

# AI-Driven Skin Disease Classification Using Deep LSTM Networks Optimized by Tunicate Swarm Algorithm

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## ABSTRACT

This study presents an innovative methodology for skin disease classification by integrating Deep Long Short-Term Memory (Deep LSTM) networks with the Tunicate Swarm Algorithm (TSA). The proposed hybrid model significantly enhances the accuracy of dermatological diagnosis using medical images. Deep LSTM networks are employed to effectively capture complex spatial and temporal patterns inherent in dermatological data, while TSA is utilized to fine-tune feature extraction and optimize model parameters, leading to improved performance and computational efficiency. This fusion of deep learning and swarm intelligence introduces a powerful framework for intelligent, automated skin disease detection in clinical settings. The experimental results demonstrate that the synergistic combination of Deep LSTM and TSA outperforms traditional classification approaches, underscoring the potential of AI-driven models in advancing precision healthcare.

**Keywords:** Deep LSTM, Tunicate Swarm Algorithm, Skin Disease Classification, Medical Image Analysis, Swarm Intelligence, AI in Healthcare.

## INTRODUCTION

In the realm of global fitness, skin disorders, which include conditions such as melanoma, psoriasis, and eczema, constitute a significant undertaking. In order to improve patient outcomes, it is essential to provide an accurate and timely prognosis. However, conventional diagnostic procedures usually rely on manual inspection, which can be time-consuming and prone to errors. Synthetic intelligence (AI) has emerged as a potent tool in automating prognosis and improving clinical selection-making. This is due to the fact that an expanding variety of scientific disciplines are turning to technology for answers. Deep Learning models, in particular Long Short-Term Memory (LSTM) networks, have demonstrated remarkable potential in pattern recognition tasks inside complicated datasets such as scientific photos[1-3]. These models are among the most promising artificial intelligence techniques. Deep Long Short-Term Memory (Deep LSTM) networks, which are a specialized form of recurrent neural network (RNN), operate exceptionally well when it comes to capturing both spatial and temporal patterns. When it comes to sequential statistics processing, such as video or time-collection assessment, these networks are unexpectedly powerful because they are built to deal with the vanishing gradient problem that is typical of regular RNNs. In the area of dermatological image analysis, Deep LSTMs have the ability to analyze pixel-level data across multiple images while maintaining context and collection. This is an essential capability for identifying and categorizing skin disorders that exhibit subtle or evolving characteristics. Figure 1 is an illustration of how artificial intelligence techniques can be applied to improve the accuracy and efficiency of skin disease diagnosis through the use of automated picture analysis and classification[4-6].

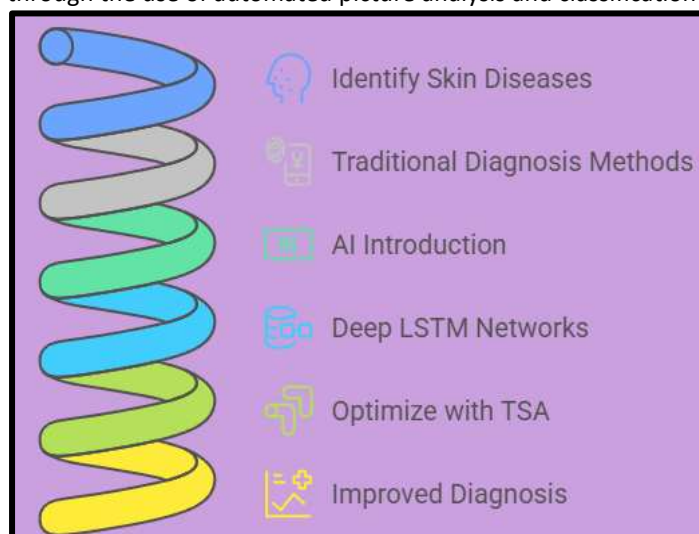


Figure :1 AI – Enhanced Skin Disease Diagnosis

In spite of the fact that LSTM networks have successfully showed their potential, their performance can be improved by the implementation of optimization algorithms. The Tunicate Swarm Algorithm (TSA), which was inspired by the behavior of tunicate swarms in nature, has emerged as a distinct optimization strategy for improving system learning methods. This is because TSA was inspired by the behavior of tunicate swarms in nature. The Transportation Security Administration (TSA), much like other swarm intelligence algorithms, is based on decentralized decision-making. This means that character dealers, which represent capacity solutions, engage with one another in the environment in order to get closer to a gold standard response. TSA's power to efficaciously explore complicated search spaces makes it an ideal device for best-tuning Deep LSTM networks in pores and skin disease kind responsibilities[7-8].

