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Developing an innovative Machine Learning-driven diagnosis system for classifying skin disease

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Abstract

Human skin is a remarkable structure. It regularly experienced several recognized and unidentified diseases. Therefore, the most complex and ambiguous area of research is the diagnosis of skin disorders in humans. The manual diagnosis of skin illnesses by medical professionals is subjective and time-consuming. Because of this, medical professionals and patients both need automated skin disease prediction, which expedites the treatment strategy. As a result, this research effectively suggested an innovative machine-learning strategy to address this issue. Initially, this study gathered an image dataset. After that, we de-noise the images using a bilateral filter (BF). Skin diseases are successfully identified by a novel Static Tree Twin Support Vector Machine (STTSVM) approach that makes use of the retrieved attributes. A number of current techniques are used to validate the suggested method's performance. The recommended technique outperforms existing approaches by effectively as demonstrated by experimental results.

Keywords: Scale Invariant Feature Transform (SIFT), static tree twin Support Vector Machine (STTSVM) approach, bilateral filter (BF), Skin disease.

1. Introduction

The most prominent role of the skin is to protect inner organs very effectively. It acts as a protective shell that shields the astronauts from extreme temperatures, ultraviolet rays, and dangerous substances. Additionally, skin-derived vitamin D carries out various life-critical functions, which include calcium absorption and the well-being of the skeleton [1]. Skin diseases are among the most common and profound illnesses that have impacts on people worldwide. Skin diseases can assume any of the dermatological carcinomas such as squamous cell carcinoma (SCC), intraepithelial carcinoma, melanoma, and basal cell carcinoma (BCC) [2]. A diagnostic system is essential due to the fact that skin problems can be observed in a variety of settings, there are insufficient and unevenly distributed dermatologists with the necessary training and experience, as well as prompt and accurate diagnosis is needed [3]. The skin is the largest organ of the human body and it is about two square meters and 3.6 kg in weight in a person of adult size. Skin with its high thermal resistance and protective function prevents the body from contact with harmful substances, ultra-violet radiation, and extreme temperatures [4]. The field of dermatology involves research on skin cancer, as well as different skin ailments and pathologies. Anatomical and physical skin properties that shape diagnosis are the first factors considered in this field of study. This is the key factor in using imaging techniques such as reflectance confocal microscopy, dermatoscopy, and ultrasound, the application of which encompasses skin disease identification [5]. Over the past ten years, there has been an increase in the emergence of skin cancer. Sunlight's ultraviolet rays induce long-term skin damage and the growth of cancer cells. These kinds of circumstances typically include unstated dangers that increase the chance of skin cancer as well as psychological discomfort and an imbalance of faith in individuals [6]. The primary goal of this research is to establish a machine learning-based skin disease detection system that will increase the accuracy of diagnosis.

The remaining research falls under the following categories: section 2 discusses related works. We provide our suggested methodology in section 3. In section 4, our method's outcomes will be evaluated. Based on the findings from the study, section 5 presents a conclusion.

2. Related works

Research [7] developed diagnostic instruments based on artificial intelligence to detect skin problems early. The recommended early diagnosis of skin illness was carried out using the ANN and FFNN algorithms. Study [8] developed a Multi-Class Multi-Level (MCML) diagnosis approach that improves illness categorization accuracy. MCML was inspired by the "divide and conquer" technique. Study [9] constructed a deep learning system (DLS) for providing an accurate diagnosis of skin diseases in clinical instances. DLS can improve the capacity of general practitioners without extra specialist training to correctly identify skin disorders. Paper [10] suggested an approach for detecting skin cancer by image processing that was a more accurate diagnosis procedure than the conventional biopsy technique.

Utilizing machine learning classification, the study [11] offered an automated image-based approach to diagnose and classify skin issues. The image data were to be analyzed, processed, and relegated using computational methods to take into account the many attributes of the processed images. Research [12] presented a computer vision approach for the automated identification of four specific groups of skin disorders. To evaluate the system's performance, images of skin conditions such as keratosis, acne, eczema herpeticum, and urticaria were taken from the DermNet collection. Research [13] presented a potential skin disease detection model utilizing MobileNet V2 and the LSTM approach. The outcome was superior when compared to other methods. A deep CNN model with a triple loss function was developed in the study [14] to enhance the classification of skin diseases. They optimize all layers of InceptionResNetV2 and ResNet152 to tackle the issue of face skin disease images. A computer-aided diagnosis (CAD) model for more prevalent skin illnesses was developed in the study [15] and it can be very beneficial for general practitioners in particular.

