Optimal Predictive Analytics of Blood Cancer (Leukemia) using Restricted Boltzmann Machine

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***Abstract*:** A predictive model utilizing deep learning is proposed to anticipate the patient health and condition of blood cancer (Leukemia). In this model, we are using the deep neural network which helps to predictive analysis on blood cancer to get optimal results. The existing model is used to predict the patient health and condition of the diabetics. In this case, a feature selection algorithm is run for the selection pro cess. The model involves deep neural network which utilizes a *Restricted Boltzmann Machine (RBM)* as an essential unit to examine the info rmation by allotting weights to the each branch of the neural network. The results increment the estimation of additional reports in light of the way that the amount of focuses done on blood cancer using a deep learning model few to none. This will predict blood cancer with considera bly more precision as showed up by the result obtained.

Keywords: *Deep Learning, Restricted Boltzmann Machine.*

1. INTRODUCTION

Leukemia are growths of the blood shaping tissues. Whit e blood cells might be delivered in exorbitant sums and can't work appropriately which debilitates the immune system.

The blood is comprised of liquid called plasma and three sorts of cells and each compose has special functions. White blood cells (additionally called WBCs or leukocytes) enable the body to battle infections and different infections. Red blood cells (additionally called RBCs or erythrocytes) convey oxygen from the lungs to the body's tissues and take carbon dioxide from the tissues back to the lungs. The red blood cells give blood its shading.

Platelets (likewise called thrombocytes) enable frame to blo od clusters that control dying.

Blood cells are framed in the bone marrow, the delicate, light focus of bones. New (immature) blood cells are called impacts. A few shoots remain in the marrow to develop. Some changes to different parts of the body to develop.

Ordinarily, blood cells are delivered in a methodical, contro lled route, as the body needs them. This procedure helps ke ep us solid. At the point when leukemia builds up, the bod y delivers expansive quantities of anomalous blood cells. In many sorts of leukemia, the irregular cells are white blood cells. The leukemia cells typically appear to be unique from ordinary blood cells, and they don't work legitimately.

Every year,* leuke*mia is analyzed in around 29,000 grown-ups and 2,000 kids in the United States.

In men and women, leukemia rate is most elevated among whites and least among Chinese, Japanese, and Koreans. The rate in men is around half higher than in ladies for all racial/ethnic gatherings aside from Vietnamese, among whom the male rates are just marginally higher. Ethnic contrasts in the frequency rates are little in the most youthful grown-up age gathering (30-54years), however turn out to be more obvious in every one of the more established age gatherings. It is discovered that youth leukemia rates are most noteworthy among Filipinos, trailed by white Hispanics, non-Hispanic whites and blacks.

1.1 TYPES OF LEUKEMIA

There are four sorts of leukemia. They are consider in two different ways. One route is by how rapidly the illness creates and deteriorates. The other path is by the type of blood cells that is influenced.

Leukemia is either acute or chronic. In acute leukemia, the unusual blood cells (impacts) stay exceptionally youthful and can't complete their ordinary capacities. The quantity of impacts increments quickly, and the ailment deteriorates rapidly. In incessant leukemia, some impact cells are available, yet when all is said in done, these cells are more develop and can do a portion of their typical capacities. Likewise, the quantity of impacts increments less quickly than in acute leukemia. Subsequently, chronic leukemia deteriorates progressively.

Leukemia can emerge in both of the two principle kinds of white blood cells — lymphoid cells or myeloid cells. At the

point when leukemia influences lymphoid cells, it is called lymphocytic leukemia. At the point when myeloid cells are influenced, the disease is called myeloid or myelogenous leukemia.

The disease appears in one of four major forms:

a) **Acute lymphocytic leukemia** (ALL) is the most widel y recognized sort of leukemia in youthful kids. This di sease additionally influences grown ups, particularly t hose age 65 and more established.
b) **Acute myeloid leukemia**(AML) happens in the two grown-ups and kids. This kind of leukemia is some of the time called acute nonlymphocytic leukemia (ANLL).
c) **Chronic lymphocytic leukemia** (CLL) consistently impacts adults past 55 years of age. It sometimes occurs in more energetic adults, yet it never impacts kids.
d) **Chronic myeloid leukemia**(CML) happens predomin antly in grown-ups. Few youngsters likewise build up this malady.