An technique to clinical photo evaluation that is synergistic is presented by the combination of Deep Long Short-Term Memory (LSTM) networks and the Tunicate Swarm Algorithm. Through the process of refining its feature extraction and parameter selection approach, the TSA's optimization capabilities serves as a complementary component to the Deep LSTM version. Consequently, this leads to a category model for skin diseases that is more accurate, environmentally friendly, and authoritative. In addition, the capability of optimizing hyperparameters, which includes accumulating knowledge about quotes, layer configurations, and activation features, enhances the capability of the version to detect skin diseases at an early stage, which is vital for the achievement of successful treatment outcomes[9].

In the field of medical imaging, feature extraction is a vital component that plays a crucial role in ensuring that relevant information is extracted from photographs for further analysis. Deep LSTM networks, when paired with TSA, make it possible to extract more accurate characteristics by understanding intricate information from dermatological images that may not be easily discernible to human observers. This is accomplished through the process of learning. It is essential to carry out this operation in order to differentiate between various types of skin disorders, which frequently share similar visual characteristics. A more nuanced understanding of the underlying patterns in skin sickness pictures is made possible by the combination of deep learning and swarm intelligence, which also contributes to a greater level of classification accuracy[10].

The ability of this integrated method to assist in the development of intelligent diagnosis structures in the medical field is yet another significant advantage. Through the process of automating the detection and classification of skin diseases, this method has the potential to significantly reduce the workload of medical professionals, hence enabling them to make treatment decisions more quickly. When applied in a medical setting, the utilization of AI-enhanced systems for the classification of skin diseases can result in a more expedient diagnosis and treatment, hence enhancing the outcomes for patients and reducing the costs associated with healthcare. In addition, the version has the potential to conform to new information methods, which means that it may develop in tandem with developments in scientific imaging and dermatological research[11].

In the field of healthcare, artificial intelligence (AI) is becoming increasingly important, and Deep Learning models are at the forefront of this transformation. In spite of this, there are still a great number of challenging circumstances that need to be addressed in order to guarantee the robustness and dependability of those models, particularly in the context of complex tasks such as medical picture class. By merging Deep Long Short-Term Memory (LSTM) with the Tunicate Swarm Algorithm, this study intends to address a number of these challenging scenarios, hence providing a solution that is more reliable and scalable for the identification of skin diseases. By incorporating swarm intelligence into the deep learning pipeline, it is possible to alleviate a lot of the limitations that are associated with standalone models. This helps to ensure that the system is both powerful and adaptable.

The findings of this study have the potential to significantly improve the capabilities of AI-driven skin disease classification systems. Through the utilization of Deep Long Short-Term Memory (LSTM) networks and the Tunicate Swarm Algorithm, this technique provides dermatologists and other medical professionals with a powerful instrument that enables them to diagnose skin diseases in a more accurate and efficient manner. As artificial intelligence continues to advance, it is projected that the incorporation of these superior techniques will play a significant role in determining the future of scientific analysis. This will allow for the provision of capacity solutions to long-term challenging circumstances in the healthcare industry[12].

A significant amount of interest has been shown in the application of artificial intelligence (AI) in the analysis of skin disorders, particularly the utilization of deep learning models to enhance diagnosis accuracy. The dermatological photo category had been assigned to the traditional device mastery procedures, which included the use of random forests and assist vector machines (SVM). Despite the fact that these procedures are effective, they frequently come into conflict with the high-dimensionality and complexity characteristic of clinical images. Convolutional neural networks (CNNs) and recurrent neural networks (RNNs), in particular, have developed as more effective equipment due to their capacity to automatically analyze capabilities from raw picture recordings. Deep learning of fashions has also emerged as a more effective method. It has been demonstrated that these

models have shown promising results in identifying skin diseases, which demonstrates the power of artificial intelligence to reconstruct clinical diagnostics[13].

