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BLOOD CELL IMAGE DIAGNOSING USING CNN AND M-SVM

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ABSTRACT : The blood related diseases involve the identification and characterization of patient's blood sample. There are automated methods for detecting and classifying the types of blood cells having important medical application. The system has convolutional neural network(CNN) and the traditional machine learning methods have shown good results in the classification of blood cells images, they are unable to fully exploit the long-run dependence relationship between certain key features of picture and their labels. To transfer the weight parameters the uses transfer-learning method that were pre-trained on ImageNet dataset to the CNN section and adopted a custom loss function to allow the network to train and converge faster with more accurate weight parameters. Experimental results will show that which network model is more accurate and efficient in classifying blood cell images. The analysis of blood cells, in magnifier pictures will give helpful information regarding the health of patients. There are three major types blood cell, erythrocytes (red), leukocytes (white), and platelets. Manual classification is time intense and liable to error because of the various morphological options of the cells. This system presents an intelligent system that simulates a human visual inspection and classification of the three blood cell types. This system comprises two phases: The features of blood cells are extracted through global pattern averaging in the image pre-processing phase, and the training is done first and then classification is carried out in the neural network arbitration phase. Experimental results suggest that SVM method performs better in identifying blood cell, regardless of their size, irregular shapes and orientation, thus providing a fast, efficient and simple scale and rotational invariant blood cell identification system which can be utilized in automation laboratory coverage.

Keywords: Blood cell subtype; Image classifications; supervised learning; Self label algorithms; etc.

I. INTRODUCTION

It is known that blood cells are of different types which include red blood cell, white blood cells platelets. Leukocyte plays an important role in the human immune system and is also called as immune cell of the body. The granulated shape and information of the leucocyte to divide white blood cells into granular cells like eosinophil, neutrophil, basophile and non-granular cells: lymphocyte and monocot is usually used by hematologist. The proportionate of these cells in the blood is different for different people and different dieses. Experts generally use these basic data to determine the type and dieses. Hence the white blood cell classification has a significance and value for medical diagnosis the bleeding in the body in the form of blood clotting. It can detect any damage in the blood vessels. Red blood cells are tiny which are also important in the body to carries fresh oxygen to the overall body over respiratory system in the body from infections. BCCD (Blood Cell Count and Detection) dataset (small scale dataset for blood cell detection) is used and processed the dataset, which then turn it into 12,444 blood cell-enhanced images (comprising 9,957 training data and 2,487 test data). In this dataset, the blood cells into 4 different types, namely, monocot, lymphocyte, and eosinophil and neutrophil.

Counting and detection of WBC in blood samples were also presented through computer-aided and mobile-cloud-assisted blood analysis. Plate counting is usually done manually but a recent

study showed that this process can be done through Circular Hough Transform in a microscopic blood cell images. In this system CNN(Convolutional Neural Network) and M-SVM(Support vector machine) are used for classifying the images. Once the classification of the images is done with both supervised learning technique are completed then the comparison is done with the accuracy values and check which technique gives the better results. UI Model (User Interface Model) is generally used to represent how the user interact with his/her own device or other devices and even check how the device responds to the user. Here in our system UI Model is used to select the images from the system and display both the techniques simultaneously and shows the results on single screen instead of a separate result. Biotechnology uses Convolutional neural networks. Neurons are like local filtering of the complete input space, and are well-organized to achieve the understanding of an image in the complete field of view. CNN (Convolutional neural networks) may extract the local and deep features of the input image.

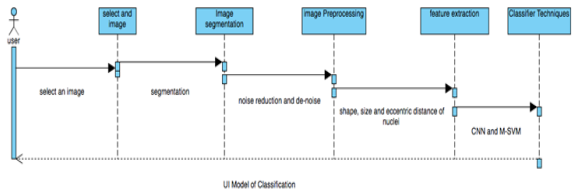

Figure 1.1 Sequence diagram

A sequence diagram is an interaction picture which shows how and in what objects would work and interact with each other. It is also called as message sequence graph construction. It demonstrates how temporally objects interact with each other. In figure 3.3 it is clearly shown how the objects interact with each other and how would they work. First the user must select an image and that image will be given for the segmentation process and that would be further given to pre-processing stage and then feature extraction stage and then finally given to the classifier and at last the classifier will give the UI model to the user at the end.