2. DEEP LEARNING

2.1 Deep Learning is a kind of machine learning in which a model makes sense of how to perform arrange errands particularly from pictures, content or sound. Deep learning is for the most part completed using a neural system engineering. The expression "deep" insinuates the amount of layers in the network the more layers the more deeper the network ordinary neural system contains only 2 or 3 layers, while deep network can have hundreds. Deep learning is tied in with taking in different level's of depiction and pondering that comprehends data.

3. LITERATURE SURVEY/RELATED WORK

In past Large number of work has been done to discover productive techniques for restorative finding for different diseases. Similarly lots of research has been done to check whether patient is blood cancer or not. Our work is an endeavour to foresee productively analysis of blood cancer with reduced number of attributes which depend on side effects that happens beginning times of blood cancer.

In 2016 T P. Kamble and Dr. S. T. Patil proposed a Deep learning based Restricted Boltzmann machine approach is used to detect whether patient is diabetic or not as Restricted Boltzmann machine is popular for classification and recognition purpose. To detect either patient is having type 1 or type 2 diabetes decision tree technique used.

In 2015 Shubhangi Khobragade, Dheeraj D Mor and Dr. C.Y.Patil proposed a technique for discovery of leukemia in patients from tiny white blood cells pictures. We have concentrated on the adjustments in the geometry of cells and factual parameters like mean and standard deviation which separates white blood cells from other blood segments utilizing handling apparatuses like MATLAB and LabVIEW.

In 2014 Mashiat Fatma and Jaya Sharma proposed a procedure for right and brisk arrangement of leukemia pictures and classifying them into their separate sorts. For this, diverse highlights are removed from the info pictures and afterward in light of these highlights an informational collection for the information pictures is made. This informational index is then used as info information to a neural system for preparing purposes. This neural system is planned and made to arrange the pictures as indicated by their comparing leukemia type.

4. PROPOSED WORK

The deep learning framework used in this project is TensorFlow. While the reference execution keeps running on single gadgets, TensorFlow can keep running on numerous CPUs and GPUs (with discretionary CUDA expansions for universally useful figuring on illustrations handling units). TensorFlow is accessible on 64-bit Linux, macOS, and mobile computing platforms including Android and iOS.

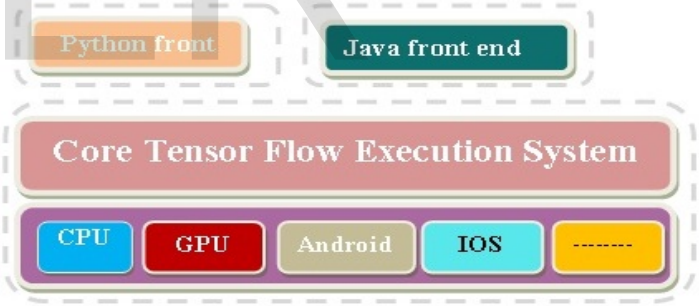

Figure 1. Deep Learning Framework – TensorFlow

The deep learning model chosen for this endeavour is a Recurrent Deep Neural Network (RNN). The most widely used neural network is a feed-forward neural network (MLP). However, that has not been chosen for this project specifically because even when both neural networks are w ell trained, a RNN uses more information than a MLP. Also, while a MLP can approximate any function to an arbitrary precision, the accuracy obtained by a RNN is much higher due to the presence of a layer that considers inputs from

different time points i.e. the recurrent formation of the neural network.

Process Flow Diagram for the Deep Learning Model is presented in figure 2.
First and foremost, the feature is selected based on the weig hts provided to the different symptoms in the deep neural n etwork. Those features are then extracted and their data val ues are applied to the Restricted Boltzmann machine for cla ssification. Restricted Boltzman machine is model which is having structure like bipartite graph (i.e., there is no intra la yer communication between the nodes of the same layer of the neural network) and it is an energy based model.

