ORIGINAL ARTICLE

An Expert System to Detect Acute Lymphocytic Leukemia in Human Tissues using Deep Learning Approach

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Abstract:

Background: The deep learning algorithm is the machine learning technique where the computers can learn from the dataset. This system builds a patterns and models from a given dataset. Expert system machine learning system and deep neural networks are considerably more efficient in detecting a cancer cell and also the nature of the cancer. Cancer prediction and identification are the challenge of our time. Cancer is the leading cause of human death. It is a problem worth solving using available technology. Methods: To train the database to classify and predict acute lymphoma leukemia with minor errors and low computational time we used round robin classification model takes a dataset with three subfolders which are Testing data (Contains both healthy and leukemia cells), training data (Contain in separate subfolders of healthy and leukemia cells), validation data (folder where the results will be saved). All the samples are in image format. All the image are in .bmp format and contain a resolution of 450x450 pixels and a 24 bit color display system. All the image data are converted into NumPy array. We will split all this data into train, test and validation purpose. After that, we train our proposed sequential CNN Model with our dataset. In our sequential model, we used tensorflow, keras, Dense, Activation, Dropout, Conv2D, numpy, pandas, shutil, time, Cv2, tpdm, sklearn, matpoltlid, seaborn, confusion matrix. Results: We made a custom dataset which we need then to examine confusion metrics, total test accuracy, precision rate, recall rate, computational time, F1-score, and MSE (Mean Squared Error) value, and error rate. We also employed model performance with train, validation accuracy, and loss for graphical depiction. We successfully achieved significant improvements in our model accuracy. Where other researchers proposed CNN models accuracy given in the accuracy table, the CNN Model accuracy was 93% and CNN Model was 92.97% accuracy on the other hand our proposed model got 78.46% accuracy and when we tried to improve our model then we got 97.19% accuracy. Conclusion: In every experiment, we used a different kind of step to increase the model performance for our dataset. That gave us a high accuracy rate, and the validation loss was low, and testing accuracy was also increased. The medical experts can benefit from the improved application of deep learning, which ensures less time and enhance reliable healthcare for patients. Machine learning will bless for the medical sector in the near future. Collecting relevant medical data for training a machine learning model is insufficient to do such research.

Introduction

Deep learning is a domain of machine learning. The deep learning algorithm is the machine learning technique where the computers can learn from the dataset. This system builds a patterns and models from a given dataset. Expert system machine learning system and deep neural networks are considerably more efficient in detecting a cancer cell and also the nature of the cancer. Cancer prediction and identification are the challenge of our time. Cancer is the leading cause of human death. It is a problem worth solving using available technology.

In medical terms, acute lymphoma leukemia (ALL) is a type of cancer. It is a cancer of the lymphoid line of blood cells characterized by the development of large numbers of immature lymphocytes. Symptoms may include feeling tired, pale skin color, fever, easy bleeding or bruising, enlarged lymph nodes, or bone pain[1]. As an acute leukemia, ALL progresses rapidly and is typically fatal within weeks or months if left untreated.

Acute lymphoma leukemia is a disease which can affect anyone at any time. It can cause premature death to children it can cause to a healthy adult human at any given time. There is no effective treatment as of writing this thesis paper. Only treatment available is chemotherapy which is not very effective in cure. The chemotherapy only helps to reduce the multiplication of affected cell. Another way to prevent this disease is to detect early stage in the disease.

ALL is the hardest leukemia to detect[2]. As the affected cells looks similar to any normal cells. For this reason along many patients get misdiagnosis at the initial stage. As a result when the disease is identified it is too late for the patient. But if ALL is identified at the very early stage there is 65% chance of the patient's survival[3]. As a result our goal is to identify this cancer cells at the very the genesis. It will be both cheap and effective for a patient who is suffering from this disease.