It has been demonstrated that CNNs have a high level of accuracy in recognizing skin conditions such as cancer, basal cell carcinoma, and other skin problems. CNNs have witnessed widespread use for the diagnosis of skin diseases. The classification of skin cancer was accomplished by Esteva et al. (2017) by the use of CNNs, which achieved diagnostic overall performance that was comparable to that of expert dermatologists. The effectiveness of CNNs can be attributed to their ability to extract hierarchical functions from picture data. This ability makes CNNs an excellent choice for identifying evident styles in dermatological photos. CNNs, on the other hand, are limited in terms of their ability to capture temporal or sequential associations in photographs, which is critical for diseases that progress over time. In the field of dermatological photo evaluation, this issue has led to the investigation of recurrent neural networks, particularly Long Short-Term Memory (LSTM) networks[14-15].

## Methodology

The proposed system performs automated skin disease classification by combining image preprocessing, Tunicate Swarm Algorithm (TSA)-based lesion segmentation, deep spatial feature extraction, and Deep Long Short-Term Memory (Deep LSTM) classification. The methodology is designed to address the major difficulties encountered in dermatological image analysis, including illumination variation, low lesion-to-background contrast, irregular lesion boundaries, visual similarity among disease categories, and class imbalance. Instead of treating segmentation, feature extraction, and classification as unrelated stages, the proposed framework integrates them into a unified pipeline in which the output of each stage is optimized for the next. The principal objective is to isolate the clinically relevant lesion region, represent it using discriminative deep features, preserve contextual relationships among local image regions, and finally predict the disease class with a reliable confidence score.

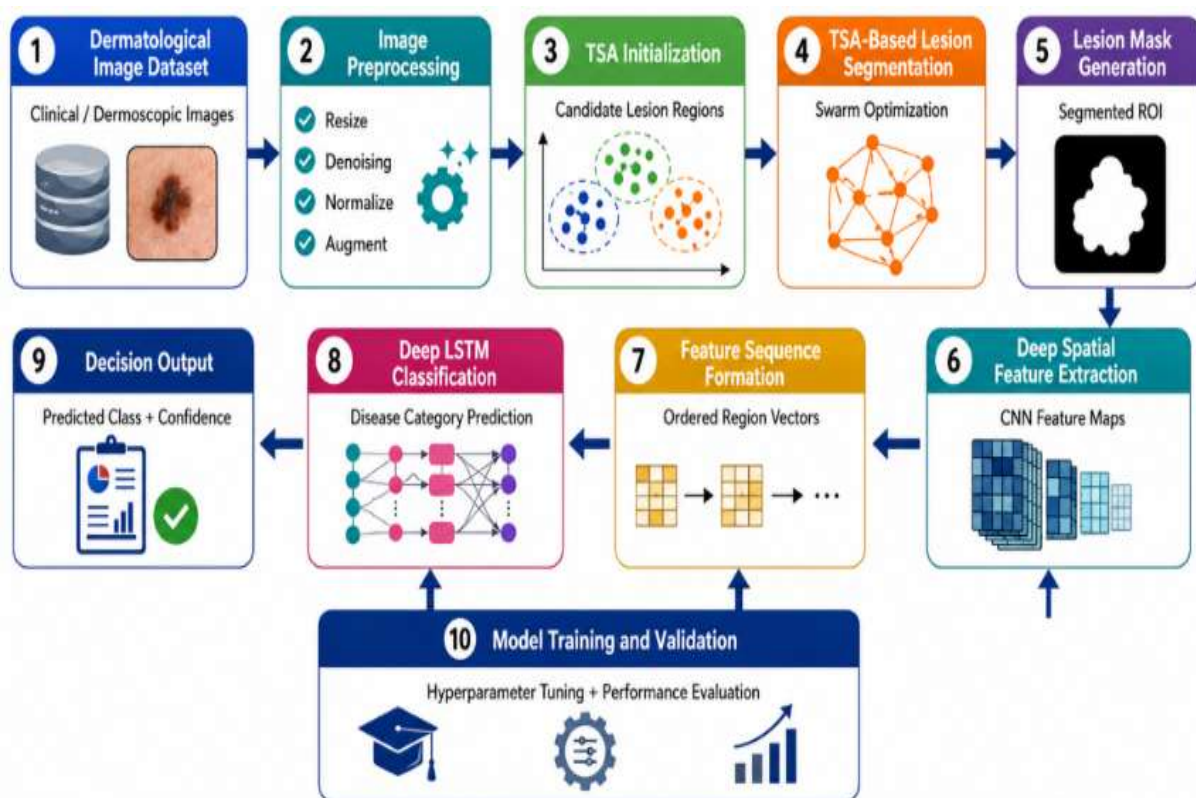


Figure 2. Overall workflow of the proposed TSA-optimized Deep LSTM framework.