The aforementioned classifier detects whether the candidat e is blood cancer or not. In the data preprocessing step, the f eatures are selected from the file on the basis of their uniqu eness. The attributes are Erythrocytes, Neutrophils, Lymph ocytes, Monocytes, Platelets.

5. METHODOLOGY

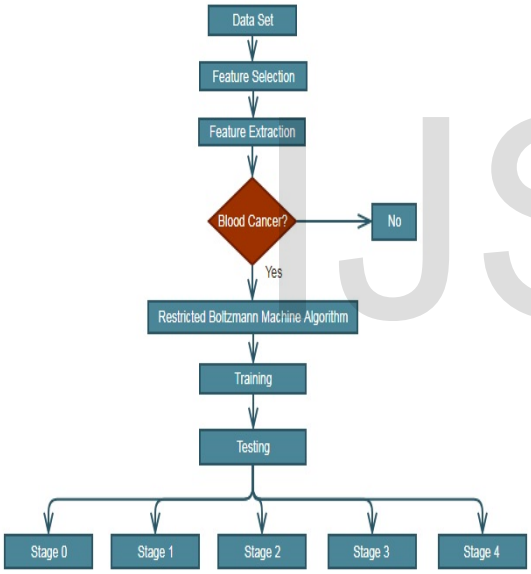

Figure 2: Process Flow Diagram

Process model consists of data process of feature selection a nd feature extraction.

5.1 Data Preprocessing:

In data pre-processing step first only the three features are selected from the file. Then that features data set is normalized to min max normalization. To get input vector range between 0 and 1 and avoid computation complexity. And next the dataset is divided into training dataset and test dataset such as 80% of training dataset and 20% of test dataset. Upper bound (UB) =1 and lower bound (LB) =0.equation number (1) is used to find min max normalization of data.

$$X\ normalized = (X\text{-}Xmin) / (Xmax - Xmin)(UB\text{-}LB) \quad .(1)$$

5.2 Restricted Boltzmann Machine for Classification

Restricted Boltzmann machine is model which is having structure like bipartite graph and it is energy based model. Its graphical structure have undirected graph. It has visible layer and the hidden layer. The input is directly clamped with the visible layer. It has a layer of visible units associated with a layer of hidden units yet no associations inside a layer Typically, RBMs utilize paired units for both visible and hidden factors. But the real valued data can be a pplied to RBM which is having structure as Gaussian Berno ulli type architecture. To show genuine esteemed informati on, a changed RBM with paired calculated concealed units and genuine esteemed Gaussian unmistakable units can be utilized.

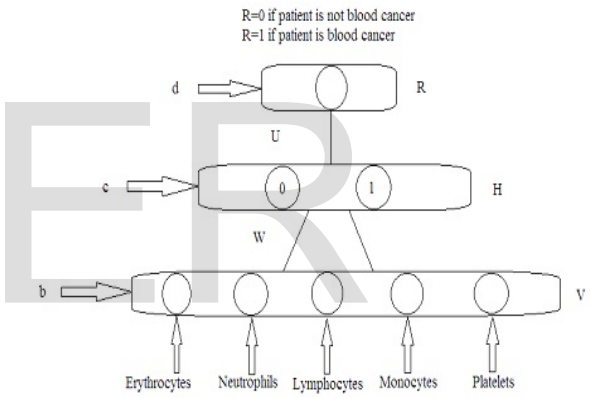

Figure 3. RBM basic structure

A Restricted Boltzmann machine is a specific kind of a Markov random field which has two layers. One layer of a RBM comprises of visible input units, v is the noticeable extending, which are associated with the other layer of shrouded stochastic units is h either 0 or 1. Figure demonstr ates the essential structure of a RBM. The appropriation of s tate {v,h} of a RBM is indicated by the accompanying vitalit y work.