As our research is primarily focused on the accurate detection of leukemia affected cell in a pool of healthy cells it is very important to use image identification for proper diagnosis. As there is lack of trained professionals in the medical industry there is a great problem in proper detection of ALL detection10. The traditional method used for acute leukemia detection is blood test, bone marrow test, imaging test, spinal fluid test. These tests are both expensive and very time consuming for most people. Besides most of the tests are inaccurate as there is lack of experience professional in the respective industry. So we will be using image recognition algorithm and pattern recognition algorithm for accurate prediction and less time consuming.

Methodology:

After study of different research works we understood most of the researchers who are involved in this field daily and successfully propose efficient solutions to machine learning problems. Many of them followed different approaches and methods to detect leukemia from medical images. Different types of CNN models are used by researchers working in this field. Some of them used transfer learning by using VGG16, RegNet50, InceptionV3, etc., in their research and successfully did it. Also, in our research work, we have to build a CNN model to propose an efficient solution for our problem. We were determined to build our improved CNN model and built a sequential model using the sequential model building method. A sequential model means building a model layer by layer, and all the model layers are arranged in sequence. We used the 'add ()' function to add a layer to our proposed model, and after adding the required layers to our model.

Because of lack of time and resource we used kaggle for data collection and Jupyter notebook IDE for code implementation. As for machine learning package used TensorFlow and Keras Library to implement our model. We reviewed many papers related to ALL detection, but we did not find publicly usable any authentic data-set. Then we try to find new data-set from different internet sources and find a combined blood test, bone marrow test, imaging test, spinal fluid test image file. In the data set, Bone, blood, and different types of cell images there, we separated blood cell image and abnormal blood cell image from there. That is our proposed data-set for our implementation.

To train the database to classify and predict ALL with minor errors and low computational time, we used round robin classification model takes a dataset with three subfolders which are testing data (contains both healthy and leukemia cells), training data (contain in separate subfolders of healthy and leukemia cells), validation data (folder where the results will be saved). All the samples are in image format. All the image are in .bmp format and contain a resolution of 450x450 pixels and

a 24 bit color display system. All the image data are converted into NumPy array. We split all these data into train, test and validation purpose. After that, we train our proposed sequential CNN Model with our dataset. In our sequential model, we used tensor flow, keras, Dense, Activation, Dropout, Conv2D, numpy, pandas, shutil, time, Cv2, tpdm, sklearn, matpoltlid, seaborn, confusion matrix9. We evaluated our model based on test accuracy, precision, f1- score, confusion matrix, recall, mean absolute error, mean square error, etc. For evaluating our model, it takes a random image as an input from the test-set and predicts that image class defined as acute lymphoma leukemia affected or normal blood cell image as the output result

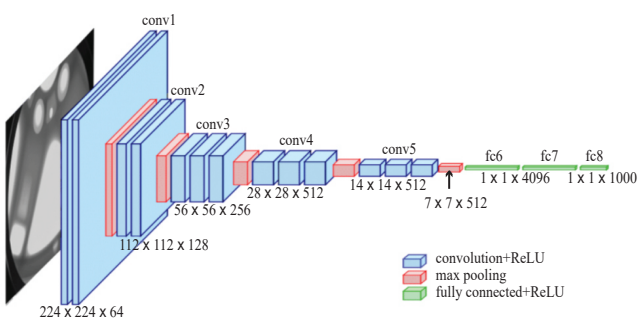

Figure 1: Our Proposed CNN System Diagram

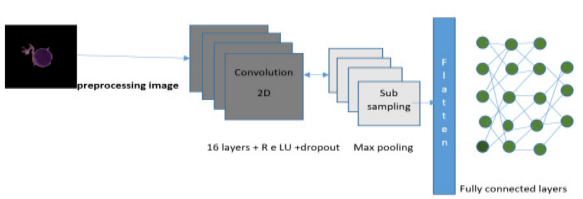

Figure 2: Technical Structure of Our Proposed CNN Model

Medical image data sets are quite rare to find. As we are finding acute lymphoma leukemia cell image so we need cell image Dataset. So, there are too much little datasets on the internet as open source. There are several leukemia related works based on private datasets. After searching the related dataset, a new dataset based on leukemia was developed. But the dataset was a combined dataset where leukemia affected and healthy cell image coexisted in a folder. So, we separated the images and made a custom dataset which we need for our implementation. The dataset were created with three subfolders which are all Folder (Contains acute lymphoma leukemia Image), hem Folder (contain normal cell Image), and validation (contain acute lymphoma leukemia identified Image).