## Image Preparation and Lesion Localization

The input to the framework is a set of clinical or dermoscopic skin images associated with known diagnostic labels. Before training, the dataset is inspected to remove corrupted, duplicate, or incorrectly labelled samples. Since images may be acquired using different cameras, magnification levels, backgrounds, and illumination conditions, all samples are converted into a uniform representation. Each image is resized to a fixed spatial resolution of  $224 \times 224$  pixels. Resizing provides a consistent tensor shape for batch processing and controls the computational cost of the deep network. RGB channels are retained because chromatic information such as erythema, pigmentation, scaling, and lesion-border colour variation is diagnostically important.

Intensity normalization is then performed so that large variations in illumination do not dominate the learning process. For an image intensity value  $I(x,y)$ , normalized intensity is obtained as shown in Equation (1).

$$I_{\text{norm}}(x,y) = \frac{I(x,y) - \mu}{\sigma + \epsilon} \quad (1)$$

where  $\mu$  and  $\sigma$  denote the mean and standard deviation of the image or training set, and  $\epsilon$  is a small constant included to avoid division by zero. In an implementation using pretrained convolutional networks, channel-wise normalization may also be performed using the statistics expected by the selected backbone. Contrast-limited adaptive histogram equalization can be applied when the lesion boundary is weak, while median or Gaussian filtering can be used to suppress acquisition noise without destroying significant edge information.

To improve robustness, online data augmentation is applied only to the training partition. Typical transformations include small-angle rotation, horizontal and vertical reflection where clinically acceptable, random zoom, translation, mild shear, brightness variation, and limited colour jitter. Augmentation generates realistic variations of the same lesion and reduces overfitting. It is particularly useful when some disease categories contain fewer images than others. The validation and test partitions are not augmented, because they must represent unseen data and provide an unbiased estimate of generalization.

After preprocessing, the Tunicate Swarm Algorithm is used to localize the diseased region. TSA is a population-based metaheuristic inspired by the jet-propulsion movement and swarm behaviour of tunicates. Each tunicate represents a candidate segmentation solution, such as a threshold set, contour parameter set, or binary lesion mask. The fitness function evaluates how well a candidate separates the lesion from healthy skin. In this work, the fitness function combines regional entropy, edge strength, compactness, and intra-region homogeneity. A general fitness expression is given by Equation (2):

$$F(X) = \alpha E(X) + \beta G(X) + \eta C(X) - \gamma V(X) \quad (2)$$

where  $E$  denotes entropy,  $G$  is the mean gradient magnitude along the boundary,  $C$  represents contour compactness or region coherence,  $V$  is intra-segment variance, and  $\alpha$ ,  $\beta$ ,  $\eta$ , and  $\gamma$  are weighting coefficients. A good lesion mask contains rich diagnostic information, strong and continuous borders, and relatively homogeneous internal pixels; therefore, the first three terms are maximized while intra-region variance is minimized.

During optimization, the location of each tunicate is updated with respect to the best solution identified so far while maintaining stochastic exploration. A simplified update mechanism can be expressed as:

$$X_i(t+1) = X_i(t) + r_1 [X_{\text{best}}(t) - X_i(t)] + A(t)\sin(Bt) \quad (3)$$

where  $X_i(t)$  is the position of the  $i$ th tunicate at iteration  $t$ ,  $X_{\text{best}}(t)$  is the current best solution,  $r_1$  is a random number in  $[0,1]$ , and  $A(t)$  and  $B$  control the magnitude and oscillation of the exploratory movement. At the beginning of the search, larger movements enable broad exploration; as the iterations progress, the movement is reduced to refine the lesion boundary. The process terminates when the maximum iteration count is reached or when improvement in fitness becomes negligible.

