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Abstract	This paper proposed a methodology that can segment, recognize, classify and detect different types of cancer cell from both RGB, CT and MRI images. In this study, partial contrast stretching is used on the preprocessed images to increase the cells' visual aspect. Otsu method is applied to enhance the stretched image and the K-means clustering method to segment the desired cancer cell. Median filtering is applied to improve the appearance of the segmented cancer cell and relevant features are extracted from the filtered cell and multi-Support Vector Machine (M-SVM) is applied to classify the test image and identified

different types of cancer cell. This paper also proposed the Convolutional Neural Network (CNN) classifier to extract features from the filtered cell and to classify the image. Then two classified results are compared to identify either equal or not. If the result is same, the extracted cancer region shown using region growing method and finally calculated percentage of detected areas of the different types of cancer cell. The Experimentation has been done on MATLAB environment on RGB, CT and MRI images.

Cancer Cell Segmentation Based on Unsupervised Clustering and Deep Learning

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Keywords: Multi SVM · Convolutional neural network · Brain · Leukemia · Lung

1 Introduction

Human bodies are rapidly producing trillions of cells that form tissues and organs such as muscles, bones, the lungs, and the liver. Genes of each cell instruct it when to grow, work, divide, and die. Sometimes these instructions get mixed up and go out of control; then, the cells become abnormal as they grow and divide but do not die in time. These uncontrolled and abnormal cells can form a lump in the body known as a tumor. Tumors are of two types, such as non-cancerous (benign) and cancerous (malignant). When cancer starts in the lungs, it is known as lung cancer, and cancer that has spread to the lungs from another part of the body might be called secondary lung cancer. Leukemia is a cancer of white blood cells, which cannot fight infection and develops bone marrow. To classify the MRI image to detect the tumor category in the patient's

brain is the purpose of brain tumor classification. Many test types can be used for brain tumor detection, such as MRI, Biopsy, and Computed Tomography scan. However, in comparison to CT scan images, MRI images are safe, and they also provide higher contrast. Moreover, MRI images do not affect the human body. It is easy to detect and classify the brain through MRI images as they have a fair resolution for different brain tissues.

Image segmentation always plays a significant part in cancer diagnosis. The actual meaning of segmentation is splitting an image into several regions and extracting meaningful information from these regions [1]. There are several segmentation techniques have been applied to the MRI images. For medical image analysis, edge detection, threshold-based, region-growing, model-based, and clustering-based segmentation techniques are the most widely used methods. All the segmentation techniques have their advantages and disadvantages, and thus, it depends on the user's choice. Besides the segmentation and detection of cancer cells, it is necessary to classify the types of cancer after segmentation to help the specialists provide the correct direction to the patient for early emergence. There have various classification methods among them multi-SVM (Multi-support vector machine) is applied in our proposed method because it is a linear learning algorithm used for classification and is a powerful supervised classifier and accurate learning technique. The Convolutional Neural Network models have been very successful for a large number of visual tasks [2]. In a word, this paper approaches benign, malignant, Leukemia, and Lung cancer detection using partial contrast stretching, Otsu, K-means, median filtering, and performs the classification of the benign, malignant Leukemia and lung using M-SVM and CNN classifier.

This system uses MRI, RGB and CT images of Brain MRI Images for Brain Tumor Detection dataset for both Benign and Malignant, SN-AM dataset for leukemia [3–6], LIDC database for lung cancer [7].

This paper is organized as follows. Section 2 summarizes the previous works completed in the fields of cancer cell detection. Section 3 gives a brief description of the methodology that has been proposed for the different types of cancer cell detection, feature extraction, classification and calculation of the detected area of cancer cell and conclusions is in Sect. 4.

2   Literature Review

Many researchers have applied different methods to segment, detect, and classify images of cancer cells. Some of the existing methods are described here.

Wang et al. [1] has presented a novel cell detection method that utilizes both intensity and shape information of a cell to improve the segmentation. Upon obtaining the cell shape information with the binarization process, they have used both intensity and shape information for local maxima generation. Lastly, the nuclei pixels are permitted to move inside the gradient vector field. The pixels will finally join at these local maxima, and the detected cells are then segmented through the seeded watershed algorithm.

Purohit and Joshi [8] introduced a new efficient approach towards the K-means clustering algorithm. They proposed a new method that produces the cluster center by reducing the mean square final cluster's error without a considerable increment in the execution time. Many judgements have been done and it can conclude that accuracy is more for dense dataset rather than small dataset.

