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Detection of stages of melanoma using deep learning

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Abstract
Human Skin is the most utilized and largest organs next to blood acts as an outer protective covering of the entire body to protect the underlying internal organs from harmful UV rays, dust and pollution. One of the major concerns of such harmful rays is its ability that affects the human skin by mutating the DNA sequence of melanocytes cells which in turn stimulates an uncontrollable rapid growth of infelicitous cells as undesirable peripheral protuberances and in later progressive, prolonged and well-infected stages, it starts to grew inwards as well and reports majority of the deaths due to a skin cancer across the world. The premature detection of the melanoma enables the complete cure of the cancer and it significantly drags down the death rate. Though many research works concentrated on detecting the melanoma, this work narrow down the scope in finding the levels of skin carcinoma by using deep learning methodologies that boosts the accuracy in the detection of melanoma and can give an appropriate treatment with respect to the level of the cancer. In this work, state-of-art techniques like Random Forest, Support Vector Machine, Artificial Neural network along with the proposed fusion-based Deep learning methodology has been experimented. Various performance metric such as Mean Square Error, Peak Signal to Noise ratio for assessing the quality of the pre-processing strategy and Accuracy, Precision and Recall for evaluating the proposed methodology. With the experimental results, it is evident that the Deep learning using the feature-fusion methodology has the accuracy of 97% than other state-of-art techniques. On comparing with recent works done using same methodology, the proposed work has 11% more accuracy than the existing well-known works.

Keywords Melanoma · Deep Learning · Skin cancer · Levels of melanoma · HAM10000

1 Introduction

According to the recent reports by World Cancer Research Fund and American Institute for Cancer Research on Skin Cancer in 2018, the Melanomic skin carcinoma is the 19th most communal disease that causing more deaths due to cancer across the world. As per the

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report, there were of about 300,000 new Melanoma patients were identified and recorded in 2018 alone which is the highest than ever before. As per the reports, the countries having the most deaths rate due to melanoma are furnished in the following Table 1. Though its counter-part, Non-melanoma skin cancer had break into the top five of all the most commonly occurring cancer across the world, it is likely an underestimate and it doesn't attract much researches. Because in the same year, it also records with an over 1 million diagnoses worldwide that makes it less harmful and less deadly. From the below table, it is very clear that the Australia and New Zealand are neck to neck and leads the table almost with 34%.

Melanoma is the most prevalent and hazardous kind of skin carcinoma that originates from the sites of pigment cells melanocytes under the skin. One of the evident and visible identification symptoms is the spread of black or brown colour moles. Interestingly, it is more commonly found in men than women since the chances of exposing to the harmful sun rays are higher to most of the men than women world-wide. By nature, the melanoma become deadly only when the early diagnosis doesn't ensure an appropriate treatment and an undiagnosed melanoma that already deepens into the skin and may successfully starts spreading to other parts/organs of the body. All the death caused by Melanomic Skin cancer is at its advanced stage by cause serious illness making an entire organ as carcinoma.

1.1 Stages on melanoma

Biologically, the human skin is including three underlying subsequent layers namely Epidermis Layer, Dermis and Hypodermis layers. The prime purpose of the skin is to shield and guard the underlying muscles, bone and organs from harmful radiations, acts as a primary sensor- actuator in most of the reflex actions and acts as a stimulus inducer and more importantly it regulates the thermal balance of the body [5].

Skin cancer is broadly classified into two categories such as Melanoma and Non-melanoma skin cancer. Of which, the Basal-cell carcinoma and Squamous-cell carcinoma were commonly called as Nonmelanoma skin cancer (NMSC). Since both the squamous carcinoma and Basal Carcinoma develops on the surface of the skin, it is directly exposed to solar UV and other harmful radiation that has no connection with melanoma [16]. The cancer cells produced in these NMSC carcinoma were found to be malignant and they were also called as Malignant Melanoma. Perhaps, the Melanoma occurs in the site of cell growth of melanin pigments, an unregulated cell growth causes irregularity protrusions of skin cells which is dangerous, harmful and life threatening if the cancer spreads deeper inside.

