Leukemia Cancer Detection Using Deep Learning

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ABSTRACT—Cancer is a disease that instils fear in many people across the globe because of its fatal nature. But in most cases, cancer can be cured if diagnosed in an early stage followed up with proper medical attention. Computer aided diagnosis is gaining popularity nowadays as it can be effectively used as a primary screening test for many diseases and especially in case of cancer. Deep learning has been applied to many areas in health care, including imaging diagnosis, classification of cancer and stromal cells, doctor assistance, etc. Cancer prognosis is to estimate the fate of cancer, probabilities of cancer recurrence and progression, and to provide survival estimation to the patients.

The accuracy of cancer prognosis prediction will greatly benefit clinical management of cancer patients. Deep learning has been suggested to be a more generic model, requires less data engineering, and achieves more accurate prediction when working with large amounts of data. The application of deep learning in cancer prognosis has been shown to be equivalent or better than current approaches, including genomics data, and clinical information in cancer studies, we believe that deep learning would potentially improve cancer prognosis. We develop a system which detects cancer from blood cell images at a level exceeding practicing medical personnel. This technology can improve healthcare delivery and increase access to medical imaging expertise in parts of the world where access to skilled medical personnel is limited.

Keywords: Deep Learning, Neural Networks, Prediction of Cancer, Transfer Learning, TensorFlow, Keras, ML.NET

I. INTRODUCTION

Blood consists of plasma, and three different types of cells and they are: White Blood Cells, Red Blood Cells and Platelets and each of these performs particular task. Red blood cells transport oxygen from the lungs to the tissues of the body and vice versa. White blood cells help the body to fight against diseases and infections. Platelets help to clot and control bleeding. Leukemia is cancer of blood cells in which number of white cells is increases numerously and those are immature cells thatinterfere with other blood cells, usually red blood cells and platelets. Our body's white blood cell ratio is 1000:1. It means thatbetween 1000 red blood cells there is 1 white bloodcell.

two types of white blood cells that get turn into leukemia and they are:
- Lymphoid cells
- Myeloid cells

Leukemia that caused due to lymphoid cells is called lymphocytic or lymphoblastic leukemia and if it is causeddue to myeloid cells then it is known as myelogenous or myeloid leukemia. Leukemia is grouped in two ways: acute or chronic, grouped according to how fast the cells are growing. The abnormal blood cells in acute leukemia are usually immature blasts (young cells) that do not work properly. These cells are growing fast. Acute leukemia gets worse quickly unless it is immediately treated. Young blood cells are present in chronic leukemia, but also mature functional cells are produced. Blasts are growing slowly in chronic leukemia. It takes the disease longer to get worse.

The four major forms of leukemia are:
1. Acute lymphoblastic leukemia (ALL)

2.   Acute myelogenous leukemia (AML)
3.   Chronic lymphocytic leukemia (CLL) and
4.   Chronic myelogenous leukemia (CML)

II.PURPOSE

The purpose of our project is to develop a system that can automatically detect cancer from the blood cell images. This system uses a convolution network that inputs a blood cell images and outputs whether the cell is infected with cancer or not. The appearance of cancer in blood cell images is often vague, can overlap with other diagnoses, and can mimic many other benign abnormalities. These discrepancies cause considerable variability among medical personnel in the diagnosis of cancer. Automated detection of cancer from blood cell images at the level of expert medical personnel would not only have tremendous benefit in clinical settings, it would also be invaluable in delivery of health care to populations with inadequate access to diagnostic imaging specialists.
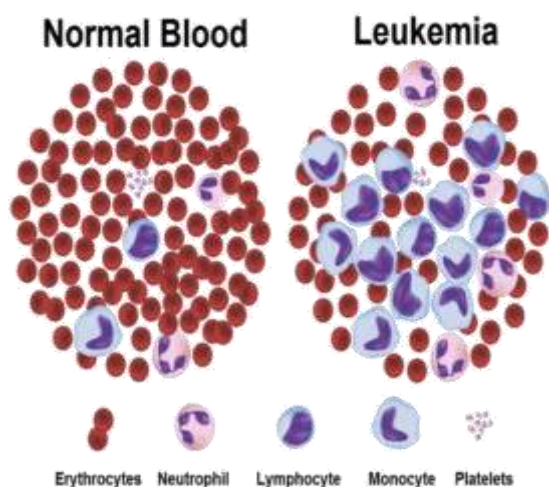
III. LITERATURE REVIEW

[1] Elham Nazari , Amir Hossein Farzin , Mehran Aghemiri and Amir Avan, "DEEP LEARNING ACUTE MYELOID LUEKEMIA DIAGNOSIS":

