TEST Engineering & Management

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

Performance Comparison of Conventional Neural Networks and Deep Learning Network For Cervical Cancer Diagnosis

[1] Chandra Prabha R, [2]Seema Singh
[1] Department of Electronics & Communication Engg., [2] Department of Electronics & Telecommunication Engg.
[1]BMS Institute of Technology and Management, [2] BMS Institute of Technology and Management
[1]chandra@bmsit.in, [2] Seemasingh@bmsit.in

Article Info
Volume 82
Page Number: 5469 - 5477
Publication Issue:
January-February 2020

Article History
Article Received*: 18 May 2019*
Revised*: 14 July 2019*
Accepted*: 22 December 2019*
Publication*: 27 January 2020*

Abstract:
Cervical cancer is the fourth-most common cause for death from cancer in women. Efforts are being made to develop more efficient techniques for the detection of cancer at the initial stage. Conventional methods require expert pathologists to examine the biopsy slide and classify it. In this regard few concerns have risen such as the deficiency of expert pathologists, lack of technical support to doctors and also lack of awareness among women especially in rural areas. Hence there is a requirement for an effective and accurate system that detects cervical cancer which can be used by health worker to detect cancer at initial stage (as a part of basic health check-up). This paper describes and compares two techniques for the cervical cancer diagnosis. The first method involves extraction of key features from complex cytology images using image processing algorithm followed by a neural network classifier with back propagation algorithm using MATLAB tool. The major challenge faced in this method is extracting the key features from complex images with overlapping cells, which is further used by neural network for classification. The other method is based on deep learning that uses inception neural network with tensor flow. A comparative analysis is presented for the same image database which is created with a Bangalore based pathology laboratory. The database is of 460 images of which 197 images are cancerous and 263 are non-cancerous images. The analysis proved that deep learning method was able to provide better classification results.

Keywords: *Image Processing, Back Propagation neural networks, Convolution Neural Networks, Inception V3, Tensor flow*

I. INTRODUCTION

The fourth most common cause of cancer death in women is cervical cancer. Developing countries like India are at a higher risk and a major percentage of cervical cancer patients are from developing and low income group countries.

Cervical cancer is caused due to abnormal cells present at the cervix which multiplies at a faster rate and grows out of control. The cervical cells transform into a precancerous state which is stated as Cervical Intraepithelial Neoplasia (CIN). Depending on the intensity of the cellular degradation it is classified as low-grade CIN and high-grade CIN. Human Papilloma Virus (HPV) is the cause for cervical cancer. Early detection of HPV can be done using either Pap test or HPV test

Liquid Based Cytology method (LBC) is one of the screening methods for cervical cancer. The samples are prepared and diagnosed in a special laboratory. The system is more accurate. As cure rate of cancer is closely related to the stage of the disease at diagnosis time, with a very high probability of fatality if it is left untreated. Therefore, timely identification of the positive cases is very crucial.

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

Current prevalent method used by pathologists for the diagnosis of cervical cancer is to manually observe the morphological changes in the cells. Due to limited number of skilled and experienced pathologist, the mass screening procedure becomes time consuming and costly. Hence an efficient algorithm is necessary to provide a technical support to the specialists. The Para-medical worker, local health visitor or lab technicians may be trained to take the smear and prepare the slide. As the number of para-medical workers is more, the screening facility may reach masses. Further the deployment of the algorithm can reduce the complexity in handling mass screening. With mass screening program supported with the proposed system, skilled pathologist can focus on critical cases only.

However, the drawback of all the methodology is that despite obtaining the samples for the purpose of testing, there is always an element of human error and hence this will lead to erroneous results. This paper proposes two techniques involved for feature extraction and classification of overlapping cancerous cells. The first method involves extraction of various key features from cervical cytology complex images by applying image processing and then followed by a neural network classifier with MATLAB tool. The other technique uses deep learning network inceptionv3 that produces a high level of accuracy in classification with less processing time (cloud computing).

L Mahanta and K Bora presents a process using pap smear images for the analysis of cervical cancer cells based on Nucleus Cytoplasm ratio which is one of the most important feature of identifying the cancer affected cells. Based on the value of Nucleus Cytoplasm ratio, a normal and an abnormal cell can be identified. This paper concludes Nucleus cytoplasm ratio of a normal cell is less compared to an abnormal cell.