The prevalent symptoms of melanoma are different shapes of skin lesions such that more than 50% of lesions doesn't match with others and of different sizes around 6 mole size. Also, the colour of the skin lesions is greatly varying with each other [18]. Though it is less common and rare, the Melanoma turns out to be a more deadly and can destroy shortly

Table 1 World-wide skin cancer rates [22]

Palce	Nation	Rate per 100,000 people
1	Australia	33.6
2	New Zealand	33.3
3	Norway	29.6
4	Denmark	27.6
5	Netherlands	25.7

the human organs more frequently than any other disease which accounts for the greatest number of death due to skin cancers. Melanoma is classified into four cases based on its severity namely Superficial, Nodular, Lentigo malignant and Acral Lentiginous [25].

The major contributions of the work are as follows:

1. To showcase a robust pre-processing methodology using a combination of Median and Gaussian Filter along with a local histogram equalization that ensures the distinction among the ROI and noises which accounts for a significant quality improvement.
2. Proposing a novel ideology of implementing KNN clustering before experimentation to ensure that it is melanoma by clustering the relate images using the property of having 50% moles has different pattern.
3. Using of a simplistic feature fusion in Deep learning strategy to improve the accuracy implementing sum rule fusion strategy.

The paper is organized as follows: In chapter 2, the problem is defined which is followed by the related state-of-art works done related to the problem in Chapter 3. Then, the Dataset used in the experiment and pre-processing done is discussed in Chapter 4 and 5 respectively. Chapter 6 exclusively deals with the GLCM features that were used in this study. Chapter 7 briefs how the intra-clustering is achieved using KNN which is a major contribution of the paper. It is then followed by brief account on the State-of-Art techniques used in the study such as Random Forest, SVM and Deep Learning in Chapter 8, 9 and 10. Which is then followed by the Performance Evaluation and Analysis of the proposed methodology in Chapter 11 and is then compared with the other recent related works to prove the superiority with the numerical results in Chapter 12. Finally, Chapter 13 concludes the study and potential areas of future scope.

2 Problem statement

From the literature, the three common symptoms of melanoma were analysed. Firstly, all the newly formed moles are different in the shape and colour from the previously existing moles. Secondly, it reports that almost half of the mole present does not match the rest half of the moles approximately. And finally, the contour or outer covering of the mole are ragged and mostly asymmetrical and looked like coarse one. This work initially makes of these features and makes use of Harlick GLCM features for more variances and standard deviation of the existing samples of other skin diseases as well and then performs Inter-Clustering KNN Clustering methodology to ensure the variances among the moles present in the body that ensures the melanoma and finally Deep learning is implemented to affirm the current stage of the melanoma.

3 Related works

Salah et al. had introduced a novel approach that calculates Proliferative Index of lymph nodes from the sample histopathological images automatically. This model is trained by the utilization of segmenting nuclei manually of Ki-67 image. The value of PI is calculated for the ROI i.e., the regions where melanoma has been identified in the lymph node images. The

PI measure and the nuclei is divided into segments by use of trained Convolutional Neural Network (CNN) model [3]. In the proposed approach, CNN that is inspired from SegNeT model proposed by [21] has been implemented to segment the stained images from Ki-67 dataset into three regions namely background region, active region and passive region. Here active and passive region is considered as ROI. This work considers the later stage of the melanoma that is the disease gets advanced severity and is either ready to spread or already spreading deep into the skin through Lymph nodes. This paper used the statistic of [6] about 2,87,723 people are diagnosed with melanoma of type invasive. The melanoma stages are measured by an activity named proliferative of the cell. In order to treat the melanoma, it is mandate to know the progression and spreading level to understand about the severity of the disease which is mandate to suggest an appropriate treatment. Proliferative Index is the value that is used to denote the progression of the melanoma. Melanoma begins with cells named melanocyte in the skin in which the growth of the cell can produce a metastatic type of melanoma that passes through the vessels to node in lymph. When the melanoma starts attacking Sentinel Lymph Nodes (SLN) which is the important stage of melanoma as in this place melanoma passes to any organ and can infect it. Here, the nuclei are classified into two types: active nuclei which possess protein Ki-67 and passive nuclei that devoid of the protein. This work gets inspired by [7] in computing the PI value as a fraction of the total active nuclei present at that instant of time to all the nuclei. A special type of stained Ki-67 is utilized to make the protein stain and find the active phase of nuclei [9]. In the stained image of Ki-67 the nuclei appear in two colors as dark brown for active phase nuclei and blue for passive phase nuclei. The result of this experiment is a method for segmenting system can segment and classify based on the complexity of computation when it is low and the error rate is average.