System Architecture

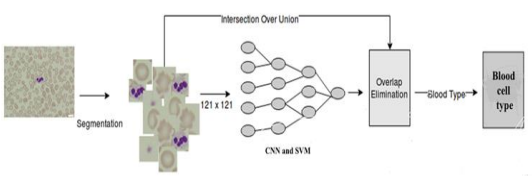

Figure 1.2 System Architecture

The blood related diseases involve the identification and characterization of patient's blood sample. The system has automated methods for detecting and classifying the types of blood cells having important medical application. The system has convolutional neural network(CNN) and the traditional machine learning methods have shown good results in the classification of blood cells images, they are unable to fully exploit the long-term dependence relationship between certain key features of image labels and images. In particular, to transfer the weight parameters the system uses transfer-learning method that were pre-trained on Image Net dataset to the CNN section and adopted a custom loss function to allow the network to train and converge faster with more accurate weight parameters. Experimental results will be displayed at the proposed network model is more accurate and efficient in classifying blood cell images compared with the other CNN models.

During feature extraction, each segmented cell is analysed to form a feature vector from color, shape, and texture features. Finally, in classification, each blood cell is labelled by the classifier according to its feature vectors as shown in figure 1.2.

II. LITERATURE SURVEY

Literature survey is a critical look at the existing research that is significant to the work that you are carrying out. It provides background information. It helps to establish importance of existing knowledge. Before developing the tool, it is necessary to determine the economy and strength of the company. Once all these requirements are satisfied, then the very next step is to find out which language and operating system (OS) can be used for building the tool. This support can be obtained from books or from senior developer or from websites. Before developing the system, the above requirements are considered for developing the proposed system. Before building the tools and its associated designing it is essential to survey and to determine the resource requirement, time factor, man power, economy, and company strength. The KNN method is closely connected to a very few number of adjacent samples in the category decision. Based on this theory, 199 cell images were experimented by Young in 1972. To segment white blood cells, he used histogram thresholds and distance classifier is used to classify them. The result was 92.46%.[12]Bayesian classification is based on statistical classification and uses its knowledge of probability statistics to classify data. In many classifications, naive Bayes algorithm can be compared with decision tree and neural network algorithm. Sinha and Ramakrishnan used Bayesian classifiers to classify cells and the result was 82.3%.[7] The linear regression LR classification method is similar to the Support Vector Machine.

This obtains a some set of weight coefficients that can be used for classification after linear representation. This first trains a hyper-plane separately, and then the boundary of the classification is the hyper plane. The classical support vector machine method is only suitable for few types of classification problems. After development, support vector machine can also be used to different classification problems. In white blood cell classification, it is essential to solve the problem of different classifications. For example, the classification problem of leukocytes the study can be solved by merging different binary support vector machine. Rezatofighi and Soltanian-Zadeh used the snake and Gram-Schmidt Orthogonal algorithms for the segmentation of 400 blood smears and classifies them using support vector machine. Their result was 90%.[6]