The suggested CAD was based on an enormous quantity of clinical images obtained from people who attended a single dermatological department. Research [16] suggested an automated deep learning-based technique for diagnosing skin illnesses utilizing Long Short Term Memory (LSTM) and MobileNet V2. With the help of low-power computing devices, MobileNet V2 architecture demonstrated that it could operate more accurately and efficiently. Deep learning was used in the study [17] to develop a system for categorizing skin cancer lesions with brown–black pigmentation. The accuracy of the method was higher than dermatologists'. It was accurate in detecting malignant melanoma as well as basal cell cancer. The study [18] suggested a CNN framework for identifying skin disorders. It was constructed using pre-trained weights from ImageNet and Google's EfficientNet-b4.

3. Methods

In this study, we gathered Image datasets. Images are de-noised using a bilateral filter and features are extracted using the Scale Invariant Feature Transform (SIFT). Next, a novel static tree twin support vector machine (STTSVM) is employed to forecast skin diseases. Figure 1 shows the process of skin disease prediction.

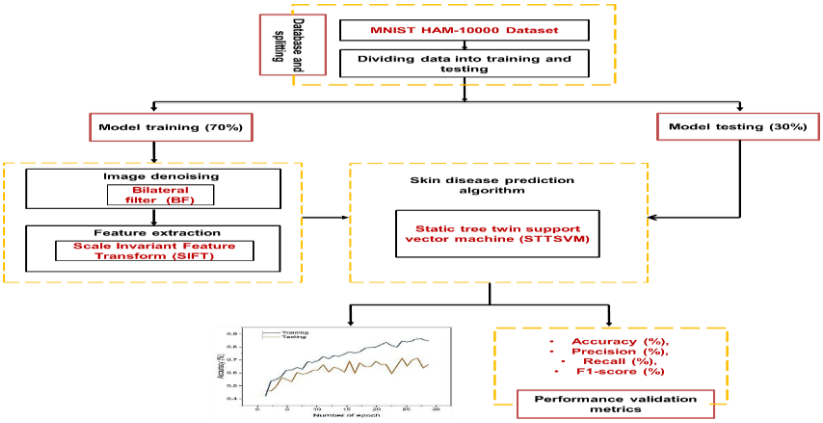

Figure 1. Skin disease prediction process.

3.1 Dataset

We utilized the skin cancer MNIST HAM-10000 dataset, which is accessible on Kaggle. It has 10030 images of skin types broken down into seven categories.

3.2 Data preprocessing

In the process of data preprocessing, this study uses bilateral filtering for image de-noising and SIFT for feature extraction.

3.2.1 Image de-noising:

Bilateral filtering has combined spatial and range filtering to ensure geometric as well as photometric locality. When we consider a 2D grayscale image with a scan-line w, the one-dimensional bilateral filtering value of w at pixel j is,

$$zj = \sum_{l=0}^{j} Q_{l,j} T_{l,j} . w_l, \quad (1)$$

Here $T_{l,j} = (T_{l,j})$ represents the spatial filtering kernel and $Q_{l,j} = Q(w_l, w_j)$ is the length of the filter kernel for determining the spatial similarity of pixels k and i. It should be noted that Eq. (1) does not include the normalizing factor $\sum_{l=0}^{j} Q_{l,j} T_{l,j}$ since it can be calculated directly from the equation by assuming w_l to be all ones.

3.2.2 Feature extraction:

The SIFT approach transforms the picture into a set of local feature vectors. It is necessary for these feature vectors to be independent of the scaling, rotation, and translation of the image. In the first stage, the feature sites are found using the local extrema of Difference of Gaussians (DOG pyramid), which is provided by Eq. (4). The DOG pyramid Eq. (3) is implemented by iteratively convolving the input picture using a Gaussian kernel. This method is repeated as long as down-sampling is feasible. An octave is a collection of identically sized photographs. The 3D function $K(W, Z, \sigma)$ represents the Gaussian pyramid, which is formed by combining all octaves according to Eq. (2).

$$K(W, Z, \sigma) = H(W, Z, \sigma) * J(W, Z) \quad (2)$$

$$H(W, Z, \sigma) = \frac{1}{2\pi\sigma^2} f^{-(w^2 - z^2)}/2 \quad (3)$$

$$C(W, Z, \sigma) = \big(H(W, Z, \sigma) - H(W, Z, \sigma) * J(W, Z)\big) = H(W, Z, L\sigma) - K(W, Z, \sigma) \quad (4)$$