Jose, Ravi, and Sambath [9] have proposed a methodology to segment Brain Tumor using K-means Clustering and Fuzzy C-means Algorithm and its' area calculation. They split the process into several parts. First of all, preprocessing is implemented by using the filter to improve the quality of the image. After that, the advanced K-means algorithm is applied, followed by Fuzzy c-means to cluster the image. Then the resulted segment image is used for the feature extraction of the region of interest. They have used MRI images for the analysis and calculated the size of the extracted image's tumor region.

Damodharan and Raghavan [10] have proposed a neural network-based procedure for brain tumor detection and classification. In their methodology, the quality rate is formed separately for segmentation of WM, GM, CSF, and tumor region and claimed accuracy of 83% using the neural network-based classifier.

In [11] Region growing algorithm proposed for segmentation of CT scan images of the lung. This algorithm starts with a seed pixel which also checks other pixels that surround it. It determines the most alike one. If it meets confident criteria, it will include in the region. The region is established by examining all unallocated adjacent pixels to the region.

Kanitkar, Thombare, and Lokhande [12] proposed a methodology that takes a CT scan image of the lung, then preprocesses the input image for smoothing using the Gaussian filter and, then enhanced using Gabor filter. Then thresholding and marker-controlled watershed segmentation methods are used to segment the processed image. They used a marker-based watershed segmentation technique to overcome the drawbacks of the watershed segmentation technique, i.e., over-segmentation. Then feature extraction and classification of cancer stages are done.

3   Proposed Methodology

Figure. 1 shows the proposed method. This method proposes the preprocessing, segmentation, detection, feature extraction and classification of cancer cells using Otsu, k-means, multi support vector machine and convolutional neural network. As the initial step, an input image is given to the system.
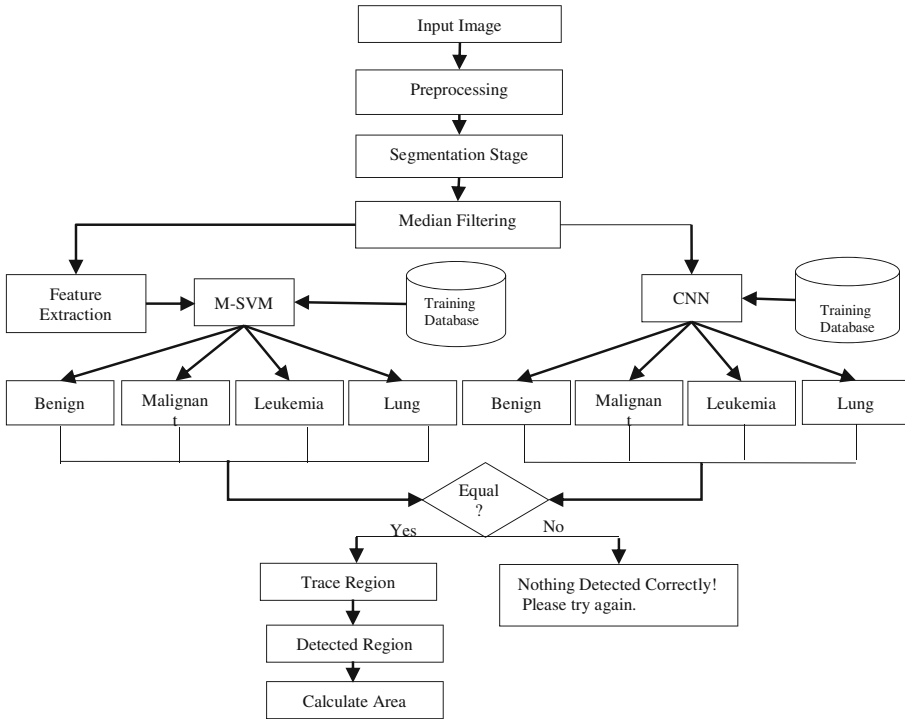
Fig. 1. Block diagram of proposed methodology.
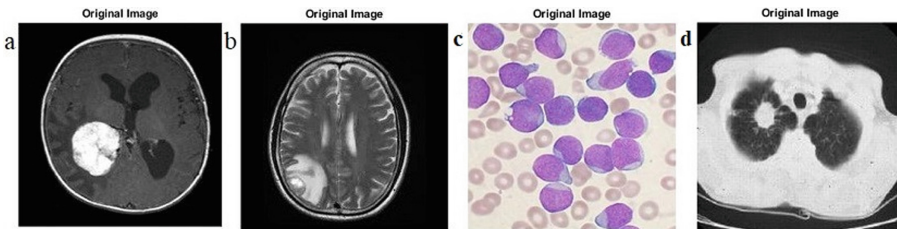
Fig. 2. (a) Original Brain test image-Benign; (b) Original Brain test image- Malignant; (c) Original Leukemia test image; (d) Original Lung Cancer test image.
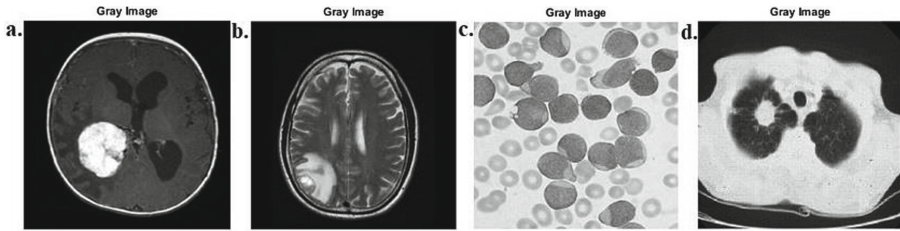
The proposed methodology contains following section:

