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ARTICLE

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DETECTION OF MELANOMA SKIN CANCER USING HYBRID MACHINE LEARNING TECHNIQUES

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Melanoma skin cancer is accountable for 75% of skin cancer mortality while only afflicting 4% of the population. It is one of the most lethal types of cancer. In this work, machine learning techniques, including Support Vector Machine (SVM) and deep learning techniques using a Convolutional Neural Network (CNN), have been applied to detect melanoma skin cancer in a more precise form. The proposed model has achieved 87.14% and 88.39% accuracy using SVM and CNN, respectively.

Introduction

The skin is the outermost part of our bodies, it is susceptible to being exposed to the elements and coming into touch with contaminants including dust, pollution, microorganisms, and UV radiation. These might be the causes of any skin conditions, and skin-related diseases are also brought on by gene instability, which makes skin conditions more complicated. The epidermis and dermis are the two principal layers of the human skin. The epidermis, or top layer of skin, is made up of three different cell types: basal cells, which give skin its round shape, SQUAMOUS cells, which are flat and scaly on the surface, and melanocytes, which give skin its color and shield it from harm. The diagnostic classification does not currently reflect the diversity of the condition, it is not possible to accurately forecast the disease's course or to treat it. In addition, cancer cells are frequently discovered and treated only after they have spread to other internal organs of the body and undergone mutations. Therapies and treatments are not particularly successful at this time. Due to these problems, heart illnesses are now the leading cause of mortality worldwide and have surpassed skin cancer in terms of the proportion of cases. Other factors that may have contributed to the disease's progression to such a terrible stage include people's ignorance, their use of home cures without first understanding the seriousness of the issue, and the possibility that these treatments may worsen the condition altogether. Skin cancer is the worst form of skin illness that affects people, out of all the other varieties. The fair-skinned are most likely to experience this. There are two forms of skin cancer: malignant melanoma and non-melanoma. Despite only affecting 4% of the population, malignant melanoma accounts for 75% of deaths from skin cancer. It is one of the most lethal types of cancer[1]. In this study, a hybrid approach combining deep learning methods with a Convolutional Neural Network (CNN) and Support Vector Machine (SVM) has been suggested for accurately diagnosing melanoma skin cancer.

The rest of this research article is organized in the following manner: In Section 2, the origin of the problem

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is mentioned. Existing gaps associated with some developed models are explained in Section 3. Strategies that are considered to develop the proposed model are described in Section 4. The proposed method, experimental analysis, and conclusion of this study are outlined in Sections 5 through 7, respectively.

Origin of the Problem

Prior research on skin cancer has solely focused on feature extraction methods like ABCD and GLCM (Gray Level Co-occurrence Matrix) and LBP individually but very few works have been done by combining these methods. Asymmetry Index (A), Border Irregularity (B), Color score (C), and Diameter (D) are the criteria used by ABCD to identify the clinical aspects of melanoma. There has been no stand-alone application to detect melanoma.

Existing Gaps in the Knowledge

J. Dagher, L.Ting, M.Bouchouicha, and M.Sayadi used a convolutional neural network and two classical machine learning classifiers K-Nearest Neighbor and SVM(Support Vector Machine), to detect melanoma skin cancer and brought accuracies of 57.3% (KNN), 71.8% (SVM), 85.5 (CNN)[1]. Using a mobile application, the system collects and recognizes moles in skin photos, and classifies them as melanoma, nevus, or benign lesions based on their abrasiveness. The testing results of the system's implementation of 11 classifiers demonstrate that the Support Vector Machine (SVM) has the greatest accuracy of 77.06%, followed by the Multilayer Perceptron at 75.15%.

A straightforward detection and diagnostic method was created by Deshpande A. S. et al.[2] and are usable by non-experts, clinicians, and physicians. According to their technique, statistical texture characteristics were retrieved using the GLCM after fuzzy C-Means (FCM) segmentation and picture pre-processing using a median filter to remove noises.

