ISSN: 0974-5823 Vol. 7 No. 5 May, 2022

International Journal of Mechanical Engineering

Generalized Softmax Regressive Feature Selected Modest Adaptive Boost Skin Disease Classification

[1]Dr.V.Umadevi, [2]S.Mohan

[1]Research Supervisor, PG and Research Department of Computer Science, Nehru Memorial College (Autonomous), Puthanampatti, Trichy(Dt). Affiliated to Bharathidasan University, Trichirappalli-24.

[2]Research Scholar, PG and Research Department of Computer Science, Nehru Memorial College (Autonomous), Puthanampatti, Trichy(Dt). Affiliated to Bharathidasan University, Trichirappalli-24.

ABSTRACT

Skin disease is the type of health illnesses experienced by the people for different ages. The skin disease identification is based on doctors and skin biopsy results. Skin disease identification and classification is carried out to improve the accuracy as well as to handle the scarcity. Skin disease classification is an essential task depends on the disease features taken to classify it correctly. Many researchers carried out their research on skin disease classification with selection of relevant features from input database. But, the accuracy level was not improved and time consumption was not minimized during skin disease classification. In order to solve these issues, Generalized Softmax Regressive Feature Selected Modest Adaptive Boost Classification (GSRMAB) Method is introduced. The main of GSRMAB Method is to perform efficient skin disease classification with higher accuracy and lesser time consumption. GSRMAB Method comprises three steps, namely data pre-processing, feature selection and classification. Data preprocessing is a data mining technique that transforms the raw data into an understandable format. After that, Generalized Softmax Regressive Feature Selection Process is carried out select the relevant features from the pre-processed input database. The softmax regression is a generalization of logistic regression to handle the multiple classification problems. Softmax regression predicts the specific class among two classes (i.e., relevant and irrelevant) according to the exponential value. After feature selection, GSRMAB Method employs Modest Adaptive Boost Classifier where each data is classified into multiple classes through designing strong classifier with higher accuracy. GSRMAB Method constructs strong classifier through reducing the training error of weak learner results for accurate skin disease classification. Consequently, GSRMAB Method enhances the skin disease classification performance when compared to existing works. The GSRMAB Method accomplishes experimental work using parameters such as classification accuracy, precision, recall and F1-score with respect to number of data. The experimental result depicts that the GSRMAB Method increases the accuracy and precision of skin disease classification when compared to state-of-the-art works.

Keyword: GSRMAB, Skin disease, Adaptive Boost Classifier

1. INTRODUCTION

Skin is the most significant part of the human body. Skin protects the body from the UV radiation infections, injuries, heat and harmful radiation. The skin plays an essential part in handling the body temperature to maintain good health and to protect body from skin diseases. A Convolution Neural Network (CNN) system was introduced in [1] for classifying the skin disease. The Eff2Net model was constructed on EfficientNetV2 in conjunction with Efficient Channel Attention (ECA) block. But, the accuracy level was not improved by CNN system.

A new classification model termed Targeted Ensemble Machine Classify Model (TEMCM) was designed in [2] for joining the suitable model in skin disease detection process. An implementable solution was obtained for IoT-led remote skin disease diagnosis. But, the classification accuracy was not improved by TEMCM. An

ensemble method was introduced in [3] with data mining techniques. The designed method comprised the data mining method with the single unit. Dermatology data was employed to classify the skin disease. However, the computational complexity was not reduced by designed method.

A two-step progressive transfer learning technique was designed in [4] through fine-tuning network on skin disease dataset. An adversarial learning was carried out with domain adaptation for increasing the recognition performance. But, the recall performance was not improved. An efficient approach was designed in [5] to identify singular type of skin diseases. An automatic technique was employed to increase the diagnosis accuracy for multitype skin diseases. But, the classification accuracy was not reduced by designed approach.

A new automated framework was designed in [6] for multiclass skin lesion classification. The designed framework comprised the augmentation and segmentation process with rotate 90, right-left flip as well as up and down flip. A self-paced balance learning (SPBL) algorithm was designed in [7] with comprehensive metric called image category complexity and recognition difficulty. The pace denoted the iteration in self-paced learning model. The mutual bootstrapping deep convolutional neural networks (MB-DCNN) model was designed in [8] for skin lesion segmentation and classification. The lesion localization maps created by mask-CN were fed into SN to transfer the localization information for accurate lesion segmentation.

An automated system was introduced in [9] depending on texture analysis for human skin disease recognition. The melanin and hemoglobin in human skin were separated by independent component analysis of skin color image. But, the recall was not improved by automated system. A support vector machine–based black widow optimization (SVM-BWO) was introduced in [10] for skin disease classification. The pre-processing was carried out to remove the noise from input images. However, the precision was not improved by SVM-BWO.

The issues identified from above literature are lesser classification accuracy, lesser precision, lesser recall, lesser F-1 score, higher computational cost, higher computational complexity and so on. In order to address these issues, Generalized Softmax Regressive Feature Selected Modest Adaptive Boost Classification (GSRMAB) Method is introduced.