$$E(v,h) = \sum_j \frac{(vi - bi)^2}{\sigma_i^2} - \sum_{i,j} \frac{vi}{\sigma i} * w_{i,j} * h_j - \sum_j c_j h_j \qquad (2)$$

where W represents to visible-to-hidden weight lattice comprising of weights wij of associations between neurons vi and hj, b represents to an visible bias vector, and a represents to a hidden bias vector. An arrangement of all parameters can be indicated by θ = {W,b,a}. The restrictive conveyance of the concealed vector h given the visibe vector v i.e. The joint probability distribution is comp uted using formula(2). The Distribution computation energ y is kept minimum to obtain maximum probability as negat ive energy is increase in probability and vice versa.

$$P(v,h) = exp(-E(v,h)) / Z \quad (3)$$

Where Z is partition function given summing all the pairs of visible and hidden unit given by below equation.

$$Z = \sum_{v,h} e^{-E(v,h)} \quad (4)$$

The contingent likelihood dissemination of every unit is given by the calculated sigmoid activation function of the input it receives using below formula:

$$P(h_j|v) = sigm(\sum_i w_{i,j} v_i + c_j) \quad (5)$$

$$P(v_i|h) = \mathbb{N}(\sum_j w_{i,j} h_j + b_i, \sigma_i) \quad (6)$$

$$Sigm(x) = 1 / (1+exp(-x)) \quad (7)$$

Computing p(r, x) is intractable, but it is possible to compute p(r|x), sample from it, or choose the most probable class under this model, for reasonable numbers of classes C this conditional distribution can be computed exactly and efficiently, below formula is used to compute energy distribution when there is classification related problem: Energy function function defines Distribution as

$$P(v,h,r) = exp(- E(v,h,r)) / Z \quad (8)$$

Using the distribution given in equation(8) the classes are predicted such as to check patient is having diabetes or not having diabetes.

Steps in training restricted boltzmann machine are as follows :

1. Take training data set clamp directly data set to visible unit.
2. To update the hidden unit states use the sigmod activation function equation number 7.
3. For ith hidden unit compute activation energy using equation number 5.
4. Set visible unit value to 1 using formula 3 and to 0 using equation number 6.
5. Compute positive statistics for edge (eij) = vi*hj
6. Reconstruct the visible units using similar technique. For each visible unit, compute the activation energy equation number 5and update the state.
7. Now update hidden units again, and compute (eij) = vi*hj which is negative statistics for each edge.

In restricted boltzmann machine the visible unit are used to find distribution of the hidden units and hidden uni ts are used to compute the distribution of visible unit until the stable state is obtained. Markov chain is important in RBM as it helps to get samples from probability distributio n such as gibbs distribution.

Markov Chain is process where the next state of system is depend on the current state of the system not on the next states of systems.

Figure 4 shows the one step in gibbs sampling.

Steps in Gibbs sampling :

1. Start updating at random state of visible unit.
2. Then update all hidden units in parallel.
3. Update or reconstruct visible unit in parallel.
4. Repeat all process for all training example.

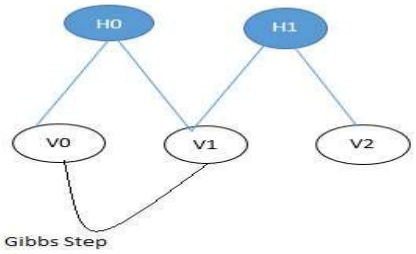

Figure 4:Gibbs sampling Step

Once the Sample probabilities of hidden layer computed using Restricted Boltzmann machine then the logistic regression is applied to classify the data as diabetic or not diabetic. In the Logistic regression binary decision task function equation (9) is used to take decision whether data belongs to class 1 or class 0.

$$0<=h(x)<=1 \quad (9)$$

Sigmod activation function is used to interpret result of logistic regression.
If h(x)>=0.7 then we can say it is class 1 data point Else if h(x)<0.7 then the data point belong to class 0
Need for Gibbs Sampling
The Gibbs sampler algorithm provides a solution to one very important problem which is sampling values from a probability distribution. As shown in the algorithm above, the Gibbs sampler gives a technique to proficiently rough a joint conveyance under one condition: we ought to effectively have the capacity to test from the contingent appropriation of every Xi.