In their publication, Nadia S. and Souhir B.[3] introduced a digital diagnostic method for early melanoma diagnosis based on a combination of the ABCD rule and the region-growing segmentation algorithm. Michal K. et al.[4] in their paper, used an SVM classifier to differentiate between melanoma and other non-melanoma cancers. The Dull-Razor method was developed by Lee et al.[5] to remove dark hair from photos. The dark hair pixels are identified using a general grayscale morphological closure method, and they are then substituted using bilinear interpolation.

Murugan, A., et al. built a system which identifies the skin cancer disease based on the image s of the skin. GLCM, Moment Invariants and GLRLM features are extracted in this research work[6].

This research concentrated on the use of multiple feature extraction techniques to improve the detection of melanoma skin cancer. A stand-alone application has been developed to address the lack of standalone melanoma detection software and increase the system's dependability and use. The data came from the International Skin Imaging Collaboration (ISIC).

Brief Outline of Methodology to be Adopted

Figure 1 represents the proposed methodology's flow diagram of detecting and classifying skin lesions both benign and malignant. The important phases include picture capture, image pre-processing, segmentation, feature extraction, and classification technique. Input to provide the network with extra training data, images are gathered from two datasets. The method known as Maximum Gradient Intensity (MGI) is used to remove the hair artifacts from the image before using image enhancement techniques to improve it. Otsu global thresholding method is used to segment the skin lesion from the picture.

***Image Acquisition*:** An appropriate dataset must be arranged for the development of an automated model for the detection of melanoma skin cancer.

***Image Preprocessing*:** Before processing, a technique called pre processing is used to correct different picture flaws. Multiple sources provide input photos, thus it is crucial to convert them to a common size, standard colour, and remove any extraneous detail like noise, bubbles, hair, etc.[7]

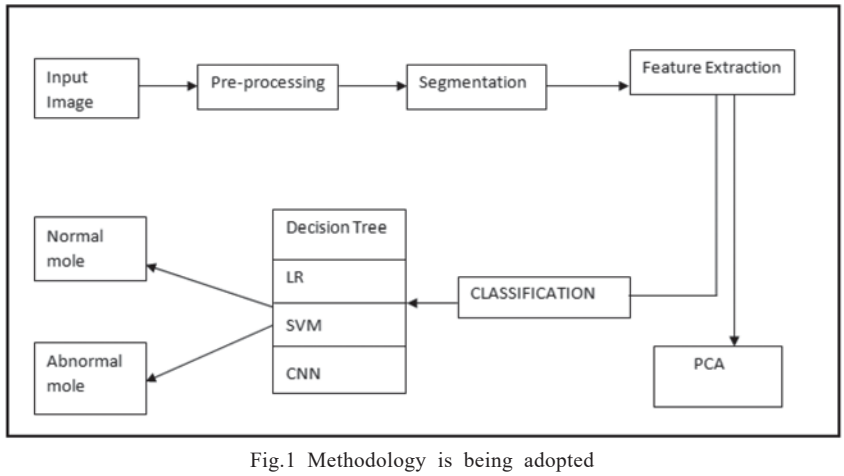

Fig.1 Methodology is being adopted

***Image Segmentation*:** Finding similar regions within an image and dividing items into discrete sections based on a threshold value are the basic goals of segmentation. Otsu's thresholding is among the best picture segmentation techniques. It is one of the global thresholding histogram-based approaches.

Proposed Methodology

The proposed method consists of two main processes to precisely detect malignant melanoma skin cancer, which are the feature extraction method and classification techniques. The features of pixels inside segmented regions of interest are frequently used for object categorization, or ROIs. Therefore, a crucial step in a successful classification process is extracting pertinent characteristics. We have used ABCD and GLCM feature extraction methods to implement the proposed method. We have employed two classification techniques, SVM and CNN, in the proposed model.