Every pixel in the DOG function is compared to its twenty-six scale-space neighbors to find its local extrema (maxima/minima). We exclude the beginning and ending pictures in each octave from the search for extrema since they don't have a scale above and below. Numerous key-point candidates are generated by the finding of scale-space extrema, some of which are unstable and unhelpful. The next stage is to do a thorough fit to the neighboring data to ascertain the precise location, scaling, and proportioning of the principal curvatures. When calculating the location of each potential key point by the interpolation of surrounding data, this information is helpful for sites with low contrast. The interpolation is carried out utilizing a quadratic Taylor expression of the Difference-of-Gaussian scale-space operation, $C(w, z, \sigma)$ with the candidate keypoint serving as the origin, as shown in Eq (5).

$$C(w) = C + \frac{\delta C^S}{\delta w} W + \frac{1}{2} w^S \frac{\delta^2 C}{\delta w^2} W \quad (5)$$

D and its derived values are assessed at the candidate's key point and the offset beyond this point is represented by the expression $w = (w, z, \sigma)$.

Next, each key point is allocated one or more orientations depending on its nearby image gradient directions. Invariance to image rotation can be achieved since the key point specification can be expressed in relation to this orientation. This is seen in the following Eq. (6) and (7).

$$n(w,z) = \sqrt{(K(w+1,z) - K(w-1,z))^2 + (K(w,z+1) - K(w,z-1))} \quad (6)$$

$$\theta(w,z) + \tan^{-1}\left(\frac{K(w,z+1) - K(w,z-1)}{K(w+1,z) - K(w-1,z)}\right) \quad (7)$$

To confirm that all calculations are scale-invariant, the Gaussian-smoothed image $K(w, z, \sigma)$ at the keypoint scaling σ is obtained first. Pixel differences are used to precompute the gradient orientation,$\sigma(w, z)$, and magnitude, $n(w, z)$ for an image sample $K(w, z)$ at scale σ.

3.3 Skin disease prediction

3.3.1 Static tree:

In general terms, a "static tree" is a tree structure in which, once the tree is built, neither the nodes nor the branches alter. In machine learning, a decision tree in every internal node denotes a characteristic or property and every branch denoting a decision rule based on that characteristic is also pointed as a static tree. Leaf nodes represent the choice or outcome. Decision trees are a type of decision assistance tool that employs a framework of decisions and their outcomes. Consequences include resource and utility expenditures, as well as random event outcomes. It is shown as a flow chart-like structure, with each node denoting an attribute, the branch pointing to the test result, and the leaf node standing in for the class title. The classification guidelines apply to leaf trails as well as roofs. Under the category of supervised learning models, tree-based learning gives predictive models stability, excellent accuracy, and interpretability. They also perform effectively when mapping non-linear connections. The phrases leaf node, decisions node, pruning, subtree, root node, parent and child nodes are frequently used in relation to decision trees. Typically, decision trees utilize a target variable that is categorical and they can be used to either:

- Determine the likelihood that a given sample falls into each of the established categories.
- To assign the sample to the class that is most likely to contain it.

There are two varieties of decision trees: a continuous-variable decision tree and a decision tree with categorical variables. The best characteristic is positioned at the root, or beginning, of the tree, according to the algorithm. Subsets of the provided training set are then created depending on the characteristics that were retrieved. Until the leaf nodes are discovered in every branch of the supplied tree, these two processes are done again.

3.3.2 Twin support vector machine:

The TSVM method is employed after all data sets have been separated into two groups based on the related l_q values by including two irregular hyperplanes in each collection of data. For all of the two clusters, there are two possible matrices. $X_1 \in R^{m\times k}$ $X_2 \in R^{n\times k}$ In each cluster, m, and n denote the number of data points, while l is the overall amount of variables included in each group of data points. A list of the irregular hyperplanes corresponding to each matrix is provided below:

$$w^t x_1 + b_1 = 0 \; and \; w^t x_2 + b_2 = 0 \tag{8}$$

Where x_1 and x_2 are standard directions to the hyper-planes b_1 and b_2 are the relevant biased terms. The hyper-planes can be computed by solving the set of functions given below:

$$\min(w_1, a_1, \xi)\frac{1}{2}\|X_1 w_1 + e_1 b_1\|^2 + c_1 e_2^T \xi \tag{9}$$

$$subjectedto(X_2 w_1 + e_2 b_1) + \xi \geq e_2, \xi \geq 0 \tag{10}$$

$$\min(w_2, b_2, \xi)\frac{1}{2}\|X_2 w_2 + e_2 b_2\|^2 + c_2 e_1^T \xi \tag{11}$$