The final TSA mask is post-processed using morphological opening and closing. Opening removes isolated false-positive pixels, whereas closing fills small holes inside the lesion. The largest connected component can be retained when the dataset contains one dominant lesion per image. The resulting binary mask  $M(x,y)$  is used to suppress irrelevant background pixels:

$$I_{\text{ROI}}(x,y,c) = I_{\text{norm}}(x,y,c) \times M(x,y) \quad (4)$$

The lesion-focused image  $I_{\text{ROI}}$  preserves the colour and texture information of the affected area while reducing interference from healthy skin, rulers, hair, shadows, and surrounding background.

## Deep Feature Representation and LSTM Classification

The segmented lesion image is supplied to a deep convolutional feature extractor. A pretrained backbone such as VGG16, ResNet50, EfficientNet, or a compact custom CNN can be used. Transfer learning is advantageous because low-level filters learned from large image datasets already represent edges, colour transitions, textures, and shapes. Early convolutional layers may be frozen during initial training, while deeper layers are fine-tuned using dermatological images. This approach reduces the amount of task-specific data required and improves convergence stability.

For an input lesion image, the convolutional backbone generates a feature tensor  $F \in \mathbb{R}^{(H \times W \times D)}$ , where  $H$  and  $W$  are the spatial dimensions and  $D$  is the channel depth. Instead of applying only global average pooling, the spatial tensor is divided into an ordered sequence of regional feature vectors. Each spatial location or patch becomes one time step:

$$S = [f_1, f_2, \dots, f_T], f_t \in \mathbb{R}^D, T = H \times W \quad (5)$$

This conversion enables the LSTM to learn dependencies among neighbouring lesion regions. Although the input is a static image, the ordered patches form a pseudo-sequence. Such a representation is useful because

diagnostic structures such as border irregularity, colour transitions, texture patterns, and asymmetry are distributed across different parts of the lesion.

The proposed classifier contains stacked LSTM layers. At time step  $t$ , the input gate  $i_t$ , forget gate  $f_t$ , output gate  $o_t$ , candidate cell state  $g_t$ , cell state  $c_t$ , and hidden state  $h_t$  are calculated as follows:

$$i_t = \sigma(W_i x_t + U_i h_{t-1} + b_i) \quad (6)$$

$$f_t = \sigma(W_f x_t + U_f h_{t-1} + b_f) \quad (7)$$

$$o_t = \sigma(W_o x_t + U_o h_{t-1} + b_o) \quad (8)$$

$$g_t = \tanh(W_g x_t + U_g h_{t-1} + b_g) \quad (9)$$

$$c_t = f_t \odot c_{t-1} + i_t \odot g_t \quad (10)$$

$$h_t = o_t \odot \tanh(c_t) \quad (11)$$

where  $\sigma$  is the sigmoid function,  $\odot$  denotes element-wise multiplication,  $W$  and  $U$  are trainable matrices, and  $b$  represents bias. The memory cell allows useful contextual information to remain available over many sequence steps while irrelevant information is discarded through the forget gate.

The final hidden representation is passed to one or more fully connected layers. Dropout is inserted between dense or LSTM layers to reduce co-adaptation. Batch normalization may be applied to convolutional features before sequence formation. The output layer contains one neuron for each disease class and uses softmax activation:

$$P(y = k | I) = \frac{\exp(z_k)}{\sum_{j=1}^C \exp(z_j)} \quad (12)$$

where  $z_k$  is the logit for class  $k$  and  $C$  is the total number of classes. The predicted class is the class having the maximum posterior probability. In addition to the class label, the highest softmax probability is reported as the model confidence.

The network is trained using categorical cross-entropy. For  $N$  training samples and  $C$  classes, the loss is:

$$L_{CE} = -\frac{1}{N} \sum_{n=1}^N \sum_{k=1}^C y_{n,k} \log(p_{n,k}) \quad (13)$$

where  $y_{n,k}$  is the one-hot target and  $p_{n,k}$  is the predicted probability. When the dataset is imbalanced, a class-weighted form of cross-entropy or focal loss can be used so that rare diseases contribute sufficiently to parameter updates. L2 regularization may also be added to limit excessive weight magnitude.