Big medical data generated as a result of recent advances in biology. Using appropriate analyzing methods led biologists to percept the complex dynamic system of life. It is one of the most critical challenges for biologists. Microarray is well known despite it is a new technology in molecular biology. It is used to monitoring genome-wide expression levels by biologists. This technology includes examining a thousand genes and protein activity on a small scale to compare the

similarity and track changes such as track decreasing or increasing gene activities and track protein samples changes in comparison to the control sample. Microarray uses include genotyping, epigenetics, translation profiling, gene expression profiling. Microarray can be replaced by aggressive cancer detection methods such as bone marrow biopsy, which is used in the accurate diagnosis of acute myeloid leukemia. Bone marrow biopsy is invasive, painful, and can cause serious complications such as infections and bleeding. Therefore, microarrays improve clinical diagnosis providing high accuracy diagnostic procedures. It can be used as a gold standard to diagnose and help to treatment progress development and understanding cell biology, especially in oncology studies. Thus, the gene expression patterns are compared in two healthy and cancerous tissues. Cancer is closely linked to genetic changes; hence, the accurate cancer diagnosis speeds up by using a pattern to classify normal and cancer cells . So, a timely and accurate diagnosis is essential.

There are many pieces of evidence that accurate cancer diagnosis is one of the most effective ways of reducing the mortality rate [7,8]. The higher number of genes (p) compare to the number of tissues (n) is the feature of the microarray. It is challenging to analyze microarray data using statistical methods to classify high-dimensional data (p>n) due to overestimation and multiple linearity problems make statistical classification of microarrays difficult. Its analyzing methods are evolving rapidly, and there is no specific way considered the best way to analyze microarrays. Recently, expert systems to diagnose cancerous gene data are increasing, and machine learning techniques are currently used more. Machine learning can help to automation and intelligence process, improve development, accuracy and reducing costs. Machine learning, ensemble methods, and deep learning are showing high performance in classifying biological data.

In this study, neural networks and deep learning were used to separate healthy and cancerous cells in leukemia related genes. Acute myeloid leukemia (AML) is the type of cancer that starts in the bone marrow, but in most of the cases, it moves to the blood very fast. This type of cancer worsens fast if left untreated.

[2].Deepika Kumar,   Nikita   Jain,   Ayush Khurana, Shwetha Mittal and Suresh Chandra Satapathi "Automatic Detection of White Blood Cancer From Bone Marrow Microscopic Images Using Convolutional Neural Networks":

Cells that comprise the blood are three types: platelets, red blood cells, and white blood

cells. Each of them is made continuously in the bone marrow and released timely in the bloodstream. The normal blood cell growth, hampered by the exponential growth of abnormal blood cells, is the main cause of blood cancer. There are three main types of blood The associate editor coordinating the review of this manuscript and approving it for publication was ShuihuaWang . cancers: leukemia, myeloma, and lymphoma. Bone marrow is the infected area for a white blood cancer type cancer called Acute Lymphocytic Leukemia (ALL). ''Acute'' indicates the fast progress of the disease, and if it does not get treated in the early stages, it might prove to be fatal within a short span [1], [2]. ALL is classified into L1, L2, and L3 [3]. Multiple Myeloma (MM) is an immature teratoma of cells called plasma, which helps to scrape off the infection [4]. It is thrice as common as ALL. The blood count remains normal in this case, unlike leukemia, but the infected one is foundto have anemia (low red blood count) because the space for RBCs is occupied by the unhealthy cells. Multiple myeloma is responsible for low platelet count in the blood, which is called thrombocytopenia [5]. It also causes erosion of bones called bone lesions diagnosed in CT scans [6]. Approximately 1500 people who died due to this disease contribute to 0.2% of the total deaths caused by cancer alone in 2019 [7]. There are nearly 20,000 people diagnosed with myeloma every year in the US. Treatment for blood cancer depends on the age of the patient, type, how fast the cancer is progressing, infected areas, etc. [8]. The blood count is one of the prime factors for the distinction for categorizing the type of blood cancer. The counting can be done manually and automatically. The manual method gives a 100% recognition rate if done by a skilled person but is also a time-consuming process [9]. On the other hand, automatic counting is a faster process but has got higher risks of the count being wrong. Thus, both methods have their pros and cons. This article gives an outline of the automatic approach to determine the type of white blood cancer. The automated method of classification is costeffective and can be deployed quickly in both rural and urban areas. The problems that are invaded through the proposed system include the inconsistencies caused due to labor work of manual classification, the requirement of a skilled professional, the errors due to cells being indistinguishable when observed under a microscope, etc. Deep learning-based methods can help in resolving all the enlisted challenges because they derive desirable features from the raw data themselves [10]. Deep Learning is known to demonstrate better functioning than

accustomed Machine Learning for processing a large number of images [11]. Convolution Neural Networks (CNNs) combine various multi-layer perceptron and display efficient results with a little pre-processing [12]. CNN's themselves act as a feature extractor as each convolution layer of the network learns a new feature that is present in the images and hence produces a high activation. In the proposed study, a robust and vigorous automated classification method for the type of white blood cancer, i.e., ALL and MM using Convolution Neural Networks is presented. The article consequently evaluates the performance of the proposed deep learning model using accuracy.

IV. EXISTINGSYSTEM

Medical history and physical examination: The record of present symptoms, and problems a person has had in the past. The medical history of a person's family also helps in diagnose leukemia.