The contribution of the are article is given as,

- The main of GSRMAB Method is to perform efficient skin disease classification with higher accuracy and lesser time consumption. GSRMAB Method comprises three steps, namely data pre-processing, feature selection and classification.
- Data preprocessing transforms the raw data into an understandable format. After that, Generalized Softmax Regressive Feature Selection Process selects the relevant features from the pre-processed input database. Softmax regression predicts the specific class among two classes (i.e., relevant and irrelevant) according to the exponential value.
- After feature selection, GSRMAB Method employs Modest Adaptive Boost Classifier where each data is classified into multiple classes through designing strong classifier with higher accuracy. GSRMAB Method constructs strong classifier through reducing the training error of weak learner results for accurate skin disease classification.

The structure of the paper is given as follows. Section 2 reviews the related works. Section 3 explains the proposed GSRMAB Method with help of architecture diagram. In Section 4, the experimental setup is presented and detailed result analysis is discussed. Section 5 presents the conclusion of the work.

2. RELATED WORKS

Skin diseases are the major global health issue linked with high number of people. With fast growth of technologies in recent years, dermatological predictive classification has become more predictive and exact. Improved Relational Network was introduced in [11] for measurement learning to recognize the skin disease classification. RPN collected and extracted the feature information through attention mechanism. But, the computational cost was not reduced by improved relational network. An automatic skin lesions classification system was designed in [12] with higher classification rate through transfer learning and deep neural network.

The transfer learning was employed with Alex-net in different ways through fine-tuning weights and replacing classification layer.

The study was carried out in [13] to discover the associations between subtypes of fingernail disease and PsA among the patients with the psoriasis. Multivariate logistic regression tested the strength of association between fingernail diseases. But, the recall was not improved. A deep learning (DL)-based amyloid PET positivity classification model was introduced in [14] from PET images through limited accessibility of amyloid position emission tomography (PET) in patients. However, the computational cost was not reduced by designed model.

A skin lesion classification method was introduced in [15] to categorize the skin lesions depending on the dermoscopic images to different diagnosis classes. The metadata comprised the patient information during data augmentation process. But, the precision was not improved by designed method. A deep learning-based application was designed in [16] for efficient skin disease classification into plaque, guttate, inverse, pustular and erythrodermic. But, the time consumption was not reduced during classification. A prototype image analysis system was designed in [17] depending on deep learning to establish whether lesion was malignant or benign depending on dermatoscopy image. However, the classification accuracy was not improved by designed system.

A new technique was introduced in [18] to combine the accurate segmentation and classification models in dermatology. The image was decomposed to normalize and to extract the high-level features. But, the F-1 score was not increased by designed technique. An image processing-based method was introduced in [19] to detect the skin diseases. The designed method considered the digital image of disease effect skin area to identify the disease type. However, the recall was not improved by designed method. A fully automatic skin disease classification approach was introduced in [20] with feature extraction and classification with first and second order statistical moments, entropy of diverse color channels and texture based features. But, the computational complexity was not reduced.

3. METHODOLOGY

Skin is the main organ of the human body made up of epidermis, dermis and subcutaneous tissues. Skin recognized the outside condition and shielded the organs as well as tissues from unsafe microscopic organisms, pollution and sun presentation. Skin gets influenced by different external and internal factors. Skin disease is caused by different problems such as fungal infection, bacteria, allergy or viruses. Skin diseases are common form of infections for peoples under all ages. A patient gets recovered from skin diseases when it is identified and treated in early stages. Early skin disease diagnosis and classification is dependent on patient attention and accurate assessment by medical practitioner. But, the skin disease classification accuracy level was not improved. In order to address these problems, Generalized Softmax Regressive Feature Selected Modest Adaptive Boost Classification (GSRMAB) Method is introduced. The main of GSRMAB Method is to perform efficient skin disease classification with higher accuracy and precision. The structural diagram of GSRMAB Method is given as, Figure 1 describes the structural diagram of GSRMAB Method. The designed GSRMAB Method comprises three processes, namely data pre-processing, feature selection and classification for efficient skin disease diagnosis with higher accuracy and precision. Data preprocessing converts the raw data into understandable format. The relevant features are chosen from the pre-processed database. After feature selection, the classification is carried out where each data is categorized into multiple classes with higher accuracy.

