia, some types of blood cells produce these weird towering cells kind of structure and this also acts as a cause for the descend in the generation of new cells. In controversy to acute leukemia affected cells, chronic leukemia affects cells that are more mature. Further classified based on, the number of white blood cells affected, they are lymphocytic leukemia and myelogenous leukemia. Lymphocytic leukemia (lymphoblastic) occurs in a type of marrow cell that leads to the formation of lymphocytes. Myelogenous leukemia (myeloid) is another one where it affects the myeloid cells which are responsible for the production of red blood cells and other types of white cells and platelets. [3-5]

Summarizing the classification, leukemia is described to be in four main forms based on the number of cells affected and the type of cells that are affected acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL) and chronic myeloid leukemia (CML), as we see in Table 1.

Table 1. Shows the different types of leukemia

	Lymphocytic leukemia	Myeloid leukemia
Acute	Acute lymphoblastic leukemia (ALL)	Acute myeloid leukemia (AML)
Chronic	Chronic lymphocytic leukemia (CLL)	Chronic myeloid leukemia (CML)

Acute lymphoblastic leukemia is a type that is mostly seen in young children but also spread across the people aging 65 and above. On the other hand, Acute myeloid leukemia is seen most commonly in adults than in children. [5] Chronic lymphocytic leukemia is more common and seen predominantly in men moreover two-thirds of the patients are men. The survival rate is 66.9% for Chronic myeloid leukemia seen in adult again. A study from the Institute of National Cancer, there about 24,500 people who died because of leukemia in the US in 2017. To tackle this situation an early diagnosis process for Leukemia is required. [6-10]

2. Existing System

In a manual or more of a traditional method in the detection of Leukemia, doctors check the microscopic images of the blood samples. This is tedious and time-consuming approach and the accuracy of the detection is mostly depending on the experience and skills of the individual, which is not reliable all the time. [5] The alternative solution is an automated process or system which can analyse the same blood sample images. It takes in the required portions of the blood sample image and does some filtering process to the images. K-mean clustering is one such approach used for finding the affected cells. [20] Next comes the histogram equalization and Zack algorithm is used for clustering the white blood cells in the blood samples. Mean, standard deviation, color, area, perimeter and the feature list go on. For the about mentioned features, the SVM classifier might be the perfect fit. The main drawback is that it just classifies the Lymphocytes and Myelocytes white blood cells for leukemia detection.

3. Proposed System for classification

3.1 Methodology

The figure I shows the workflow that shows the entire process carried out for the classification of leukemia from the blood sample images. The process starts with loading the dataset from the file to the program. Then separating the images for testing and training process. (figure 1) Then these loaded images are once verified before passing those images into the modified CNN.

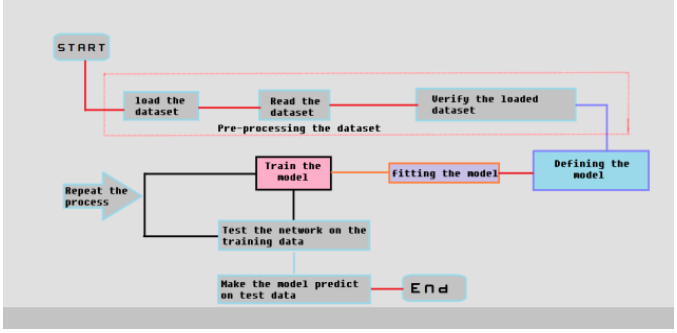

Figure 1. Flow of Process

The model is then defined with the various CNN layers for the classification of leukemia. After the creation of the model, the fitting of the model takes place. Fitting is the process where the parameters of the model is declared. [11] The parameters like the loss function used in the network and the metrics that are to be calculated are given. The training is then started with the provided parameters and the metrics to be calculated. Initially, the network is trained for about 100 epochs and then the accuracy, the loss is obtained from training the model [14-15]. These values are then plotted in the form of graph to better visualize the result. This process is again repeated for another 100 epochs and the graph is plotted. After the training is done to a sufficient accuracy the model is then tested with the testing set for the evaluation. Then the model is made to predict the unseen image. This is the entire process from the start to the end.