Directories Name	Number of Images
all	7,272
hem	3,389
validation	1,867
Total	12,528

Table- I: Dataset Info

The dataset folder is stored in kaggle as a zip file using that unique id, we downloaded the zip file from the website and used that file after unzipping. We imported all of the essential libraries to process and created the classification and test the model after downloading the Dataset. NumPy, Keras, TensorFlow, CV2, OS, and matplotlib libraries we reutilized in Kaggle for this implementation.

The data set used in this project was found on the internet and there were some garbage data so we had to remove it. There were two sub folders ALL images and healthy cell images but our need was only leukemia images. So, we focused on only leukemia images and split all the leukemia images into two sub folders: all (leukemia affected cell images) and hem (normal cell images). All the cell images into “RGB” color format and a default image shape size for all the images which was 450 x 450. Images were converted into array format using python NumPylibraries and NumPyarrays to perform all the machine learning operations of our model and can operate faster and NumPyarrays consume less memory while computing. Labels were added into all the images of both all and hem folder one by one for data preprocessing.

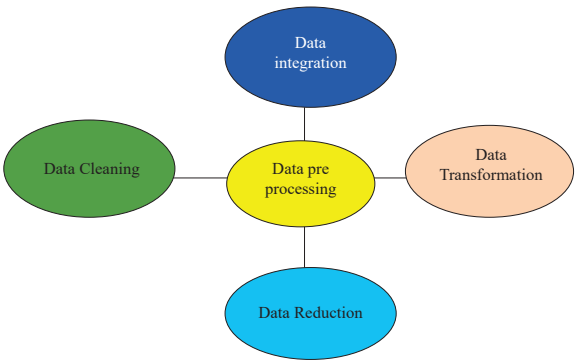

Figure 3: Data Pre-processing Technique

Training is the essential part of implementing a model where we build our model to train and classification leukemia. We have created a binary classification model for classification purposes. 2D convolution layer with32 filters of 3*3 kernel size with activation function ReLU, pulling, and dropout layer was used. After that, we add a max-pooling 2D layer with pool size 2*2, Flatten layer for multi-dimensional input into a single dimension. Multiple Dense layers and Dropout for better accuracy and the sigmoid function in last layer because proposed model based on binary classification, so result would predict between 0 to 1.

For evaluation of our CNN model, we track some parameters and while training the model we track accuracy for better training accuracy. And better training accuracy only ensures maximum test accuracy of our model. Besides, we calculated the confusion matrix (TP, TN,FP, FN), monitor validation and training accuracy, validation loss, and training loss. Also, we generated a heat map for better understanding of confusion matrix visualization.