An innovative method for automated system for the diagnosis of cervical cancer by extracting various features from cervical cytology images using MATLAB image processing tool is proposed.in this paper the features like nucleus-to-cytoplasm ratio, shape and color intensity were used to train the neural network using Back-propagation algorithm. The cytology cells were then successfully classified as non-cancerous, low- grade and high- grade cancer cells. Nucleus Cytoplasm ratio is very high for cancerous cells and less for non-cancerous cells. Depending on the shape, the cancer cells are of two types, low-grade which are mostly circular and High-grade which are tapered and possess spindle like structure. Cancerous and non-cancerous cells have distinctively different color intensity distribution.

Z. Lu, G. Carneiro, and A.P. Bradley applied an algorithm for accurate segmentation of the individual cytoplasm and nuclei from a clump of overlapping cervical cells. Existing methods do not provide such a complete segmentation due to severe overlap and poor contrast. In this paper, a scene segmentation is performed to highlight the free-lying cells, cell clump and their nuclei. This segmentation is performed using a joint level set optimization on all detected nuclei and cytoplasm pairs. This technique is constrained by the length and area of each cell, cell shape, the amount of cell shape overlap and the expected grey values within overlapping regions.

Christian Szegedy et. al. applied deep convolutional neural network architecture code called Inception, classification and detection in the Image Net Large-Scale Visual Recognition Challenge. The architectural decisions were based on the Hebbian principle and multi-scale processing for optimization of quality.

Karen Simonyan, Andrew Zisserman investigated the effect of the convolutional network depth for accuracy in a setting that involves large scale image recognition. Their main contribution is a complete evaluation of networks which rises in depth using very small 3 x 3convolution filters.

An enormous amount of work is carried out in the area of cervical cancer diagnosis using neural network with various combination of input features.

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

However, the slides directly from the pathologist were not used. This work proposes two different approach for the classification of same database which is created with a Bangalore based pathology laboratory. The first approach of classification involves extraction of different key features from cervical images using image processing followed by a neural network classifier. The other technique uses deep learning using inception that produces a high level of accuracy in classification and processing time. Based on the comparative analysis of two approaches, usage of deep learning network is appreciated for this application.

II. METHODOLOGY

The two techniques i.e. neural network classifier and deep learning works with the same data set to classify cervical cancer images into cancerous and non-cancerous cells.

The following sections discusses the description of data set used and different method of classifier

DATA SET

Data Set has been obtained from a pathologist:

Total Images collected	460 images
Cancerous images	197 images
Non-cancerous images	263 images
Image size	2040x1528
Horizontal and vertical resolution	96dpi

A. Technique 1: Image processing and neural networks algorithms

Image processing and neural network algorithm are applied to identify cancerous and non-cancerous cells. The following steps are involved. The Fig. 1 describes the flow of steps involved in the process.

Pre-processing

The purpose of pre-processing is to improve the image data by suppressing the unwanted distortions or to enhance some image features. Using the MATLAB tool, pre-processing is done on the images attained.

RGB-to- Grey Conversion

The input images are of high-resolution and in JPEG format. The collected colour image is changed to a grey scale image.

Scene segmentation

There are two stages in Scene segmentation processes: 1) The segmentation of cell clumps. 2) The detection of nuclei and respective cell segmentation.

1) Segmentation of cell clumps

There are four stages in segmentation of cell clumps

Stage 1: Super Pixel Map

The amount of grey value similarities and spatial proximity is determined by finding local maxima using quick shift algorithm. The algorithm segments an RGB image by identifying clusters of pixels in the joint spatial and colour dimensions. Segments are local (super pixels) and it can be applied as a base for further processing. Given an image, the algorithm calculates a forest of pixels whose branches are considered with a distance. This specifies a hierarchical segmentation of the image, with segments corresponding to sub trees. The informative super pixels can be recognised by cutting the branches whose distance label is above a specified threshold (the threshold can be either fixed by hand, or determined by cross validation).

Stage 2: Edge Map

The second stage is applying a canny edge detection on this super-pixel map to detect super-pixel edges and removes most of the background data. Canny edge detection provides good detection, clear response and good localization.