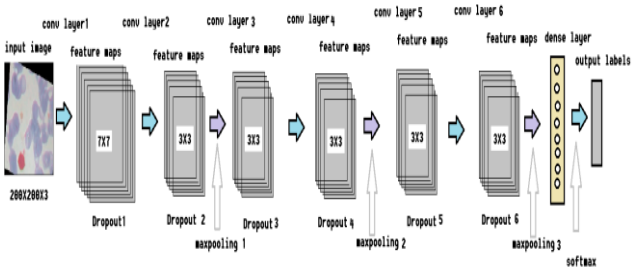

Figure 2. Proposed CNN architecture design

The model is built by arranging various layers of CNN in order, such that the model exhibits high performance. The input image size is 200x200 with the RGB color format. The input layer is then passed on to a convolution layer having filters that are specified in our function declaration and then attaches the Batch Normalization layer, after thatan activation function ReLU is used, and then another convolution layer is stacked in. Now, this combination is repeated and for the output layer the input is flattened. [21] This step is necessarily to be done to match the layer sizes of both the layers that are going to be converged. As an add on max-pooling layer is added and also dropout layer is used to avoid any over fitting that could occur in the network. There is a total of six layers used in the design of this complex model. (figure 2) Each of those layers contains several layers such as a Convolution layer, Activation layer, dropout layer and then the max-pooling layer. Finally, these layers are converged to the fully connected dense layer which is made to process the images to their respective labels. This classification involves a total of four classes. [22]

3.2 Convolutional Neural Networks (CNN)

In deep learning, CNN's are specifically applied for computer vision application that involves image classification and object recognition. To recognize the different types of leukemia, a model must be trained with a larger set of images, so that it could predict accurately the types of leukemia after the model is trained. This way of prediction of images through training the images by labels is termed as "supervised learning" which requires a dataset of images with labels to predict the label of an untrained image.[19]

$$G[m,n] = (f * h)[m,n] = \sum_{f} \sum_{k} h[j,k]\, f[m-j,\ n-k] \quad (1)$$

Subsequent feature map values are calculated according to the above formula, where the input image is represented by f and kernel by h. (1)

CNN consists of a stack of different types of layers that akes in input data, performance some of the mathematical and logical (in some cases) operation (matrix addiction and vector addiction) and predict the type or probabilities at the output. Instead of using standard hand-crafted feature extraction methods, CNN stakes in the raw pixel data of the input image as the input is fed as a flattened vector. For example, a [200x200] color image will be fed into the input layer. CNN analysis the input image and derives complex feature maps that are present in the input image using various layers which has auto learning filters and comes up with a combination of feature maps the model can predict the type of image that is fed in [18]. The neurons in a CNN layer need not necessarily be connected to all the other neurons of the next layer, only a few neurons are left out unconnected. The first layer of the convolution layer detects some minimal or primary features such as corners and edges in the image [16-17].

The upcoming layers might pick up and detect middle-level features such as shapes and textures, and finally, higher-level features will be detected by the next higher layers in the network.

3.3 Pooling Layer

Besides convolution layers, CNNs fairly often use supposed pooling layers. They are used primarily to scale back the dimensions of the tensor and speed up calculations. These layers are unit straightforward - we want to divide our image into totally different regions, and then perform some operation for each of these elements. As an example, for the scoop Pool Layer, we tend to choose the most worth from every region and place it within the corresponding place within the output. As within the case of the convolution layer, we've got2hyper parameters accessible — filter size and stride. However, if you 'reper forming pooling for a multi-channel image, the pooling for every channel has to be done individually.

For a feature map having dimensions nh x nw x nc, (2) the dimensions of output obtained after a pooling layer is

$$(n_h - f + 1) / s \times (n_w - f + 1) / s \times n_{c(2)}$$

n_h-Height of the image map
n_w-Width of the feature map
n_c - Number of channels in the feature map
f -Size of filter
s - Stride length

4. Results and Discussion

4.1Plots of Training and Validation Accuracy

Training accuracy is calculated after the training is done. The plot shows how the data is being fitted into the model for each epoch. Training accuracy predominantly keeps on increasing as the epochs go on. The training accuracy for the proposed architecture is 98.8%.

