Classification Of Skin Disease Using LSTM With Feature Selection Method

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Abstract

Objective: Skin diseases are an important public health issue that affects a large number of individuals across the world. As a result, it is vital to forecast the disease sooner in order to prevent the disease from progressing to a more critical stage. In recent years, the advancement of dermatological predictive categorization has grown more predictive and accurate, thanks to fast technological advancements and the implementation of various deep learning approaches.

Methods: In this work, diagnosis of skin diseases using Long-Short Term Memory is proposed which is one of the best deep learning techniques used for classification. Here, the informative Dermatology data is used to analysis and classify the skin disease with the help of the LSTM. The proposed work comprises of three steps. The procedure begins with data preprocessing, which prepares the dataset for classification. In addition, the novelty has been made in the feature selection process which is the second step of the proposed work. The recursive feature reduction approach is employed to select 10 key characteristics that play a key role in prediction. Final step is classification which is performed by the LSTM. It consists of six layers.

Conclusion: When compared to other classifier methods, the presented work on Dermatology datasets gives better outcomes. From the observation, the suggested research provides a more accurate prediction result and effective way to anticipate skin diseases.

Keywords: LSTM, Skin diseases, deep learning

1. Introduction

The skin is the most significant part of human body. The skin protects the body from UV radiation infections, injuries, heat and harmful radiation, and also helps in the manufacture of vitamin D. The skin plays an important role in controlling body temperature, so it is important to maintain good health and protect the body from skin diseases [1].

However, skin diseases can be developed to become chronic and seriously develop into skin cancer. Thus, early detection is required to reduce patients' development risks. Currently, there are many different machine learning models have been proposed to support automatic dermatological tool development. However, these experiments sent confusing conclusions because of using different image dataset, comparing a subset of learning models and unique data processing methods or pre-trained model [2].

The diagnosis of skin diseases is very challenging due to the symptom of skin disease is an extended and continuously transforming process with occurring in certain areas of the skin. In order to diagnose skin disease, a lot of clues such as specific lesion anatomy, physical assortment, scaling, shade, and arrangement can be used [3]. Sometimes the classification by using the image dataset is complex and result in less accuracy. So, the use of clinical features which is got by the deep analysis of human tissue. The clinical features are provides better prediction result than the image processing.

Deep learning technology recently attracts many researchers' attention on the object classification detection and other fields [4]. In this work, deep learning technique is proposed for classifying the skin disease. Long Short Term Memory is used for the skin disease classification in this study. A variation in the recurrent network by using memory blocks is called Long Short Term Memory blocks or LSTM. LSTM has the input layer, hidden layers and output layers. The hidden layers have memory blocks which are also called cells. Memory blocks contain information in a gated cell which is outside the normal flow of the recurrent network.

The three gates present in the LSTM are the input gate, the output gate and the forget gate. The memory cells contain the same input and the same output gate, forming a structure called memory cell block. All the data or information can be stored in a memory cell block as in computer memory. The functions, like data (read, write and erase), are performed by the cells through the open and close operation of gates. The gates are analogue, a sigmoid function multiplies element wise and provides range 0-1 [5]. The gates have a differentiable property due to its analogue nature so it can be used for the back-propagation. The gates of LSTM perform a similar task like a node in Neural Network.

As a classifier, the LSTM approach provides better performance. LSTM has more parameters and gating units that control the flow of information easily and provide higher accuracy in classification. Moreover, the multiplicative gates of LSTM allow the memory cells to access and store the information over a long period. Finally, the computational cost of LSTM is lower than the other techniques [6].

In proposed system, effective skin disease classification was achieved with the help of the LSTM model. Before classification the dataset was goes under the preprocessing step, then for improving the accuracy rate the features are limited. Then the LSTM with six layers are used for the classification.