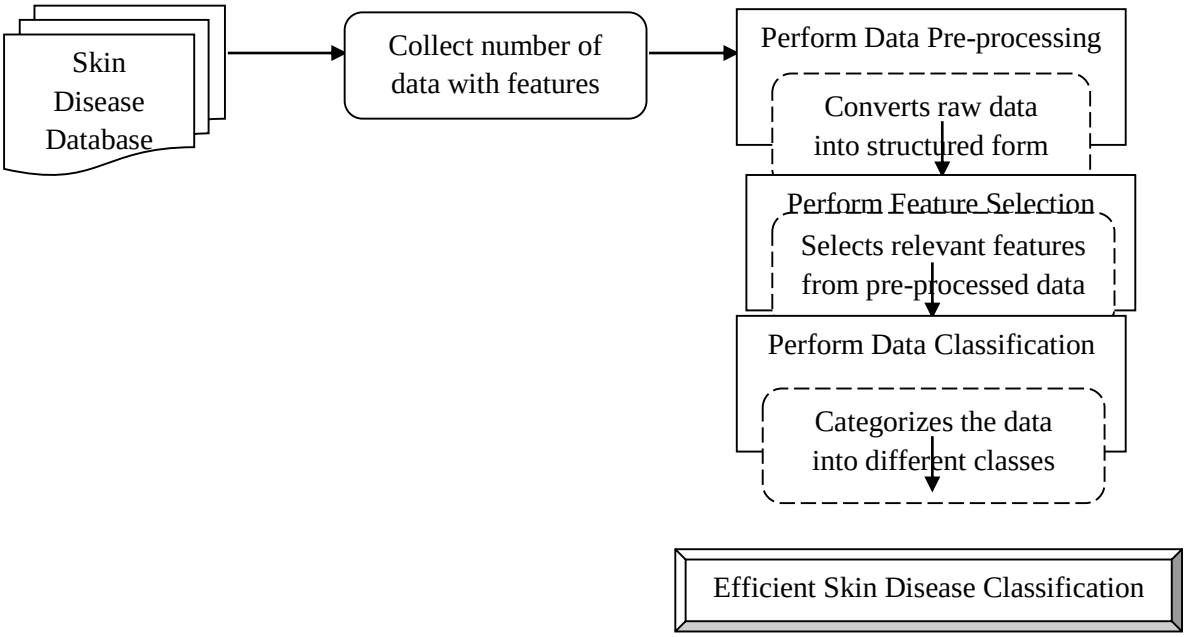

Figure 1 Structural Diagram of GSRMAB Method

3.1 Data Pre-processing

In GSRMAB Method, Data Pre-processing is a data mining method used to convert the raw data into useful format. The data comprises the irrelevant and missing parts. The data cleaning is carried out to handle the missing data and noisy data. The missing data is handled through tuple ignorance and filling missing spaces. Noisy data is a meaningless data that are not interpreted by machines.

3.2 Generalized Softmax Regressive Feature Selection

Feature selection is defined as the process of choosing the necessary features from database for future processing. In GSRMAB Method, the number of features is considered as an input for performing classification. Generalized softmax regression is used to perform feature selection through choosing the relevant features from the input database. Generalized softmax regression analysis is carried out between the dependent and independent variables (i.e., features) to attain two outcomes, namely '0' and '1'. In Generalized softmax regression analysis, the decision tree is built with the root node, internal node, and leaf node. The root node performed the correlation based on the connection measure. The internal node represents the results and the leaf node presents the output class label. Generalized softmax regression analysis with features is illustrated in figure 2.

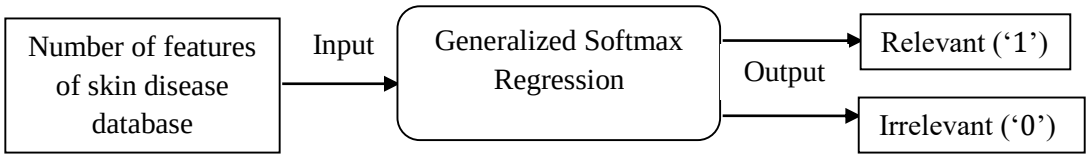

Figure 2 Generalized Softmax Regression

Figure 2 illustrates the generalized softmax regression analysis with the number of features. It is formulated as,

$$GSR = \frac{1}{1+exp\,(-\rho_0+\rho_1\theta)} \quad (1)$$

From (1), 'GSR' denotes the generalized softmax regression output. 'ρ_1' represent the regression coefficient. 'α_0' is considered as the zero. 'θ' symbolizes the explanatory variable. When the regression tree output is '0',

then the feature is considered as irrelevant feature. Depending on the regression analysis, the tree makes the decision output as '1' to select the relevant features. After that, the relevant features are selected in GSRMAB Method for performing the skin disease classification.

3.3 Support Vector Modest Adaptive Boost Classification

After performing the feature selection, the classification process is performed in GSRMAB Method by using Support Vector Modest Adaptive Boost Classifier. The designed classification method is a machine learning and ensemble learning technique that combines the weak learners to form the strong ones. A weak learner is considered as the classifier that is difficult to attain the true classification results. An ensemble technique is the strong learner where the classifier provides true classification results with minimum error. Therefore, the GSRMAB Method uses Support Vector Modest Adaptive Boost Classifier to improve the accuracy and reduce the inaccurate classification. The structure of Support Vector Modest Adaptive Boost Classifier is illustrated in figure 3.