Figure 5: Login page for the blood cancer

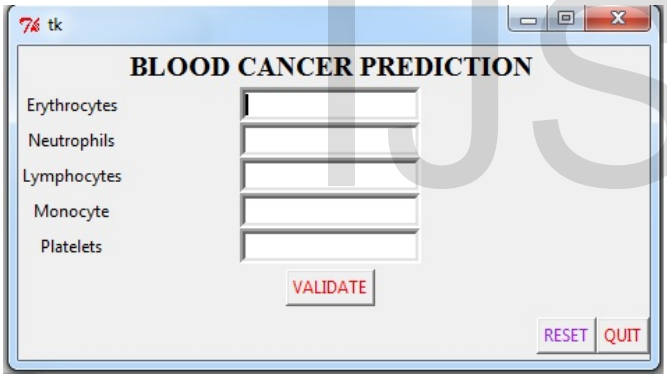

Figure 6: Prediction page for blood cancer

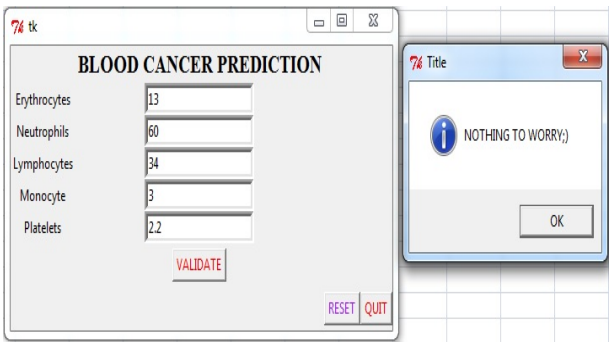

Figure 7: The prediction shows the result about normal patient.

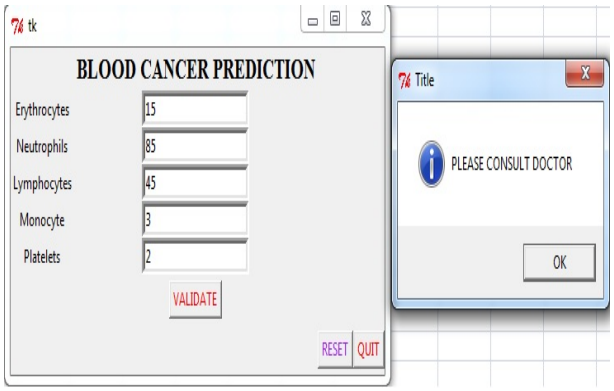

Figure 8: The prediction shows the result about cancer patient

Figure 7 & Figure 8

Consist of whether the patient belongs to blood cancer disease or not.
To detect Blood cancer or not the GUI is used as shown in figure 7 and 8, if patient is Blood cancer then it intimate to consult doctor else it replace don't worry.
GUI For the system is as follows to detect Stage 0 to Stage 4 blood cancer as shown in figure 7 & 8.if patient belong to which stage it will show the details of which stage click the validate to find the stage of blood cancer.

6. Performance and evaluation setup

Initial Result obtained after applying logistic regression on data generated from Restricted Boltzmann machine.

i.	Correctly Classified Instances	: 192 (80%)
ii.	Incorrectly Classified Instances	: 48 (20%)
iii.	Correlation coefficient	: 0.8085
iv.	Mean absolute error	: 0.2663
v.	Root mean squared error	: 0.306
vi.	Relative absolute error	: 53.1654 %
vii.	Root relative squared error	: 61.0731 %
viii.	Total Number of Instances	: 240

GRAPHS AND TABLES

This graphs consists of x and y axis. On the x axis, we are consider attributes of the blood samples and on y axis it consists of ranges of the blood samples.

Stage 0 :

The blood cancer at stage 0 too many lymphocytes in the blood but no other symptoms.

Attributes	Normal	Stage 0
Platelets	5	5
Monocytes	8	9
Erythrocytes	18	18
Lymphocytes	40	41
Neutrophils	70	71

Table 1: The table consists of attributes and ranges of blood cancer of stage 0.