- Complete blood count (CBC): Blood is taken and checked under the microscope for the number of RBCs, WBCs and platelets.
- Bone marrow aspiration: Bone marrow is removed with the help of a needle from breastbone. The removed sample is observed under a microscope to look for abnormal cells.
- Cytogenetic analysis: Cytogenetic test takes blood or bone marrow to help identify individual chromosomes. It shows abnormalities in chromosomes, which help to diagnosis and identify the type of leukemia. Results are usually available within 3 weeks.
- Immunohistochemistry: Blood sample of cells are treated with special antibodies in immunohistochemistry. Under the microscope the change in color can be seen. It helps in determining the types of cells that are present.
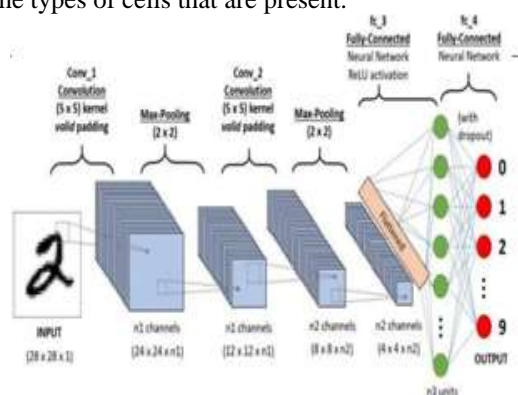

V. PROPOSEDSYSTEM.

We develop a system which detects cancer from blood cell images at a level exceeding practicing medical personnel. This technology can

improve healthcare delivery and increase access to medical imaging expertise in parts of the world where access to skilled medical personnel is limited. In the proposed research, an optimized CNN model for classification of the type of cancer has been deployed.. Convolution Neural Networks (CNNs) are majorly used for analyzing visual imagery. CNN's are the heart of image classification algorithms. They work fast and efficient for image classification.

In comparison to other image classification algorithms,

they use a little pre-processing. A CNN model is comprised

of an input layer, an output layer, and multiple hidden layers.The model, containing three types of layers, namely convolution layer, max pool, and fully connected layer, is trained on the training set, and then it is used for prediction on the testing set.
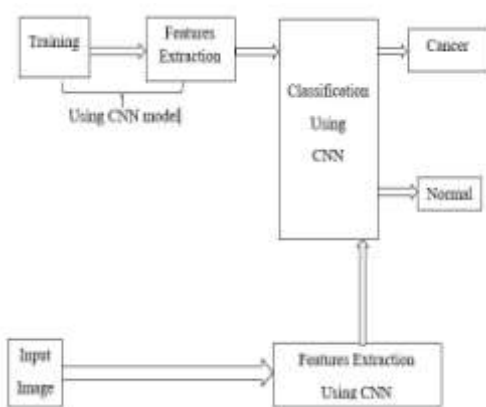

VI. METHODOLOGY AND ALGORITHM

In deeplearning a neural Network(**CNN/ConvNet**) is a class of deep neural networks, most commonly applied to analyse visual imagery. Now when we think of a neural network we think about matrix multiplications but that is not the case with ConvNet. It uses a special technique called Convolution. Now in mathematics **convolution** is a mathematical operation ontwo functions that produces a third function that expresses how the shape of one is modified by the other.

Convolutional neural networks are composed of multiple layers of artificial neurons. Artificial neurons, a rough imitation of their biological counter parts, are mathematical functions that calculate the weighted sum ofmultiple inputs and output an activation value. When youinput an image in a ConvNet, each layer generates several activation functions that are passed onto the next

layer.

VII. EXPERIMENTAL RESULTS

Aftertraining convolutional neural network architectures, we perform experiments to evaluate the loss and accuracy. We perform extensive evaluation usingvarious metrics and the results graphicsplotted asshown below.
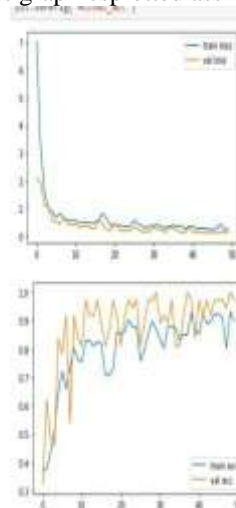
VIII. CONCLUSION

The proposed model annihilates the likelihood of blunders in the manual procedure by utilizing a profound learning strategy in particular convolutional neural system. The model pre-forms the pictures and concentrates the best highlights out of them followed via preparing the model with the changed Convolutional neural system structure.

In the end, it predicts the type of cancer in the given image. A baseline comparison with some state of art methods like Support Vector Machine (SVMs), Decision Trees, Random Forests, Naïve Bayes, etc. was also performed and presented. The proposed model performed better than these baseline methods. A clear comparison between the model and some existing proposed models is also shown over three discrete datasets where the former performed better in terms of accuracy. Therefore, the model can be utilized viably as an apparatus for deciding the sort of cancer. However, we have to admit that a broader experimental study considering the dependence on the size of the databases has not been performed and presented here.

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