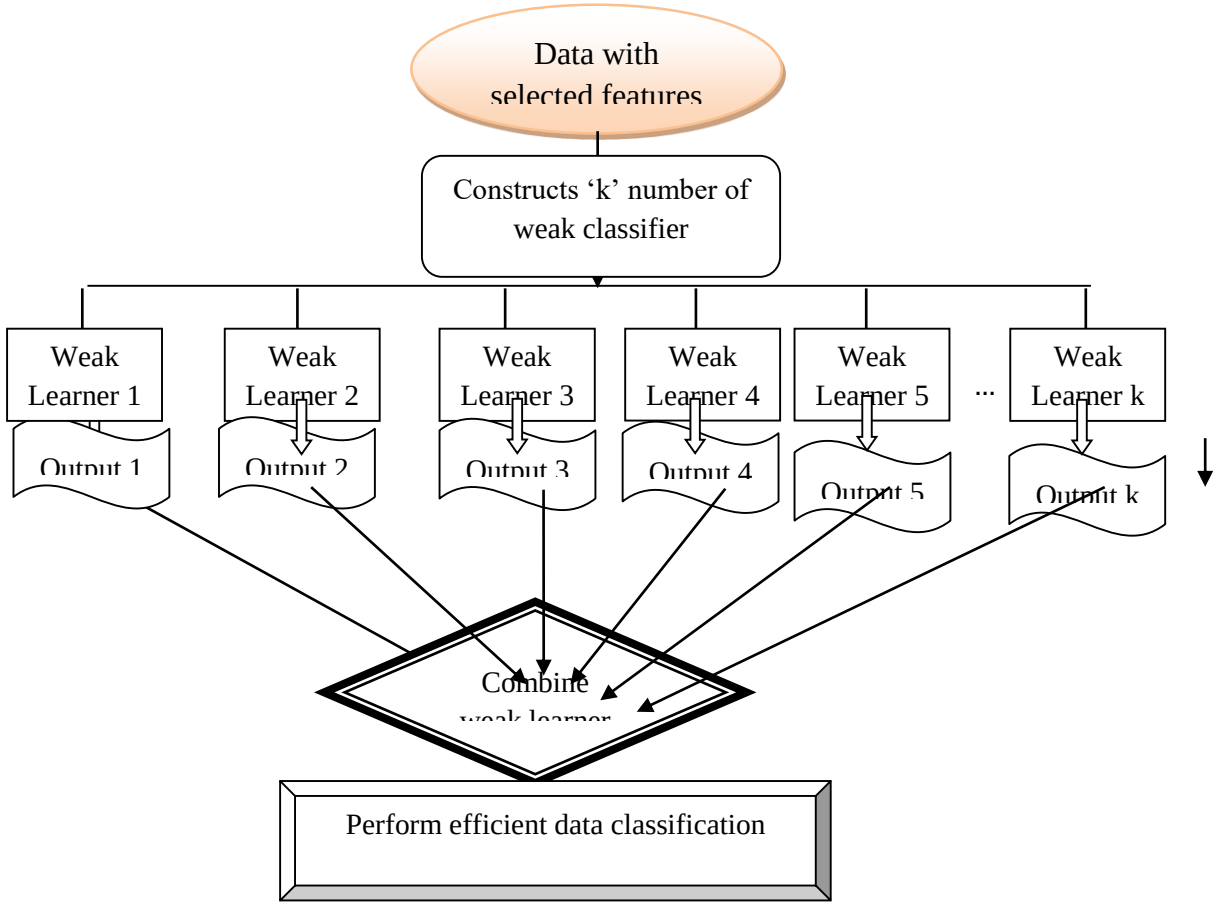

Figure 3 block diagram of the Support Vector Modest Adaptive Boost Classifier

Figure 3 describes the block diagram of Support Vector Modest Adaptive Boost Classifier to obtain an accurate skin disease classification. Support Vector Modest Adaptive Boost Classifier considers the training set $\{TD_i, E\}$ in which '$TD_i = d_1, d_2, \ldots, d_n$' symbolizes the training data. 'E' illustrates the ensemble classification results. As illustrated in figure 3, the ensemble classification constructs the 'k' weak learners '$P_1, P_2, P_3, \ldots . P_k$' and corresponding output results are '$R_1, R_2, R_3, \ldots . R_k$' are combined to attain the strong classification results. Modest Adaptive Boost Classifier used Support Vector Machine as the weak learner to categorize the patient data. A support vector classifier examines the testing and training data in GSRMAB Method to attain the final

classification results with the hyperplane. For each training data, the hyperplane is used to determine the ruzicka similarity. It is formulated as,

$$\alpha = \frac{min(D_{tr}, D_{ts})}{max(D_{tr}, D_{ts})} \quad (2)$$

From (2), 'α' denotes the ruzicka similarity coefficient. 'D_{tr}' represent the training data. 'D_{ts}' symbolizes the testing data. The similarity coefficient (α) presents the resultant value ranging between 0 and 1. The hyperplane examines the similarity value of data and categorized results on upper or lower side of the hyperplane. The separating hyperplane (H_s) is symbolized as,