The contributions of this proposed work are summarized as follows:

- ✓ To obtain the high accuracy, in this work the features are reduced into 10 number of features. The classification process with low impact features are leads to less accuracy. By using the recursive feature elimination method the low impact features are discorded.
- ✓ To achieve better classification result, here clinical dataset is used for the prediction process. Because certain picture datasets have noise data and resolution issues, incorrect prediction is possible. So the proposed work uses the clinical features for the disease prediction.
- ✓ To obtain effective classification process in this proposed work, LSTM is used for classification. Because the LSTM network can remember and connect previous information to data obtained in the present.

The rest of the work is organized as follows: The related works in the fields of deep learning based classification, skin disease prediction and feature selection methods were presented in Section 2. Section 3 defines the proposed LSTM based skin disease classification. Section 4 contains result and discussion which shows the efficiency of proposed work. Conclusion of the research work is discussed in Section 5.

2. Literature Survey

The study [1] presented a new method, which applies five different data mining techniques and then developed an ensemble approach that consists all the five different data mining techniques as a single unit. The proposed ensemble method, which is based on machine learning was tested on Dermatology datasets and classify the type of skin disease in six different classes like include psoriasis, seborrheic dermatitis, lichen planus, pityriasis rosea, chronic dermatitis, pityriasis rubra. The results show that the dermatological prediction accuracy of the test data set is increased compared to a single classifier. Ensemble method gives more accurate and effective skin disease prediction.

The author [7] proposed a new method that can reduce the number of class association rules produced by classical class association rule classifiers, while maintaining an accurate classification model that is comparable to the ones generated by state-of-the-art classification algorithms. More precisely, they proposed a new associative classifier that selects "strong" class association rules based on overall coverage of the learning set. The advantage of the proposed classifier is that it generates significantly smaller rules on bigger datasets compared to traditional classifiers while maintaining the classification accuracy.

Authors in [8] proposed method consists of five subsequent blocks of layers, each having convolutional, and drop-out, and max-pooling layers. The performance of the introduced classification system is validated on colorectal cancer histology image dataset which consists of RGB-colored images belonging to eight different classes. The experimental results confirm the higher performance of the proposed convolutional neural network against existing different machine learning models with the lowest error rate.

The authors of [9] proposed a novel multi-instance learning algorithm based on Long and Short-Term Memory neural network with attention mechanism (ALSTM-MIL). Firstly, by using the Pyramid Overlapping Grid Division (POGP), a multi-instance modeling scheme is designed to convert Chinese painting images into multi-instance bag, thereby transforming the problem of Chinese painting image classification into a MIL problem. Secondly, an efficient sequence generator is designed. It selects discriminative instances from the positive bags, construct a discriminative instance set (DIS), and convert multi-instance bags into equal-length ordered sequences. Thirdly, an LSTM network model with an attention mechanism is designed to perform semantic analysis on multi-instance bags to obtain their memory coding features, and then combined with the Soft max classifier to achieve semantic classification of traditional Chinese painting images.

The study [10] proposed a bilinear CNN model based on the mid-level and high-level feature fusion (FB-CNN) for classifying the fruit fly image. At the first step, the images of fruit fly are blurred by the Gaussian algorithm, and then the features of the fruit fly images are extracted automatically by using CNN. Afterward, the mid- and high-level features are selected to represent the local and global features, respectively. Then, they are jointly represented. When finished, the FB-CNN model was constructed to complete the task of image classification of the fruit fly. Finally, experiments data show that the FB-CNN model can effectively classify four kinds of fruit fly images. It has a disadvantage that is, it cannot able to classify the image with the natural background.

Authors in [11] proposed an alternative approach where 21 temporal features in lieu of the temporal signal are collected from the 12 lead data to reduce redundancy and class imbalance keeping the vital information intact. Then these extracted features are fed into a detection model consisting of a one dimensional convolutional neural network and a bidirectional long short-term memory (bi-LSTM) layer which classifies into three classes, namely: HC, MI, and non-myocardial infarction (non-MI) subjects for a realistic and reliable assessment.

