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Leukemia detection in short time duration using machine learning

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Abstract: Leukemia (blood cancer) begins in the bone marrow and causes the formation of a large number of abnormal cells. The most common types of leukemia known are Acute lymphoblastic leukemia (ALL), Acute myeloid leukemia (AML), Chronic lymphocytic leukemia (CLL) and Chronic myeloid leukemia (CML). This thesis makes an effort to devise a methodology for the detection of Leukemia using image processing techniques, thus automating the detection process. Our project consists of development of a machine learning algorithm to detect cancer using microscopy image.

Keywords—LeukemiaDiagnosis,convolutional neural networks, Leukemia types

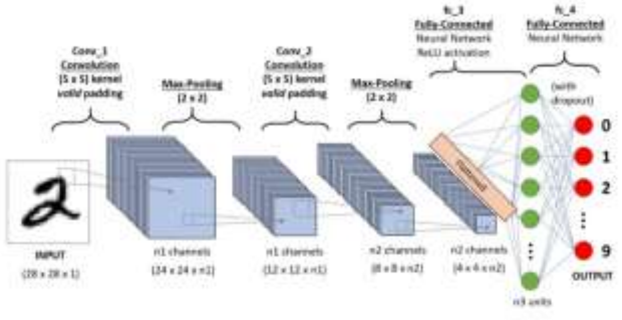
I. INTRODUCTION

Cancer is a fatal illness often caused by genetic disorder aggregation and a variety of pathological changes. Cancerous cells are abnormal areas often growing in any part of human body that are life-threatening. Cancer also known as tumor must be quickly and correctly detected in the initial stage to identify what might be beneficial for its cure. Even though modality has different considerations, such as complicated history, improper diagnostics and treatment that are main causes of deaths. The study highlights how cancer diagnosis, cure process is assisted using machine learning with supervised, unsupervised and deep learning techniques. Several state of art techniques are categorized under the same cluster and results are compared on benchmark data sets from accuracy, sensitivity, specificity, false-positive metrics. Finally, challenges are also highlighted for possible future work.

II. ALGORITHM

CONVOLUTION NEURAL NETWORK(CNN)

Convolution neural network*The field of machine learning has taken a dramatic twist in recent times, with the rise of the Artificial Neural Network (ANN). These biologically inspired computational models are able to far exceed the performance of previous forms of artificial intelligence in common machine learning tasks. One of the most impressive forms of ANN architecture is that of the Convolutional Neural Network (CNN). CNNs are primarily used to solve difficult image-driven pattern recognition tasks and with their precise yet simple architecture, offers a simplified method of getting started with ANNs. The agenda for this field is to enable machines to view the world as humans do, perceive it in a similar manner and even use the knowledge for a multitude of tasks such as Image & Video recognition, Image Analysis & Classification, Media Recreation, Recommendation Systems, Natural Language Processing, etc. The advancements in Computer Vision with Deep Learning has been constructed and perfected with time, primarily over one particular algorithm — a Convolutional Neural Network**.**



A CNN sequence to classify handwritten digits

A Convolutional Neural Network (Conv Net/CNN) is a Deep Learning algorithm which can take in an input image, assign importance (learnable weights and biases) to various aspects/objects in the image and be able to differentiate one from the

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other. The pre-processing required in a Conv Net is much lower as compared to other classification algorithms. While in primitive methods filters are hand-engineered, with enough training, Conv Nets have the ability to learn these filters/characteristics. The architecture of a Conv Net is analogous to that of the connectivity pattern of Neurons in the Human Brain and was inspired by the organization of the Visual Cortex. Individual neurons respond to stimuli only in a restricted region of the visual field known as the Receptive Field. A collection of such fields overlaps to cover the entire visual area. A Conv Net is able to successfully capture the Spatial and Temporal dependencies in an image through the application of relevant filters. The architecture performs a better fitting to the image dataset due to the reduction in the number of parameters involved and reusability of weights. In other words, the network can be trained to understand the sophistication of the image better. The role of the Conv Net is to reduce the images into a form which is easier to process, without losing features which are critical for getting a good prediction. This is important when we are to design an architecture which is not only good at learning features but also is scalable to massive datasets.

III.METHODOLOGY

The system consists of 2 parts
A: Training of machine learning module with data sets

B: Diagnosis of cancer

A: Training of machine learning module with data sets:
The neural machine learning module is created using keras library and python in google Collab editor for training the module 1000's of images of cancerous and noncancerous sample are collected and stored in a file. The file is divided into two parts training datasets and testing data sets. Training data sets is used to train the machine learning module. It consists of cancerous and noncancerous images labeled respectively. These images will be fed into machine learning module and trained module is extracted.

