Acute Lymphoblastic Leukemia Detection Using Sequential, Lenet and Vggnet Models

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Abstract

The purpose of this research is to develop a web-based application for blood cancer cell detection using deep learning to provide accurate identification of acute lymphoblastic leukemia (ALL) and its subtypes. A conclusive diagnosis of acute lymphoblastic leukemia (ALL), as the most prevalent cancer, necessitates intrusion, expensive, and diagnostic test takes a long time. It is a tedious process to analyse acute lymphoblastic leukemia if the number of patients is quite high. In order to prevent mortality, it is important to identify acute lymphoblastic leukemia at an early stage. In the primary separating cancer from non-cancer instances, images of peripheral blood smear using ALL diagnosis plays an important role. Laboratory users' examination of these PBS pictures is plagued with issues such as diagnostic mistakes, as the wrong status of ALL symptoms frequently leads to an incorrect diagnosis. Taleqani Hospital (Tehran, Iran) takes the responsibility of preparation of images of this dataset. It is handled by their bone marrow laboratory. The blood samples from 89 patients are taken from peripheral blood smear, where 64 patients show the symptoms of ALL and rest of the people are healthy. The total image used in this dataset is 3256.All photographs were captured using and saved in JPG format. Haematologist find it helpful to identify the accurate condition of the patient in a quick and easy way. There are two classes namely benign and malignant. Pro-B, Early Pre-B and Pre-B cells are subtypes of Malignant. In this project, microscopic blood cell images are taken as input. The models used are Sequential Model, VGGNet and LeNet. Based on the comparison between these architectures, a conclusion has been arrived that LeNet is the most suitable architecture as it produces an accuracy of 95.75% and takes less computational time.

Keywords Deep Learning, Segmentation, Feature Extraction, Classification, Prediction, Acute Lymphoblastic Leukaemia, Microscopic Blood Cell Image, Haematology, Vignette, Lent and Sequential model.

1 Introduction

Acute lymphocytic leukemia (ALL) is a type of cancer which is seen in white blood cells. It is predominantly seen in children and the success rate for recovery is high. It is also seen in adults. ALL in adults cannot be cured and the mortality rate is high. In people over the age of 20, Acute Lymphoblastic Leukemia accounts for 15% of all cases. In the United States, 2 in 1 million persons are diagnosed with ALL at some point in their lives. ALL has an overall 5-year rate of survival of 69 percent. The figures are broken down further into 90 percent for youngsters and it ranges from 31-41 percent for adults. According to the study, 6,151 cases reported of ALL will be identified in 2020, yet 1,521 individuals will die from it. Other factors influencing survival are age, type of ALL, treatment response, WBC count. The creation of blood cells becomes aberrant, and the bone tissue creates an excess of b - lymphocytes. These cells are dysfunctional and push out the healthy ones. Being exposed to chemotherapy and radiation during past cancer treatment, high amounts of radioactivity such as those seen during nuclear accidents, genetic abnormalities such as Down's syndrome, and having a sibling, particularly a twin, with ALL are all common triggers for ALL. In order to prevent mortality, it is important to identify acute lymphoblastic leukemia at an early stage. General malaise or exhaustion, dizziness, breathlessness, tanned skin, repetitive or chronic infectious diseases,

flu or sweats, irregular heartbeats, tiny, bruised patches of skin, risen haemorrhage ,decreased cravings, spine or muscle aches, bulging or clots in lymph nodes have been some of the signs of ALL (neck, underarm, abdomen). Since there are 0 procedures to diagnose ALL early, it's crucial to keep attention to body language for any suspected signs. If you report these probable signs to a licensed doctor, you will receive prompt screening testing. Most of these symptoms aren't specific to ALL and will need to be investigated further. After you've informed your healthcare provider about your worries, they'll do a healthcare examination, as well as lab tests and blood smears. An enhanced amount of Leucocytes and inflammation caused in the bloodstream may indicate the creation of a large number of lymphoid cells. The majority of ALL patients will have a skeletal bone extraction and test to verify the diagnosis and define the kind of leukemia they have. Swollen lymph nodes or lymphocytes spreading to other afflicted regions are frequently detected using a chest X-ray and scanning. Leukemia cells can sometimes be seen in cerebrospinal fluid. ALL are handled differently based on the patient's age, illness stage, and subtype. Chemotherapy is typically the processing technique applied for ALL in adults. Chemotherapy is a cell-killing drug. Intravenous drugs are given in high doses. Stem cell transplant is another option for treating ALL. This involves injecting healthy stem cells into the patient's circulation from a donor. The patient's immune system can be rebuilt with the new healthy cells. Radiation treatment is another viable option.