The authors of the study [12] proposed Deep Learning assisted Efficient Adaboost Algorithm (DLA-EABA) for breast cancer detection has been mathematically with advanced computational techniques. In addition to traditional computer vision approaches, tumor classification methods using transfers are being actively developed through the use of deep convolutional neural networks. This study starts with examining the CNN based transfer learning to characterize breast masses for different diagnostic, predictive tasks or prognostic or in several imaging modalities, such as Magnetic Resonance Imaging (MRI), Ultrasound (US), digital breast

tom synthesis and mammography. The classification and error estimation that has been included in a fully connected layer and a soft max layer.

The study [13] proposed a new framework that performs both segmentation and classification of skin lesions for automated detection of skin cancer. The proposed framework consists of two stages: the first stage leverages on an encoder-decoder Fully Convolutional Network to learn the complex and inhomogeneous skin lesion features with the encoder stage learning the coarse appearance and the decoder learning the lesion borders details. The second stage proposed a novel FCN-based Dense Net framework that is composed of dense blocks that are merged and connected via the concatenation strategy and transition layer.

The authors of [14] proposed a hybrid Automatic Incident Detection method using Random Forest-Recursive Feature Elimination (RF-RFE) algorithm and Long-Short Term Memory (LSTM) network optimized by Bayesian Optimization Algorithm (BOA) Firstly, a relatively comprehensive set of initial variables is constructed using basic traffic variables and their combinations. Secondly, feature variables are selected from the initial variables using the RF-RFE algorithm. Then, the feature variables are used for training the LSTM network, and the hyper-parameters of the LSTM network are optimized by BOA. In addition, Synthetic Minority Over-Sampling Technique (SMOTE) is employed to solve the problem of imbalance between incident sample size and non-incident sample size.

3. Methodology

In this work, the proposed system model consist of three major phases namely Data Preprocessing, Feature Selection and Classification as shown in the figure 1.



http://www.webology.org

Figure 1. Proposed system model

Data Preprocessing: In this phase, the dataset used for classification is transformed into a proper format by applying some preprocessing techniques.

Feature Selection: Only important features which plays a key role in classification is selected in this phase. This process improves the classification accuracy.

Classification: Finally, in this phase based on the patient's record and the selected important features, the skin disease was diagnosed.

In general, classification of skin disease was performed in two different ways. In first type, the image data is used to diagnosis the disease and the second type is skin disease identified from the clinical data which is obtained by the analysis of human tissue. Among these two types, classification using clinical data has high accuracy than image processing method. Because the images has the great similarity which give the characteristics to other type of skin disease at some point. Low image resolution and high noise rate are the additional problems related to image data classification. Due to above drawback of image data, in this work clinical data are used for the classification.

The proposed model classify the skin disease into 6 various classes such as psoriasis, seborrheic dermatitis, lichen planus, pityriasis rosea, chronic dermatitis and pityriasis rubra. The classification process of proposed model is explained as follow:

Data Preprocessing:

This is the first step of the proposed model. In this phase, the raw data that is clinical feature dataset and patient records are collected. The gathered data are not ready for the classification process. Because those raw data are contains noise information. To remove the noise data from the gathered dataset preprocessing was performed. The preprocessing is the process that transform the raw dataset into the form which is suitable for the perfect classification process.

Data cleaning, Normalization and Aggregation processes are used in this preprocessing phase. Cleaning method is nothing but remove the irrelevant values and duplicate values, concentrate of missing values, eliminate non-sense answers & unreadable data and check patient records are formatted correctly. Arrange the records in database correctly and verify only relevant information are kept in the database by the normalization technique. After preprocessing, the feature dataset and patient record dataset are ready for the classification in proper format without noisy data.