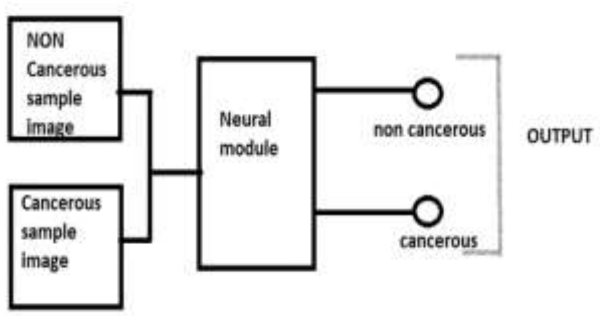

Figure:2 Block diagram of training process

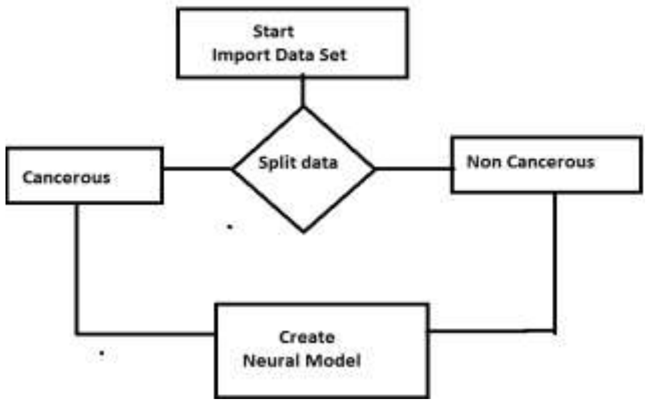

Figure 3: flow diagram of training neural model

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B: Diagnosis of cancer:
The diagnosis of cancer starts with the collection of blood sample at the laboratory, the microscopy image is then passed into trained neural module for diagnosis.
The trained machine learning module will give output whether the sample is cancerous or noncancerous based on prediction value.

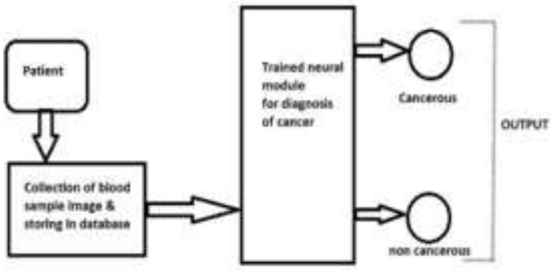
Patient
Collection of blood sample image & storing in database
Trained neural module for diagnosis of cancer
Cancerous
non cancerous
OUTPUT

Figure 3: diagnosis of cancer

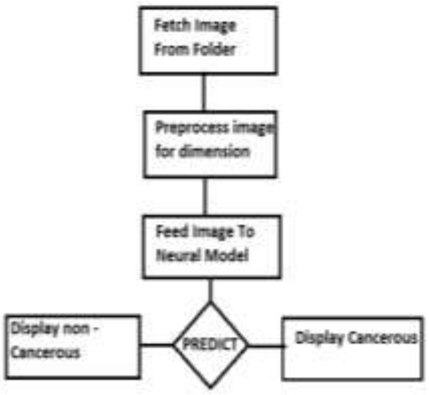

Figure 4: flow diagram of diagnosis procedure

IV.CONCLUSION

Due to modern lifestyle, pollution and other factors cancer is becoming more of common disease. With conventional methods of detection of cancer takes time because transport of sample tissue (biopsy) to a cancer diagnosing facility, since cancer is fast spreading disease early treatment will likely increase the chances of survival of cancer patient. With the help of machine learning, results are fast and accurate which helps in early detection and also the diagnosing process can be done at low cost.

RESULT

1: Collecting images for training the model Linking the image directory in code.