Stage 3: Convex Hull and Clump Boundary

To find candidate cell clumps, the third stage applies an unsupervised binary classifier, where the classes are “background” and “cell clump”. The first assignment is provided by building a convex hull around the connected components of the edge map computed in stage 2.

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

Stage 4: Clump Boundary Using Gaussian Mixture Models

Gaussian Mixture Models (GMM) starts with an initialization step which will be the convex hull input from stage 3, which assigns the parameters to values based on the

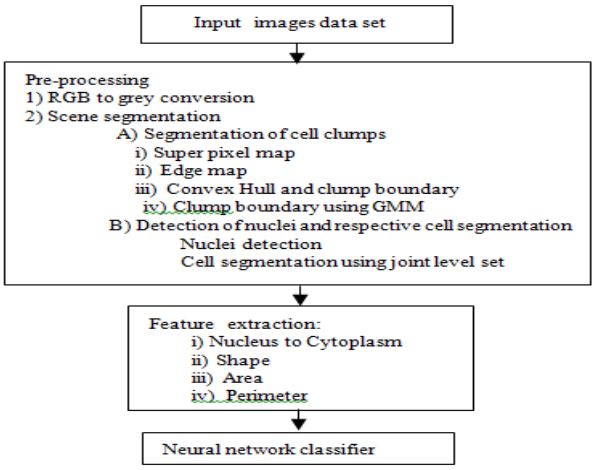


Fig.1. Different stages involved in image processing and neural networks

data. Then, the model iterates over the Expectation (E) and Maximization (M) steps until the parameters estimates converge; where Expectation is given by stage 2.

The result of the convex hull map stage is taken and re-estimated using the GMM. This is iterated until the GMM is stable. In practice, iterating this re-estimation process 10 times produces stable results. At the end of this step the cytoplasm boundaries will be obtained. As the number of iterations for noise removal increases, processing time also increases.

2. Nuclei detection and cell segmentation

Nuclei detection

Nuclei can be described by comparatively low grey values, similar texture, and circular borders. The nuclei detection is primarily an experimental procedure using a thresholding function. After this step all the nuclei of a particular image will be detected. This is then labelled as Nuclei mask and used for later processing.

Cell Segmentation Using Joint Level Set

The segmentation of overlapping cells uses the set of nuclei described in previous section as the initial guess for each level set function. Level Set can be used to efficiently address the problem of curved surfaces/edges propagating in an implicit manner. Thus, by using the nucleus as the initial guess(actual contour), and the obtained cytoplasm mask after GMM as final guess, about 40 or more iterations are performed to get the required accurate cytoplasm mask. For each iteration cytoplasm is considered to be an ellipse.

B. Feature Extraction

Different features need to be extracted from each segmented cell. The extracted features are put in a proper vector form which is used to train the neural network for further classification. Presented in Fig.5.

The pre-processing steps, Nuclei Mask and CytoMask, have to undergo before feature extraction using the steps. Presented in Fig. 2.

Step 1: CytoMask is complimented such that detected Cytoplasm is given by bit 1(white) and background is given by bit 0(black).NucleiMask are such that detected nucleus is represented by bit 0(black) and background is represented by bit 1(white).

Step 2: CytoMask and NucleiMask are given as inputs to the AND function to get a Fused image. Thus, each individual cell is obtained separately.

Step 3: The Fused image and NucleiMask are given as inputs to XOR function to get nucleus of each cell separately. Features of Nucleus can be extracted.

Step 4: From step 2, on applying fill holes function, cytoplasm of each cell is extracted separately. Features of
cytoplasm can now be extracted.

TEST Engineering & Management

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

The pre-processing is followed by the feature extraction which is used to distinguish between the cell images.

Nucleus-to-Cytoplasm ratio: Separation of the nuclei from the cell involves the following steps: a) converting the RGB image to grey- scale, applying a 'Gaussian' filter and setting a threshold to separate nuclei. The threshold value is set by observing the intensity values of the nuclei using 'impixel' function in MATLAB. Area of nuclei and cell is calculated using 'regionprops'. Ratio of these areas are calculated. A threshold value for the ratio is set to distinguish cancerous and non-cancerous cells.