## TSA-Based Parameter Optimization, Training, and Decision Generation

In addition to lesion segmentation, TSA is used to optimize selected model hyperparameters. A candidate tunicate may encode the learning rate, number of LSTM units, number of stacked LSTM layers, dropout rate, batch size, dense-layer width, and the number of trainable convolutional blocks. Each candidate configuration is trained for a limited number of epochs on the training partition and evaluated on the validation partition. Its fitness is defined using validation loss and, when needed, a complexity penalty:

$$J(\theta) = \lambda_1 L_{val}(\theta) + \lambda_2 [1 - A_{val}(\theta)] + \lambda_3 C_{model}(\theta) \quad (14)$$

where  $\theta$  denotes the hyperparameter vector,  $L_{val}$  is validation loss,  $A_{val}$  is validation accuracy or macro F1-score,  $C_{model}$  represents model complexity or inference time, and  $\lambda_1$ ,  $\lambda_2$ , and  $\lambda_3$  control their relative importance. The candidate with minimum  $J$  is selected as the optimal architecture. This prevents optimization from selecting an unnecessarily large network solely because it produces a marginal accuracy increase.

The dataset is divided into training, validation, and testing subsets using stratified sampling so that every disease category is proportionally represented. Patient-level separation should be maintained whenever multiple images from the same patient are available; otherwise, similar samples from one patient may appear in both training and testing and produce an overly optimistic result. The selected model is trained using an optimizer such as Adam. Early stopping monitors validation loss and restores the best weights when no improvement is observed for a predefined number of epochs. A learning-rate scheduler reduces the learning rate when convergence slows. During each training iteration, an image batch is normalized and augmented, lesions are isolated using the optimized TSA segmentation parameters, and the lesion images are converted into deep feature sequences. The LSTM predicts class probabilities, cross-entropy loss is computed, and gradients are propagated through the dense, recurrent, and trainable convolutional layers. The process continues until the stopping criterion is reached. After training, all parameters are fixed and the independent test set is processed without augmentation. Performance is assessed using accuracy, sensitivity, specificity, precision, recall, F1-score, and the confusion matrix. Because accuracy alone may hide poor recognition of minority classes, macro-averaged precision, recall, and F1-score should also be reported. For binary interpretation, the measures are calculated from true positives, true negatives, false positives, and false negatives:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (15)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (16)$$

$$\text{Recall} = \frac{TP}{TP + FN} \quad (17)$$

$$\text{F1-score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (18)$$

For multiclass classification, the metrics are calculated for each class and then macro- or weighted-averaged. Receiver operating characteristic and area-under-the-curve values can be reported using one-versus-rest evaluation.

For a new image, the same preprocessing and segmentation operations used during training are applied. The lesion is converted into a sequence of deep features and passed through the trained LSTM. The system produces the most probable disease class, its confidence score, and optionally the segmented lesion mask for visual verification. In a clinical decision-support setting, low-confidence predictions can be flagged for expert review rather than being treated as definitive diagnoses. This confidence-aware mechanism improves safety and enables the system to support, rather than replace, dermatologists.

The integrated methodology therefore uses TSA at two complementary levels. At the image level, it improves lesion localization by searching for a segmentation that maximizes region quality and boundary information. At the model level, it searches for hyperparameters that produce strong validation performance with acceptable computational complexity. The Deep LSTM then models relationships among spatial lesion regions and converts the optimized representation into a disease prediction. This combined strategy is expected to provide more stable segmentation, more discriminative features, and improved classification performance compared with standalone clustering, conventional machine-learning classifiers, or a non-optimized deep network.

**Table 1: Proposed Operation**

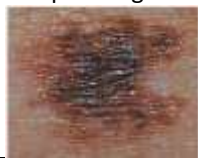
| Step | Operation                                                                         |
|------|-----------------------------------------------------------------------------------|
| 1    | Acquire labelled clinical or dermoscopic skin images and remove unusable samples. |
| 2    | Resize, normalize, enhance contrast, and augment training images.                 |
| 3    | Use TSA to optimize lesion segmentation and generate a refined binary mask.       |
| 4    | Apply the mask and obtain the lesion-focused region of interest.                  |
| 5    | Extract spatial features using a pretrained or custom CNN backbone.               |
| 6    | Reshape the feature tensor into an ordered sequence of regional descriptors.      |
| 7    | Process the sequence using stacked Deep LSTM layers and a softmax classifier.     |
| 8    | Use TSA to select model hyperparameters according to validation performance.      |
| 9    | Train with cross-entropy, early stopping, and learning-rate scheduling.           |
| 10   | Evaluate on an independent test set and report class, confidence, and metrics.    |