Training Data Argumentation

```
[illegible]
```

Test Data Set Argumentation

```
[illegible]
```

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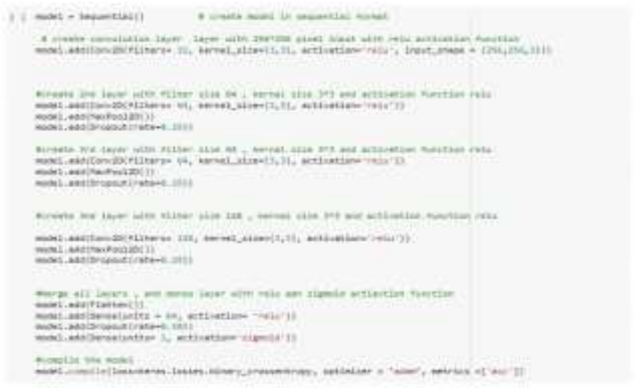
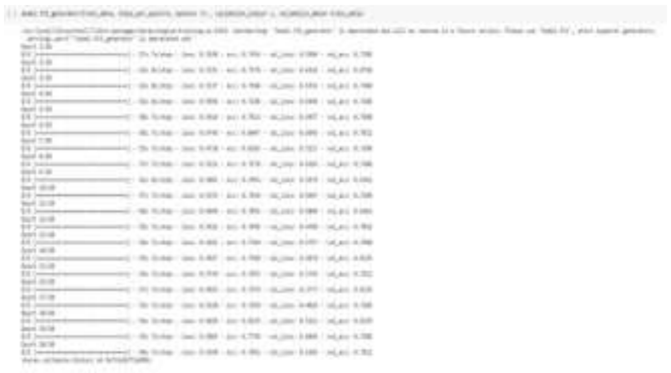
2**:** Creating the neural model with 5 layers and compiling the layer verifying the compilation status



```
[ ]  model = Sequential()          # create model in sequential format

      # create convolution layer  layer with 256*256 pixel input with relu activation function
     model.add(Conv2D(filters= 32, kernel_size=(3,3), activation='relu', input_shape = (256,256,3)))


     #create 2nd layer with filter size 64 , kernel size 3*3 and activation function relu
     model.add(Conv2D(filters= 64, kernel_size=(3,3), activation='relu'))
     model.add(MaxPool2D())
     model.add(Dropout(rate=0.25))

     #create 3rd layer with filter size 64 , kernel size 3*3 and activation function relu
     model.add(Conv2D(filters= 64, kernel_size=(3,3), activation='relu'))
     model.add(MaxPool2D())
     model.add(Dropout(rate=0.25))


     #create 4nd layer with filter size 128 , kernel size 3*3 and activation function relu

     model.add(Conv2D(filters= 128, kernel_size=(3,3), activation='relu'))
     model.add(MaxPool2D())
     model.add(Dropout(rate=0.25))


     #merge all layers , add dense layer with relu and sigmoid activation function
     model.add(Flatten())
     model.add(Dense(units = 64, activation= 'relu'))
     model.add(Dropout(rate=0.50))
     model.add(Dense(units= 1, activation='sigmoid'))

     #compile the model
     model.compile(loss=keras.losses.binary_crossentropy, optimizer = 'adam', metrics =['acc'])
```

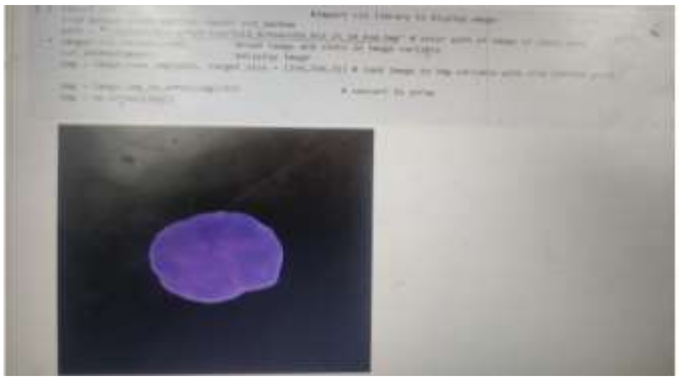
3: Training the neural network with different epoch values and noting down the accuracy after each epoch



```
[illegible]
```

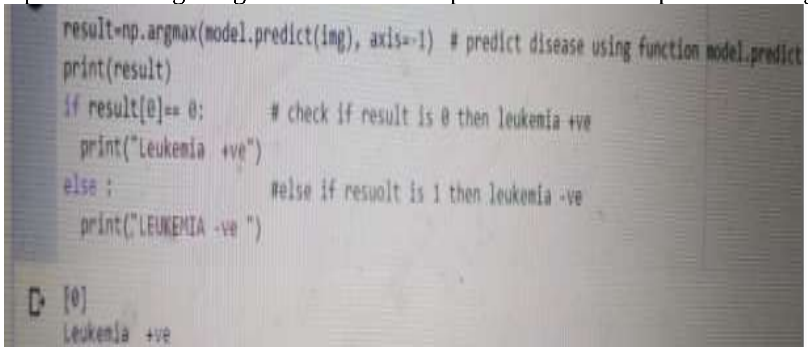
OUTPUT

1.Importing the x-ray image of patient whose diagnosis for leukemia has to be conducted. Linking the path and displaying the image



```
[illegible]
```

2: Feeding the image to predictor and getting result whether the patient is leukemia positive or negative



```
result=np.argmax(model.predict(img), axis=-1)  # predict disease using function model.predict
print(result)
if result[0]== 0:          # check if result is 0 then leukemia +ve
  print("Leukemia  +ve")
else :                     #else if resuolt is 1 then leukemia -ve
  print("LEUKEMIA -ve ")

[0]
Leukemia  +ve
```

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