3.1   Preprocessing

RGB2GRAY
In the preprocessing stage firstly the input image checked either RGB or gray. If the testing image becomes a RGB image it converts the true color RGB image into gray scale by eliminating the hue and saturation information while retaining the luminance.

Fig. 3. Gray image- (a) Benign; (b) Malignant; (c) Leukemia; (d) Lung Cancer.

Remove Noise
Gaussian filtering method used to smooth the testing images so that it looks more meaning full for segmentation. Filtering method helps to improve certain parameters of testing images such as improving the signal-to-noise ratio, enhancing the visual appearance of testing image, removing the irrelevant noise.
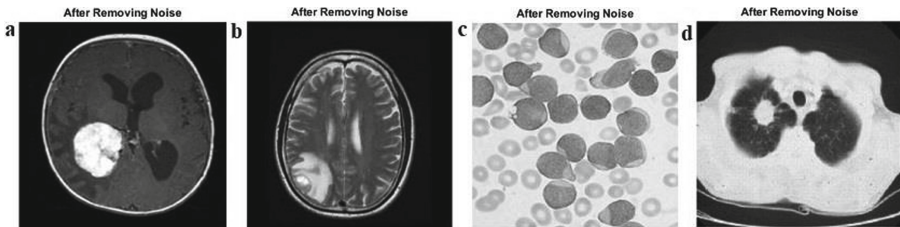
Fig. 4. Removed Noise- (a) Benign; (b) Malignant; (c) Leukemia; (d) Lung Cancer.

Partial Contrast Stretching

In medical science, images used for the diagnosis may have their own weakness such as blurred or low contrast. To solve this problem a contrast enhancement technique such as partial spatial starching is used so that it can improve the image quality and contrast of the image. It is implemented by stretching and compression process and applying this technique, the pixel range of lower threshold value and upper threshold value will be mapped to a new pixel range [13].
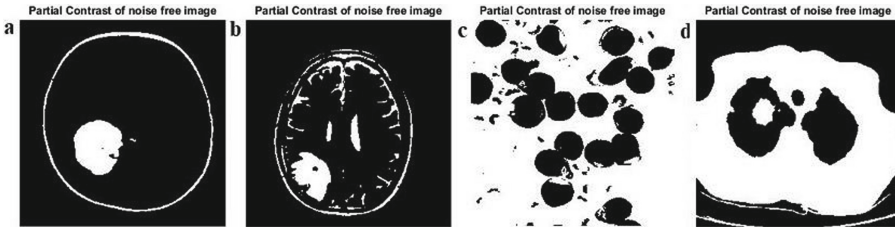
Fig. 5. Partial Contrast Stretched- (a) Benign; (b) Malignant; (c) Leukemia; (d) Lung Cancer.

Enhancement Using Otsu

Otsu's method is one of the most successful methods for image threshold-based enhancement. The algorithm provide idea that the image to be threshold contains two classes of pixels or bi-modal histogram then calculates the optimum threshold separating those two classes so that their combined spread is minimal. The main objective of Otsu method is to implement binary algorithms for converting gray image into monochrome image or binary image. Consequently, it is playing the vital rule to enhance the image.
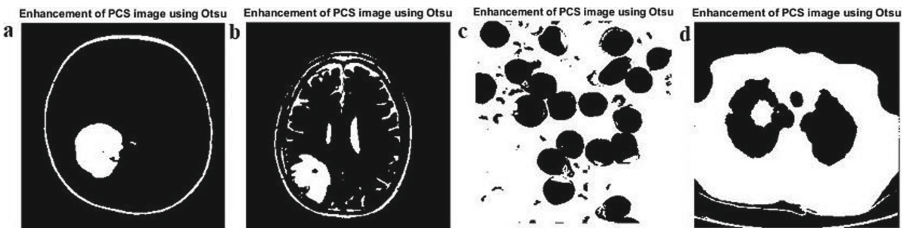
Fig. 6. Enhanced using Otsu Method (a) Benign; (b) Malignant; (c) Leukemia; (d) Lung cancer.
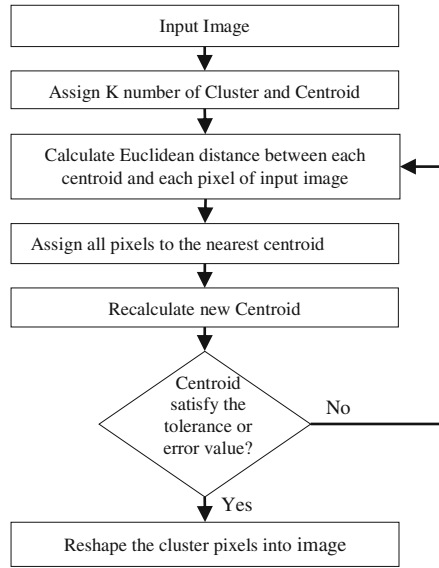
Fig. 7. K-means Clustering.