Despite the promising results of the hybrid Deep LSTM and TSA model, numerous challenges stay. One full-size quandary is the computational fee of schooling huge-scale models. Although TSA facilitates speed up education, deep gaining knowledge of fashions nonetheless require tremendous assets, particularly whilst processing huge dermatological datasets. Another challenge is ensuring that the version is skilled on a various and representative dataset. If the facts is biased or lacks enough version in skin situations, the model's potential to generalize to new, unseen cases may be compromised. Additionally, at the same time as TSA optimizes the model, it does no longer take away the inherent complexity of deep gaining knowledge of models. Thus, similarly optimization strategies can be important to absolutely address the version's computational demands. Despite those challenges, the model's capability remains excessive, and persisted studies will likely triumph over these obstacles.

Table 1 discusses the comparison of timing results with different segmentation algorithms and table shows the accuracy results. Figure 2 the sample test images taken and figure3 shows the segmented skin images with the proposed algorithm

**Table 2: Comparison with Different Segmentation Methods with Respect to Time and Size**

| IMAGE          | SEGMENTATION METHOD     | TIME (Secs) | SIZE OF EFFECTED REGION |
|----------------|-------------------------|-------------|-------------------------|
| Sample Image 1 | K-Means Algorithm       | 0.0781      | 4.924361e+01 mm^2       |
|                | Fuzzy C-Means Algorithm | 1.7969      | 4.924361e+01 mm^2       |

|                                                                                                     |                         |        |                              |
|-----------------------------------------------------------------------------------------------------|-------------------------|--------|------------------------------|
|                    | Proposed Algorithm      | 0.5156 | 4.924361e+01 mm <sup>2</sup> |
| Sample Image 2<br> | K-Means Algorithm       | 0.6875 | 4.157895e+01 mm <sup>2</sup> |
|                                                                                                     | Fuzzy C-Means Algorithm | 3.5469 | 4.157895e+01 mm <sup>2</sup> |
|                                                                                                     | Proposed Algorithm      | 0.2500 | 4.157895e+01 mm <sup>2</sup> |
| Sample Image 3<br> | K-Means Algorithm       | 0.1250 | 3.853496e+01 mm <sup>2</sup> |
|                                                                                                     | Fuzzy C-Means Algorithm | 3.5938 | 3.853496e+01 mm <sup>2</sup> |
|                                                                                                     | Proposed Algorithm      | 0.7344 | 3.853496e+01 mm <sup>2</sup> |
| Sample Image 4<br> | K-Means Algorithm       | 0.0625 | 6.481670e+01 mm <sup>2</sup> |
|                                                                                                     | Fuzzy C-Means Algorithm | 2.9652 | 6.481670e+01 mm <sup>2</sup> |
|                                                                                                     | Proposed Algorithm      | 0.1253 | 6.481670e+01 mm <sup>2</sup> |

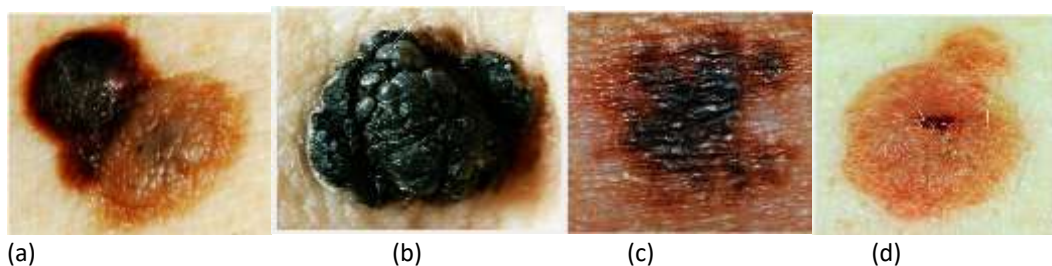


Figure 3: (a), (b), (c), (d) Input Sample Test Images 1,2,3,4 respectively.