Recently, convolutional neural networks have been widely implemented in various image classification fields. In particular, convolutional neural networks (ConvNets) [2] achieved unprecedented results in the 2012 ImageNet large-scale visual recognition challenge, which included classification of natural images in the ImageNet dataset into 1000 fine-grained categories [1]. This can also improve the presentation of various medical imaging applications [17], [18], such as classification of lymphnodes and lung diseases in CT images [19], [20], segmentation and pixel intensity of brain tissues using MRI [21], fundus images for vessel segmentation[23], and detecting cervical intraepithelial neoplasia (CIN, particularly CIN2+) at patient level based on Cervigram images or Multimodal data [22]. In addition, ConvNets showed superior performance in cell image classification such as pleural cancer [24] and human epithelial cell images [25].The blood related diseases involve the identification and characterization of patient's blood sample. The system has automated methods for detecting and classifies the different types of blood cells having important medical application. The system has convolutional neural network(CNN) and the traditional machine learning methods have shown good results in classifying the blood cell images, and are unable to fully exploit the long-term dependence relationship among certain key features of images and image labels. In particular, to transfer the weight parameters the system uses transfer-learning method that were pre-trained on Image Net dataset to the CNN section and adopted a custom loss function to allow the network to train and converge faster with more accurate weight parameters. Wang Shitong and Wang Ming has used a new Detection Algorithm based on Fuzzy Cellular Neural Networks (NN) for white blood cell(WBC) detection and the work involves fuzzificatiion of the features derived from leukocytes. 2006 [3]. Understanding of blood cell images with visual subjective method and image analysis mediated objective methods have their own limitations. Hence medical image processing techniques such as image enhancement and edge detection are done prior to segmentation of WBC (white blood cells) from blood smear .Pre-processing methods use a small neighbourhood of a pixel in an input image to get a new brightness value in the output image. The concerned research scholar has collected the microscopic blood cell images from blood smear and bone marrow, cells affected with leukaemia and other malarial parasites from radiologist and oncologists and have database of them. Blood cell image acquisition requires 100 x magnifications on the blood smear and pre-processing requires the application of frequency domain filters and edge detection by using cellular automata. The scholar has applied advanced image enhancement techniques and presented them as papers in national and international conferences. The scholar has implemented de-noising filters such as Gaussian filter & Gabor filter and compared it with conventional filters such as median, laplacian and average filter. Since the image is stored as a collection of discrete pixels it is necessary to produce a discrete approximation to the Gaussian function before the convolution can be performed. It is found that Gaussian filter algorithm is an extremely versatile sharpening tool that improves the definition of fine detail by removing low-frequency spatial information from the original image. Next step in medical image processing after pre-processing is edge detection which identifies the sudden intensity changes that are observed by the boundaries of object image produced something like a line drawing of an image. Hough transform based edge operator & Sobel edge operator are implemented and compared with conventional edge operators like Prewitt and Canny operators. Hough transform algorithm uses an array called accumulator to detect the existence of a line. Hough transform is also a feature extraction technique concerned with the identification of arbitrary shapes or ellipse and it has performed well compared to Sobel and Canny operators. Segmentation is done to divide the unique disjoint regions of the image or to partition the image into meaningful regions that corresponds to objects within the scene, distinguishing one element from other is very difficult when occlusion, staining reagent or illumination is inconsistent. The scholar has implemented one new segmentation technique based on fuzzy cellular neural network(FCNN) using New Detection Algorithm (NDA). This New Detection Algorithm combines the advantages of threshold segmentation mathematical morphology (TSMM) and fuzzy logic method. The binary segmentation is performed as the main step due to the gray value of the WBC nuclei is the tiniest in the image. (16) Then the individual WBC (white blood

cells) are detected quickly according to their shape feature. In this new detection method both gray and homogeneity information are taken into account. However more number of parameters needed to be determined by statistics. K means clustering was used as a segmentation technique using various color models Performing differential WBC (white blood cell) counts in a bone marrow preparation is a cruci l step in diagnosing various disease states. It is a difficult task to locate, identify, and count these cells. The watershed algorithm can be used to perform an over segmentation of the image where each primitive component. Memberships is assigend in order to obtain more consistent labels for merging into cell objects. The watershed algorithm with the help of morphological pre-processing provides useful patch information which helps preserve geometric structures in bone marrow cell images. This patch information is used to build a patch graph and the graph guides the relaxation process by providing context information to the fuzzy rules. It produces highly over segmented results if an image contains noise or texture. o, time tasking is high. The proposed method supposes that the blood cell image consists of two regions. One is the interest region which contains all white cells and the other is of no interest region which contains back ground and red blood cells. The idea of this method is to subtract the back ground first and eliminate the red blood cell and small disturbing objects. It was possible to segment almost all the white blood cells and it was found that the running speed was high and the algorithm was comparatively adaptable. Feature extraction is extraction of a vector in multidimensional space from a image, where each dimension represents an attribute of the image that is believed to carry information that helps in classification of the image. Features such as nucleus and cytoplasm area, average color co-ordinates and number of pixels in the nuclear perimeter are used. Accurate classification of human blood cells plays an important role in the diagnosis and treatment of diseases. Haematological disorders refer to the diseases caused with the changes in blood cells or blood system such as Leukemia, Anemia, Malaria and Azotemia. White blood cell composition of the blood gives valuable information and plays a major role in the diagnosis of different diseases like Leukemia. Leukemia is a rapid proliferation of abnormal white blood cells (leukocytes). Anemia can be detected the reduction in the morphology of red blood cells (erythrocytes). Thalassemia, a type of malaria is that is caused due to the abnormality in red blood cells [6] Azotemia is another type of hematological disorder caused by excessive nitrogen compounds can be detected by the change in micro morphological features from blood cell. New and already done (by the scholar) and some other existing segmentation algorithms will be compared for their accuracies, to determine the optimal algorithm finally to be adopted for the next stage of work. After the segmentation of leukocytes soft computing classifiers are used to classify using the extracted morphological indexes as Neutrophils, Basophils, Eosinophils, Lymphocytes and Monocytes [4]. Fuzzy C means clustering (FCM) will be used for the classification of pixels which is an unsupervised fuzzy classification algorithm. Separation of the classes can be done using three most relevant features such as cell and nucleus area and the gray intensity of the cytoplasm.