3.2 Segmentation

K-means clustering is an unsupervised clustering method that classifies a given set of data into k number of disjoint clusters. It is also an iterative method which is used to partition an image into K clusters. Firstly, it takes k number of clusters and k centroid where the value of k is defined as 2 and initial 2 centroids are chosen randomly, then it calculates the Euclidean distance between the center and each pixel of the input image [14]. Here Euclidean distance is used to define the distance of the nearest centroid and assigns each point to the cluster which has nearest centroid from the respective data point. After assigning all data points it recalculates the new centroid of each cluster and using that centroid, a new Euclidean distance. So, K-means is an iterative algorithm, it repeats the process and calculates new centroid in each iteration until it satisfies the tolerance or error value. In our proposed system we divide the whole region into two clustered. Best clustering region is taken as region of interest from two clustered e.g. the white cancer cell cluster is taken as segmented with black background [15].
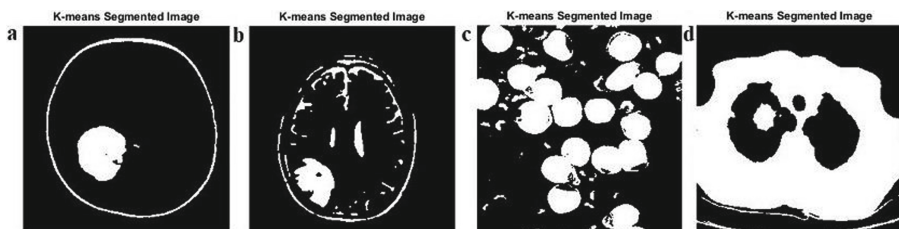
Fig. 8. K-means Segmented-(a) Benign; (b) Malignant; (c) Leukemia; (d) Lung cancer.

3.3   Median Filtering

After segmentation, the segmented image may contain some noise. So, to detect the affected region perfectly median filtering method is applied on the segmented image. Median filter can provide excellent noise reduction capabilities with considerably less blurring than linear smoothing filters of similar size. After completing the clustering process, the resultant clustering image was filtered by using 7×7 pixels median filter to improve the segmented images [16]. In the median filtering process, firstly read the test image and place a 7×7 neighborhood Kernel around each pixel in the image. After sorting the neighboring pixels according to the pixel value, the median value becomes the new value for the central pixels. Then move over the neighborhood kernel to the next pixel in the image. Repeat place a 7×7 neighborhood Kernel and sorting the neighboring pixels and also move over the neighborhood kernel are until all the pixels in the image being processed. Until all the pixels in the image being processed, repeat place a 7×7 neighborhood Kernel and sorting the neighboring pixels and also move over the neighborhood kernel.
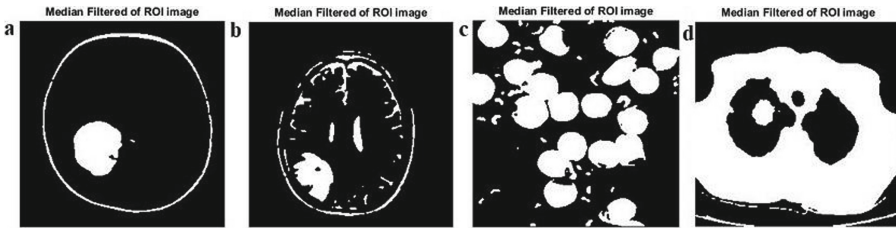
Fig. 9. Median Filtering of- (a) Benign; (b) Malignant; (c) Leukemia; (d) Lung cancer.