It is a prolonged process to analyse acute lymphoblastic leukemia if the patients are large in number. This proposed method involves the design and development of an automated system. That will help the medical professionals to diagnose acute lymphoblastic leukemia more precisely. It assists haematologists to determine the accurate state of the patient in a quick and easy way. In this project, microscopic blood cell images are taken as input. Microscopic Blood cell image is segmented or divided as red, blue, green channels. Region-based segmentation is used here where segments with equivalent pixels are grouped together to form matrix labels. The next step is extracting the features. Microscopic blood cells are extracted by comparing the features. The three architectures used are: Sequential model, VGGNet and LeNet which filters the input image and extracts the features. These features are transferred to fully integrated layers. Classification is done along with it. Output is obtained as cancerous or not. If cancerous, then the particular type is displayed using Graphical User Interface (GUI).The deformation is detected using the reflection of Red Blood Cells on Nano-Particle in blood stream and to provide the design for selected drug delivery; detection of vascular disease and the deformability is treated [1]. However, extensive restraints such as only 2-dimensional simulation model is used. It is a prototype model and cannot be used in real world application. As a result, the Deep Learning approach is utilized to precisely and quickly determine the distortion of cells.

2 Related Work

In these papers, deformability in blood cells is found and diagnosed using various techniques.

Y. Sun, R. Zhang and Y. Chen [1] discovered that the projection of Red Blood Cells on nano-particle motion in the blood arteries was used to discover the deformation of Red Blood Cells (RBC). It also allows for the creation of custom medication delivery systems and the identification of vascular disease. Red blood cell deformation is modelled and cross-checked. The immersion boundary approach is used to create a numerical model. Blood flow curve, apparent blood viscosity, and Fahraeus-Lindqvist effect, Blood Flow Model, Deformation State of Red Blood Cells, and Nano-Particles Propagation Model are among the methods employed in this study. Additional methods used for Single and Multiple Red Blood Cells are Aggregation Detection, Deformation and Numerical Simulation model. There are some limitations to modelling and simulation settings. In fact, a two-dimensional model is impossible to detect the deformation of RBC.

S. Sadiq et al. [2] found that Thalassemia is an inherent disease. It is a type of blood related disease which is tedious to identify. Children are 25 % more likely to develop ß thalassemia if both parents are infected by this disease. The rate of mortality is high, if found at delayed phase. To diagnose this disease, a procedure known as liquid chromatography should be performed to increase the performance. It is a prolonged and expensive procedure. Four protein chains are present in the haemoglobin of the RBCs. A pair of beta and alpha globin chains is present. Any modification that takes place in any single chain results in thalassemia. Dataset used here is the Punjab Thalassemia prevention project lab report from 5066 patients. Three tree-based ML algorithms are used. They are Gradient boosting machine, Random Forest and Support Vector machine. The evaluation of ß

thalassemia is done based on voting indices of RBC. The accuracy achieved here is 93%.

K. AL-Dulaimi, J. Banks, K. Nugyen, A. Al-Sabaawi, I. Tomeo-Reyes and V. Chandran [3] found that White blood cell differentiation is an essential phase in haemato-oncology that can aid in the diagnosis of illnesses like leukemia. Different colors are used to stain the cells. Quantitative and qualitative analysis was crucial. This was familiar territory for pathology researchers. Analysis and acquisition of images of WBCs can be used to support and assist in diagnosing the progress of the disease. Computer Aided Diagnosis (CAD) improves accuracy and efficiency. It helps patients with early and increased diagnosis accuracy. Each kind of Leukocyte has distinct morphological characteristics which can result in the appearance of one or more species depending on how its unique granules respond during the staining process.WBC computations and classification are carried out with these features. The K-based Colour-space method is used. The accuracy obtained is 91%.

D. Krijgsman et al [4] found that ERpositive invasive breast cancer in postmenopausal women were treated additionally. There has been increasing interest in tumor microenvironments (TME) as potential biomarkers for diagnostic and prognostic purposes for various types of cancer because it provides an insight into how the immune system interacts with the tumor. Selective estrogen receptor modulators (SERMs) like tamoxifen or aromatase inhibitors (AIs) like exemestane are used for treatment, on their own or combined together. Hematoxylin-eosin (HE) and immunohistochemistry (IHC) images were used to quantify CD8-positive lymphocyte infiltrate in the central tumor (CT) as well as invasive margins (IM). Based on tissue type detection on HE, a region of interest is defined and based on the nucleus detector on IHC, CD8-positive cells can be identified. The technique defines the key tumor and intrusive margin of a tumor by using a supervised neural cell kind classification method to a hematoxylineosin stained tissue segment.

S. Khan, M. Sajjad, T. Hussain, A. Ullah and A. S. Imran [5] found Medical Image Analysis (MIA) has been proven to be useful in identifying a variety of disorders, including haemoglobin, cancer, and influenza. Neural and Artificial Learning are two strategies utilized in MIA. MIA works with a wide range of picture types, including Blood Smear photos. TML and DL are essential for cellular separation, cancer detection, segregation, clinical picture categorization, and recover the data utilizing computer-aided diagnostics (CAD). To discriminate Leucocytes in stained blood pictures, various approaches have evolved. Traditional methods take a long time. They too are prone to mistakes. By analyzing leucocytes, Autocad systems automatically identify AIDS and Leukemia. Due to shifting feature kinetics, selecting the best feature extractor is difficult. The increased adoption of DL approaches has led in elevated MIA models based on blood smear pictures in recent years.