Mini puri and Jyoti pana used stem cell regional localization in their research paper for the cancer detection. The malarial parasitic detector can use a Bayesian pixel classifier to mark the stained and unstained classes of pixels using conditional probability density functions. Early identification of leukaemia, malarial parasites and other haematological disorders can greatly increase the probability of recovery. Blast cells, for instance are characteristics of a certain type of leukaemia and would indicate further tests if found in blood. Features are to be extracted according to an efficiency criterion on the basis of classification or recognition tasks. Being able to automatically able to classify these and flag samples accordingly could be a great boon to haematologists. This would of course require leukemic blood with unusual evidence to be available and manual classification by haematologists for the training data set.

TECHNOLOGIES USED

Python

Python is high-level, interpreted, and general-purpose programming language.Released first in 1991 by Guido van Rossum. Its object-oriented approach aims the programmers to write clear, logical code for large and smallscale development. It is a garbage collected and dynamically typed. This language contains a substantial body of documentation, abundant of it contributed by various authors. The markup used for the Python documentation is restructured text, developed by the docutils project, amended by custom directives and using a toolset named sphinxto post-process the Hypertext Mark-up Language (HTML) output.

UI Model

UI Model (User Interface Model) is generally used to interact with the user easily. This is present in all the programming language. In this system, UI is implemented using python.. This is also known as native technologies. In this system, the console of Spyder and UI is connected with the help of pipe and this helps the builder to connect the related information for his choice of select and put in the UI for ease of understand. Generally, UI is used for

the user to understand easily and this helps a person who has no knowledge regarding the system can also understand with the help of this. Hence this is used in this system.

III. EXISTING SYSTEM

In the existing system,an architecture that combines CNN and RNN is proposed it integrated the features extracted from CNN and RNN for blood cell classification. CNN and RNN are considered as two different branches. First, the pre-trained CNN model is freezed, use the pre-processed training data as the input of the RNN model, extract features are obtained and saved,at last CNN and RNN features are combined. The weight parameters are constantly updated during the training of RNN. In the CNN model, different size and weight matrix windows in order to generate multiple feature maps [13], [3] are applied. The features extracted from the two models are combined according to the elements. And atlast, the classification results are displayed using Softmax [21]. In addition, a fine-tuning strategy to retrain the CNN-RNN framework is also used, and finally obtains the results of classification. The existing system four major contributions of blood cell classification as follows.

First Contribution: This is the first application that combines CNN and RNN classifiers to classify the blood cells. This can be effectively use the spatial and temporal characteristics of data to achieve a good classification results.

Second Contribution: By using the pre-trained results of the CNN model, where the chosen weights are closer to local optimum, so that they are kept within a high gradient range and they can be effectively fine-tuned.

Third Contribution: RNN is a neural network that captures dynamic information in serialized data by hiding the periodic connections of nodes in layers, and can classify serialized data [14], [15]. Different from other forward neural net- works, RNN can save the context state, and even can store in any arbitrarily long context window, learn and express relevant information, and is no longer limited to the spatial boundaries of traditional NN. Based on the above theory, a RNN with memory function is introduced to generate a continuous time outputs of states, for the features extracted from the CNN model. In addition, because the LSTM (a special type of RNN network, Long Short-Term memory networks) [17], [18] this can re-solve the problem of gradient disappearance during traditional RNN network training, our network model can have more layers.

Forth Contribution: The existing system adjusts the loss function and activation function of RNN, and introduces the RMSProp [23] and Adam optimizers to train the network. At the same time, a fine-tuning strategy to train the CNN-RNN framework is introduced. The CNN and RNN combination method will give an accuracy of 90.79. since there are other several methods which will give better results than these combinations in the existing system it compares the classification techniques which gives the best results among them.