Prashant and et al. Proposed a technique for the classification of skin based on the type namely malignant and benign. Among 200 types different cancer malignant is the hazardous of skin cancer and prospects is good as it can be cured it is found in early stage. This paper uses images from the clinical by cameras with high speed is used to identify melanoma in the initial stage. This technique is based on the calculation of Total Dermoscopic Score (TDS) by preprocessing and segmentation is done by OTSU's method. The OTSU's method is used to classify the skin cancer as Benign and Melanoma. This paper is worked on the dataset with 30 lesions of images in which 16 malignant image and 14 benign images. The detection system of melanoma is utilized to detect the malignant type of cancer from the given dataset. In this technique frequently three steps are used namely finding the region of unhealthy, descriptive feature computing and labeling based on the classification. In the proposed work, the intent is to re-iterate the method to all the skin lesions present in the body to find out whether melanoma is present or not [8].

Reshma and et al. has introduced two methodologies for the automatic melanoma identification. In the first method, the total area and other statistical features are employed to ensure the skin lesion as melanoma and to predict the current stage of advancement of the disease with the previous similar scores of the same subject. The intent of the model is to rapidly analyze the advancement of the disease and severity of the cancer so as to treat the patient immediately before the cancer cell spreading to other parts of the body. The second method is to find whether the skin lesions are melanoma or not for an appropriate diagnosis. First the input image is loaded and preprocessing involves of transformation RGB2 and median filter usage. The colored images from the dataset initially converted into the

gray scale without any information loss to the lamination and saturation. Next is to pre-process the resultant grey scale image to free from air bubble noises, removing hairs and to removing black frame. Median filter is employed to de-noise the preprocessed image. Then, finally, four important features were exploited for the classification such as Irregularity, Contour coarseness, Color variation and indifferent similarities. These features were later very important to predict the severity of the disease in first method and to identify the current stage of melanoma [23].

Shalu and et al. Proposed technique is developed using dataset of digital image namely MED-NODE. The raw image collected from the dataset contain more noisy objects and preprocessing is used to remove all the noisy objects and active contour segmentation is used for the extraction of interest region. From the segmented part features of the color are extracted and performance of the system is analyzed by thy Naïve Bayes, Decision Tree and KNN classifiers. The Decision tree classifier has more accuracy than the all other classifier. In this proposed work first preprocessing and segmentation technique is used. Here most of the features is extracted from color spaces. The proposed system varies more in specificity than sensitivity as the system more specifically identify benign cancer and the accuracy of the model is also high than all other model [24].

Hiam et al. has claimed a novel system used for the detection and classification of collected dermoscopy image, preprocess, segment and extraction is done. In the proposed model, the dataset samples were processed so as to detect any kind of skin lesion by using the extracted features from the test images from the dataset. The technique uses Support vector machine (SVM) classifier based on the features selected from principal component analysis (PCA). The performance of the classifier is used for separating the type of benign and malignant skin lesion. In this method is for detection, extraction and classification of skin lesion using Support vector machine and principal component analysis but accuracy is high for principal component analysis for the selected features [2].

Muhammad and et al. has put forth a novel model for the skin cancer classification of melanoma by using the conventional K-means algorithm. The technique is implemented by clustering using the centroid selection. Feature extraction like Color and textural techniques are used for classification. In texture classification, the fusion of GLCM and LBP features were done along with the color features to achieve the better accuracy for the classification of the images from the sample dataset [12].

Adekanmi and et al. has introduced a model that implements the idea of deep convolutional network for segmenting the ROI and to predict whether the ROI is melanoma or other skin lesions. This proposed model is characterized as consistent and organized with hop routing and the work has significant contribution in reducing the size of the test cases and henceforth computational resource such as time and memory can be greatly reduced. The proposed deep CN has been built with many layers wherein every layer is responsible for handle feature learning and extraction of image. Pixel based classification is done in softmax classifier which has a goal for decreasing the limitations of deep learning classifier. The processing time of the image is very less for dermoscopy. This system has high accuracy [1].