Feature Extraction: For the suggested model, we used two feature extraction techniques, which are as follows:

ABCD feature extraction method: The ABCD rule stands for the asymmetry index (A), border irregularity (B), colour score (C), and dimension (D) of the lesion. While symmetrical lesions are more typical in benign lesions, asymmetrical lesions on the skin are more likely to be cancerous. The following equation is used to determine the Index of Asymmetry (AI)[8].

$$AI = \frac{\Delta A}{A} \tag{1}$$

Here, A stands for the total picture area and denotes the lesion's area relative to the entire image. A melanoma lesion's border seems to be rough, erratic, and blurry. The circularity or compactness index (B1) determines the border's irregularity by,

$$B1 = \frac{4\pi A}{p^2} \tag{2}$$

$$B2 = \frac{A}{P} \tag{3}$$

$$B3 = A * P \tag{4}$$

This reveals the smoothness of the lesion boundaries. Since a circle is the smallest structure, its compactness is considered to be 1, and for all other shapes, it ranges from 1 to 0. The B1 result is zero because the melanoma lesion's margin is ragged, uneven, fuzzy, and unpredictable. Area to perimeter ratio is represented by B2, while area and perimeter multiplication is represented by B3. These characteristics will be more important for malignant melanoma. The score for a characteristic depends on how many colours are present in the lesions. Another early sign of melanoma is a change in the colour of the lesion. The benign ones include many fewer colours than the malignant ones do. Ratings range from 0 to 6, with 1 being the highest rating for each of these hues. The fact that a melanoma-affected mole enlarges more than a typical mole is one of the most crucial factors. A malignant lesion has a diameter of more than 6 mm. The lesion's average diameter D1 is computed using,

$$D1 = \frac{D1' + D1''}{2}$$

where

$$D1' = \sqrt{\frac{4A}{\pi}}$$

$$D1'' = \frac{D + d}{2}$$

$$D2 = D - d$$

The difference between the main axes is shown by D2. The main axis is D, while the minor axis is d. D1 and D2 will have higher values for malignant melanoma than for benign melanoma.

GLCM feature extraction method: The frequency of pixel pairings in a picture that have the same grey value is what is meant by the GLCM technique. The relationship between the reference pixel and the pixels around it is established in order to assess the texture of the image. Energy, contrast, correlation, and homogeneity are a collection of traits taken from uniform symmetrical directional GLCMs for texture characterization.

GLCM values are computed using following methods:

- Contrast: Determines the degree of textural roughness between a pixel and its surrounding pixels throughout the whole image.

$$\sum_{i=1}^{N}\sum_{j=1}^{N}(i,\ j)^2 P_{ij}$$

- Correlation: Measures the homogeneity of the textural distribution between 0 and 1.

$$\sum\nolimits_{i=1}^{N}\sum\nolimits_{j=1}^{N}(i, j)\left(P_{ij} - \mu_i\mu_j\right)\Big/\sigma_i\sigma_j$$

- Energy: The amount of disruption or non-homogeneity is quantified by energy.

$$\sum_{i=1}^{N}\sum_{j=1}^{N} P_{i^2 j}$$

- Homogeneity: Refers to how a pixel's surroundings affect the overall composition.

$$\sum_{i=1}^{N}\sum_{j=1}^{N} P_{ij} \Big/ \left(1+(i-j)^2\right)$$

Classification Method : The two most popular classifiers, named Support Vector Machine (SVM) and Convolutional Neural Network (CNN) have successfully applied in the proposed model for classification purposes.

Support Vector Machine (SVM) : Support Vector Machine (SVM) is a well-known and widely used supervised learning technique to solve various classification problems. In our proposed model we have employed SVM as a classifier to detect malignant melanoma precisely.

If the data can be linearly separated, the SVM plane is linear but if data cannot be separated linearly, the data will be divided into benign and malignant categories using kernel SVM with radial basis function. m

Let $\{(x_1, y_1), ..., (x_m, y_m)\} \subset X \times \{\pm 1\}$ a set of empirical data, where X is a non-empty set with the patterns x_i.

Let the function $f : X \to \{\pm 1\}$. Considering the class of hyper plane

$$(w.\, x) + b - 0$$

Where, $w \in R^N, b \in R$.