Fig. 2. (a) Nuclei Mask (b) Cyto Mask (c) Fused Image

The key features extracted are shape, area, perimeter, eccentricity, solidity and extent

Shape: The ratios of major-axis length and minor-axis length of the cell are computed. Presented in Fig.3.

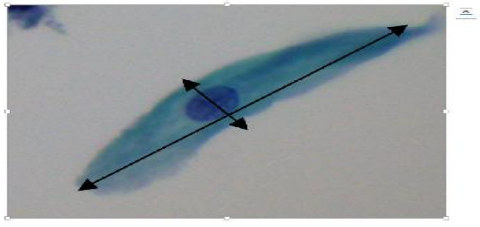


Fig. 3. Major and Minor Axis indicated for a cell

Area: It is the degree of entire number of pixels present in each cell of the image. Presented in Fig.3.

Perimeter: It is distance around the boundary of the region. Its obtained computing the distance between each adjoining pair of pixels around the border of the region.

Eccentricity: It is a scalar whose value is between 0 and 1. It is the ratio of the distance between the foci of the ellipse and its major axis length.

Solidity: It is a scalar specifying the proportion of the pixels in the convex hull that are also in the region. Convex hull is a p-by-2 matrix that specifies the smallest convex polygon that can contain the region. Each row of the matrix contains the x- and y-coordinates of one vertex of the polygon.

Extent: The ratio of pixels in the region to pixels in the total bounding box is specified as extent which is a scalar.

C Neural Network Classifier

Back propagation algorithm is used as a classifier. The method gradient of a loss function is computed with respects to all the weights in the architecture. The computed gradient is fed to the optimization method to update the weights continuously in order to minimize the loss function. Propagation and Weight update are two phases of back propagation. Presented in Fig.8. The other types of cancer can also diagnosed using neural networks.

D Technique 2: Deep learning networks

Deep learning is a model which uses neural network architecture to classify the images directly. A conventional neural network contains only 2 or 3 layers, while deep networks can have more layers.

Convolutional Neural Network (CNN) is a powerful tool that can classify visual inputs into different classes [4]. The CNN is widely successful in the task of classification is because the network can be modelled on animal visual perception to perform classification.

CNN contains an input layer, an output layer, and many hidden layers in between. The Feature Detection Layers implements convolution, pooling, or rectified linear unit (ReLU) operation which are executed repeatedly over tens or hundreds of layers, with each layer detecting distinct features.

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

Convolution lays the input images through a set of convolutional filters, each of which initiates certain features

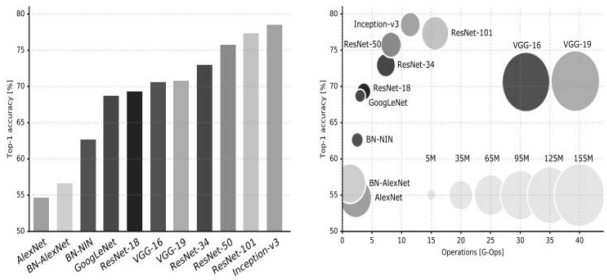


Fig. 4. Comparison of Inception V3 with other CNN models

from the images. Pooling performers nonlinear down sampling to reduce the number of parameters that the network needs to learn about. Rectified linear unit (ReLU) permits for faster and more effective training by mapping negative values to zero and maintaining positive values. After feature detection, the next task is to classify.

The a fully connected layer (FC) which outputs a vector of N dimensions where N is the number of classes that the network will be able to detect. This vector contains the possibilities for each class of any image being classified.

The last layer of the CNN architecture uses a softmax function to provide the classification output.

CNN has less processing time (cloud computing) compared to other image classification methods. Hence the filters are learned instead of being hard-coded in traditional algorithms. In this regard, the Inception V3 which is one of the best image classifier among CNN. The Fig. 4. presents an understanding into the performance of the Inception V3 with respect to other CNN models.

Architecture of inception V3

Inception V3 is one finest image classifiers in CNN [4]. A deeper and wider network improves the quality of the network.

Computational cost in Inception is lower in comparison to other CNN's [12]. Inception networks are applied in processing large amount of data at practical cost or situations where memory or computational capacity is limited.