Feature Selection:

Feature selection process is nothing but, it take only important features or attribute from the large dataset. Feature selection method remove the unwanted or low impact features and remove the redundant data. The purpose of feature selection is, to improve the accuracy of classification process by removing of unrelated features. There are number of feature selection techniques are available. Among those techniques recursive feature elimination technique is used in this proposed work.

***** Recursive Feature Elimination:

Recursive feature elimination process is one of the feature selection technique in which the unimportant features are eliminated until the particular number of features are obtained. For example, if the user specified 12 important features are needed. Then the recursive feature elimination technique is remove the least important features recursively until 12 features are obtained. This technique first, ranking the features by its importance and discard the least important features from the dataset.

In this proposed technique, only 10 important features are selected for the skin disease classification. Those 10 important clinical features are selected by the recursive feature elimination technique. The features and the feature extraction concept by using recursive feature elimination is shown in the figure 2.

Analysis of Dataset

The database used in this study is taken from the UCI machine learning repository (http://archive.ics.uci.edu/ml). Briefly, this dataset was formed to examine skin disease and classify the type of erythemato-squamous diseases. This dataset contains 34 variables; in this dataset, 33 variables are linear and 1 variable is nominal. These six classes of skin disease include the following: C1- psoriasis; C2- seborrheic dermatitis; C3- lichen planus; C4- pityriasis rosea; C5- chronic dermatitis; C6- pityriasis rubra. Biopsy is one of the basic treatments in diagnosing these diseases. A disease may also contain the properties of another class of disease in the initial stage, which is another difficulty faced by dermatologists when performing the different class of diagnosis of these diseases. Initially, patients were first examined with 12 clinical features, after which the assessment of 22 histopathological attributes was performed using skin disease samples. Histological features were identified by analyzing the samples under a microscope. If any of the diseases is found in the family, the family history attribute in the dataset constructed for the domain has a value of 1, and if not found, the value is 0. The age of the patient is used to indicate age characteristics. All other attributes (clinical and histopathological both) were assigned a value in the range from 0 to 3 (0 = absence of features; 1, 2 = comparative intermediate values; 3 = highest value). There are six classes of erythemato-squamous disease, with 366 instances and 34 attributes in the domain.

Erythema, melanin incontinence, scaling, eosinophils in the infiltrate, definite borders, PNL infiltrate, itching, fibrosis of the papillary dermis, Koebner phenomenon, exocytosis, polygonal papules, acanthosis, follicular papules, hyperkeratosis, parakeratosis, oral mucosal, clubbing of the rete ridges involvement, knee and elbow, elongation of the rete ridges, scalp involvement, thinning of the suprapapillary epidermis, family history, spongiform pustule, age, munro microabscess, focal hypergranulosis, disappearance of the granular layer, vacuolization and damage of basal layer, spongiosis, the saw-tooth appearance of rete ridges, follicular horn plug, perifollicular parakeratosis, inflammatory mononuclear infiltrate, band-like infiltrate





Original Dataset

Figure 2. Feature Extraction

Classification:

After feature selection, the classification process was performed by using the deep learning technique. In this study, the skin disease classification was done with the help of the Long-Short Term Memory. The proposed LSTM network consists of six layers:

- ➤ Input Layer
- Feature Mapping Layer
- ► LSTM layer
- ➢ Soft max Layer
- Classification Layer and
- ➢ Output Layer.

Input Layer:

I hope he will The first layer of proposed LSTM is an input layer where inputs are feed to the network. Two type of inputs were used,

- Patient Record and
- Clinical Feature details.

Both the patient record dataset and details about clinical feature dataset are given to this input layer which forward those into next layer. The clinical feature dataset contains only 10 important features which is obtained after feature selection process.

Feature Mapping Layer:

This is the second layer of proposed LSTM. This layer takes input data from input layer and map features from those data. Patient record and clinical feature dataset are the input for this layer. The patient record contains all the features which is obtained by their tissues. That is, there may be possibility for all 34 features, but the feature dataset has only 10 important features. So, from the patient record only selected 10 important features are considered.