R. A. Welikalaet al. [6] found that mouth cancer is most common variety of cancer, with a high mortality rate when diagnosed late. Mouth Oral cancer, malignancies and OPMDs are all detected automatically using images. CNN has made good advances in acquiring content from natural photography sites such Pascal VOC and Common Context. Convolutional neural network and the latest Mask R-CNN are examples of CNN algorithms that can produce a broad range of components. Faster R-CNN was evaluated by obstetricians at a diagnostic medical centre for colon polyp identification. This research exemplifies cross-sector collaboration by providing healthcare professionals the tools they need to provide detailed annotations. This study also explored how to use binding box from a large number of doctors. The dataset contains 2155 images. This study uses this method to analyze two ways for automatically detecting and separating the depth of oral ulcers: picture-based image classification. This paper offers various methods for applying binding box annotations from a large number of doctors. ResNet-101 is used to classify images. Faster R-CNN is used for object detection. For image processing that included lesions, the classification performance was 87.07 %, and for image processing that needed referral, it was 78.30 %.

S. Pang, Y. Zhang, M. Ding, X. Wang and X. Xie [7] found that study employs DL to classify the carcinoma kinds based on Computed Tomography scans of individuals. It faces two difficulties: Such pragmatic demands cannot be met by Artificial Intelligence classifiers which were equipped using public databases. Furthermore, the amount of patient data gathered is restricted. Rotation, translation, and transformation methods are employed to tackle this problem. The training data is broadened and adjusted. The method employs Dense Network. The tumor is divided into three types of carcinoma include squamous cell, adeno, and small-

cell. The adaptive boosting (AdaBoost) technique is utilized at the end. It helps with multiple categorization aggregation. As a result, categorization performance improves. It is possible to obtain an accuracy of 89.85%. In other words, it outperforms Dense Net. That's without the use of ResNet, VGG16,AdaBoost or AlexNet. This non-invasive technology is effective in the identification of lung cancer.

M. Zhang, X. Li, M. Xu and Q. Li [8] found that division and classification of RBC images are difficult based on the various size and shape of cells. Semantic segmentation using DL techniques are used. These are used for classification of images. The image noise levels are reduced using the U-network design. It has enhanced with the inclusion of deformed convolution layers. Sickle cell disease (SCD) is a genetic disease. Size varies from other standard cells. Binary and multi-class semantic segmentation has been used to identify sickle cell disease with high accuracy and background noise reduced by deformable layers. Ten layered CNN is used to identify single-cell patches with normalization. The accuracy obtained is 89%. Dataset used here is a multi-institutional RBC microscopic image.

P. K. Das, S. Meher, R. Panda and A. Abraham [9] found that Sickle cell disease arises in a person who has two abnormal copies of haemoglobin genes. The cells lifespan is for about 10 to 20 days. The healthy cells lifespan is 120 days. Automatic segmentation methods like region based, threshold based, and cluster based are used to find sickle cell disease from healthy cells. Proper segmentation between the touching and overlapping, done for identification and recognition. Pre-processing and image uplifting assists in the eradication of undesirable noise and suppress distortion. Feature extraction is done based on morphological features. KNN was used to classify sickle cells. The accuracy obtained is 80.6%. The accuracy obtained in deep Convolutional Neural Network is 89.9%.

P. Pandey, P. A. P, V. Kyatham, D. Mishra and T. R. Dastidar [10] discovered that microscopic images are achieved by peripheral blood smear (PBS), manual counting, and classification. It helps in resolving the issues faced in the manual laborious process. The accurate identification of subtypes is difficult as staining is undone properly. Deep CNN helps in the proper identification and accurate classification of the images based on unsupervised training of data. When evaluated on multiple data sets from which it is trained, the automatic categorization of camera-based microscopic pictures suffered from domain shift serious deterioration. The problem encountered by CNN is solved by unsupervised domain adaptations (UDA). The UDA needs access to unlabelled target data. They propose a theoretical closet clone and do not need target data during training. The UDA uses ResNet-50 and VGGNet-16 architecture and preserves an accuracy of 92%.

A. Shah, S. S. Naqvi, K. Naveed, N. Salem, M. A. U. Khan and K. S. Alimgeer [11] found that Leukemia is a disease. It causes quick creation of abnormal WBCs. It affects the bone marrow and blood vessels. It results in the loss of haemoglobin. It can be tested and found using a complete blood count (CBC). These manual methods are time consuming and less dependable. The computer aided diagnostic approach is adopted for the automatic identification and classification of leukemia. The pre-processing of leukemia cells is done with histogram equalization and contrast stretching techniques. The segmentation method used here is Utah's thresholding. Feature extraction is done based on the shape, area, circularity, and perimeter. Classification uses the k-nearest neighbours (KNN) algorithm. The accuracy obtained is 93%.