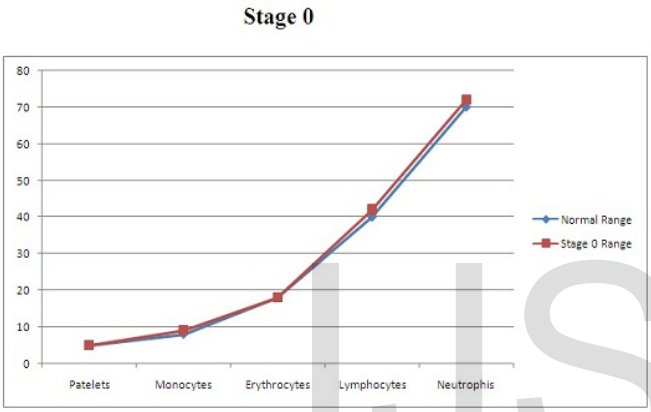

Figure 9 : Shows the graph of "Table 1" attributes

Stage 1

The blood cancer first stage incorporates the development of the lymph nodes. This happens in view of the sudden increment of the quantity of the lymphocytes. The risk at this stage is low as the growth isn't yet spread or influenced some other physical organ.

Attributes	Normal	Stage 1
Platelets	5	6
Monocytes	8	10
Erythrocytes	18	20
Lymphocytes	40	43
Neutrophils	70	73

Table 2: The table consists of attributes and ranges of blood cancer Stage 1.

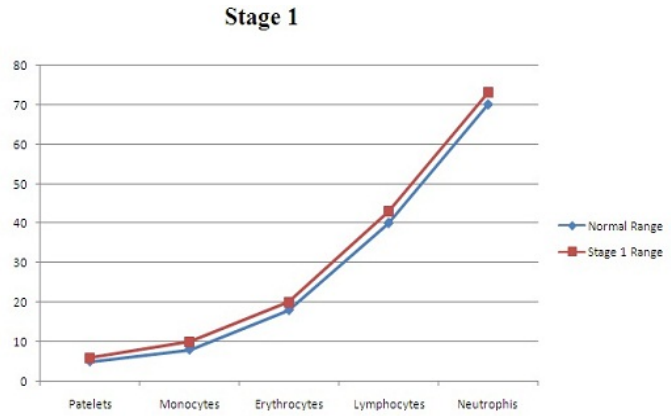

Figure 10 : Shows the graph of "Table 2" attributes

Stage 2:

In the blood cancer second stage, spleen, liver and lymph hubs get developed. It isn't fundamental that every one of these organs get influenced in the meantime; notwithstanding, this stage incorporates one of these organs without a doubt. The development of the lymphocytes is high in this stage.

Attributes	Normal	Stage 2
Platelets	5	6
Monocytes	8	10
Erythrocytes	18	25
Lymphocytes	40	45
Neutrophils	70	75

Table 3: The table consists of attributes and ranges of blood cancer Stage 2.

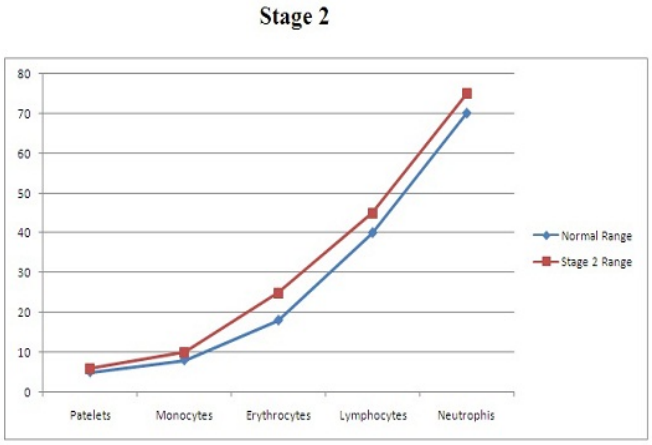

Figure 11 : Shows the graph of "Table 3" attributes

Stage 3

In the blood cancer third stage, anemia creates in the third stage or more said organs are as yet discovered amplified. It is certain that in excess of two organs get influenced in this stage.