After every epoch, the model is put into a testing kind of a phase where the model is tested against the unseen data. Validation accuracy describes how accurate the model makes the predictions on the data that the model is not trained on. The validation score or accuracy is about 97% for the proposed CNN architecture and the validation accuracy plot is shown in (figure 3) & (figure 5)

Figure 3. Training and validation accuracy on first 100 epochs

4.2 PLOTS OF TRAINING AND VALIDATION LOSS PLOTS

Training loss is the error that occurs during the training process of the CNN model with the training dataset. The training loss for the proposed architecture is about 0.07 and the training loss plot is shown in (figure 4) & (figure 6)

Validation loss is the error made while fitting the model with the dataset after every epoch. The validation loss is about 0.38 and the validation loss plot is shown in (figure 5)

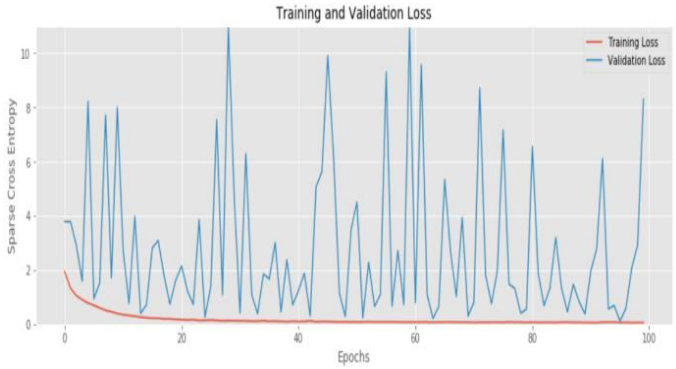

Figure 4. Training and variation loss of first 100 epochs

Next 100epochs –

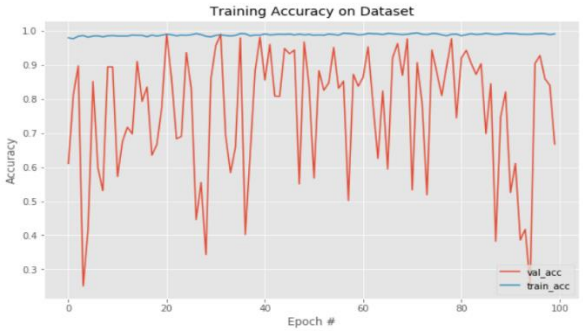

Figure 5. Training accuracy on next 100 epoch

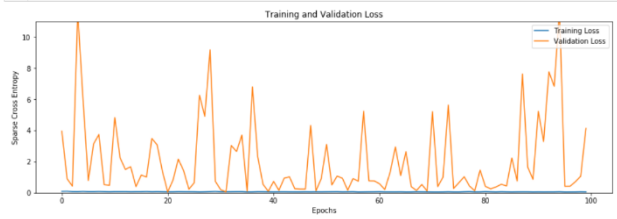

Figure 6. Training and validation loss on next100 epoch

Figure 7. Confusion Matrix of the model

A confusion matrix is a kind of a tabulated summary of the prediction results on a classification problem. The numbers of correct and incorrect predictions are tabulated with values denoting the different classes. (figure 7) This is the key to the confusion matrix. The confusion matrix displays the way in which the model is trained when it makes predictions. It gives insight not only on the errors being made by the model but more importantly the different errors that are being done while predicting [23].

Figure VII shows the confusion matrix that is obtained after the model is trained with the image dataset. The labels ALL, CLL, CML, AML are represented as 0,1,2,3 respectively. Randomly selected 200 images are predicted with the trained model and the confusion matrix is plotted based on the predicted result.

5. CONCLUSION

The proposed model is to identify the types of leukemia using CNN. The obtained results show the effectiveness of CNN for identifying the types of leukemia. The accuracy is greater than 98% for a dataset with a small number of classes. In the future works, the CNN can be designed in such a way to effectively classify and predict the different forms of blood sample images.

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