K. AL-Dulaimi, I. Tomeo-Reyes, J. Banks, and V. Chandran [12] found that an edge-based geometric contour is used to divide white blood cell nuclei using degrees of set forces. White blood cell fragmentation is difficult owing to changes in color, shape, backdrop, cell overlapping, and altering cell topologies. Morphological opening and closing operations are used to improve cell pictures. The picture intensity of the color is standardized using this method. Remove the lobe-to-cell bulge connections. The WBC nucleus area is cropped out using segmentation. It occurs in the cytoplasm and cell wall. Curvature, vector field-based level set forces, standard direction, and edge-based geometric active contours are all combined in this theory. The suggested segmentation approach is compared to and benchmarked against existing nucleus shape identification techniques. Curvature, standard direction, and vectors field are the three-level set forces studied. This is achieved by using edge-based geometric active contours with F-indices of 92, 91, and 90 percent. For all indices, the recommended segmentation method is more successful than alternative approaches.

Tharwat [13] found that Abstract Classification Technique applied to many applications. This

Technique helps to evaluate classification algorithms. Measures like Scalar Metrics and Graphical Methods are analysed to interpret different learning algorithms. The graphical approaches presented are receiver operating characteristics (ROC), Precision Recall, and Detection error trade off (DET) curves. This article clarifies confusion matrix problems in binary and multi-classification and demonstrates how to construct measures in binary and multi-classification situations. It also discusses the accuracy of these computations when compared to balanced and unbalanced data. Pre-processing procedures for plotting ROC, PR, and DET curves are described in detail.

Z. Li et al. [14] found that it enhances the patient's health, lung cancer division was performed precisely on the pathological section. Deep learning is the foundation of this system. A dataset of 200 patients includes training: testing ratio of 3:1. Lung cancer is detected using a computer-assisted diagnostic approach. Precision, Accuracy, Sensitivity, DC coefficient, and specificity are some of the criteria used to evaluate the methods. The DC coefficient was between 73 and 83 percent. Overall, the multi-model strategy outperforms the single approach, with mean DCs of 79% and 75%, respectively. Pathologists can still use deep learning to find suspicious areas of lung cancer that need to be investigated further. Breast cancer is detected with Big Data using kernel support vector machine with the Gray Wolf Optimization algorithm[15]. Machine learning methods are matched with Early Detection of Lung Carcinoma. The outcome of the classification provides 94.3% accuracy, which is the highest precision rate in comparison with the conventional methodologies[16-17]

3 Proposed Work

On comparing Sequential Model, VGGNet and LeNet, it is inferred that an accuracy of 93% and an error value of 7% is observed. In VggNet, the accuracy value is observed to be 34% and the error value is 66%.It requires more computational time. It works efficiently with large number of datasets. In LeNet, the accuracy value is observed to be 95.75%and error value is 4.25%.It is the shortest architecture and requires less time to process the data and provides the best result. Based on comparison it is concluded that LeNet is the most suitable architecture. Designing and creating an automated system to aid medical personnel in appropriately detecting acute lymphoblastic leukemia is the proposed technique. Acute lymphoblastic leukemia is classified as non-cancerous or Cancerous. Pro-B, Early Pre-B, and Pre-B are the three subtypes of malignant tumors. For image analysis, feature extraction, and classification, CNN is utilized. Microscopic blood cell image is taken as input. The input dataset for Acute lymphoblastic leukemia is taken from Kaggle. These images are taken from the peripheral blood smears of 89 patients. In which 64 patients have been observed with the symptoms of Acute lymphoblastic leukemia. The remaining 25 healthy persons are classified under Benign(non-cancerous). In total it consists of 3256 images. The dataset is collected by observing the patient of Taleqani Hospital (Tehran, Iran). The dataset is divided into 4 directories namely Benign (504 images), Early Pre-B cells (985 images), Pre-B cells (963 images), and Pro-B cells (804 images) in that there are 3256 train data and 1052 test data. This dataset is used to train the model.