The decision of SVM corresponds to the results of the following formula:

$$f(x) - \text{sgn}\left((w.\, x) + b\right)$$

To construct an optimal hyper plane, one solves the following optimization problem:

$$Minimize_{w,b}\ 1/2||W|^2$$

Subject to $\mu_i.\left((W.x_i) + b\right) > 1, i = 1...m$

Algorithm of SVM to detect melanoma skin cancer using the combination of ABCD and GLCM features is as follows:

Step 1. The ISIC dataset of skin lesion images, including both melanoma and non-melanoma lesions, is used.

Step 2. Preprocess the images, including resizing, cropping, and normalization, to prepare them for feature extraction.

Step 3. Extract the ABCD features from each image. The ABCD features refer to Asymmetry, Border irregularity, Color variegation, and Diameter. Asymmetry is measured by dividing the lesion into two equal parts and comparing them for symmetry. Border irregularity is measured by examining the contour of the lesion and checking for any irregularities. Color variegation refers to the variation in color within the lesion. Diameter is the size of the lesion in millimeters.

Step 4. Extract the GLCM features from each image. GLCM stands for Gray-Level Co-occurrence Matrix, which is a statistical method that quantifies the spatial relationship between pixels in an image. GLCM features include Contrast, Energy, Homogeneity, and Correlation.

Step 5. Extract the LBP features from each image. LBP stands for Local Binary Patterns, which is a texture descriptor that captures the local structure of an image. LBP features include Uniformity, Entropy, and Contrast.

Step 6. Combine the ABCD, GLCM, and LBP features into a feature vector for each image.

Step 7. Split the dataset into a training set and a test set.

Step 8. Train the SVM model using the training set and the feature vectors.

Step 9. Evaluate the performance of the SVM model using the test set. Performance metrics can include accuracy, precision, recall, and F1 score.

Step 10. Use the trained SVM model to classify new skin lesion images as melanoma or non-melanoma based on their feature vectors.

Convolutional Neural Network (CNN) : CNN is a type of deep learning model for processing data that has a grid pattern, such as images, which is inspired by the organization of animal visual cortex and designed to automatically and adaptively learn spatial hierarchies of features, from low- to high-level pattern.

Algorithm of CNN to detect melanoma using the combination of ABCD,GLCM features is as follows:

Step 1. Load and preprocess the melanoma skin cancer image dataset. Divide the dataset into training, validation, and testing sets.

Step 2. Extract the ABCD, GLCM, and LBP features from each image in the dataset. Normalize the feature values.

Step 3. Design a CNN architecture that takes the extracted features as input. The CNN architecture should have multiple convolutional layers, pooling layers, and fully connected layers. Use rectified linear unit (ReLU) activation function in the convolutional and fully connected layers. Use softmax activation function in the output layer for predicting the class probabilities.

Step 4. Train the CNN on the training set.Use cross-entropy loss as the loss function.Use stochastic gradient descent (SGD) as the optimizer.Use batch normalization to speed up training and improve accuracy.

Step 5. Evaluate the trained CNN on the validation set.

Step 6. Test the trained CNN on the testing set. Calculate the accuracy, precision, recall, and F1-score of the CNN on the testing set.

Step 7. Visualize the learned features and filters in the CNN to understand how the CNN is detecting melanoma skin cancer.

The convolutional operation for the sequential CNN model architecture is as follows:

i) The Rescaling layer rescales the input image pixel values between 0 and 1.

ii) The first convolutional layer uses 32 filters of size 3x3 with a ReLU activation function. It produces feature maps by convolving each filter across the input image.

iii) The first max pooling layer performs max pooling with a pool size of 2x2. It reduces the spatial dimensions of the feature maps by taking the maximum value within each 2x2 window.

iv) The second convolutional layer uses 64 filters of size 3x3 with a ReLU activation function. It produces feature maps by convolving each filter across the output of the first max pooling layer.

v) The second max pooling layer performs max pooling with a pool size of 2x2. It reduces the spatial dimensions of the feature maps by taking the maximum value within each 2x2 window.