From the Table 2, the inspiring related works were discussed to identify their short-falls and the work is carried out to address all those demerits. By choosing a vast dataset, it is possible to have more training-validation subsets. Adopting the idea of hybridizing GLCM features and implementing in DL, almost addresses the issue of misclassification in lesion segmentation and identification.

Table 2 Summary of some state-of-art works

S.No	Literature	Methodology	Demerit(s)
1	[1, 7, 9, 21, 24]	Calculating proliferative Index (PI)	This work considers the later stage of the melanoma
2	[8]	Calculating Total Dermoscopic Score (TDS), using OTSU segmentation	Though it attempts to detect early stages of melanoma, the model is evaluated using a dataset having only 30 images.
3	[23]	Using Statistical values as features	A benchmark work motivates this research, yet it uses only 4 measures yielding less accuracy
4	[24]	Decision Tree	Best in class accuracy is achieved. But, its not suitable for either larger datasets or to consider more features due to dimensionality issues of decision tree model and consumes more space.
5	[2]	SVM over PCA.	Though claiming of better accuracy, no word on other metrics and the quality of pre-processing metrics like PSNR or MSE. Also, experiment is carried out using lesser validation subsets.
6	[12]	Using Texture features i.e., LBP features	Dermis dataset has only 397 images. Better accuracy but the higher misclassification despite having better accuracy of 94%. Inspired by hybrid of different features to boost accuracy.
7	[1]	Using DCNN	Inspiring work yet it consumes more time for multi-feature classifications and it requires more memory as well. Ignoring time and space complexities, it doesn't ensure that the lesions are not other skin diseases prior to the ROI computation.

4 Dataset used

The training of the proposed deep neural networks for the automated diagnosis of stages of melanoma initially done with PH2 dataset having 140 melanomas along with 160 non-melanoma images. The performance of the model is not satisfactory since the dataset consists of only a limited number of subjects and thus it seems PH2 dataset has only limited variety of features can be extracted from its images. In order to address this, relatively bigger HAM10000 (Human Against Machine with 10000 training images) dataset that includes of about 10015 skin lesion images which are acquired from different kinds of subjects having distinct modalities. This dataset is archived publicly by ISIC freely. The actual images of the dataset were acquired by using MoleMax HD system with a non-quadratic 1872x1053 resolution. They were later on either cropped with lesions i.e., ROI as centre or shall be compressed to a quadratic pixelate 800x600 resolution images possessing atleast 72DPI [10].

In this experimental setup, 10-cross validation is followed on 1113 malignant melanoma images. Thus, a subset composed of 111 images is used to validate and the rest of 1002 images were separated into 10 bins and training and validation is randomly occurred. The mean value is considered as the optimal value of the feature in every layer separately and is transferred to next layer of DCNN to identify the lesion.

5 Pre-processing

The pre-processing of raw images from the dataset is the foremost and predominant step for the three basic reasons. The primary intent is to reduce the size of the images to an adequate 400 × 300 while preserving the 720 DPI by either cropping manually and is then compressed to 64 × 64 images. Since, the training involves many images, it is mandate to reduce the size to an adequate quality. Secondly, the process of denoising, that is the removal of unwanted pixels from the images without disturbing other. In this case, hairs, scratches and bubbles were considered as noises. Here, the Median filter is used first and is followed by Gaussian filter to remove the fine-grained noises.

The Median filter is a non-linear filter that considers the neighbour pixel values to fill the missed value or replace a noisy pixel and is most used one because of its straight forward approach. It has a characteristic feature of removing noise whereas meanwhile keeping edges intact. Unlike median filter, the Gaussian filter is a linear filter and is work on the basis of initially introduce a gaussian blur to neutralize the noisy pixels. The Gaussian low-pass filter is used so that it preserves even low-frequency edges while pre-processing. The key work is to introduce a CLAHE algorithm i.e., Contrast Limited Adaptive Histogram Equalization which is a well-known local histogram equalization method that addresses the noise intensification problem while increasing the contrast of the image.