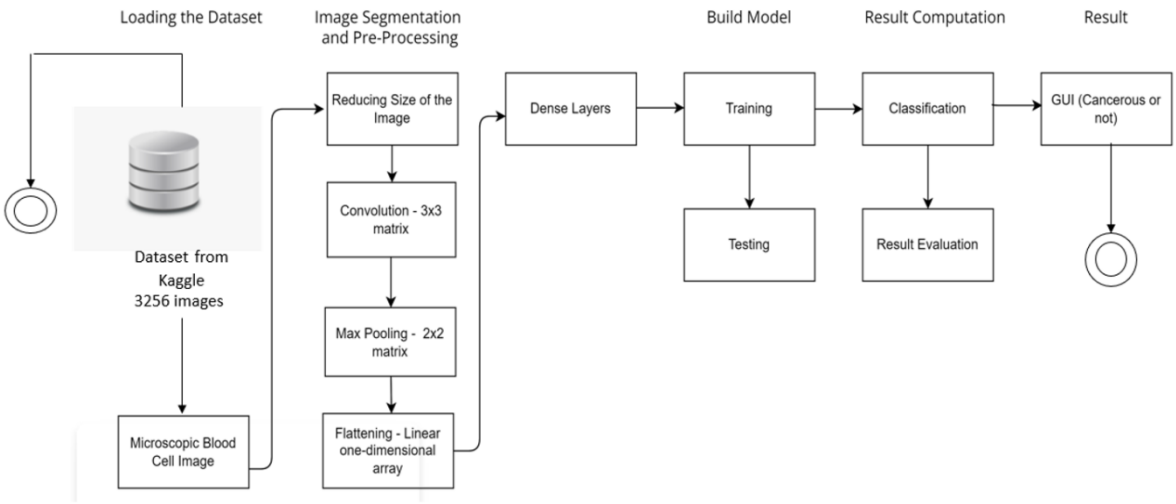

Fig1. Overall flow of system architecture

Fig 1. depicts overall system. In this, the dataset is taken from kaggle. The microscopic blood cell image is preprocessed and segmented and it passes through various filters like Convolution, Max pooling 2X2 matrix, Flattening and Dense Layers Then, dataset is used trained using Sequential, VGGNet and LeNet architectures. Based on the model trained, the sample input is tested. The result is predicted and depicted in user interface.

The input image is seen by computers like a pixel. This will perceive the picture as a, x, b, x, c (a = Height, b = Width, c = Dimension) depending on the image resolution. The picture is a 224 x 224 x 3 matrix of color values. The dimension of the photo is reduced in phases to reduce computing effort while maintaining image quality. Region-based segmentation is performed on the images to identify the similarities between the pixels, color pattern, edges, and shape of microscopic blood cells. Each pixel has a unique color value and it ranges from 0 to 255. It is calculated by the formula 1/color value. The value range lies between 0 to 1. The color and group of similar pixels are observed together. In the convolutional layer, there is a 3x3 filter grid over the image. Stride means the shift in pixels over the images. The filters are shifted one pixel at a period whenever the step is 1. The dot product is being used to minimize image size while maintaining image quality. Negative pixels are converted to zero by Rectified Linear Unit. The same amount is kept if the image value is larger than 0. When the photos are too huge, the pooling layers portion would lower the number of parameters. The dominating feature is examined in Max pooling, and the Pixel value is lowered for faster calculation. It features a number of filters that may be used to identify different aspects of an image. The feature extraction and classification are done using Sequential Model, VGGNet (Visual Geometry Group Network), and LeNet. Output is obtained as cancerous or not. If cancerous, then a specific type is displayed in Graphical User Interface.

Sequential Model

In sequential model, the layers is arranged in sequence. In sequential model, 1 convolutional 2d, 1 max pooling 2d, 1 flattening and dense layers are used. In this, the image is compressed and the features are extracted. Then, it passes through dense layer based on the neural connection and the bias value the result is predicted.

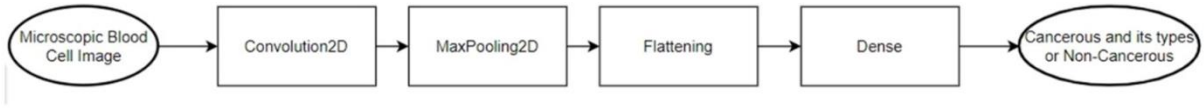

Fig2. Sequential Model Diagram

Fig 2 depicts Sequential Model. Microscopic blood cell image is taken as input and it passes through Convolution2D, Maxpooling 2D, Flattening, Dense layers and the output is obtained as Cancerous or not. If Cancerous, the type is also displayed.

VGGNet Architecture

The VGGNet structure has 16 segments. There seem to be 13 convolutional layers, 5 max pooling layers, and 3 dense layers in this photo. The filter size increases in from 64,128,256 and 512 order respectively. It can accept large number of data and as it has many filters the prediction rate is more precise. The main drawback is it requires high configuration system and the accuracy of VGGNet is less when compared to other architectures that uses similar dataset.