3.4   Classification

In this stage this study proposed multi SVM and Convolutional Neural Network (CNN) for classification. Multi-SVM has two steps. Firstly, relevant features have extracted from the filtered image. Secondly, the extracted features have feed the multi-SVM to classify the test image. The process of two classifier is described below.

Feature Extraction
Collecting higher level information of an image such as shape, texture, color and contrast is known as feature extraction. The analyzing methods that have been done so far has used the values of pixel intensities, pixel coordinates and some other statistic features namely mean, variance or median, which have error in determination process, low precision and low efficiency in classification [10]. Gray Level Co-occurrence Matrix (GLCM) is one of the most widely used image analysis applications. This procedure follows two steps so that it can extract features from the medical images. For this purpose, firstly the GLCM is computed, and in the other step, the texture features based on the GLCM are calculated. In the proposed system the GLCM texture features chosen are contrast, correlation, energy, homogeneity and features like mean, standard

deviation, RMS (Root Mean Square), entropy, variance, smoothness, kurtosis, skewness, IDM. After extracting the features from segmented image, all features fed to the multi-SVM and CNN classifier to classify the segmented image. Those features are extracted from datasets to train the multi-SVM and also extracted from test image to classify it. Again, CNN features are extracted using fc1000 layer from both datasets and test image, while the test image is being classified using CNN.

Classification the Test Image
Multi-SVM is used to classify the input image as Benign, Malignant, Leukemia or Lung cancer, a systematic technique for four class problems [17]. It needs two stages, training and testing. The Multi-SVMs can be trained by features given as an input to its learning algorithm and while training, it finds the suitable margins between two classes. When extracted features are feat to the multi-SVM, it performs the steps to classify. In this methodology, multi SVM works as a two class SVM repeatedly. When an input image features are fed to the multi-SVM, it classifies the input image from first two class. After classifying from two class, it takes the classified class and take the next third class two classify the input image. It also gives a classified class. Lastly, the classified class and fourth class is used to classify again. From this last classification, we get the correct classified class where the input image belongs to. In testing phase, the multi-SVM produces 90.75% to 95.55% accuracy.

Convolutional neural networks (CNN) are important tools for deep learning, and also especially useful for image classification, object detection, and recognition tasks. Deep learning uses convolutional neural networks to learn useful representations of data directly from images [18]. Neural networks combine diverse nonlinear processing layers, using simple elements operating in parallel, biological systems and deep learning models are trained using a large set of labeled data [19]. Again, neural network architectures that contain many layers, usually include some convolutional layers. The cell images are fed into a CNNs model to extract deep-learning features. The CNN based classification is divided into two phases such as training and testing phases. The number of images is divided into different category by using labels name such as benign, malignant, leukemia and lung. In the training and testing phase, preprocessing is done for image resizing. Further, passing the input dataset to all the layers mentioned the classification network undertakes training. The convolution neural network is used for automatic cancer cell classification and for forecasting the class label of a new test image.

Firstly, cancer cell database is loaded which create an image data store to manage the data. Then it calculated images and the category labels associated with each image. The labels are automatically assigned from the folder names of the image files and adjust unequal number of images per category so that the number of images in the training set is balanced. Using the resnet-50 function from Neural Network, we Load `ResNet-50' pretrained network. To avoid biasing the results, randomize the split and the training and test sets processed by the CNN model. Then prepare training and testing set for CNN. It can easily extract features from one of the deeper layers using the activations method and extract training features using 'fc1000' layer. CNN image features used to train a multiclass SVM classifier. To extract image features from test set, repeat the procedure used earlier and test features can then be passed to the classifier to measure the accuracy of the trained classifier. Finally, newly trained