$$H_s \rightarrow wt.(TD_i) + bias = 0 \quad (3)$$

From (3), 'wt' denotes the normal weight vector to the hyperplane. 'TD_i' symbolizes the training data in GSRMAB Method. The hyperplane categorizes the data above or below with help of two marginal planes. It is given as,

$$MP_1 = wt.(TD_i) + bias > 0 \quad (4)$$

$$MP_2 = wt.(TD_i) + bias < 0 \quad (5)$$

From (4) and (5), 'MP_1' and 'MP_2' symbolizes the two marginal hyperplanes (i.e., above and below the hyperplane). The data with higher similarity is categorized above the hyperplane. Or else, the data are categorized below the hyperplane. By this manner, weak learner categorizes the data into multiple classes in GSRMAB Method. But, the weak learner results have some training error without providing the accurate results. The ensemble technique joins all weak learners to make the strong one. The ensemble of the weak learner is given as,

$$E = \sum_{j=1}^{k} R_j(d) \quad (6)$$

From (6), 'E' denotes the ensemble classification result through linear combination of the weak learners $\sum_{j=1}^{k} R_j(d)$. Then, the weights are initialized to every weak learner. It is symbolized as,

$$E = \sum_{j=1}^{k} R_j(d) * r \quad (7)$$

From (7), 'r' symbolizes the integer to validate the classification performance of weak learner. The weak learner with training loss is measured as,

$$Loss = (A - P)^2 \quad (8)$$

From (8), '$Loss$' symbolizes the training loss. 'A' denotes the actual classification result. 'P' symbolizes the predicted classification results. Depending on loss value, the weight gets updated in GSRMAB Method. Lastly, the gradient function identifies the weak learner with lesser loss value than the other. It is given as,

$$GF = arg\ arg\ [Loss\ ] \quad (9)$$

From (9), 'GF' denotes the gradient descent function. '$arg\ min$' represent the argument of minimum function. '$Loss$' denotes the training loss of weak learners. Consequently, the weak learner with minimal training loss is considered as the final classification results in GSRMAB Method. Depending on the classification results, the skin disease data is correctly classified with higher accuracy. The algorithmic process of Modest Adaptive Boost Classification is given as,

\\ **Algorithm 1: Modest Adaptive Boost Classification**
Input: Number of training data '$TD_i = d_1, d_2, \dots, d_n$', Selected features
Output: Improves classification accuracy
Begin
1. Collect a number of data with selected features
2. **for each** data 'TD_i'
3. Construct a weak learners $P_1, P_{2,} P_{3,} \dots . P_k$
4. Measure the similarity between training and testing data
5. Classify the patient data
6. **End for**
7. Combine the set of weak learners results '$E = \sum_{j=1}^{k} \quad R_j(d)$'
8. **For** each weak learner 'R_j'
9. Assign the weight value
10. Measure the training loss
11. Update weight value
12. Apply gradient descent function
13. Identify the weak learner with minimal training loss
14. Attain the strong classification results
15. **End for**
End

Algorithm 1 explains the step-by-step process of skin disease classification in GSRMAB Method with higher accuracy. An ensemble classifier has taken the number of training data as an input. For every patient data, the ensemble technique constructs the number of weak learners. The weak learner uses ruzicka similarity for examining the testing and training data. Depending on the similarity analysis, a hyperplane classifies the data into multiple classes. The weak learner results are joined to attain the strong results. The weight is initialized to the weak learner results. After that, the training loss is determined depending on the actual and predicted classification results. The gradient function is used to identify the weak learner results with lesser loss value. This in turn increases the skin disease classification performance.

4. EXPERIMENTAL EVALUATION

In this section, experimental evaluation of GSRMAB Method and existing Convolution Neural Network (CNN) system [1] and Targeted Ensemble Machine Classify Model (TEMCM) [2] is carried out using JAVA software with Dermatology Data Set. The URL of the dataset is given as https://archive.ics.uci.edu/ml/datasets/Dermatology. The dataset comprises 34 attributes and 366 instances. The attributes are classified into two types, namely Clinical Attributes and Histopathological Attributes. Among 34 attributes, 33 attributes are linear valued and one is nominal. The six classes of skin disease include:

- C1 - Psoriasis
- C2 - Seborrheic dermatitis
- C3 - Lichen planus
- C4 - Pityriasisrosea
- C5 -Chronic dermatitis and
- C6 - Pityriasis rubra

Biopsy is considered as the fundamental treatment in diagnosing skin diseases. The performance metric of GSRMAB Method are discussed with four metrics such as

- Classification Accuracy,
- Precision,
- Recall and
- F1-score

4.1 Impact on Classification Accuracy

Classification accuracy is defined as the ratio of number of correctly classified predictions to the total number of predictions. The classification accuracy is calculated as,

$$Classification\ Accuracy = \frac{Number\ of\ correct\ classified\ prediction}{Total\ number\ of\ predictions} \qquad (10)$$

From (10), the classification accuracy is computed. When the classification accuracy is higher, the method is said to be more efficient.