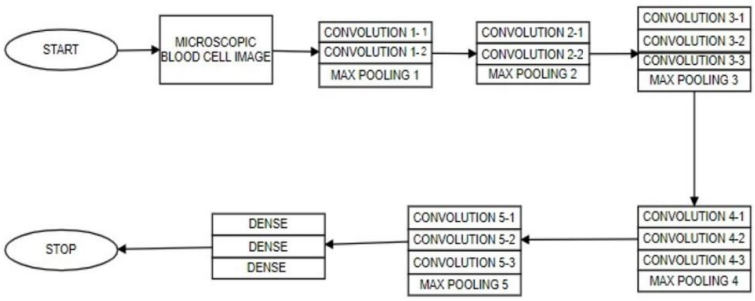

Fig3.VGGNet Architecture Model

Figure 3 depicts VGGNet Architecture. The VGGNet uses an image input size of 224×224. It is a very good architecture for benchmarking on a particular task. Microscopic blood cell image is taken as input. The convolutional layers have input in form of 3×3. There is a 1×1 convolution filter for linear transformation of the input. The activation function used here is Rectified Linear Unit. It's a nonlinear linear function that produces the same outcome as the source if the source is favorable , otherwise, the value is 0. Rectified Linear Unit is used in all hidden nodes. Locally Responsive Normalization is not used by VGGNet since it increases memory usage, training time, and accuracy level is not increased. VGGNet contains three main parts that are all linked. Any of the first two levels has 4096 streams, whereas the third stage contains one thousand streams.

LeNet Architecture

LeNet-5 takes a 32-bit grayscale picture as input and runs it through the first convolutional layer, which has six feature maps or filters with a size of 55 and a stride of one. The picture size has been reduced from 32x32x1 to 28x28x6 pixels. A sub-sampling layer with a filter size of 22 and a stride of two is then applied by the LeNet-5. The picture size is reduced to 14x14x6 as a result. The second convolutional layer is composed of 16 feature maps with a size of 55 and a stride of 1. A pooling layer with a filter size of 22 and a stride of 2 is the fourth layer. Because this layer comprises 16 feature maps, the output will be 5x5x16.The fifth level is a convolutional layer with 120 feature maps that is fully linked. All of the 5x5x16 with in forth network are connected to every one of the 120 cells in the 5 layer. A fully linked layer is the sixth layer. Finally, a SoftMax output layer having values in comparison to the digits 0 to 9 is fully linked.

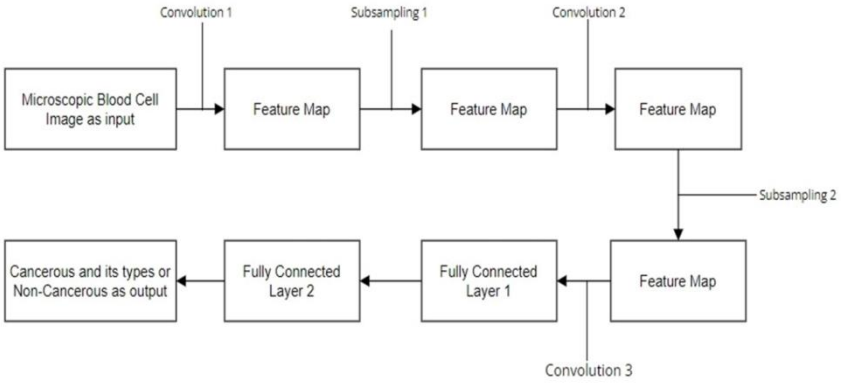

Fig4. LeNet Architecture Model

Fig 4 depicts LeNet Architecture. Microscopic blood cell image is taken as input. The image undergoes convolution, sub-sampling and feature mapping iteratively and the output is predicted.

4 Performance Evaluation

Sequential Model

This graph represents the performance of the model. The epochs are now on the horizontal axis, while the overall accuracy is on the vertical axis.

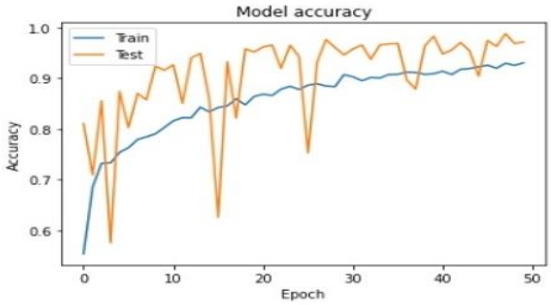

Fig5. Accuracy Graph

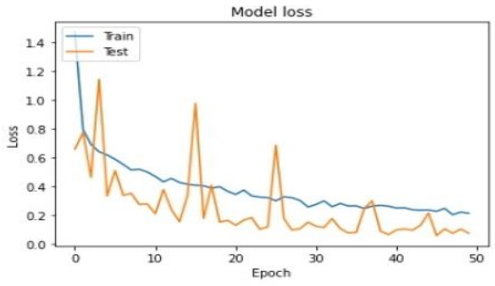

Fig6. Loss Graph

Sequential architectures are suited for simple stacks of layers since each layer has precisely one incoming and outgoing tensor. When the model contains multiple inputs or outputs, or when some of your

levels has numerous inputs or outputs, a sequential model isn't really acceptable. If this is the case, layer sharing is required. (Referred from: https://deepchecks.com)

$$Acc = \frac{No.of\ correct\ predictions}{Total\ no.of\ predictions}$$

p = 0.93 indicates that the item corresponds to category 1 (or plus class).

