

Accurate Recognition of Leukemia Sub-types by Utilizing a Transfer Learned Deep Convolutional Neural Network

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Abstract—Leukemia has been causing more than 350,000 deaths per year despite holding a notable number of studies on the prognosis, diagnosis, and therapy for Leukemia. Computerized Leukemia disclosure may change the circumstances, as steps can be obtained instantly, hence, precise identification of Leukemia has been a domain of concern for researchers for nearly a decade now. Lately, many contributions have been bestowed to the scientific society concerning the identification of Leukemia. But with the expansion and development of the datasets, the demand for accurate identification of Leukemia is becoming more demanding every day. In this research, we examined a Leukemia sub-types dataset that consists of three kinds of Leukemia individuals. We introduced and implemented a modified DenseNet-201 design and produced an overall accuracy of 99.56% which exceeded all the previous investigations.

Index Terms—Leukemia Classification, Leukemia Sub-types Dataset, Transfer Learning, Deep Convolutional Neural Network, Modified DenseNet-201 Architecture, Augmentation

I. INTRODUCTION

Leukemia is a combination of blood fatalities that commonly begin in the bone essence and emerge in large amounts of abnormal blood cells [1]. Some blood cells are not fully seasoned and are identified as leukemia cells [2]. Symptoms may include bleeding and bruising, seeming vulnerable, raised temperature, and extensive risk of infections [2]. Those symptoms appear because of the lack of normal blood cells [2]. The particular cause of leukemia is indistinguishable [3]. A blend of family servings and environmental elements is supposed to perform a function [3]. Risk factors include smoking, ionizing radiation, certain elements e.g. benzene, previous chemotherapy, and down symbol [3], [4]. People with a family history of leukemia are additionally at more prominent exposure [4]. Leukemias and lymphomas both lead to a more comprehensive compilation of tumors that affect the blood, bone marrow, and lymphoid organization recognized as tumors of the hematopoietic and lymphoid tissues [5], [6].

In kids under fifteen, the five-year persistence rate is greater than 60% or even 90%, regarding the sort of leukemia [7]. In kids with acute leukemia who are recovered from cancer after five years, the cancer is unlikely to return back [7]. In 2015, leukemia was found in 2.3 million people worldwide and caused nearly 353,500 deaths [8], [9]. In 2012, it was

again obtained in approximately 352,000 personalities [9]. It is the most common variety of cancer in children, with 75% of leukemia cases in children being the acute lymphoblastic type [4]. Nonetheless, over 90% of all leukemias are diagnosed in adults [4], [10]. It occurs more commonly in advanced areas of the globe [11].

In this research, we analyzed a Leukemia sub-type dataset which has samples from three sub-types of Leukemia. After implementing augmentation, we implemented a modified DenseNet-201 design on the dataset and obtained an overall accuracy of 99.56% which surpassed the previous research outcomes by a distinct boundary.

II. LITERATURE REVIEW

Earlier, diverse approaches and systems have been exercised by researchers for the automated perception of Leukemia to identify sub-types [12] and a semi-automated lesion identification [13]. Orlov et. al. [12] studied a computer vision system for the quantitative classification of image features. From the measurement of identification enforcement, it was determined that the best recognition accuracy was 98% on the three lymphoma classes [12]. Furthermore, Sertel et al. obtained an accuracy of 90.3% with three groups [14]. One research proposed an accuracy of 89% taking four types into consideration [15]. Tuzel et al. also produced an accuracy of 89% with five types [16] Another study proposed an accuracy of 78% but this time two subtypes were under judgment [17]. Tabesh et al. produced 96.7% accuracy with two groups [18]. 79% accuracy was obtained with two groups by Monaco et al. [19]. The overall accuracy of 99% for three groups was obtained in one study as well [20] but the version of the dataset was older. A recent paper has obtained an accuracy of 97.33% for the same fresh dataset examined in this research [21].

III. MATERIALS AND METHODS

A. Dataset Description

In this study, we examined a Leukemia sub-type dataset including a total of 334 picture examples for three sub-types of Leukemia [22]. There are 113, 139, and 122 samples for chronic lymphocytic leukemia, follicular lymphoma, and mantle cell lymphoma respectively. All the pictures are in TIF form and the kind of pictures is RGB.