It is certainly possible to mitigate parts of these issues by applying specialized solutions to target memory use, or by improving the execution of certain steps through computational tricks. These modification comes with added difficulties. Furthermore, these methods may be applied to enhance the Inception architecture and increase the efficiency gap.

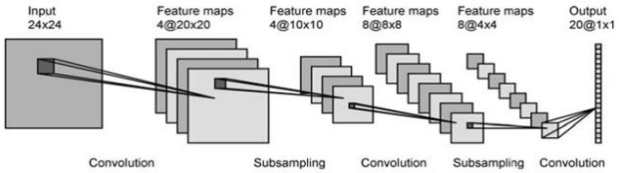


Fig. 5. Convolutional neural network architecture

E Labelling the Images

One of the visual clues to detect a cancerous slide is the nucleus to cytoplasm ratio, which is very high for cancerous cells. Another thing to note in the images is the dense clustering of the cells which is common for cancerous cells.

The neural network is been trained to classify two classes cancerous and non-cancerous. The images are trained using

Supervised learning algorithm, wherein the images are labelled and the classifier learns the special features from the images fed to it.

F Training the Architecture

The network is trained for 1500 steps which results the cross entropy of 0.13201, which is the loss function in machine learning and optimization [8]. Increasing steps results in smaller cross entropy values, leading to more accurate results.

III. RESULTS

A Conventional Neural Network

In this method, processsing time and computational required for the classification of images is high,intermediate image processing results

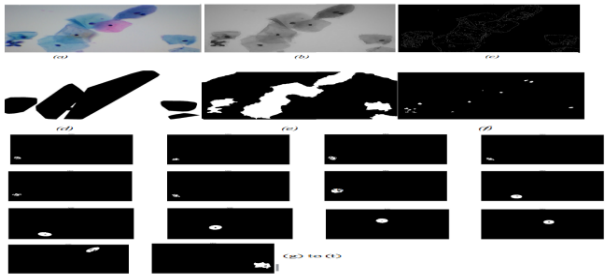
TEST Engineering & Management

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

can be verified. Here each cell can be classified

Factors	Conventional Neural Networks	Inception neural networks
Platform	Windows	All Platforms as docker platform has been used
Processing Time	Timing differs based on number of clumps and nuclei in image. If there 10 nuclei (overlapped cells)It takes 1 hour.	500 training images, 2 test images timing: *Creating bottle neck-5min 18s *500 training steps -54s *total training time- 6min 12s *Display of results -10s
Images processed at a time	One image to be loaded at a time, if more images are loaded computation time increases.(8GB Processor, 2.8GHz)	200 images
Image Processing	Intermediate steps can be recorded to the pathologists for verification	No image processing algorithms used
Status of each cell in the image	Each cell can be classified separately as cancerous /non-cancerous	Not possible: the complete image is classified as cancerous/ non-cancerous

separately as cancerous/non-cancerous. Processing of complex images consumes huge amount of time. The Fig.6. describes the outputs of each stages of method 1



	A	B	C	D	E	F	G	H
1	Cyto Area	Nuc Area	Cyto/Nuc Ratio	Major/Minor	Perimeter	Solidity	Eccentricity	Extent
2	9428	1686	5.591933571	1.621739222	386.508	0.950403	0.787259406	0.6951264
3	16024	2193	7.306885545	1.413473696	537.784	0.903524	0.706736461	0.7512424
4	18399	2525	7.286732673	1.555926186	548.456	0.919031	0.766114583	0.6638404
5	9756	1717	5.682003494	1.97766603	421.954	0.916401	0.862740731	0.6088747
6	10726	2035	5.270761671	1.178665975	395.193	0.942365	0.529328777	0.6726452
7	9503	2104	4.516634981	2.048955931	428.851	0.889211	0.872813746	0.5846561
8	23016	1262	18.23771791	1	609.788	0.963577	0.378360393	0.7524273
9	20782	292	71.17123288	1.055517582	516.044	0.985957	0.32004452	0.7821898
10	24848	292	85.09589041	1.244695517	591.959	0.976768	0.595427105	0.7524225
11	26314	757	34.76089828	1	645.318	0.977779	0.403542312	0.7656541
12	24792	118	210.1016949	1.095222674	585.209	0.980734	0.40783346	0.7416904
13	21211	732	28.97677596	1.132529427	521.041	0.987293	0.469411993	0.7769597
14	20149	1817	11.08915795	2.694068096	610.668	0.960345	0.928558589	0.51411
15	43928	1020	43.06666667	1	1037.284	0.810525	0.592948587	0.6364071