The final part is the identification of Region of Interest. ROI is identified by using thresholding methodology that works straight-forward and simple to implement. Also, since the ROI is a centred mass, it is adequate to use the conventional thresholding method.

6 Haralic – GLCM features

The features extracted here are three folded. Firstly, the size attributes were extracted such as Area and Perimeter whereas area attribute represents the total number of pixels falls inside the ROI and the perimeter denotes the contour of the ROI. The contour of the ROI is later used to find the stage of the carcinoma.

Second, the colour features are extracted to ensure the anonymity and similarity of the colour of the ROI. The features used in this work are Mean, Standard Deviation and Kurtosis. All of them are computed in HSI colour space.

Mean is calculated as follows:

$$\mu = \sum \frac{x_i}{N} \tag{1}$$

Standard Deviation is computed by:

$$\sigma = \sqrt{\frac{1}{n} \sum_{i=1}^{N} (x_i - \mu)^2} \tag{2}$$

Kurtosis is computed by:

$$\frac{1}{N}\sum_{i}^{N}\frac{(x_i-\mu)^4}{\sigma^4} \tag{3}$$

Finally, the third set of features includes the Haralic introduced texture features as follows:
Energy is computed by

$$\sum i \sum j\{p(i,j)\}^2 \tag{4}$$

Contrast is computed by

$$\sum i \sum j(i,j)^2 P(I,j) \tag{5}$$

Correlation is computed by

$$\sum i \sum j \frac{p[i,j]}{1+p[i,j]} \tag{6}$$

Variance is computed by

$$\sum i \sum j(i-\mu)^2 p(i,j) \tag{7}$$

Homogeneity is calculated by

$$\sum i \sum j \frac{p(i,j)}{1+(i-j)^2} \tag{8}$$

Sum Average is calculated by

$$\sum_{i=2}^{2N_p} P_{x+y}(i) \tag{9}$$

Sum Variance is calculated by

$$\sum_{i=2}^{2N_p} P_{x+y}(i)(i-f6)^2 \tag{10}$$

Entropy is calculated by

$$-\sum i \sum j P[i,j] log P[i,j] \tag{11}$$

Sum Entropy is calculated by

$$-\sum_{i=2}^{2N_p} P_{x+y}(i) log_2[P_{x+y}(i)] \tag{12}$$

Difference Entropy is calculated by

$$\sum_{i=0}^{2N_{g-2}} P_{x-y}(i) log_2[P_{x-y}(i)] \tag{13}$$

Difference variation is calculated by

$$-\left[\sum_{i=o}^{2N_{g-2}} i^2 P_{x-y}(i)\right] - \sum_{i=o}^{2N_{g-2}} i P_{x-y}(i) \tag{14}$$

Information measure of correlation is calculated by

$$\frac{HXY - HXY1}{max(H_x, H_y)} \tag{15}$$

Maximal correlation Coefficient is calculated by

$$(2^{nd} \quad \text{largest} \quad \text{eigen} \quad \text{value} \quad \text{of} \quad \text{Q})^{1/2}$$

7 K-Means clustering

The idea behind the algorithm is to identify the local center from the randomly formed groups initially and the process is continued to find the actual center of the new subsets with respect to the given criterion. Initially, the preliminary centers were arbitrarily chosen as certain points falls in the area of the interested search-space. In each reiteration step, a new center is computed by calculating the Euclidean distance and by considering the inter-intra clustering distances [17].

The following procedural steps were carried out recursively:

1. Disassociate the points those where positioned on the centers C(i), i.e., detect the centers for all the points included in the dataset to which they were closely associated. Here, the points are divided based on the Euclidean and Jacobian distance from the current centers.
2. Compute a new centroid $c(i+1) \in C(i+1)$ from the already divided clusters so that the new centroid will be either the mean or closer to the mean of the entire points that are closest to $c(i) \in C(i)$.

The above two procedures were re-iterated to n times till the k-clusters are well disassociated among the other with less intra-cluster score of similarity meanwhile possessing the maximum inter-cluster similarity i.e., dissimilar to the other clusters whereas strongly associated within the cluster. The abovesaid clustering procedure will converge only when C(i) and C(i – 1) becomes same [20].