Category 0 (or minus class) probability = 1 – p = 1-0.93 = 0.07.

$$\hat{x} = \begin{bmatrix} \widehat{x0} \\ \widehat{x1} \\ \widehat{x2} \\ \widehat{x3} \\ . \\ . \\ . \\ . \\ \widehat{x999} \end{bmatrix}$$

The categorization probability for the associated class is indicated by the above vector. The picture is assigned to category 0 with such a frequency of 0.25, category 1 with a frequency of 0.25, category 2 with a frequency of 0.25, and category 3 with a frequency of 0.25.

To increase the probabilities to 1, SoftMax function is used. The below is the explanation of SoftMax function:

$$p(x = b|\theta^{(a)}) = \frac{e^{\theta^{(a)}}}{\Sigma_{b=0}^{c}\theta_c^{(a)}}$$

$$Where\ \theta = w_0\, y_{0+}\ w_1\, y_1 + \ldots. + w_c\, y_c = \int_{a=0}^{c} w_a\, y_a = w^t{}_y$$

1. Our aim is to estimate if the training set of characteristics y; within each weight matrix, are indeed a class of b provided a net input variable in the shape of the one encoded matrix θ. A one-hot matrix is made up of binary numbers, with 1 indicating an element in the column's a th position and 0 representing the remainder

2. The exponent of the input variable and the summation of exponentially variables of any and all known values inside the inputs are computed in the formula. The proportion of the exponent of the variable and the summation of exponent parameters is the Softmax function's output.

VGGNet Architecture

This graph represents the performance of the models. The epochs are on the horizontal axis, while the accuracy rate is on the vertical axis. Epoch used is 10 and batch size is 128.The accuracy obtained is 34.4%.

The dataset consists color-channeled images with such a fixed size of 224*224. As a conclusion, the input tensor is (224,224,3). This model takes input image and produces a 1000-value vector. (Referred from: https://www.geeksforgeeks.org)

3. θ, at a high level, is the total of the scores of each item in the vector that occurs. We state that θ is the transposition of the weight matrix w multiplication by the feature y in a generalized form.

4. The phrase w_0y_0 refers to the bias that must be introduced to each iteration.

Error function as follows:

$$E = \frac{1}{n}\sum_{c} \min_a d(j_a, G_c)$$

$$where\ d = 0a\ f\ j_a = G_k\ else\ d = 1$$

Here j is probable candidate in vector, G is ground truth vector, E is the error function

So, the loss function for this instance is:

$$E = \frac{1}{3}(min_a d(j, G_a) + min_a d(j_a, G_2) + min_a d(j_a, G_3))$$

So,

$$E = \frac{1}{3}(0 + 0 + 0)$$

$$E = 0$$

Because all of the categories in the ground truth are

contained inside the Predicted best classification matrix, the loss is zero.

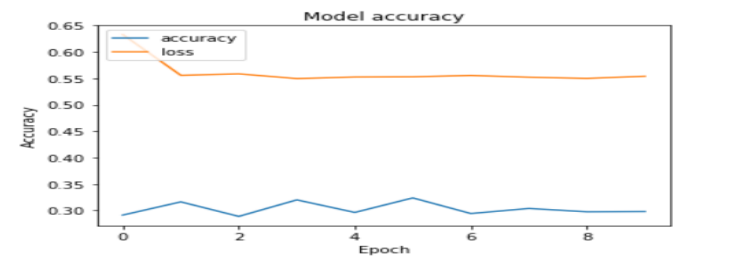

Fig7. Accuracy Graph

LeNet Architecture

This graph represents the performance of the models. The epochs are on the horizontal axis, while the accuracy rate is on the vertical axis. (Source: "Facial Expression Recognition Using Improved LeNet")

The following is the full network's computation procedure given the input:

The convolution method for the Y input of the convolution layer:

$$con = f(\sum_{a,b\in M} X_{a,b} + Q_{m-a,n-b} + i)$$

Where y is an element in the convolutional region M of input Y, w is an element in the convolutional network, m n is the size of a convolutional network, f (.) is the activation function, and I is the offset,

The pooling process again for pooled layer input X is as follows:

$$pool = down(\text{maxpool}(X_{a,b})), a, b \in p$$

Where x denotes the component inside the pooling region p in the pooling layer feed X, and down(.) denotes the down sampling procedure, which keeps the pooled area's highest value.

Input Z for the fully linked layer:

$$full = (q \times z + i)$$

Where z is the input element, q denotes the weight, I denotes the offset, and f (.) denotes the activation function.

Input Y for the output layer:

$$p(x = b|y; q) = \frac{e^n}{\sum_{a=1} o}$$

The weight variable, c is indeed the total number of varieties, and its error function is the hypothetical function of a Softmax, which determines the likelihood when the input is categorized into category b q.

Where 1 value is a genuine indication = 1, 1 value is a genuine indication = 0, and 1 value is a genuine indication = 0.

The following is the back propagation procedure: To get the real output after inputting the sample, you must first compute the feedback transmission error of each layer.