classifier used to classify the desired segmented image. A general block diagram of the Convolutional neural networks (CNNs) is shown in Fig. 10.
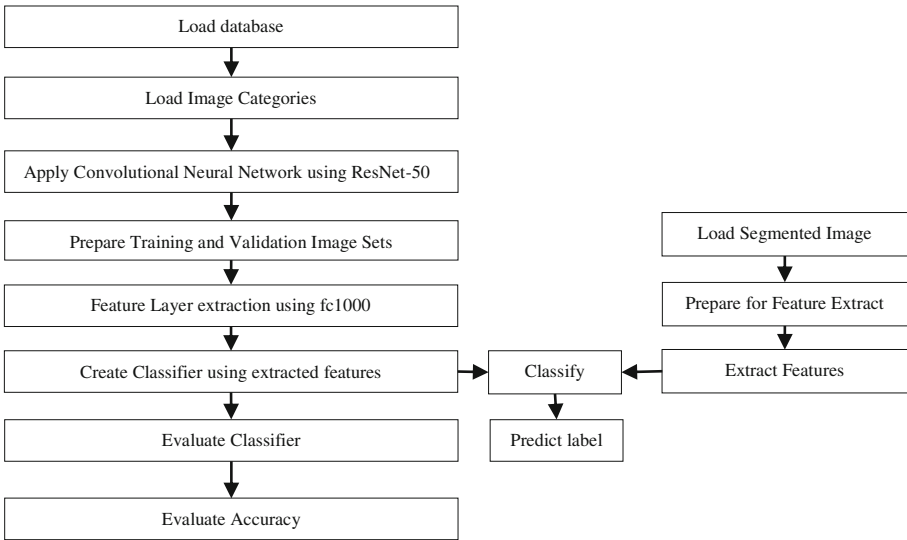
Fig. 10. Process of Convolutional neural networks.
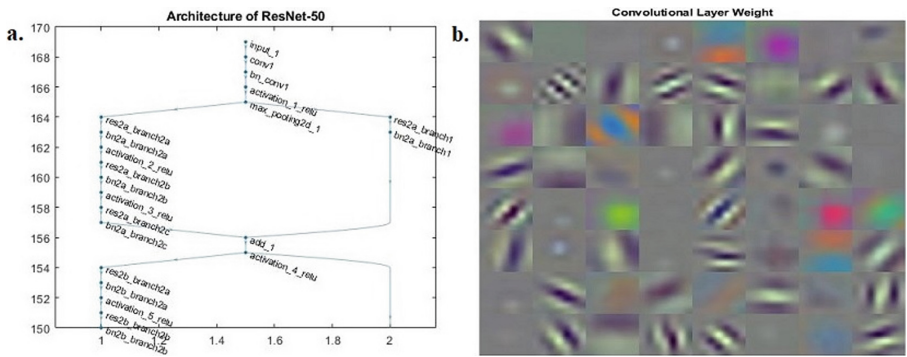
Fig. 11. (a) Architecture of ResNet-50 (b) Convolutional Layer Weight.

Confusion matrix is a square matrix which describes the performance of a classifier based on the test data set to observe the relationship between the classifier and the true ones. It predicts results of a classification problem counting the number of correct and

incorrect predictions of each class given by the classifier. It provides use the errors and types of errors being made by the classifier. The CNN classifier produces approximately 87.5% to 100% accuracy.

$$\text{Accuarcy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \tag{1}$$

a

	Predicted Class: Benign	Predicted Class: Malignant	Predicted Class: Leukemia	Predicted Class: Lung
Actual Class: Benign	TP 1	FN 0	FN 0	FN 0
Actual Class: Malignant	FP 0	TN 1	TN 0	TN 0
Actual Class: Leukemia	FP 0	TN 0	TN 1	TN 0
Actual Class: Lung	FP 0	TN 0	TN 0	TN 1

b

	Predicted Class: Benign	Predicted Class: Malignant	Predicted Class: Leukemia	Predicted Class: Lung
Actual Class: Benign	TN 1	FP 0	TN 0	TN 0
Actual Class: Malignant	FN 0	TP 1	FN 0	FN 0
Actual Class: Leukemia	TN 0	FP 0	TN 1	TN 0
Actual Class: Lung	TN 0.2500	FP 0	TN 0	TN 0.7500

c

	Predicted Class: Benign	Predicted Class: Malignant	Predicted Class: Leukemia	Predicted Class: Lung
Actual Class: Benign	TN 1	TN 0	FP 0	TN 0
Actual Class: Malignant	TN 0	TN 1	FP 0	TN 0
Actual Class: Leukemia	FN 0	FN 0	TP 1	FN 0
Actual Class: Lung	TN 0	TN 0	FP 0	TN 1

d

	Predicted Class: Benign	Predicted Class: Malignant	Predicted Class: Leukemia	Predicted Class: Lung
Actual Class: Benign	TN 0.7500	TN 0	TN 0	FP 0.2500
Actual Class: Malignant	TN 0	TN 1	TN 0	FP 0
Actual Class: Leukemia	TN 0	TN 0	TN 1	FP 0
Actual Class: Lung	FN 0.2500	FN 0	FN 0	TP 0.7500

Fig. 12. Confusion matrix-(a) Benign; (b) Malignant; (c) Leukemia; (d) Lung cancer.