8 Random forest

Random forest (RF) is one of the algorithms comes under supervised learning for making decision that is utilized for both regression and classification but in most case, it used only for classification. In Random forest, large number of dimensional data can be handled in the ensemble method. The featured of random forest are estimation of missing data is effective, the method named weighted random forest is utilized for balancing the imbalanced data and also utilized for the estimation of type of variable used in the problem [15].

The working function of random forest has four main steps. They are

1. Random samples are selected from the given dataset.
2. Decision tree is constructed for all samples in the dataset and predicted result can be estimated from all decision tree.
3. For all decision tree, the method of voting can be accomplished.
4. The conclusion is made based on the predicted result which is more voted.

The advantages of random forest are variance is minimum, has more flexibility, has good accuracy even the data is not scaled and high quantity of missing data and has ability to overcome the overfitting problem by the use of combining the result of the various types of decision tree. The disadvantage of random forest is complexity, construction, time consuming, requires more computational resources and prediction process consume more time as verify all the decision tree.

9 Support vector machine

Support Vector Machine (SVM) is the widely used and popular bi-classification and supervised learning algorithm. Over the years, it can be both utilized for classification as well as regression whereas it is well suited for classification problems. SVM has the ability to handle numerous amounts of categorical and continuous variables. The working is based on the illustration of various types of classes of hyperplane in many dimensions. The mechanism of SVM is to fragment the dataset based on the class labels that are used to find the Maximum Marginal Hyperplane (MMH) which is done in two steps. The first steps is that the SVM will create the hyperplane in a iterative manner that is used to separate out the classes and nest step is to select the hyperplane that is used to separate the classes [26].

SVM includes the main concept namely support vectors, hyperplane and margin. Support vector is referred as the point in the data which is near to the hyperplane. These points are used to spate the lines. Hyperplane is referred as place or space used for the decision that is separated by the group of objects having various types of classes. Margin is referred as a slit in between two lines on the data points of various types of classes which is closest. The calculation is done based on the perpendicular distance from the line. When the margin is large it is said as good margin and small it is said to be bad margin. The advantage of SVM is it has more accuracy, large dimensional space and utilizes less memory space. The disadvantage of SVM is not suited for huge dataset and overlapping of classes [14].

10 Deep learning

By making use of the state and thinking process of humans and deploying a synthetic ANN, a new subfield has emerged as Deep learning making the extended neural network of a human thinking process. There are three types of learning is available for promoting self-learning ability in a machine namely supervised learning, semi-supervised learning and unsupervised learning. There are different hybridized versions of Deep Learning architecture are available namely deep-convolutional neural networks, deep-belief networks, deep-neural networks and recurrent-neural networks. The model put forth by Deep learning is capable of producing and behaviors similar to that of humans and in some cases, they were well ahead in defeating the human accuracy, speed and diligence. Hence, it exhibits an outstanding performance than human. This ability makes the researchers to deploy the architecture of neural network in the brains of humanoid robots. Artificial neural networks (ANNs) working mechanism is based on how the biological communication taken place in human neurons and how they will be communicated in a distributed node in a highly distributed environment accurately. Even though, many simulations were made, still the tradeoff among the error and time complexity is too large and sometimes it approaches none which means it still a complete chaos. It is not possibly to expect the desired way how it

could be behaved and is not possible until disclose all the mysteries of the mechanism of how human brain works.

From the Fig. 1, it is not restricted with the four deep layers only, the deeper it iterates the more refining will be the results. Also, if there is no such related information is available in the dataset as classification labels, it starts the trick part of the DL. It tries to make use of a closer similarity and henceforth it carries the knowledge on classifying the pixel in every layer. The only thing is that it cannot be ensured until it grows deeper. This is overcome by the extensive training cases. And this is the reason why we are choosing a vast dataset for the experimental purposes with HD images.

There is an interesting and important feature of Deep Learning is that it adapts itself automatically for self-learning to gain the more knowledge from every cases and thus it is capable of generating its own set of rules constructs for as many hidden layers as possible provided the model is trained with huge pile of related data and is availed with powerful computational resources. In our work, the concatenation based DenseNet-161 network model is considered for evaluation of DL.