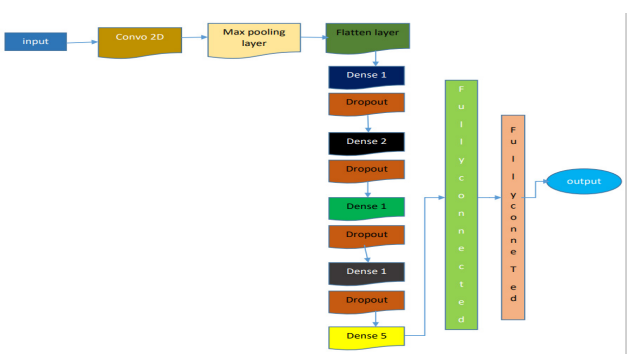

Figure 4: CNN Model Layers Visualization

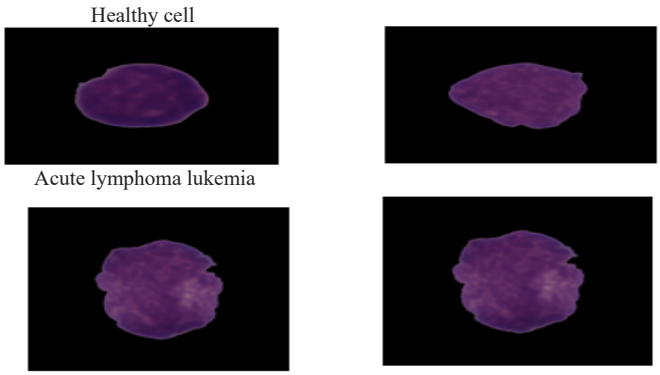

Fig-5: Images of ALL cell by DLA

For image recognition and acute lymphoma leukemia detection, several models and approaches have previously been established. All of them have good production for a certain criterion. We sought to develop a CNN model to get the best accuracy rapidly utilizing the CNN-based technique. To increase the amount of image, we altered our training model. In addition, we employed the ReLU (Rectified Linear Unit) activation function and max-pooling in our model design. Another non-linear activation function that has gained popularity in the deep learning sector is the ReLU function. ReLU stands for Long Measure Rectified. The most significant value of using the ReLU function over other activation functions is that it does not activate all the neurons at an equal moment. We can create a model more effectively in the future to boost the efficiency of the model.

Results:

To check the effectiveness a normal cell dataset combined with leukemia data-se was used. In the data set there several image in normal cell and leukemia to examine confusion metrics, total test accuracy, precision rate, recall rate, computational time, F1-score, and MSE (Mean Squared Error) value, and error rate. We also employed model performance with train, validation accuracy, and loss for graphical depiction.

Accuracy is a way of estimating the performance of a model. This table represents the comparison of our proposed CNN models and other researchers

proposed CNN models. We successfully achieved significant improvements in our model accuracy. Where other researchers proposed CNN models accuracy given in the accuracy table, the CNN Model[19] accuracy was 93% and CNNModel[34] was 92.97% accuracy on the other hand our proposed model got 78.46% accuracy and when we tried to improve our model then we got 97.19% accuracy.

Accuracy comparison:

Medical image data sets are difficult to find out. We required blood sample dataset since we need an ALL cell on a cell image. As a result, there are far too many little data sets available as open source on the internet. We discovered a novel dataset based on leukemia cell after searching the associated dataset. However, the data set was a composite one that included both normal healthy cell and leukemia infected cell images. As a result, we segregated the normal cell image and created a new data set for our implementation. The Folder named all (contains acute lymphoma leukemia Image), Folder named hem (contains Normal cell Image), and validation (contain ALL detected Image) are the three sub-folders inthedata set.

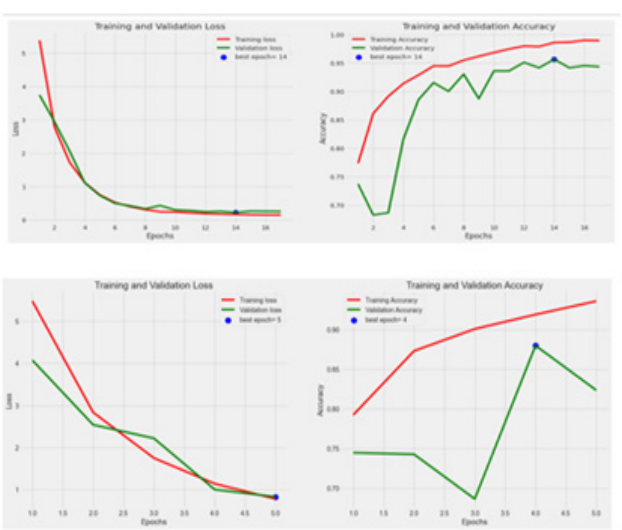

Figure-1: Training and validation loss and accuracy curve for CNN Model

Model Name	Recall Rate
CNN Model [31]	0.97
CNN Model [36]	0.9
Rocket Man (Proposed CNN Model)	*Result for '0'= 0.57*
	Result for '1'= 0.60
God's Gonna Cut You Down (Improve CNN Model)	***Result for '0'= 0.66***
	Result for '1'= 0.69