The symbol denotes the multiplying of the corresponding pixel inside the matrices or vector, and the symbol reflects the response transmission fault of every layer of the network.

$$\delta_b^{(1)} = h'(z_i^{(1)}) \sum_{o=1}^{m1+1} Q_{ob}^{1+1} \delta_o^{(1+1)}$$

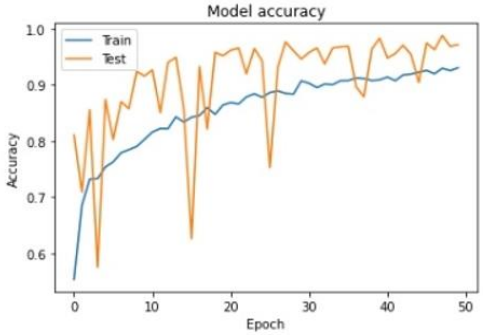

Fig8. Accuracy Graph

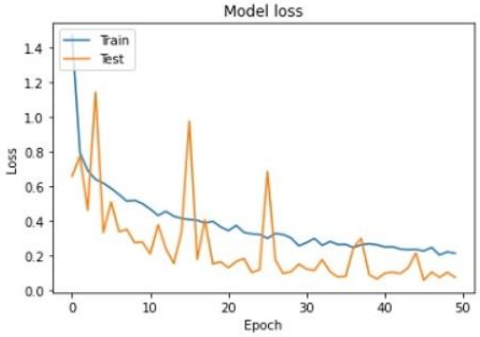

Fig9. Loss Graph

The aim of LeNet Learning Algorithm is to create precise prediction with minimum number of layers for the given datasets.

The structure of LeNet learning Algorithm is presented as Alg1.

Algorithm 1: LeNet Learning Algorithm

Training Dataset D = $\{x_i, y_i, z_i a_i\} i = 1 \ldots . n$

Set Img_dim

Set epoch(Ep)

Set Batch_Size

$E_p = \{1 \ldots n\}$

Procedure classifier.fit_generator (T_D, E_P, V_A)

$H(x) = T_D$//Batch_Size

for E_P=1…n do

V_A=Sampling(E_p)

return t, l,V_L

V_A=E_p(minimum value of t,l,V_L)

return H(x)

return V_A

This algorithm represents the process flow of LeNet. Where the training dataset is represented a D.It comprises of four classes where x_i represents the benign, $y_i$represents the pre-B, $z_i$represents the early pre-B, a_i represents the pro-B.The i denotes the numbers of images used in each class from 1 to n. Img_dim is used to set the dimension of the image to specific size and the value is set to 150. Epoch(E_p) is the number of passes of entire training dataset and its value is set to 40. Batch_Size is used to train the dataset and the value is set to 32.The epoch is iterated from 1….n. Procedure classifier.fit_generator (T_D, E_P, V_A) is a deep learning library which can used to train deep learning models.T_D represents the training dataset,$E_P$represents the epoch and V_A represents the validation accuracy. H(x) denotes the history where the history is calculated using the formula complete training dataset (T_D)//Batch_Size. Complete training dataset = 3256 and the Batch_Size =32. H(x) = T_D//Batch_Size =>3256//32 =101. The epoch is iterated starting from 1 to the end of image. The sampling value is calculated for each epoch to determine the validation accuracy (V_A).As a result, we obtain time (t), loss (l) and validation loss (V_L).Validation accuracy(V_A) is calculated based on the loss (l), accuracy loss(V_L) and the time (t) taken to execute one epoch cycle.The H(x) and the V_A is returned.

Prediction Results

The image file is chosen from the dataset. The specific class name is displayed as the output based on the prediction results.

Fig10. Output screenshot

Fig 10 depicts output displayed in the user interface. In first page, the user is requested to provide an image. The selected image name is displayed. In second page, the selected image is displayed after clicking the result button, it displays whether it is as benign or malignant and if malignant then the particular stage is displayed.

5 Conclusion and Future Works

Acute lymphoblastic leukemia has become life-threatening if it is not diagnosed. Hence, there is a demand to develop a system with high reliability and accuracy. A survey is performed on various techniques used for blood cancer detection and diagnosis. Studies show that Deep Learning is preferred over manual diagnosis, as it is less time-consuming, more accurate, and easily accessible at no cost. Comparing the three architectures (Sequential, VGGNet, LeNet), the best architecture is LeNet. The accuracy of LeNet is 95.75% and the loss is 4.75%.Convolutional Neural Network is most commonly used for Blood cancer cell classification. Furthermore, due to the importance and complex nature of the analysis of the type of cancer, a lot of

work is required to understand and analyze the images. In the future, architecture can be designed that is compatible with minimum setup and resources. The system must accept images of different size that are taken from various sources. Even with distinct set of images from dataset, the model should be able to process and provide accurate result within a stipulated time frame. Various architectures are used for one particular types of leukemia called Acute Lymphoblastic Leukemia and would like to collect the dataset and advance our system for other leukemia types. Other models and architectures can be incorporated into the system for higher performance as further research.

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