Patient	Absence of feature	Intermediate	Highest Value
		value	
P1	F3, F8	F10	F1
P2	F4	F14, F3	F2
P3	F5	F7	F6, F3

Table 1. Mapping process in LSTM

For example the feature dataset contains 10 important features (F1, F3, F2, F7, F6, F10, F4, F5, F14 and F8) and patient's record contains all 34 features. From the two records, only selected important 10 features are considered for all patients. Then the features are mapped with corresponding patient according to their values like absence, presence or intermediate presence.

LSTM Layer:

And he has all This is the third layer of proposed LSTM. This layer processes the previous layer input and provides the identified skin disease along with value (%). For example, the patient P1 was 99.9% affected by the skin disease C1.In this study, a single LSTM layer with numerous LSTM blocks is employed which is shown in figure 3. Input gate, Output gate, and Forget gate are the three types of gates used in a LSTM block. Eq. (1), (2), and (3) are the equations for the input gate, output gate, and forget gate, accordingly. The input gate determines the quantity of new information added to the cell state, the forget gate determines the information to be deleted from the cell, and the output gate determines the information to be output. LSTM uses the three gate architectures for information control and protection. The sigmoid and tanh functions are used extensively in the LSTM cell structure [15].Finally, it filters the cell state before passing it via the activation function, which forecasts what part of the current LSTM unit's output should occur at time (t).



Figure 3. Structure of single LSTM block

The equations [15] for the three gates in L STM are:

$\mathbf{i}_t = \sigma(\omega_i[\mathbf{h}_{t-1}, \mathbf{x}_t] + \mathbf{b}_i)$	(1)
$f_t = \sigma(\omega_f[h_{t-1}, x_t] + b_f)$	(2)
$o_t = \sigma(\omega_o[h_{t-1}, x_t] + b_o)$	(3)

Here, i_t stands for input gate, f_t stands for forget gate, o_t stands for output gate, σ represents sigmoid function, ω_x stands for weight for the corresponding gate (x) neurons, Output of the previous LSTM block (at timet – 1) is indicated as h_{t-1} , Input at current timestamp is indicated as x_t , Biases for the corresponding gates (x) are denoted as b_x .

The cell state, candidate cell state, and final output equations are as follows [15]:

$$\begin{aligned} \tilde{c}_t &= \tanh(\omega_c[h_{t-1}, x_t] + b_c) \quad (4) \\ c_t &= f_t * c_{t-1} + i_t * \tilde{c}_t \quad (5) \\ h_t &= o_t * \tanh(c_t) \quad (6) \end{aligned}$$

Here, c_t denotes the cell state (memory) at timestamp (t), \tilde{c}_t represents candidate for cell state at timestamp (t), and h_t is an output of current LSTM block (at timestamp (t)). Then the output h_t from current LSTM block is passed through the soft max layer to get the predicted disease of the patient.

Soft max Layer:

The soft max layer convert the LSTM layer's output into the values between 0 and 1. For example, the output of LSTM layer is, patient P2 98.6% affected by the disease C3. Then the predicted

disease is convert into value 1 and remaining diseases are convert into 0. Eq. (7) shows the formula for soft max layer,

$$\vec{\sigma(d)}_i = \frac{e^{d_i}}{\sum_{j=1}^{K} e^{d_j}}$$
(7)

Where all the d_i value is the predicted disease in previous LSTM layer. The normalized factor at the bottom of the calculation ensures that all of the function's output values add to 1, resulting in a proper probability distribution.

Classification Layer:

The classification layer produces the predicted output along with the features and patient detail. For example, the patient P1 has the characteristics F1, F10, which is the illness class C6's 96.8% symptom.