Table 1 Comparison of Classification Accuracy

Model	Classification Accuracy
CNN system	0.8449
TEMCM	0.88.97
Proposed GSRMAB Method	0.9298

Table 1 discusses the classification accuracy of three different methods, namely GSRMAB Method and existing Convolution Neural Network (CNN) system [1] and Targeted Ensemble Machine Classify Model (TEMCM) [2]. The classification accuracy of the proposed method is higher than other conventional techniques. The graphical representation of classification accuracy is given in figure 4

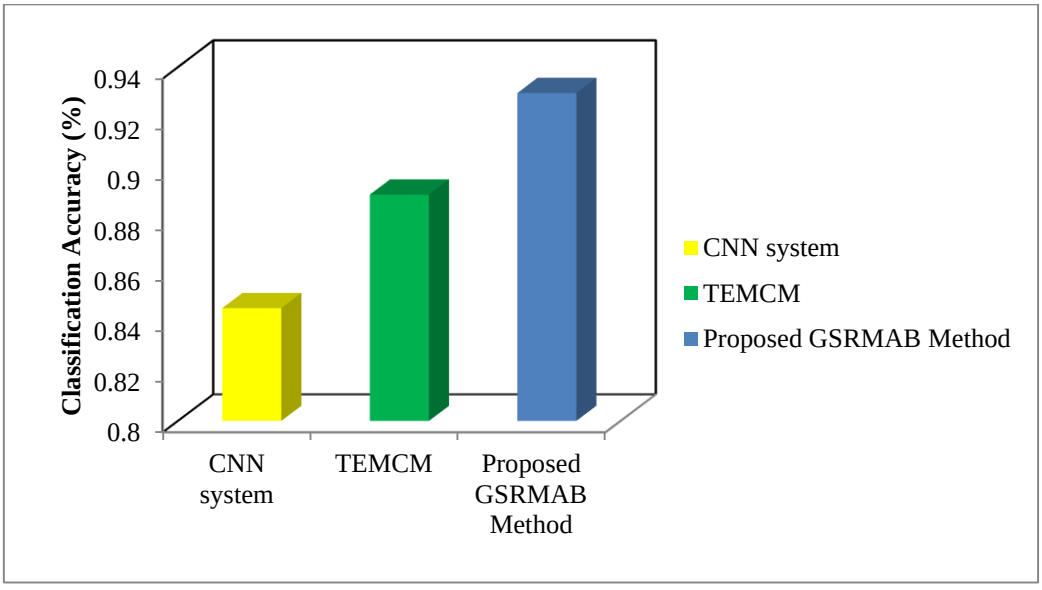

Figure 4 Measurement of Classification Accuracy

Figure 4 explains the diagrammatic representation of classification accuracy. From figure, the horizontal axis represents different methods and the vertical axis symbolizes the classification accuracy. The blue color bar represents the classification accuracy of proposed GSRMAB method. The yellow and green color bar denotes the classification accuracy of CNN system and TEMCM. The classification accuracy performance is higher when compared to other methods. This is due to the application of preprocessing, generalized softmax regressive feature selection and modest adaptive boost classification. In the proposed method, only 10 important features are chosen for the classification with lesser complexity and high accuracy rate. The unwanted features are eliminated to enhance the skin disease classification. Therefore, the classification accuracy of proposed GSRMAB method is 10% higher when compared to CNN system and 5% higher when compared to TEMCM.

4.2 Impact on Precision

Precision is described as the ratio of total number of positives to the total number of correctly positive observations. Therefore, the precision denotes the correct prediction of skin disease and it is represented as,

$$Precision = \frac{Total\ Positives}{Total\ Positives + False\ Positives} \quad (11)$$

From (11), the precision is determined. True positive denotes skin disease identified for patient and it is correctly classified into prediction list. False positive represents the skin disease not identified for patient. True negative represents the disease not identified for patient and it is correctly classified into non-prediction list or not considered. False negative indicates the disease identified for the patient but it is wrongly classified into non-prediction list.

4.3 Impact on Recall

Recall is the described as classifier capacity to identify all the successful data. Recall indicates the capability to identify the skin disease and it is represented by below formula,

$$Recall = \frac{Total\ Positives}{Total\ Positives + False\ Negatives} \quad (12)$$

From (12), the recall is calculated.

4.4 Impact on F1-Score

F1-Score generates the single score that joins the precision and recall problems into a single value. It is computed as

$$F - 1\ score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (13)$$

From (12), the F-1 score is calculated. Precision, Recall and F-1 Score values for proposed GSRMAB method, CNN System, TEMCM are stated in Table 2. Figure 5 show that the proposed model attains higher performance than other technique in all three parameters.