Fig.7. Features Extraction

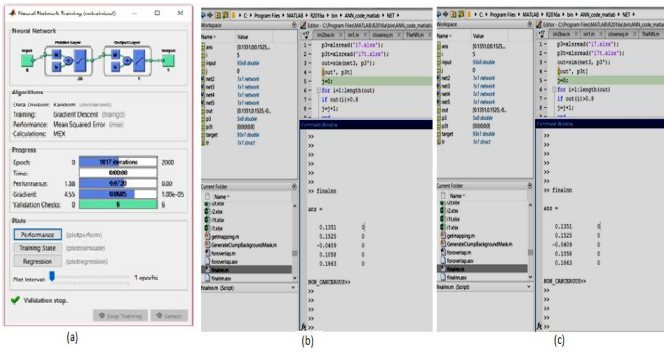


Fig. 8. Neural Network Classifier: (a) Neural Net Training, (b) Cancerous Image,(c) Non-Cancerous Image

B Deep Learning Network

The result of the classifier is very accurate with less processing time and computational cost. By increasing the number of steps smaller cross-entropy can be achieved, which results in better outputs i.e. at step 1499, the cross entropy is 0.013201.

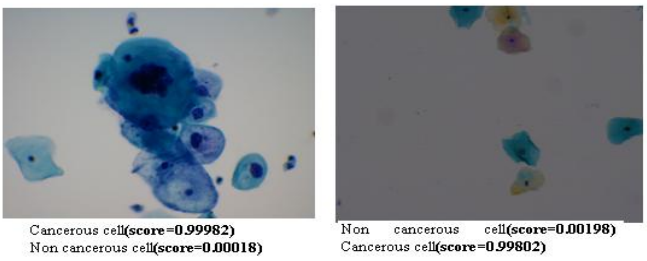


Fig. 9. (a & b) Result scores of Cancerous Image and non-cancerous Image

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

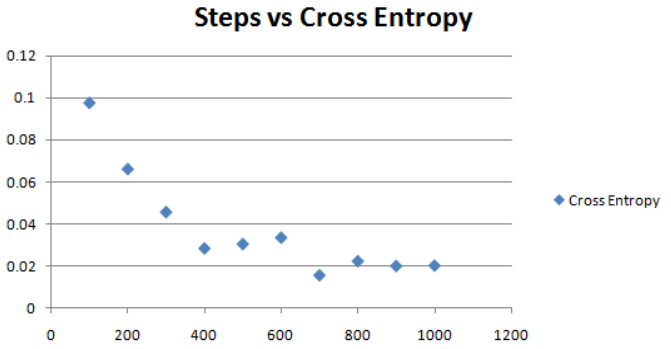


Fig. 10. Performance Curve Of Training Process

C Comparative analysis of simulation results

TABLE I. Comparative analysis of two approaches

The two methods have been explored for the classification of images as cancerous or non-cancerous. A comparative study of the same for the parameters like processing time, computational cost, platform, cloud support, etc. is presented in the table I.

From the table I, it is observed that Inception Neural Network is the better than conventional neural networks. Due to low processing time and high accuracy, inception neural network is able to process highly complex cervical images with large number of clumps and nuclei

IV. CONCLUSION

The cervical cancer diagnosis is done with the manual observation of morphological changes in the cells, which is very subjective and rises several concerns. Implementation of neural network algorithm and deep learning network in cervical cancer diagnosis for classification of complex images with overlapping cells image into cancerous and non-cancerous cells can reduce critical problems faced by pathologists. This paper presents a comparative analysis of biomedical image classifier for cervical cancer using two different methods for the same dataset of images created with a Bangalore based pathology laboratory. The database has 460 images out of which 197 images are cancerous and 263 are non-cancerous images.