IV. PROPOSED SYSTEM

The proposed system contains the comparison between the supervised learning techniques for blood cell image classification. The classification techniques that are implemented in the proposed system are CNN and M-SVM. The images are classified with the help of classifiers and these classifiers are the supervised techniques in the machine learning. The classification process is mainly involved in the few basic techniques like pre-processing, segmentation, feature extraction of image. The convolutional neural network is generally a layered structure where the input of the images is given to the first layer and the output of the first layer will be the input to the second layer and similarly for the next layers. The main part of the CNN is the activation function and the activation function used in this system is relu. The M-SVM will be directly implemented with the help of the functions and can get the results directly. The last part is comparing the two classifiers and check which one would give the best results in classification so to make this easy the UI model is used at the end to display the results of both the classifiers simultaneously to make the user get the information easily.The system contains several modules like image acquisition, pre-processing, segmentation, and classification techniques. The feature extraction plays a major role, the features extracted here are shape, size and eccentric distance of the nuclei, back ground colour. And finally, the classification is done based on these extractions.

V. OBJECTIVES

The aim of this project is to automate the classification of Blood Cells using Segmentation and Classification methods, ease the working of the pathologist, to help the doctor make a better diagnosis. The following are the formulated objectives:

i. To develop automated blood cell counting system using segmentation and classification method.
ii. To test the segmentation and classification, performance for system accuracy and

reliability for different classification techniques.

The system is designed to comparing the classification techniques.

- Image acquisition
- Image preprocessing
- Image segmentation
- Feature extraction
- Classification techniques

Image acquisition: the image intensity, grey level, brightness are collected and these are same for all the images to make sure that there would not be any difference in the images elected from the user.

Image pre-processing: aim of the pre-processing is to improve the image data that suppresses unwanted distortions or enhances some features. In this system the intensity and the grey scale transformation for the pre-processing are used.

Image segmentation: The image segmentation is used to segment the image with certain range into different other images and this can be used for feature extraction and each segment cell is hopped based on the window size and here the window size for all the images are 2.

Feature extraction: features like shape, size and eccentric distance of the nuclei, back ground colour is extracted in the system. These are later used to classify the images.

Classification techniques: CNN and M-SVM are the classification techniques used for the classification of images in this system.

VI. MODULE DESCRIPTION

Image Acquisition

The images are collected from microscope which is equipped with DinoEye Eyepiece Camera, and this process of capturing the image will involve the blood smear process to prepared sample. Blood smear is the process of preparation of blood specimen on the slide that is observed under microscope. The process for displaying the RBC image will involve digitization of image from the optical image with 40 times (40X) objective which equal to approximately 400 magnifications. The shapes of the blood cells are also used here.

Image Pre-processing

This stage includes reduction of noise and constant enhancement of required image. This is essential to perform in order to perform the segmentation. De-noising of images are generally degraded by various other noises in the transmission. De-noising is generally done to get the important data from the image and some of them are as follows feature extraction, segmentation, recognition will result in the removal of the noise data. The median filtration is a digital filtration technique(no-linear) and is rottenly used for the removal of the noise. The main aim is to run on a single entry on entry and replacing the other with the previous one. This will not only remove the noise and can keep the shape and edge details of the image as well and the corresponding results will also be illustrated.

Feature Extraction

The recognition of objects may be accomplished for several applications by identifying an un-known object as the member of the set of known objects. These features are typically identified and these will be different for different images. These features can be uniquely identified for different cells in the blood. In this project, the object information is extracted through a sample of normal/abnormal cell by relying on the object's geometrical features which are compactness and moment invariant. Compactness is a common shape measurement techniques are based on the information from the perimeter (L) and area (A). The compactness provides information about how the object is form in term of the smoothness circle shape. When the compact value become higher, it shows that the object's shapes is more complex. Such property is really useful to distinguish between the normal and abnormal cell since for, the abnormal cell shape is quite complex compare to the normal cell. However, relying on a compactness value alone is not enough since when cell shape becomes more oval, the compactness value become higher even though the shape is not complex. Because of that, a second feature information is extracted which is moment invariant values. Formerly, moment method has been used in the analysis and recognition of object shape. One advantage suggested by moment method is that they can easily, equipped to be invariant in 2D transformation such as translation, rotation, reflection and scaling. This property is very convenient since such transformations are very common for RBCs in blood smeared images. Furthermore, because the invariant does not provide any or less information than the original moment values, the features that might be require for classification is reduced, and thus decrease the complexity of the learning problem. For this project, seven HU moment features are used [15] to represent the RBC shape.