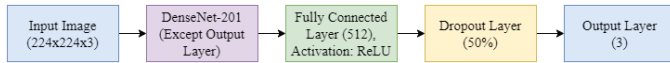


Fig. 1: Proposed Modified DenseNet-201 Architecture

B. Convolutional Neural Network

The convolutional neural network, also recognized as CNN, is one of the most common types of deep neural systems which is usually studied for interpreting optical pictures of various research fields [23]. Convolutional neural networks are utilized for the identification of pictures and videos, picture classification, recommender systems, natural language processing, medical picture study, and economic study [24], [25], [26]. If we regularize the multilayer perceptrons, we will obtain the convolutional neural networks. In multilayer perceptrons, the neurons of the individual layer are correlated to all the other neurons of the previous layer, therefore, it makes a fully associated progression among two layers. But the term fully-connectedness enables us to include overfitting to the system. On the contrary, Convolutional Neural Network also exercises regularization but by collecting patterns with the assistance of easier and fewer patterns instead of utilizing fully-connectedness. Because of getting the benefit of hierarchical designs of data, CNNs don't require huge pre-processing steps. CNNs are competent in obtaining important knowledge from the data and acquire the filters which are not common in traditional machine learning algorithms. In conventional algorithms, the inputs are custom engineered or extremely preprocessed in a separate step. CNNs were motivated by the relationship among neurons that can be observed in the primate cortex and are generally exercised for picture identification or recognition in diverse domains of research.

Typically a convolutional neural network is constructed with an input layer and an output layer simultaneously with many hidden layers. The hidden layers of a convolutional neural network can include a series of many convolutional layers that are connected via multiplication or a dot product. An activation function is exercised and it is followed by additional convolutions such as pooling layers, hidden layers or normalization layers, and fully connected layers. These layers are utilized in the chain to gather more knowledge from the input data. Although these layers are described as convolutions, it is simply a custom. In terms of calculation, it is truly a cross-correlation or a sliding multiplication. It maintains significance for the contents in the matrix, in which it involves by which way measurement is provided at a distinct index point.

C. Transfer Learning

Transfer learning focuses on gathering knowledge collected while fixing one barrier and performing it to another but comparable perplexity [27]. For example, the knowledge gained while discovering to classify cars could be used while the perception of vans. This domain of research reveals an extraordinary connection to the magnificent archives of cerebral

investigation on the transfer of knowledge, though established relationships among the two sections are incompetent. From a practical viewpoint, carrying or conveying information from formerly accomplished jobs for the training of fresh jobs has the ability to dramatically intensify the individual achievement of an operator [28].

D. Proposed Modified DenseNet-201 Architecture

The common foundation of the Convolutional Neural Network (CNN) can be discovered in [29]. However, in a conventional Convolutional Neural Network, all layers are uniformly connected which makes the network challenging to grow larger and deeper, as it may spread beyond difficulties of either misclassifying or gradient missing elements. After that, ResNet proposed an approach to joining the bypass attachment by jumping at least two layers. Then, DenseNet additionally increased the model by concatenating all the characteristic patterns in series instead of the addition of the output characteristic charts from all previous layers. In this investigation, we've established a modified DenseNet-201 architecture which is represented in Figure-1. After the implementation of DenseNet-201 basic layers, we added a fully connected layer of size 512 accompanied by a dropout layer of 50%. Lastly, an output layer is connected with having a size of 3. While training by this design, no layer was held frozen.

E. Augmentation

Insufficient data has always been a remarkable barrier while performing deep learning structures like convolutional neural systems. Furthermore, imbalanced datasets in terms of groups can be an extra hurdle. While there can be adequate data for some groups, consistently significant, but the under-sampled groups will undergo ineffective group-specific enforcement or effectiveness. This aspect is consistent. If the model studies from fewer examples or events of a presented class, it is less feasible to prophesize the class label or the test label. Image augmentation artificially creates training photographs via various methods of processing or association of multiple processing, such as random rotation, shifts, shear, and flips, etc. [30].

Augmentation has been proved efficient in several obstacles like data augmentation accompanied by expert insight [31] and more comprehensive image augmentation [32] also has verified in achieving effective results in picture identification. Modest players in the AI business often lack passage to notable volumes of data. The impulse of our dilemma is both comprehensive and precise which motivates the practice of data augmentation in this research. Among various data augmentation techniques some popular approaches are flipping, twisting, resizing, cropping, altering, combining Gaussian noise, etc.

IV. EXPERIMENTAL ANALYSIS

A. Preprocessing

Because of feeding photographs to a convolutional neural network, a substantial preprocessing of the photos was

TABLE I: Class-wise accuracy, precision, recall, f-score, and support of each of the classes

Classes	Class-wise Accuracy	Class-wise Precision	Class-wise Recall	Class-wise F1-Score	Class-wise Support
CLL	1.00	1.00	1.00	1.00	300
LLF	0.99	0.99	1.00	0.99	300
MCL	0.99	1.00	0.99	0.99	300