Attributes	Normal	Stage 3
Platelets	5	6
Monocytes	8	12
Erythrocytes	18	25
Lymphocytes	40	50
Neutrophils	70	80

Table 4: The table consists of attributes and ranges of blood cancer Stage 3.

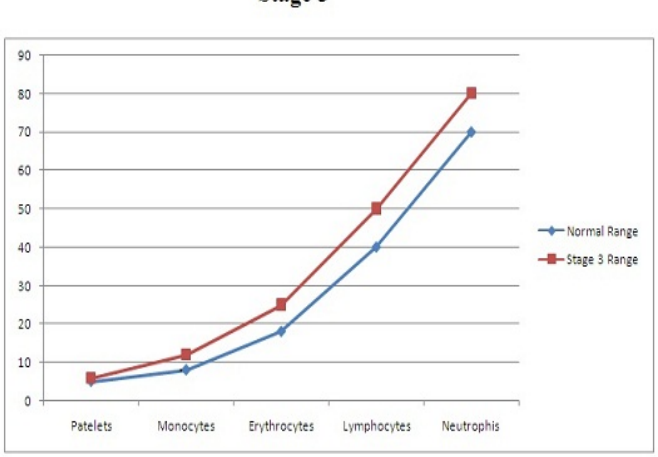

Figure 12 : Shows the graph of "Table 4" attributes

Stage 4

The blood cancer fourth stage is the last stage with the most noteworthy risk proportion. The rate of blood cells begins falling quickly. The harmful cells begin influencing the lungs including alternate organs which as of now began getting influenced in the before stages. Frailty, in this stage, will probably be acute.

Attributes	Normal	Stage 4
Platelets	5	8
Monocytes	8	15
Erythrocytes	18	30
Lymphocytes	40	60
Neutrophils	70	85

Table 5: The table consists of attributes and ranges of blood cancer Stage 4.

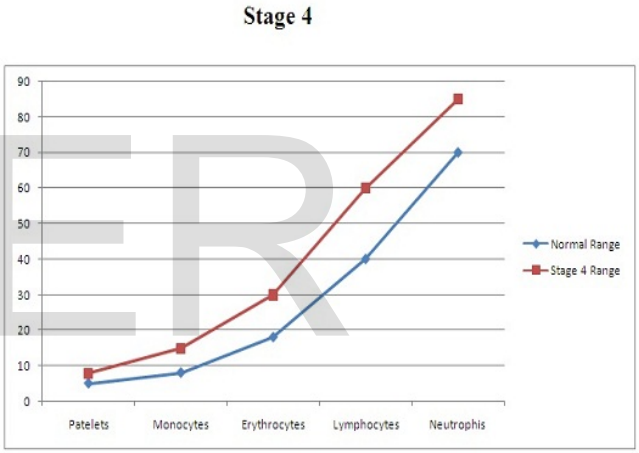

Figure 13 : Shows the graph of "Table 5" attributes

Attributes	Assigned weights
Erythrocytes	13 - 18 gms%
Neutrophils	40 - 70%
Lymphocytes	20 - 40%
Monocyte	2 – 8%
Platelets	1.5 - 5 L

7. Future Work

This is a rich theme to take a shot at and a great deal of furt her work should be possible to enhance the effectiveness of the neural system regarding both speed and precision. Add itionally, utilizing profound learning, AI frameworks can b e made that can anticipate the beginning of blood cancer cer tainly before a patient is determined to have it. At long last, a similar model utilized as a part of this paper can likewise be connected to an assortment of other medical issues, for example, heart diseases, strokes, respiratory issues and even annoy bladder illness.

8. Conclusion

The deep neural system was effectively prepared, tried and executed on the informational collections. The outcomes go t were above satisfactory and can be additionally enhanced by expanding the measure of the information index by addi ng to it the data accumulated by approaching patients in a healing center or in a system of doctor's facilities. Besides, t he forecast of blood cancer can likewise rely upon different variables which are absent in said informational collection. Thinking about these variables will additionally enhance th e exactness of the proposed framework. Additionally, the c orrelation demonstrates that the profound learning models are certainly more successful as far as accuracy than the un pleasant set hypothesis display.

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