3.5 Trace and Detect Region

After classification, based on the classified results of multi-SVM and CNN (Convolutional Neural Network) are equal, then morphological operation applied on the segmented image to trace and detect the cancerous region. Several types of image property measuring and area measuring methods are applied to trace regions. In phase-contrast microscopy images, noncancerous cells appear to be darker than the background after observing the most exposures. On the other hand, cancerous cells appear to be brighter than the background. Therefore, by creating a new averaged image via taking the mean of all exposure images, pixels at cell regions should have low intensities, and pixels at cancer regions should have high intensities. Applying the MSER (Maximally Stable Extremal Regions) method, the cancer region is traced. Finally, detected regions are shown with a red boundary. The detected regions of tested images are given below.
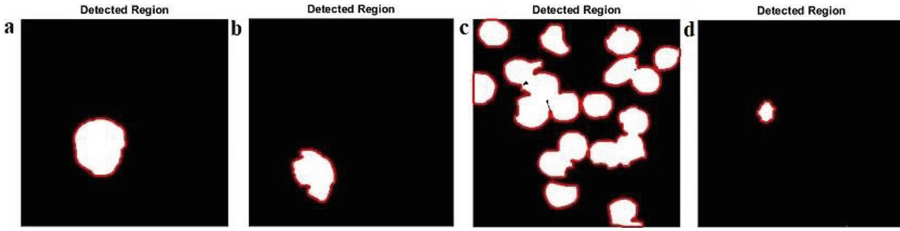
Fig. 13. Detected region of-(a) Benign; (b) Malignant; (c) Leukemia; (d) Lung cancer.

3.6   Area Calculation

The main task for area calculation of test image is the global threshold processes, which has examination pixel not equal to 0. Regionprops function measure properties of image regions. It returns a set of property measurements for each 8-connected component (object) in the binary image. Regionprops can also use in contiguous regions and discontiguous regions. If the properties argument does not specify, then Regionprops returns the 'Area', 'Centroid', and 'BoundingBox' measurements. The label image specified a numeric array of any dimension. Pixels labeled 0 are the background. The label image specifies an array of numeric values with different dimensions. Different pixel labels identify different objects, such as pixel labeled 0 for background, and pixel labeled 1 for one object, pixel labeled 2 for another object, etc. One of the critical characteristics of Regionprops is that it treats the negatively valued pixels as background and round down input pixels that are not integers. The actual number of the pixels in the region are returned as scalar. The bwarea value differs slightly from this value as it weighs a different pattern of pixels differently. The equation of the area has represented the result of the total pixel.

$$Area = \sum_{i=1, j=1}^{n,m} P(i,j) \tag{2}$$

The area of detected area is obtained by counting the number of affected regions pixels. The ratio of cancer cells area was calculated using the formula:

$$Ratio = \frac{Area\ of\ Cancer\ cell}{Area\ of\ Test\ image} \times 100\% \tag{3}$$

Here, the benign tumor has a 7.4% affected region where the test image has 49295 pixels area, and the detected benign tumor region is 3663 pixels. The malignant has a 4.6% affected region where the test image has a total of 51790 pixels area and detected malignant region is 2399 pixels. Leukemia has a 31.4% affected region where the test image has 65536 pixels area, and the detected leukemia region is 20561 pixels. The lung has a 31.4% affected region where the test image has 54231 pixels area, and the detected lung region is 814 pixels.

4 Conclusions

This research developed a methodology that can identify and classify different types of cancer cell using unsupervised clustering method and deep learning more specially multi SVM and Convolutional Neural Network and can also be able to segment perfectly compare to the results from current methodologies. In comparison with found results to those of current studies, it must be pointed out that this methodology is not limited to a fixed. Moreover, the current methods recognized on a specific type of class or a specific type of cancer dataset. This experimental results indicate that the proposed approach is an improved method and it can significantly generate accurate and automatic detection of cancer cells than existing methods. This research has shown that the overall accuracy of the system is approximately 93%. One of the primary challenges of this research is the expected centroid of clusters, need initial knowledge of the image and more awareness to train dataset.

In future research, it will give some directions such as developing better segmentation technique, selecting better feature extraction, clssification process when optimal learning algorithms are applied on different feature descriptors. This research will open a pathway to implement and analyze different areas of image segmentation in future.