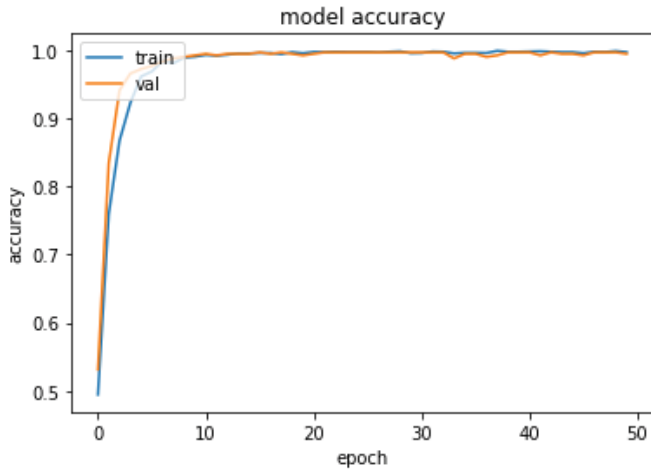


Fig. 2: Training accuracy and validation accuracy of our proposed architecture

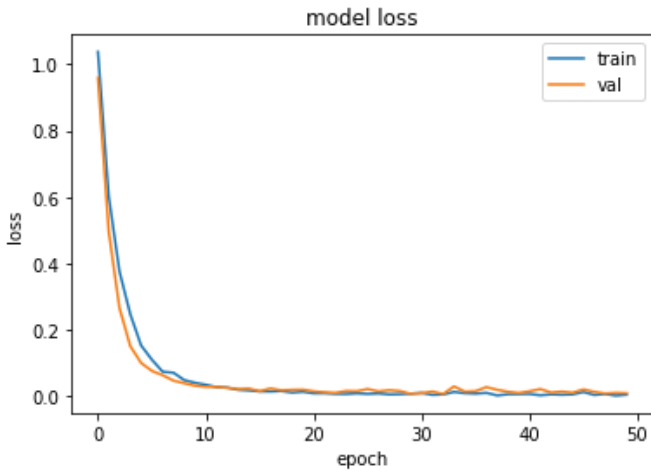


Fig. 3: Training loss and validation loss of our proposed architecture

hopped as CNN is a compelling system that can recognize estimable characteristics from raw photos. Nevertheless, some preprocessing steps were expected. The input photographs were in different aspects, therefore, they were resized to 224x224x3. For more specific identification, augmentation was implemented with the compensation of the Augmentor Library [33]. While utilizing the method of augmentation, the max left rotation, the max right rotation, and the probability of rotation of the rotation function was anchored to 3, 3, and 0.4 respectively. The values of grid width, grid height, probability,

TABLE II: Comparison between our proposed work and notable previous works

Classifier or Work Reference	Overall Accuracy
Sertel et al [14]	90.30%
Foran et al [15]	89.00%
Tuzel et al [16]	89.00%
Nielsen et al [17]	78.00%
Tabesh et al [18]	96.70%
Monaco et al [19]	79.00%
Rucha et al [21]	97.33%
Nikita et al [20]	99.00%
Proposed	99.56%

and magnitude of the random distortion function were adjusted to 4, 4, 0.4, and 4 respectively. Moreover, the percentage ranges and the probability of the zoom random function were adjusted to 0.9 and 0.2 respectively. After the augmentation method, we had 1200 images per group, a total of 3600 images for three groups of Leukemia.

B. Design of Experiment

The model was trained for 25 epochs with a batch size of 24 as after that the validation loss shifted almost constant for the rest of the epochs. Adam optimizer [34] with the learning rate of 0.0001 was employed to maximize the error function. A categorical cross-entropy function was utilized for the loss or error function. For bypassing overfitting, the dropout technique was followed.

C. Result Analysis

Firstly, the augmented dataset was divided into the train set and test set. 80% of the data were stored in the train set and the rest of the 20% data was saved to the test set. Later, the proposed modified DenseNet-201 architecture was employed to the train set. Figure-2 represents the training accuracy and validation accuracy of our proposed design. On the other hand, Figure-3 represents the training loss and validation loss of our proposed design. Table-1 represents the class-wise accuracy, precision, recall, f-score, and support of each of the sub-types of Leukemia. Our proposed design produced an overall accuracy of 99.56% for the Leukemia dataset. Table-2 represents the comparison among our proposed work and distinguished previous attempts. From Table-2 it can be remarked that our proposed design exceeded all the previous strategies by a distinguished boundary, hence, our model is proficient in identifying the examined subtypes more precisely.

V. CONCLUSION

In this research, we examined a Leukemia sub-types dataset. Leukemia is one of the most popular diseases worldwide which is causing a large number of losses each year. Computerized disclosure of Leukemia sub-types with the assistance of the blood cell picture sample is essential to seek quick actions against Leukemia. In our research, we implemented a modified DenseNet-201 architecture and produced an overall accuracy of 99.56% which exceeded all the previous outcomes. Furthermore, we analyzed three sub-types of Leukemia and our dataset was the most updated one. From the result interpretation, we remarked that our proposed approach can be employed for precise recognition of Leukemia with only 4 misclassifications.

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