$$subjectedto(X_1 w_2 + e_1 b_2) + \eta \geq e_1, \eta \geq 0 \tag{12}$$

The numbers, slack variables, and penalty variables are represented by the variables c_1 and c_2. Moreover, e_1 and e_2 are two vectors with the right dimensions as their values are both ones. By decreasing the complexity of the problem, Lagrange multipliers facilitate problem-solving. The following is the stated function for decision-making and each data sample will be grouped according to the hyperplane's perpendicular distance:

$$class\ i = \min|x^T w_i + b_i| \; for\ i = 1{,}2 \tag{13}$$

3.3.3 Proposed method:

The Static Tree Twin Support Vector Machine (STTSVM) is a skin disease prediction tool that combines medical diagnostics with machine learning to increase the precision of skin disease diagnosis. Static tree structure used for STTSVM helps in the organization as well as optimization of feature space for classification, which is usually evaluated by the typical SVMs. To reduce the misclassification and allow the trained model to be interpretable, SVMs and trees with the ability to adapt well to noisy environments are combined and this is done by STTSVM. Its twin structure SVM of sequential classifier with entire class margin supports the problem of maximizing the class margin and minimizing the error in classification at the same time. Accurate diagnosis and customized treatment plans can be achieved through the STTSVM application for skin disease prediction in clinical practice. Through funding early detection and optimal patient treatment STTSVM has the potential to present a full paradigm shift in the future of dermatology. That can be achieved by handling all kinds of data and delivering results that are

easy to understand. The STTSVM can serve as beneficial for addressing and diagnosing skin conditions earlier

4. Result

In order to evaluate the efficacy of the suggested methodology, it is necessary to employ an array of quantitative metrics, including F1-score (%), recall (%), precision (%), and accuracy (%). The suggested method's efficacy is assessed against other existing techniques, including Convolutional Neural Network (CNN) [20], Gradient Boosting Tree (GBT) [20], K-Nearest Neighbor (K-NN) [19], and Support Vector Machine (SVM) [19]. Table 1 illustrates the experimental setup.

Table 1: Component and its specification

Component	Specification
Operating System	Windows 10
Processor	Core i7
RAM	8 gigabytes DDRAM
Graphics Card	GeForce MX150 NVIDIA
Storage	500-gigabyte solid-state drive (SSD)
Integrated Development Environment (IDE)	Anaconda

Accuracy, Loss:

Accuracy: Prediction accuracy is the degree of agreement between the model's estimated values and the real values. It assesses the model's accuracy; more accurate forecasts are more reliable and credible.

Loss: The error in the model is shown when the loss is contrasted to the anticipated values, which quantify the difference between expected and actual outcomes. To provide accurate forecasts, it minimizes loss and specifies the variation using a preset measure. Figure 2 shows the results of accuracy and loss.

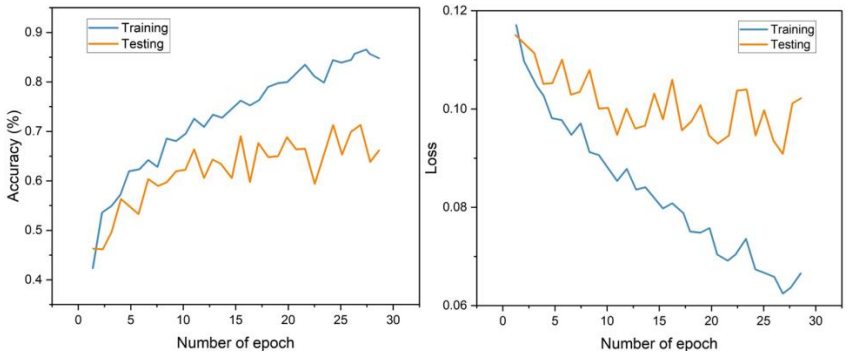

Figure 2. Accuracy and Loss results.

The percentage of accurately diagnosed skin disorders among all patients is known as accuracy. It is computed as the proportion of instances that are properly categorized to all cases. The corresponding accuracy rates reached by SVM, K-NN, GBT, and CNN were 90.7%, 67.1%, 73.44%, and 88.83%. The accuracy percentage that our suggested method (STTSVM) achieved was 95.3%. The outcomes demonstrate that our recommended strategy outperforms the existing strategy. Figure 3 shows the result of accuracy.