vi) The third convolutional layer uses 128 filters of size 3x3 with a ReLU activation function. It produces feature maps by convolving each filter across the output of the second max pooling layer.

vii) The third max pooling layer performs max pooling with a pool size of 2x2. It reduces the spatial dimensions of the feature maps by taking the maximum value within each 2x2 window.

viii) The Dropout layer randomly sets 50% of the input units to 0 at each update during training, which helps prevent overfitting.

ix) The Flatten layer flattens the output of the third max pooling layer into a 1D array, which can be passed to a fully connected layer.

x) The Dense layer has 128 neurons with a ReLU activation function.

xi) The Dropout layer randomly sets 25% of the input units to 0 at each update during training, which helps prevent overfitting.

xii) The output Dense layer has a number of neurons equal to the number of classes and uses a softmax activation function to produce class probabilities.

xiii) Epoch value=20

xiv) Activation function(1st,2nd, 3rd convolution layer) = ReLU

Activation function (Dense Layer) = Softmax function

Pool size=2X2

Kernel Size=3X3

Result and Performance Analysis

The proposed model is written in Python, and the simulated program is run on an Intel i7-7500U processor with a Nvidia GTX 1080 GPU and 16GB of DDR4 RAM in the Ubuntu 20.04 LTS operating system with glibc 2.17 version. The ISIC dataset has been used for training and testing of the proposed model.

Using SVM, an accuracy of 87.14% has been obtained on the ISIC dataset. The proposed work gives better accuracy compared to[9,10], as shown in Table 1 and Figure 2.

Using CNN an accuracy of 88.39% has been obtained on the ISIC dataset. The proposed work gives better accuracy compared to[11,12], as shown in Table 1 and Figure 2.

Table 1: Comparison of proposed work with other

Models	Accuracy achieved using CNN (%)	Accuracy achieved using SVM (%)
Proposed	88.39	87.14
1	NA	75.29
2	NA	85.72
3	81	NA
4	85.5	NA

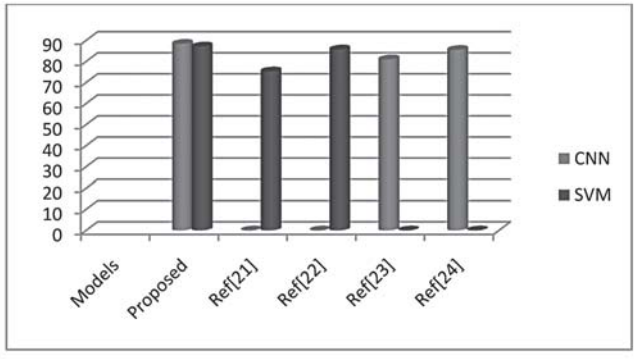

Fig. 2 Graphic relationship of the proposed work with other related works.

Mathematical terminologies considered for the proposed model : The goal of SVM is to find a hyperplane that separates two classes with the largest margin. In the case of binary classification for detecting melanoma skin cancer, we have two classes: benign and malignant.

The objective function of SVMs for binary classification is to minimize the following equation: minimize (1/2 * ||w||^2 + C * sum (max (0, 1 - y_i * (w * x_i + b)))) where ||w||^2 is the squared Euclidean norm of the weight vector w, C is the regularization parameter, y_i is the class label of the i-th data point (either 1 or -1), x_i is the i-th data point, and max(0, 1 - y_i * (w * x_i + b)) is the hinge loss function that penalizes misclassification. The objective function seeks to find the optimal values of w and b that minimize the sum of hinge losses while also maximizing the margin between the two classes.

The decision function of SVMs for binary classification: Once we have trained an SVM model using the objective function, we can use it to predict the class label of new data points. The deci-sion function of SVMs for binary classification is given by: f(x) = sign(w * x + b) where x is a new data point, w is the weight vector obtained from training, b is the bias term obtained from training, and sign() is the sign function that returns 1 if the argument is positive, -1 if the argu-ment is negative, and 0 if the argument is zero.