Table 2 Precision, Recall and F-1 Score for CNN System, TEMCM and Proposed GSRMAB method

Models	Parameters		
	Precision	Recall	F1 Score
CNN System	0.81	0.86	0.84
TEMCM	0.85	0.89	0.86
Proposed GSRMAB Method	0.95	0.97	0.97

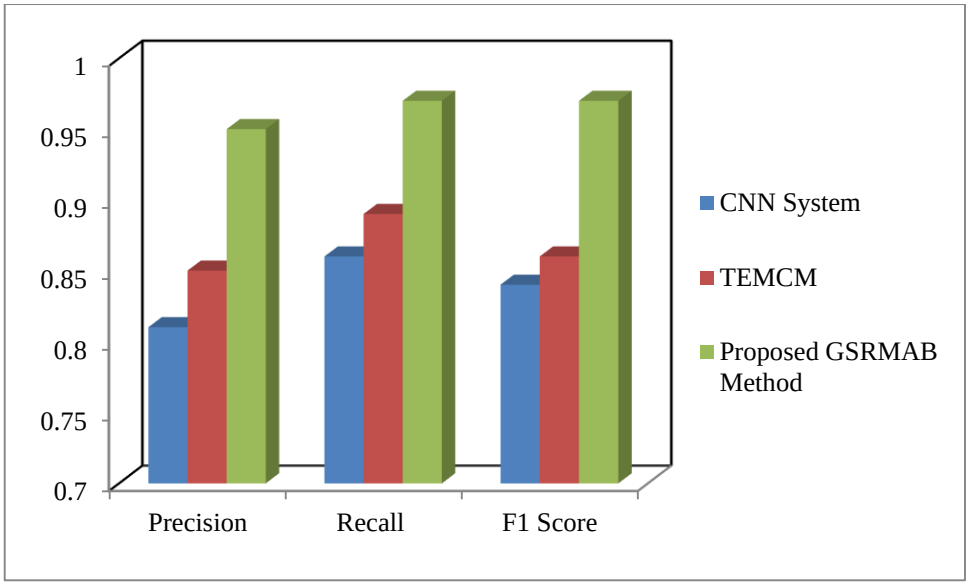

Figure 5 Measurement of Precision, Recall And F-1 Score

From the Table 2 and Figure 5, the proposed GSRMAB Method attains higher precision, recall and F-1 score values when compared to other techniques. This is because of applying generalized softmax regressive feature selection and modest adaptive boost classification. The feature selection process selects the relevant features and eliminates the unwanted features to enhance the skin disease classification. After that, modest adaptive boost classification uses the hyperplane to classify the data into multiple classes. The weak learner results are joined to attain the strong results. Therefore, the precision of proposed GSRMAB method is 17% higher when compared to CNN system and 12% higher when compared to TEMCM. In addition, the recall of proposed GSRMAB method is 13% higher when compared to CNN system and 9% higher when compared to TEMCM. Consequently, the F-1 score of proposed GSRMAB method is 15% higher when compared to CNN system and 13% higher when compared to TEMCM.

5. CONCLUSION

A new method termed GSRMAB Method performs efficient skin disease classification with higher accuracy and lesser time consumption. Data preprocessing transforms the raw data into an understandable format. Generalized Softmax Regressive Feature Selection Process selects the relevant features from the pre-processed input database. After feature selection, GSRMAB Method employs Modest Adaptive Boost Classifier where each data is classified into multiple classes through designing strong classifier with higher accuracy. GSRMAB Method constructs strong classifier through reducing the training error of weak learner results for accurate skin disease classification. Consequently, GSRMAB Method enhances the skin disease classification performance when compared to existing works. Experimental result shows that the proposed GSRMAB Method outperformed better than existing techniques in terms of precision, recall, F1 Score, and classification accuracy.

REFERENCES

[1] Karthik R, Tejas Sunil Vaichole, Sanika Kiran Kulkarni, Ojaswa Yadav and Faiz Khan “Eff2Net: An efficient channel attention-based convolutional neural network for skin disease classification”, Biomedical Signal Processing and Control, Elsevier, Volume 73, March 2022, Pages 1-15

[2] Hong Qing Yu and Stephan Reiff-Marganiec, “Targeted Ensemble Machine Classification Approach for Supporting IoT Enabled Skin Disease Detection”, IEEE Access, Volume 9, March 2021, Pages 50244 - 50252

[3] Anurag Kumar Verma, Saurabh Pal, and Surjeet Kumar, "Classification of Skin Disease using Ensemble Data Mining Techniques", Asian Pacific Journal of Cancer Prevention (APJCP), Volume 20, Issue 6, 2019, Pages 1887–189

[4] Yanyang Gu, Zongyuan Ge, C. Paul Bonnington and Jun Zhou, "Progressive Transfer Learning and Adversarial Domain Adaptation for Cross-Domain Skin Disease Classification", Volume 24, Issue 5, May 2020, Pages 1379 – 1393