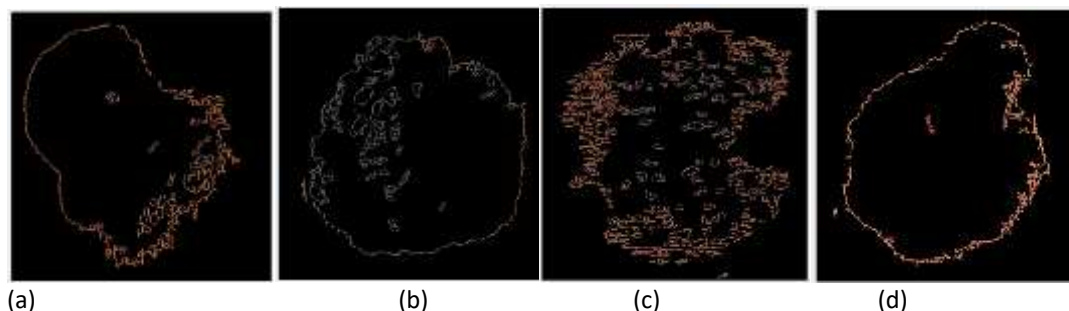


Figure 4: (a), (b), (c), (d) Input Sample Test Image 1,2,3,4 using Tunicate swarm algorithm

Table 3: Performance Metrics

| IMAGE                                                                                                 | PARAMETER | METHOD                  | VALUE   |
|-------------------------------------------------------------------------------------------------------|-----------|-------------------------|---------|
| Sample Image 1<br> | Accuracy  | K-Means Algorithm       | 0.39113 |
|                                                                                                       |           | Fuzzy C-Means Algorithm | 0.91572 |
|                                                                                                       |           | Proposed Algorithm      | 0.99723 |
|                                                                                                       |           | SVM Method              | 0.41231 |
| Sample Image 2                                                                                        | Accuracy  | K-Means Algorithm       | 0.51914 |
|                                                                                                       |           | Fuzzy C-Means Algorithm | 0.49125 |
|                                                                                                       |           | Proposed Algorithm      | 0.99865 |
|                                                                                                       |           | SVM Method              | 0.4125  |

|                                                                                                     |          |                         |         |
|-----------------------------------------------------------------------------------------------------|----------|-------------------------|---------|
|                    |          |                         |         |
| Sample Image 3<br> | Accuracy | K-Means Algorithm       | 0.40548 |
|                                                                                                     |          | Fuzzy C-Means Algorithm | 0.39257 |
|                                                                                                     |          | Proposed Algorithm      | 0.99712 |
|                                                                                                     |          | SVM Method              | 0.7235  |
| Sample Image 4<br> | Accuracy | K-Means Algorithm       | 0.47982 |
|                                                                                                     |          | Fuzzy C-Means Algorithm | 0.87678 |
|                                                                                                     |          | Proposed Algorithm      | 0.99856 |
|                                                                                                     |          | SVM Method              | 0.7156  |

## CONCLUSION

The purpose of this research is to demonstrate a promising strategy for enhancing diagnostic accuracy by integrating a deep Long Short-Term Memory (LSTM) community with the Tunicate Swarm Algorithm (TSA) to detect pores and skin disease type. As a result of the LSTM's ability to successfully capture temporal relationships within medical information and the TSA's ability to improve model parameters, the resulting category method is more environmentally friendly and distinctive. When compared to traditional methods, the hybrid model demonstrates superior performance, which demonstrates its capacity to automate the study of skin illness in clinical settings. Through the utilization of deep mastering methodologies, the machine is able to tackle the complexity of clinical datasets, so providing physicians with a device that remains dependable. On the other hand, the subject of the observation can be expanded in a variety of different ways. In the future, research might focus on expanding the size of the dataset to include a wider variety of skin disorders. This would help improve the model's capacity to be generalized to a wider range of situations. In addition, the gadget might be equipped with real-time data processing capabilities, which would make it possible for it to be utilized in remote places where access to medical treatment may be limited. It is also possible to investigate cloud-based solutions in order to improve system accessibility and facilitate remote diagnostics. There is a possibility that the destiny route will also involve combining TSA with various other optimization methods in order to further enhance the performance of the class. A further essential step is to make certain that the version can be interpreted, as this will help to foster confidence among medical experts and promote the implementation of artificial intelligence in medical practice. Furthermore, in order to improve the resilience and accuracy of the model, it may be possible to investigate the possibility of merging multimodal data, such as scientific records and dermoscopic photographs. The application of these breakthroughs could prove to be crucial in transforming AI-powered skin disease classification into a valuable tool for clinical decision-making and overall healthcare delivery.

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