Patient		Features						Predicted Disease			
	F1	F2	F3	F4	F5	F6	F7	F8	F10	F14	
P1	\checkmark	-	\checkmark	\checkmark	-	-	\checkmark	-	\checkmark	-	C3
P2	\checkmark	-	\checkmark	-	\checkmark	\checkmark	-	\checkmark	-	\checkmark	C5
P3	-	\checkmark	-	\checkmark	-	-	\checkmark	-	\checkmark	-	C1

Table 2. Example classification layer output

Output Layer:

This is the last layer of the proposed model. The simplified and easy understanding output was produced by the output layer. For example, Patient P1 affected by the skin disease class C4.

Table 3. Skin disease classification

Patient	Skin Disease
P1	C1
P2	C5
Р3	C2

4. Result & Discussion

The effectiveness of the proposed model is analyzed by comparing it with the other existing classification techniques namely CNN [8] and ensemble techniques [1]. The following terms are used for the efficiency analysis of proposed work:

Precision, Recall and F1 score

Classification Accuracy

4.1 Precision, Recall and F1 Score

Precision is defined as the ratio of properly predicted positive observations to the total number of correctly anticipated positive observations. Here precision indicates the correct prediction of skin disease and it is represented by below formula,

$$Precision = TP/(TP + FP)$$

The recall refers to the classifier's capacity to identify all successful data. Here recall indicates the capability to identify the skin disease and it is represented by below formula,

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

F-Measure generates a single score that combines precision and recall issues into a single value. Both False Positive (FP) and False Negative (FN) are consider for this calculation. It is represented by below formula,

F1 score =
$$2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

For above scenario, True Positive (TP) indicates the skin disease which is identified for the patient and it is correctly classified into prediction list. False Positive indicates the skin disease which is not identified for the patient but it is wrongly classified into prediction list. True Negative (TN) indicates the disease which is not identified for the patient and it is correctly classified into non prediction list or not considered. False Negative indicates the disease which is identified for the patient but it is wrongly classified into non prediction list. The Precision, Recall and F1 Score values for proposed work, CNN and ensemble techniques are stated in Table 4. Fig. 4 shows that the proposed model is outperformed than other technique in all three parameters.

Table 4. Precision, Recall, F1 Score for CNN, Ensemble Techniques and Proposed LSTM

	Parameters				
Models	Precision	Recall	F1 Score		
CNN	0.79	0.85	0.82		
Ensemble Techniques	0.83	0.88	0.83		
Proposed LSTM	0.92	0.94	0.94		

From the Table 4 and Figure 4, the proposed system has high precision, recall and F1 score values when it is compared with other techniques. From the analysis, the proposed LSTM outperforms than other models.





4.2 Classification Accuracy

The ratio of correct classifications, that for an independent test set or employing some form of the cross-validation principle, is known as classification accuracy. The classification accuracy of the proposed LSTM is compared with the existing work for efficiency analysis. Table 5 and figure 5 shows the classification accuracy analysis. The accuracy is calculated through the following formula,

 $Accuracy = \frac{Number of correct classified prediction}{Total number of predictions}$

Table 5.	Comparison	of	classification	accuracy
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Model	Classification Accuracy
CNN	0.8331
Ensemble Techniques	0.8741
Proposed LSTM	0.9077

The classification accuracy of the proposed model is higher than other models. The main reason for the highest accuracy is feature selection and use of clinical dataset for classification. In this proposed work, only 10 important features are selected for the classification which results in low complexity and high accuracy rate. Unwanted and low impact features are eliminated at starting which enhances the skin disease classification.

Figure 5. Comparison of Classification accuracy



5. Conclusion

The Long Short Term Memory with feature selection method is proposed in this work for efficient skin disease classification process. The recursive feature elimination technique is used in this study which improves the accuracy level of classification. Additionally, a real world dermatology dataset which contains 34 clinical features are used for this work, which provides the correct prediction rate. The proposed work is compared with existing convolution neural network model and ensemble techniques. Result shows that the proposed technique LSTM with feature selection is outperformed the existing techniques in terms of, precision, recall, F1 Score, and classification accuracy.

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