[5] Li-sheng Wei, Quan Gan, and Tao Ji, "Skin Disease Recognition Method Based on Image Color and Texture Features", Computational and Mathematical Methods in Medicine, Hindawi Publishing Coorporation, Volume 2018, 2018, Pages 1-10

[6] Mehak Arshad, Muhammad Attique Khan, Usman Tariq, Ammar Armghan, Fayadh Alenezi, Muhammad Younus Javed, Shabnam Mohamed Aslam and Seifedine Kadry, "A Computer-Aided Diagnosis System Using Deep Learning for Multiclass Skin Lesion Classification", Volume 2021, 2021, Pages 1-15

[7] Jufeng Yang, Xiaoping Wu, Jie Liang, Xiaoxiao Sun, Ming-Ming Cheng, Paul L. Rosin and Liang Wang, "Self-Paced Balance Learning for Clinical Skin Disease Recognition", IEEE Transactions on Neural Networks and Learning Systems, Volume 31, Issue 8, August 2020 Pages 2832 - 2846

[8] Yutong Xie, Jianpeng Zhang, Yong Xia and Chunhua Shen "A Mutual Bootstrapping Model for Automated Skin Lesion Segmentation and Classification", IEEE Transactions on Medical Imaging, Volume 39, Issue 7, July 2020, Pages 2482 – 2493

[9] S. Arivazhagan, K. Divya and M. P. Subadevi, "Skin Disease Classification by Extracting Independent Components", Computer Science, 2012, Pages 1-15

[10] D. Naveen Raju, Hariharan Shanmugasundaram and R. Sasikumar, "Fuzzy segmentation and black widow–based optimal SVM for skin disease classification", Medical & Biological Engineering & Computing, Springer, Volume 59, 2021, Pages 2019–2035

[11] Xue-Jun Liu, Kai-li Li, Hai-ying Luan, Wen-hui Wang and Zhao-yu Chen, "Few-shot learning for skin lesion image classification", Multimedia Tools and Applications, Springer, Volume 2022, 2022, Pages 1-14

[12] Khalid M. Hosny, Mohamed A. Kassem and Mohamed M. Foaud, "Classification of skin lesions using transfer learning and augmentation with Alex-net", PLoS ONE, Volume 14, Issue 5, 2019, Pages 1-17

[13] Ran Cui, Hua Zhang, Miao Chen, Qian Wang, Qiang Tong, Zhiyong Chen, Ke-Xiang Yan, Yang-Feng Ding and Sheng-Ming Dai, "Unequal relevance between different subtypes of fingernail psoriasis and psoriatic arthritis", Clinical Rheumatology, Springer, Volume 2022, 2022, Pages 1-18

[14] Suhong Kim, Peter Lee, Kyeong Taek Oh, Min Soo Byun, Dahyun Yi, Jun Ho Lee, Yu Kyeong Kim, Byoung Seok Ye, Mi Jin Yun, Dong Young Lee and Yong Jeong, "Deep learning-based amyloid PET positivity classification model in the Alzheimer's disease continuum by using 2-[18F]FDG PET", EJNMMI Research, Springer, Volume 11, Issue 56, 2021, Pages 1-15

[15] Qilin Sun, Chao Huang, Minjie Chen, Hui Xu and Yali Yang "Skin Lesion Classification using Additional Patient Information", BioMed Research International, Hindawi Publishing Corporation, Volume 2021, 2021, Pages 1-18

[16] Syeda Fatima Aijaz, Saad Jawaid Khan, Fahad Azim, Choudhary Sobhan Shakeel and Umer Hassan, "Deep Learning Application for Effective Classification of Different Types of Psoriasis", Journal of Healthcare Engineering, Volume 2022, 2022, Pages 1-15

[17] V. Ramesh, Abdulsattar Abdullah Hamad, Mohanad Fadhil Jwaid, M. Sathyabama, Mustafa Mahdi Abdulridha, Noor Mohammed Kadhim, and Assaye Belay "Early Recognition of Skin Malignancy in Images Based on Convolutional Networks by Using Dynamic System Model", Journal of Nanomaterials, Hindawi Publishing Coorporation, Volume 2022, 2022, Pages 1-15

[18] Ha Min Son, Wooho Jeon, Jinhyun Kim, Chan Yeong Heo, Hye Jin Yoon, Ji-Ung Park & Tai-Myoung Chung, "AI-based localization and classification of skin disease with erythema", Scientific Reports, Springer, Volume 11, Issue 5350, 2021, Pages 1-18

[19] Nawal Soliman, AL Kolifi and AL Enez, “A Method of Skin Disease Detection Using Image Processing and Machine Learning”, Procedia Computer Science, Elsevier, Volume 163, 2019, Pages 85-92

[20] Usama Ijaz Bajwa, Sardar Alam, Nuhman ul Haq, Naeem Iqbal Ratyal and Muhammad Waqas Anwar, “Skin Disease Classification using Neural Network”, Current Medical Imaging, Volume 16, Issue 6, 2020, Pages 711 – 719