Classification

In order to be able to discriminate between normal and abnormal RBC in the image by using

the selected features, a robust classifier should be used. The classification module is performed by using convolutional neural network (CNN) classifier. The CNNs are a mathematical approximation of a biological brain, and have been identified as a useful framework for precise modelling of nonlinear response. It comprises a number of neurons connected together to form a network. The weights that linked between the neurons, i.e. Wij and Wjk are where the functionality of the network resides. Before the network can be useful, it needs to be trained. Basically, the training session will alter the weights so that the error between the inputs and targets can be minimized. One of the fastest training approaches is Levenberg Marquardt algorithm with mean square error (MSE) cost function. Here from the RBC features the data is feed, i.e. [compactness and seven HU moments invariant] [15], to the input neurons, and normal/abnormal RBC type to the targets neuron during the training process. The networks setting is considering optimal for the highest recognition rate in both training and validation set.

VII. RESULTS AND DISCUSSIONS

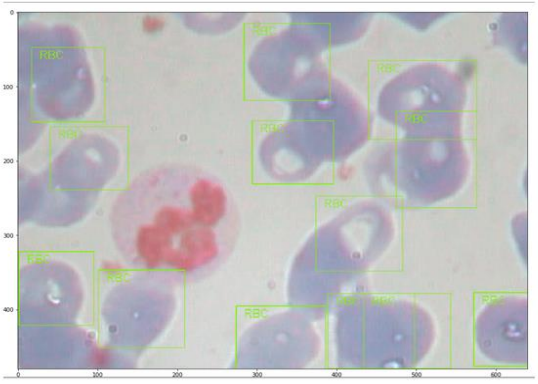

Figure 7.1 Image Segmentation

In the figure 7.1 after an image is selected from user the image will be segmented and these segmentations will be done on the overall image.

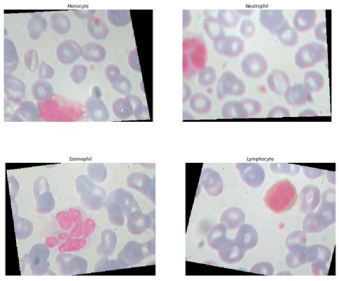

Fig 7.2 Plotting the image

The data that is there in the dataset will be labelled and plotted as shown in figure 7.2. With these the user can easily understand what kind of data is there in the dataset and can be accessed easily.

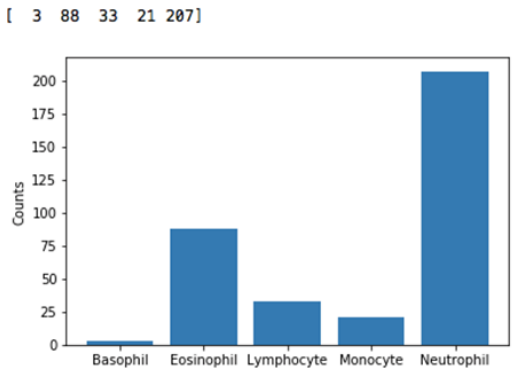

Fig 7.3 Count of bell cell images in the data set

The counting of data present in dataset is done based on the labels and these labels are counted these count is displayed as shown in figure 7.3.

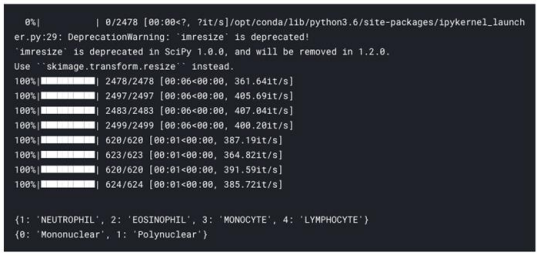

Fig 7.4 Image transformation part

The image transformation is done for the preprocessing stage of the data and is done as shown in figure 7.4.