The key mathematical forms that are used in the proposed model for CNNs to detect melanoma are:

Convolution operation: The convolution operation is the core operation in a CNN. It involves sliding a filter over an input image and computing the dot product between the filter and the cor-responding patch of the image. The resulting output is then passed through an activation function to obtain the final output. Mathematically, the convolution operation can be expressed as:

$z[i,j] = (f * x)[i,j] = \sum\sum x[m,n] * f[i-m, j-n]$, where f is the filter, x is the input image, and z is the output feature map. The summation is taken over all valid indices of m and n.

Pooling operation: Pooling is a downsampling operation that reduces the size of the input feature map while preserving important features. The most common type of pooling is max pooling, which involves taking the maximum value within each pooling window. Mathematically, max pooling can be expressed as: y[i,j] = max(z[i*stride:i*stride + pool_size, j * stride:j * stride + pool_size]) , where z is the input feature map, y is the output feature map, pool_size is the size of the pooling window, and stride is the stride length.

Activation function:An activation function is applied element-wise to the output of a convolutional or pooling operation to introduce non-linearity into the model. The most commonly used activation function is the ReLU (Rectified Linear Unit) function, which is defined as: f(x) = max(0, x)

Softmax function: The softmax function is used to convert the output of the last layer of a CNN into a probability distribution over the different classes. Mathematically, the softmax function can be expressed as: $p_i = e^{z_i} / \sum e^{z_j}$, where z is the output of the last layer, p is the resulting probability distribution, and the summation is taken over all possible classes.

These mathematical formulas are combined and applied in a series of convolutional and pooling layers to extract important features from input images, followed by fully connected layers and a softmax activation function to produce the final classification output.

Measures of Performance Evaluation That Are Generally Accepted : The most generic method of comparing algorithms is to compare classification performance without focusing on a class. It does not prefer any one application over another. A new learning challenge will invariably focus on its domain without providing a thorough analysis. As a result, the most common empirical measure of accuracy does not differentiate between the quantity of accurate labels for the various classes.

The following metrics will be considered in the stated research proposal to assess how well the various classification techniques perform:

True positives (TP) = the number of instances where a good outcome was actually anticipated.

False positives (FP) =instances that were projected to be positive but turned out to be negative.

True Negative (TN) =number of cases that were projected to be negative yet turned out to be negative

False negatives (FN) = the number of instances in which the expected outcome is positive.

Accuracy: This is the total number of records that the classifier successfully categorized. The proportion of test set tuples properly categorised by the model is what is known as a classifier's accuracy.

$$Accuarcy = \frac{TF + TP}{TP + FP + FN + TN} \times 100\%$$

We have achieved 87.14% accuracy using SVM and 88.39% accuracy using CNN for the proposed model.

Sensitivity: Refers to the actual positive rate, or the percentage of accurately detected positive tuples[24].

$$Sensitvity = \frac{TP}{TP + FP} \times 100\%$$

For the experimental analysis, SVM and CNN, respectively, obtained sensitivity levels of 84.34% and 85.57%..

Specificity: Indicates the rate at which a test or diagnostic method sets a correct (i.e negative) diagnosis for a patient who is not ill.

$$Specificity = \frac{TN}{TN + FP} \times 100\%$$

For the proposed model, we have achieved 88.19% and 89.275 of specificity using SVM and CNN, respectively.

Conclusion

Malignant Melanoma is the most severe type of skin cancer, spreads very fast, and can target any organ in the human body. Furthermore, distinguishing between malignant and non-malignant melanoma tumours is difficult for medical professionals. In order to accurately diagnose melanoma skin cancer, a hybrid approach combining deep learning techniques using a Convolutional Neural Network (CNN) and Support Vector Machine (SVM) has been taken into consideration. From the experimental analysis, it is seen that the suggested model achieves satisfactory results in terms of Accuracy, Sensitivity, and Specificity on the ISIC dataset. In the future, other classifier techniques as well as some other performance evaluation metrics, such as Balanced Accuracy, Precision, and F-measure, may be incorporated into the proposed model. ❐

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