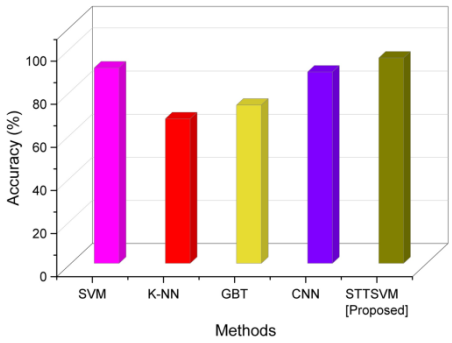

Figure 3. Result of Accuracy

The ability of the model among all cases that have been classified as positive to consistently identify positive occurrences is sometimes referred to as true positives. The proportion of genuine positives to the sum of false positives and true positives is used to calculate it. SVM, K-NN, GBT, and CNN achieved precision values of 91%, 72.8%, 68%, and 91.07%. Our suggested method (STTSVM) achieved a precision score of 94.2%. The outcomes demonstrate that our recommended strategy outperforms the existing strategy. Figure 4 shows the result of precision.

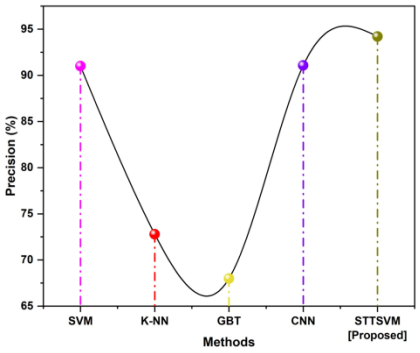

Figure 4. Precision results

The recall with, which the model distinguished genuine positive instances from positive cases. The difference in the percentage of true positives to the aggregate of false negatives and true positives is employed for determining it. The recall rates for SVM, K-NN, GBT, and CNN were, respectively, 90.8%, 67.1%, 73%, and 87.68%. With our suggested method (STTSVM), a recall value of 93.7% was obtained. Our recommended strategy outperforms the existing approach, according to the results. Figure 5 shows the result of the recall.

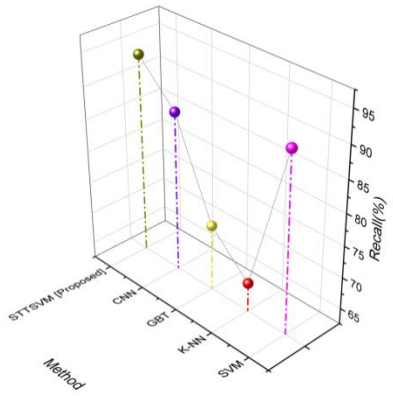

Figure 5. Result of Recall

A balance between the two metrics is provided by the harmonic mean of recall and accuracy. It is calculated as follows: divide both the recall and precision ratio by the sum of the two. Recall rates were 90.8%, 68.4%, 70%, and 89.32% for SVM, K-NN, GBT, and CNN, in that order. With our suggested method (STTSVM), a recall value of 94.3% was obtained. Our recommended strategy outperforms the existing one, according to the results. Figure 6 shows the F1-score results.

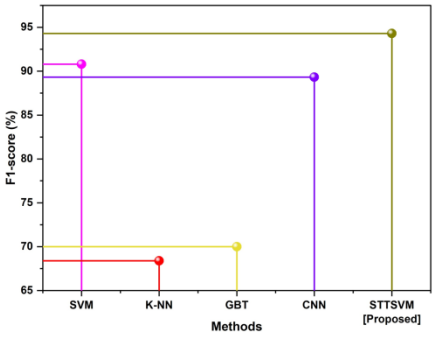

Figure 6. Result of F1-score

5. Conclusion

The identification and classification of skin diseases such as dermatitis, eczema, and melanoma is accomplished by utilizing a skin disease detection system. It helps with early diagnosis and therapy by assessing aspects including texture, color, and morphology, improving healthcare efficacy and accessibility. This study introduces an innovative approach employing machine learning techniques for detecting skin disease. Initially, we gather the dataset and de-noising with a bilateral filter and feature extraction using SIFT, followed by classification with STTSVM, this method offers a promising solution. Experimental results demonstrate its superiority over existing diagnostic procedures, highlighting its potential to expedite diagnosis and treatment planning for skin diseases. The proposed STTSVM method achieves higher rates of accuracy (95.3%), f1-score (94.3%), recall (93.7%), and precision (94.2%). The scalability and applicability of STTSVM for identifying skin disorders to varied datasets can be limited by its static nature. To increase its application and diagnosis accuracy, future studies might concentrate on scalability improvements and dynamic adjustments.

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