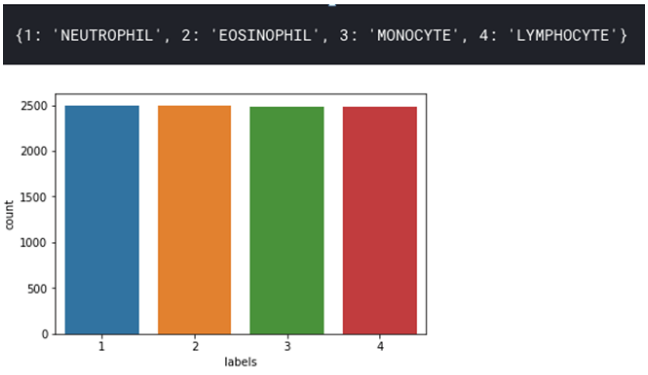

Fig 7.5 Images after resizing in the data set

Once this data is done with the pre-processing then the data is resized as shown in figure 5.5.

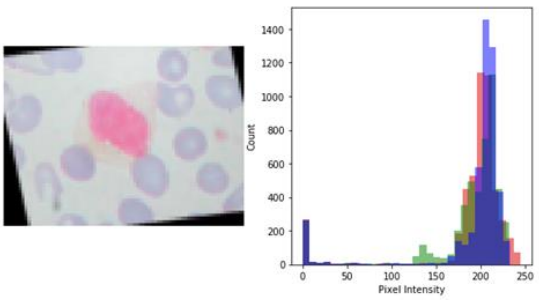

Fig 7.6 Image's pixel intensity that is selected

In figure 7.6 the image's pixel intensity that has been selected from the user is given.

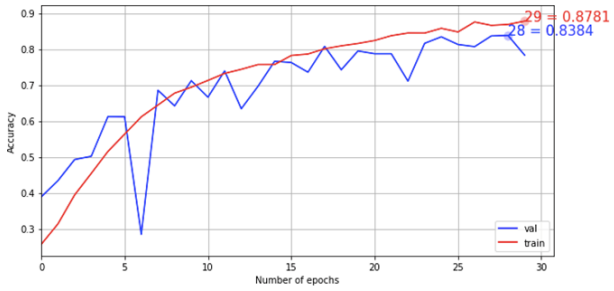

Fig 7.7 Number of epochs VS accuracy of CNN
The learning and epoch curve of the CNN classifier is as shown in figure 7.7. Accuracy of CNN: 0.7832730197024528

	precision	recall	f1-score	support
NEUTROPHIL	0.57	0.88	0.69	624
EOSINOPHIL	0.96	0.53	0.68	623
MONOCYTE	0.84	0.81	0.83	620
LYMPHOCYTE	0.97	0.92	0.94	620
avg / total	0.83	0.78	0.78	2487

Fig 7.8 Precision, recall, f1-score, support for CNN of all four cells

Generally, comparison of classification techniques is done based on the precision, recall, f1-score, support. The above values of the CNN are as shown in figure 7.8.

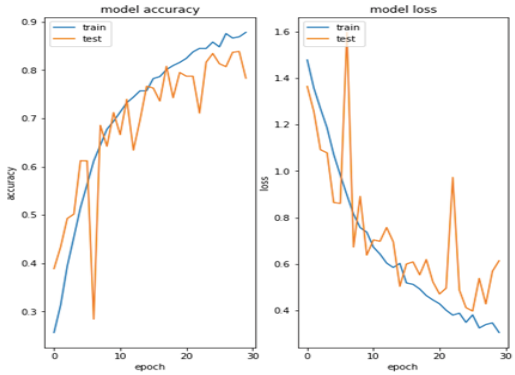

Fig 7.9 Model accuracy and model loss of CNN.

The CNN accuracy and loss curve is as shown in figure 7.9.

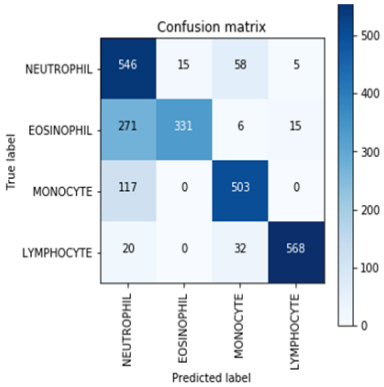

Fig 7.10 Confusion matrix for CNN with all four data variables

Confusion matrix of the CNN with five different labels are as shown in figure 7.10.

Accuracy of M-SVM= 0.92848009

	precision	recall	f1-score	support
Mononuclear	1.00	0.88	0.93	1240
Polynuclear	0.89	1.00	0.94	1247
avg / total	0.94	0.94	0.94	2487

Fig 7.11 Precision, recall, f1-score, support of M-SVM with two nuculer cell

The precision recall f1-score and support of the M-SVM with two nuclear cell is as shown in figure 7.11.