Conventional Neural network method uses image processing algorithm to extract features from complex images with overlapping cell. The key features extracted are area, perimeter, eccentricity, nucleus-to cytoplasm ratio, major axis-to-minor axis ratio of the cells. Further, extracted features are fed to neural network architecture with the structure of 8-20-1. After training, the best performance goal (error) of 0.0738 was achieved. Further the trained network was tested on the unknown cell images to achieve significant accuracy. However, it faces a major issue in extracting the feature from overlapping cells and influences the computational time due to hardware constraints. Deep learning is computationally intensive and complex. However it is capable of giving better accuracy for highly complex images with overlapping cells also. With the support of Cloud computing, deep learning network classifies images as cancerous and non-cancerous with less processing time and computational cost. By increasing the number of steps smaller cross-entropy is been achieved, which results in better output. The deep learning network provides a good accuracy and is robust in comparison with the other image processing techniques used. In order to assist pathologist and to support mass screening with reduced human error, the deep learning network can be used on site. This method can also be used to classify other kinds of cancerous cells after training with those respective cell images.

V. REFERENCES

[1] L Mahanta, and K Bora. "Analysis of malignant cervical cells based on N/C ratio using pap smear images." International Journal of Advanced Research in Computer Science and Software Engineering 2, no. 11 (2012): 341-346.

[2] S Seema, V. Tejaswini, R P Murthy, and A Mutgi. "Neural network based automated system for diagnosis of cervical cancer." In Deep Learning and Neural Networks: Concepts, Methodologies, Tools, and Applications, pp. 1422-1436. IGI Global, 2020.

[3] Z Lu, G Carneiro, and AP Bradley. "Automated nucleus and cytoplasm segmentation of overlapping

January - February 2020
ISSN: 0193 - 4120 Page No. 5469 - 5477

cervical cells." In International Conference on Medical Image Computing and Computer-Assisted Intervention, pp. 452-460. Springer, Berlin, Heidelberg, 2013.

[4] C Szegedy, W Liu, Y Jia, P Sermanet, SReed, D Anguelov, DErhan, V Vanhoucke, and A Rabinovich. "Going deeper with convolutions." In Proceedings of the IEEE conference on computer vision and pattern recognition, pp. 1-9. 2015.

[5] K Simonyan, and A Zisserman. "Very deep convolutional networks for large-scale image recognition." arXiv preprint arXiv:1409.1556 (2014).

[6] K He, X Zhang, S Ren, and J Sun. "Spatial pyramid pooling in deep convolutional networks for visual recognition." IEEE transactions on pattern analysis and machine intelligence 37, no. 9 (2015): 1904-1916.

[7] Y LeCun, B Boser, J S Denker, D Henderson, R E. Howard, W Hubbard, and L D. Jackel. "Backpropagation applied to handwritten zip code recognition." Neural computation 1, no. 4 (1989): 541-551.

[8] I Sutskever, J Martens, G Dahl, and G Hinton. "On the importance of initialization and momentum in deep learning." In International conference on machine learning, pp. 1139-1147. 2013

[9] S Singh, J Harini, and B R Surabhi. "A novel neural network based automated system for diagnosis of breast cancer from real time biopsy slides." In International Conference on Circuits, Communication, Control and Computing IEEE, pp. 50-53.2014

[10] Sam Abrahams, DanijarHafner, Erik Erwitt, Ariel Scarpinelli.,"TensorFlow for Machine Intelligence", Bleeding
Edge Press, Santa Rosa, CA 95404.

[11] C Szegedy, A Toshev, D Erhan ."Deep neural networks for object detection." In Advances in neural information processing systems, pp. 2553-2561. 2013

[12] D C Ciresan, U Meier, J Masci, L M Gambardella, and J. Schmidhuber "High-performance neural networks for visual object Classification." arXivpreprint arXiv:1102.0183 (2011).

[13] A Karpathy, G Toderici, S Shetty, T Leung, R Sukthankar, L Fei-Fei "Large-scale video classification with convolutional neural networks." In Proceedings of the IEEE conference on Computer Vision and Pattern Recognition, pp. 1725-1732. 2014

[14] Y LeCun, F J Huang, and L Bottou,"Learning methods for generic object recognition with invariance to pose and lighting." In CVPR (2) , pp. 97-104. 2004.