Model Name	F-1 Score
CNN Model [31]	0.97
CNN Model [36]	0.91
Rocket Man (Proposed CNN Model)	*Result for '0'= 0.62*
	Result for '1'= 0.64
God's Gonna Cut You Down (Improve CNN Model)	***Result for '0'=0.80***
	Result for '1'= 0.81

Table- I: Comparative recall rate and F-1 score

In every experiment, we used a different kind of step to increase the model performance for our dataset. That gave us a high accuracy rate, and the validation loss was low, and testing accuracy was also increased. But we got some over fitting problems because of the data set problem. However, it was not satisfactory at all. Then we tried to tune our parameters for the experiment. If we used a high epoch, the Tensor Flow runtime environment was likely to be crashed16. We adjusted the epochs according to TensorFlow and altered the learning rate, the dropout rate, and the optimizer. In the future, we will try to use the cross-validation technique to increase the performance of our model.

Discussion:

The proposed method consisted of training an image dataset of acute lymphoma leukemia developing a model to predict cancer from an input image by comparing it to the learned images, with the leukemia class name shown alongside a sample image as an output. We employed an enhanced Convolution Neural Network model to train this picture dataset, which contains a relatively simple Conv2D layer to improve the efficiency of training

and testing26. It acts as a regularized and helps to reduce over fitting while training a machine learning system. We employed sequential models to train our algorithm, and inside the central CNNmodel architecture, we used Conv2D layers with the same padding size. We trained our model using the EfficientNetB3 architecture, which is quicker and has less convergence than other architecture. Our model also includes activation, dense, and flattens layers. To evaluate our model, we employed test accuracy, precision rate, recall rate, MSE (Mean Square Error), RMSE (Root Mean Square Error), and other parameters. We utilized graph over accuracy and loss for visual depiction. In our experiments, we attained the most significant test and precision rate, recall and accuracy of 98.4% for detecting acute lymphoma leukemia. From an input picture, it can anticipate leukemia. We employed only a few images and epochsin our model for training purposes, which were not used in other studies. After all, we developed an effective model for increasing acute lymphoma leukemia detection6.

Conclusion:

Deep learning models will never be capable of taking over for doctors and medical professionals. It might, however, have a considerable influence on image processing and analysis automation. Computer-assisted approaches for medical picture segmentation have made significant progress in recent years, advancing medical research and clinical applications. Recent breakthroughs in deep learning have revealed that differentiating leukemia variation is improving.

In recent years, deep learning algorithms had a considerable influence in detecting research difficulties in several applications. The medical experts can benefit from the improved application of deep learning, which ensures less time and enhance reliable healthcare for patients. Machine learning will bless for the medical sector in the near future. Collecting relevant medical data for training a machine learning model is insufficient to do such research.

Though there are types of leukemia, our model can detect acute lymphocytic leukemia. Data sets for other leukemia can be worked on in the future to detect all kinds of leukemia. Based on our proposed model, any medical device or mobile application can be created.

The World Health Organization reported a doctor's proportion ratio, which is 1:250 per thousand[28]. The number of doctors globally is negligible compared to the number of patients. Since the number of doctors is much less than the number of patients, doctors work under a lot of pressure and handle many patients in less time. If our model can bring better output through proper training, it will triumph in medical science. It will assist doctors in detecting the patient's stock in a short time. And the doctor will be able to take care of the patient in a very short time through automation.

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