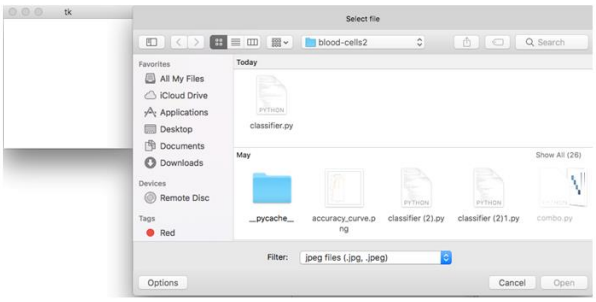

Fig 7.15 selecting an image from the system using UI model

Image selection from the system using an UI model and these will help for the next processes in the model is shown in figure 7.15.

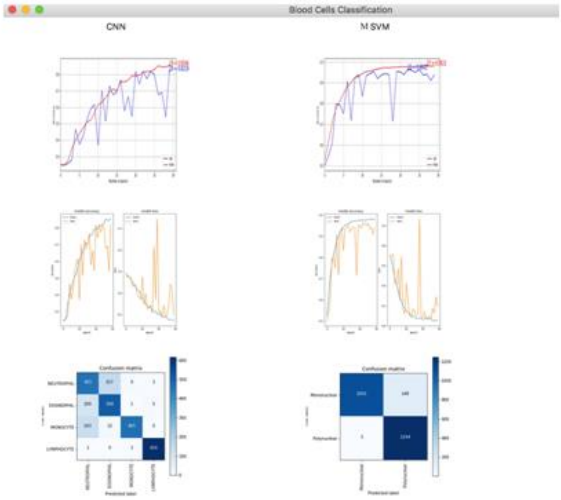

Fig 7.17 CNN and M-SVM classification analysis.

In figure 7.17 the CNN and M-SVM classification analysis in done here and these are displayed with the help of UI model using pipe. Here the confusion matrix, model accuracy and loss curve, epoch curve are displayed.

	precision	recall	f1-score	support
NEUTROPHIL	0.64	0.73	0.68	624
EOSINOPHIL	0.75	0.82	0.78	623
MONOCYTE	0.97	0.75	0.85	620
LYMPHOCYTE	0.99	0.99	0.99	620
micro avg	0.82	0.82	0.82	2487
macro avg	0.84	0.82	0.83	2487
weighted avg	0.84	0.82	0.83	2487

	precision	recall	f1-score	support
Mononuclear	1.00	0.88	0.94	1240
Polynuclear	0.89	1.00	0.94	1247
micro avg	0.94	0.94	0.94	2487
macro avg	0.95	0.94	0.94	2487
weighted avg	0.95	0.94	0.94	2487

In figure 7.18 the precision, recall, support and f1-score values of CNN and M-SVM are shown respectively. These values are taken from the console as text and shown here.

CONCLUSION

In this work, a depth neural network architecture convolutional neural networks and M-SVM is proposed. The model prevents the temporal and spatial information of image features and can learn structured information of image features. Unlike other feature extraction methods, which rely on cytoplasmic/nuclear segmentation, this method can automatically classify and extract the deep features embedded in cell image patches. Compared with the previous existing methods, the proposed technique achieved the highest performance of classifier is based on the blood cell dataset. This segmentation-free, highly accurate cell classifier method and can be used to develop medical-aided diagnostic systems for blood-related diseases in the future.

A framework for automatically classify the RBC into overlap, normal and abnormal cluster is proposed system and consists of combination of blocks. Mainly of three main blocks which are feature extraction block and classification block and segmentation and processing block. Each of algorithms in blocks gave a good performance during task completion with an acceptable error. For the feature extraction, fusion of compactness and HU moment invariant are able to distinguish the normal and abnormal shape with a low computational resources and high discriminate power. The M-SVM frameworks can effectively identified the clustered blood cell when sufficient sample cells were supplied has been showed. The trained network is optimal in term of classifying training and validation dataset. The results for CNN, 79% of accuracy over all precision, recall and F1-score is 83%,78%,78%. The result for M-SVM, 92% of accuracy over all precision, recall, F1-score is 94%,94%,94. In future, the system can be improved by counting and recognising the number of cells in the overlap region. This can be done by using marker based watershed segmentation with distance transform.

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