11 Performance evaluation

The system is analysed for its performance with respect to two aspect. First aspect is to exhibit the pre-processing quality of the image and the later one is to exhibit the classifying

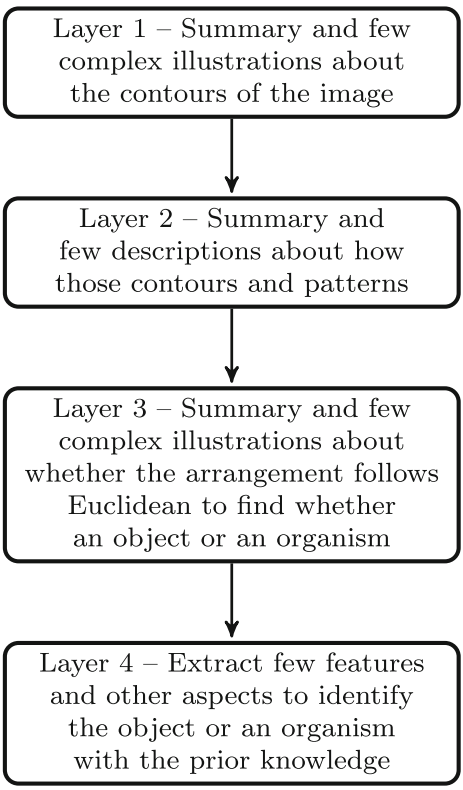


Fig. 1 Deep learning approach in computer vision

and detecting capacity of the proposed deep learning system to the conventional similar systems that automatically detects the stages of the deadly disease Melanoma.

The pre-processing quality has been computed using many metrics of which two widely accepted and utilized more accurate metrics namely Mean Squared Error (MSE) and Peak Signal to Noise ratio (PSNR) were used in this work. For a better pre-processing, the value of MSE should b as low as it can be. Since PSNR and MSE are inversely proportional, the lower MSE will yield better PSNR.

Sum of Squares Due to Error is computed using:

$$SSE = \sum (y_i - \hat{y}_i)^2 \tag{16}$$

The Mean Squared Error (MSE) is an imperative measure that is widely used to exhibit the quality of the pre-processed image by comparing every individual pixel values of the original image to the respective pre-processed one to find out the maximum deviation and is called as error pixel. The important step of MSE is it considers only the average of squared "errors" among all of the actual image and processed image so as to avoid the neutralization of negative and positive index errors since it was a cumulative score.

Mean Square Error (Estimate of σ^2) is calculated using:

$$s^2 = MSE = \frac{SSE}{n-2} \tag{17}$$

TThe value of Peak Signal Noise Ratio (PSNR) is computed as the instantaneous maximum power of the signal to the square root of the respective Mean squared error i.e., its peak error.

The mathematical representation of the PSNR is as follows:

$$PSNR = 20log_{10}\left(\frac{MAX_f}{\sqrt{MSE}}\right) \tag{18}$$

where the MSE (Mean Squared Error) is:

$$MSE = \frac{1}{mn}\sum_{0}^{m-1}\sum_{0}^{n-1}||f(i,j) - g(i,j)||^2 \tag{19}$$

For a better reconstructive pre-processing, the value of MSE should be minimal and since MSE and PSNR are inversely proportionate, the respective PSNR should be maximum. From the following table, the execution time also measured to carry out the calculations.

From the Table 3, it has been clear that the proposed deep learning model has been outperformed all the recently proposed similar models. In the following analysis, True Positive is the case where the disease has been identified accurately and True Negative is the cases where the model correctly rejects the images without melanoma correctly. The other two metrics, False Positive and False Negative are the cases where the images doesn't have melanoma is falsely deemed as positive possessing melanoma and leaving the images

Table 3 Performance analysis

Technique	RMSE	PSNR	Execution time (in sec)
KM+FCM [27]	4.20	27db	89.4
GMM+CNN [4]	2.66	25db	56.6
Otsu+SVM [13]	1.50	59db	15.7
CNN [11]	0.73	NA	13.8
Proposed DL	0.56	86db	14.2

that actually having melanoma as negative respectively. In Medical Application system, the accuracy doesn't only claim the aspect of identifying the disease perhaps it must also should have a robust discriminating ability to claim Positive and negative cases.