References

1. Wang, M., Zhou, X., Li, F., Huckins, J., King, R.W., Wrong, S.T.C.: Novel cell segmentation and online learning algorithms for cell phase identification in automated line-lapse microscopy. biomedical imaging from Nano to Macro. In: ISBI 2007 4th IEEE International Symposium, pp. 65–6 (2007)
2. Nandagopalan, S., Kumar, P.K.: Deep convolutional network based saliency prediction for retrieval of natural images. In: Vasant, P., Zelinka, I., Weber, G.W. (eds.) Intelligent Computing & Optimization. ICO 2018. Advances in Intelligent Systems and Computing, vol. 866. Springer, Cham (2019). https://doi.org/10.1007/978-3-030-00979-3_51
3. Gupta, R., Mallick, P., Duggal, R., Gupta, A., Sharma, O.: Stain color normalization and segmentation of plasma cells in microscopic images as a prelude to development of computer assisted automated disease diagnostic tool in multiple Myeloma. In: 16th International Myeloma Workshop (IMW), India, March 2017
4. Duggal, R., Gupta, A., Gupta, R., Wadhwa, M., Ahuja, C.: Overlapping cell nuclei segmentation in microscopic images using deep belief networks. In: Indian Conference on Computer Vision, Graphics and Image Processing (ICVGIP), India, December 2016
5. Duggal, R., Gupta, A., Gupta, R.: Segmentation of overlapping/touching white blood cell nuclei using artificial neural networks. CME Series on Hemato-Oncopathology, All India Institute of Medical Sciences (AIIMS), New Delhi, India, July 2016
6. Duggal, R., Gupta, A., Gupta, R., Mallick, P.: SD-Layer: stain deconvolutional layer for CNNs in medical microscopic imaging. In: Medical Image Computing and Computer-Assisted Intervention − MICCAI 2017, MICCAI 2017. Lecture Notes in Computer Science, Part III, LNCS 10435, pp. 435–443. Springer, Cham. https://doi.org/https://doi.org/10.1007/978-3-319-66179-7_50
7. Armato, I.I.I., Samuel, G., McLennan, G., Bidaut, L., McNitt-Gray, M.F., Meyer, C.R., Reeves, A.P., Clarke, L.P.: Data from LIDC-IDRI. Cancer Imaging Archive (2015). https://doi.org/10.7937/K9/TCIA.2015.LO9QL9SXArchive

8. Purohit, P., Joshi, R.: A new efficient approach towards k-means clustering algorithm. Int. J. Comput. Appl. **65**(11), 0975–8887 (2013)
9. Jose, A., Ravi, S., Sambath, M.: Brain segmentation using k-means clustering and fuzzy C-means algorithm and its area calculation. Int. J. Innov. Res. Comput. Commun. Eng. **2**(2) (2014)

AQ1

10. Damodharan, S., Raghavan, D.: Combining tissue segmentation and neural network for brain detection. Int. Arab J. Inf. Technol. **12**(1) (2015)
11. Mesanovic, N., Grgic, M., Huseinagic, H., Males, M., Skejic, E., Smajlovic, M.: Automatic CT image segmentation of the lungs with region growing algorithm
12. Kanitkar, S.S., Thombare, N.D., Lokhande, S.S.: Detection of lung cancer using marker - controlled watershed transform. In: proceedings of the IEEE Conference on Pervasive Computing, 978–1–4799–6272–3/15 (2015)
13. Abdullah, A.S., Rosline, H.: Improving color leukemia images using contrast enhancement techniques. In: 2010 IEEE EMBS Conference on Biomedical Engineering and Sciences IECBES 2010, Kuala Lumpur, Malaysia (2010)
14. Abdul Nasir, A.S., Mashor, M.Y., Harun, N.H., Abdullah, A.A., Rosline, H.: Improving colour image segmentation on acute myelogenous leukaemia images using contrast enhancement techniques. In: 2010 IEEE EMBS Conference on Biomedical Engineering & Sciences (IECBES 2010), Kuala Lumpur, Malaysia (2010)
15. Dhanachandra, N., Manglem, K., Chanu, Y.J.: Image segmentation using K-means clustering algorithm and subtractive clustering algorithm. Article in Procedia Computer Science, December 2015. https://doi.org/10.1016/j.procs.2015.06.090
16. Abd Halim, N.H., Mashor, M.Y., Abdul Nasir, A.S., Mustafa, N., Hassan, R.: Color image segmentation using unsupervised clustering technique for acute leukemia images. In: International Conference on Mathematics, Engineering and Industrial Applications 2014, Proceedings 1660, 090038–1–090038–10. https://doi.org/10.1063/1.4915882,2015
17. Rejintal, A., Aswini, N.: Image processing based leukemia cancer cell detection. In: IEEE International Conference on Recent Trends in Electronics Information Communication Technology, 978–1–5090–0774–5/16 (2016)
18. Joshua Thomas, J., Pillai, N.: A deep learning framework on generation of image descriptions with bidirectional recurrent neural networks. In: Vasant, P., Zelinka, I., Weber, G.W. (eds.) Intelligent Computing & Optimization. ICO 2018. Advances in Intelligent Systems and Computing, vol. 866. Springer, Cham (2019). https://doi.org/10.1007/978-3-030-00979-3_22
19. Ghoneim, A., Muhammad, G., Hossain, M.S.: Cervical cancer classification using convolutional neural networks and extreme learning machines. Future Generation Comput. Syst. **102** (2020) 643–649 (2019)

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