Accuracy The metric accuracy is a very important performance measure and it represents how well the model correctly identifies and correctly rejects the test cases. It is calculated with the following terms in our work as follows:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{20}$$

Here, TP represents True Positive means disease is correctly identified, TN represents True Negative i.e., rejecting the normal lesions correctly, FP represents False Positive i.e., mistakenly predicting a normal skin lesion as Melanoma and FN represents False Negative i.e., rejecting melanoma as normal melanoma.

From the Table 4, it is clear that the proposed deep learning model outperforms all the conventional models and possessed of about 97% of accuracy while considering all the features such as size, colour and texture features. So, the proposed model is so accurate than others.

12 Discussion

This section deals with the discussion on how the proposed methodology achieves all the shortfalls of literature in two aspects. Firstly, the lesion is ensured as melanoma by KNN clustering and is then pre-processed to remove hairs and filters introduced fine grained noises as well. The deployment of CLAHE ensures that artefacts are not treated as noises and noises were not be over-intensified while limiting the contrast of the image. The quality has been assessed and compared with the literature to prove the superiority of the image reconstruction using Table 3. The second prospect, the superiority of the proposed hybrid feature fusion model for DL has been established by showcasing the comparison with the almost similar kind of recent work done in the Table 5.

The above Tables 4 and 5 demonstrates the performance of the proposed model that uses feature fusion methodology using sum rule fusion for every layer out performs it previous layers by considering fewer features. Using the similar dataset and instances, the proposed model produces a significant increase in accuracy of over 10% with additional 100 samples in the ISIC 2018 dataset. By analysing the results furnished in Table [4], while considering more number of features there is a linear increase in all the classifiers. But the lower side of the sum fusion is the time consuming especially using Densenet. Since the application is very sensitive to false predictions, time consuming tradeoff would be at the choice of

Table 4 Performance comparison

Features	Accuracy (%)		
	RF	SVM	Proposed DL
Size	75.3	82.6	89.5
Size + Colour	79.6	89.5	93.3
Size + Colour +Texture	95.75	91.2	96.7

Table 5 Performance comparison

Comparison	Model	Dataset Used	Instances	Accuracy (%)
[19]	Inception –v4	ISIC 2017 Challenge Dataset	1019	82
	ResNet-152			83
	DenseNet-161			86
Proposed DL	Random Forest	ISIC 2018 Challenge Dataset	1113	85.7
	Support Vector Machine			91.2
	DenseNet-161 (DL)			96.7

physician whether the decision of the model is used as supportive claim or preliminary claim for proceeding with further tests or treatment.

13 Conclusion

As the report of World Cancer Research Fund and American Institute for Cancer Research on Skin Cancer suggests, the Continuous Update Project Panel arbitrated that there is strong evidence that drinking of arsenic contaminated water propels greatly the risk of skin cancer particularly malignant melanoma. Interestingly, the report also suggests that intaking of high supplements beta-carotene doesn't had any significant consequence on propelling or regulating the risk of non-melanoma skin carcinoma. Alongside, there exists evidences suggesting that drinking coffee might decrease the risk of malignant melanoma in women and reducing the risk of basal cell carcinoma in men and women. Similarly, by consuming alcohol will upsurge the vulnerability of acquiring malignant melanoma and basal cell carcinoma.

From the above Table 4 and 5 exhibiting experimental results, the proposed model using deep learning exhibits a higher performance than all the other conventional similar models. It is also understood that the above model propels higher accuracy of about 97% while using all the features combined together. In this study, the sum rule fusion method is used to consider all the features for classification and thus it consumes more time. To address this, the model can be designed to find alternate way to extract features and train the model. One expected let-off of the work is its time complexity but it is a natural tradeoff while expecting a higher accuracy. Also, it is interesting to boost the performance of straightforward and simplistic approaches like RF and SVM using meta-heuristic approach that can be implemented as less time and space complexities.

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