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***Research paper***



# An Effective Detection of Skin Cancer Using A Multi-Module CNN

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**Abstract**

In modern years, Deep Learning (DL) systems, predominantly Convolutional Neural Networks (CNNs), have shown hopeful outcomes in computer-aided diagnosis and classification of skin lesions. In this paper, an advanced methodology for skin cancer detection is proposed that leverages preprocessing and classification-based multi-module CNN. The proposed method begins with preprocessing and data augmentation steps for improving the resolution of the skin lesions, including noise reduction and contrast enhancement, which optimize the input data for subsequent analysis. Subsequently, a multi-module CNN architecture is employed, consisting of interconnected modules designed to capture diverse features crucial for accurate classification. The overall proposed work is implemented in Python software, and a comparative analysis is carried out with the existing approaches to show the prominence of the developed work. The results of the investigation show that the model created has a high accuracy of 97% and a short classification time, which makes it a useful tool for helping dermatologists detect skin cancer early.

***Keywords***: *Skin Cancer; Early Detection; Preprocessing Steps; Multi-Module Convolutional Neural Network; Python Software.*

## 1. Introduction

With rising incidence rates and potentially fatal consequences, skin cancer is a serious worldwide health concern [1-2]. For successful treatment and better patient outcomes, early identification of skin cancer is essential [3]. To identify skin lesions, dermatologists use visual inspection and specialized knowledge; however, this method is both arbitrary and subject to human error. Therefore, there is a growing demand for computer-aided diagnosis systems to assist dermatologists in accurately identifying and classifying skin cancer [4-5]. Computer-assisted diagnosis helps medical professionals analyze dermoscopy operations, but it presents considerable obstacles and weariness for patients when skin illnesses are identified manually, particularly in instances of limited expertise or professional availability during the diagnostic process, which offers a solution for reducing both inter- and intra-variability in dermatological image categorization [6-8]. However, contemporary computer-assisted systems in dermatology face two primary challenges. There is a deficiency of adequate data, and the imaging process presents a formidable obstacle, as skin images are acquired using a specialized instrument known as dermoscopy [9-10], as opposed to other medical imaging types like histology and biopsy images, which are produced by microscopic analysis and biopsy. Modern methods require substantial preprocessing and classification procedures to properly classify skin images [11]. Machine learning (ML) methods play a pivotal role by eliminating the need for manual feature extraction and enhancing the efficiency of classification tasks [12].In the current era, there has been a surge of interest in leveraging ML strategies for aiding in precise cancer detection. Notably, it has markedly augmented cancer prediction accuracy, exhibiting an improvement of 15% to 20% over the past few decades [13]. However, ML methods require preliminary information and complex image preprocessing. Some CNN-based classifiers have demonstrated capabilities on par with dermatologists in classifying skin cancer images [14]. CNNs with simple architectures are prone to overfitting on limited training datasets [15-16]. Table 1 represents the existing technique for skin cancer detection along with its accuracy.

**Table 1:** Literature Review Summary

| Reference | Methodology | Dataset | Accuracy |
|---|---|---|---|
| MdShahin Ali[17] | DCNN | HAM10000 dataset | 93.16% |
| Saket [18] | MobileNet | HAM10000 | 91.36% |
| Walaa Gouda[19] | CNN | ISIC2018 | 83.2% |
| LishengWei [20] | Lightweight CNN | ISBI 2016 | 96% |

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| | | | |
|---|---|---|---|
| Natasha Nigar[21] | Explainable Artificial Intelligence | (ISIC) 2019 | 94.47% |
| MostafizAhammed [22] | SVM | HAM10000 | 91.2% |
| Lixin Liu[23] | RF | HMI | 95.2% |
| Tri-Cong Pham [24] | EfficientNetB4-CLF | CIFAR-10 | 89.97% |

Many approaches using CNNs [17-19] often suffer from limited feature extraction capability when compared to more advanced or deeper architectures, leading to lower accuracy, particularly on complex datasets. Lightweight models like the one proposed in [20] achieve high accuracy but may trade off robustness in real-world settings due to reduced parameter space. Classical machine learning approaches such as SVM [22], [23] lack deep feature learning and depend heavily on handcrafted features, making them less effective for large and diverse datasets. While explainable AI models [21] offer interpretability, they may increase computational complexity and have slower inference times. Moreover, models in [24], trained on non-medical datasets like CIFAR-10, are not directly applicable to dermatology tasks due to domain mismatch. Considering transformer-based models, they require large amounts of labeled data to effectively learn complex representations, which is often a challenge in the medical domain due to data scarcity and annotation costs. They also tend to be computationally expensive, requiring significant resources and longer training times compared to traditional CNNs, making them less accessible for low-resource settings or real-time clinical deployment [25], [26]. Moreover, transformers lack the inductive biases like spatial locality and translation invariance inherent in CNNs, which can be advantageous in medical imaging, where structural features are critical. Without sufficient data, this can lead to overfitting or suboptimal generalization [27], [28]. With the goal of enhancing the proposed system's accuracy and performance, the Multi-Module CNN approach is proposed in this paper, which provides high accuracy and performance indices, thereby the skin cancer is predicted early than the other topologies. Moreover, the contributions to the developed work are illustrated below.

- To improve both the quality and clarity of skin lesion images, a preprocessing stage is carried out that enhances the visibility of important features for subsequent analysis, and it contributes to the more precise detection of skin cancer.
- The multi-module CNN architecture for skin cancer detection, which leads to improved accuracy in the detection process, enabling more reliable and precise detection of malignant skin lesions.
- The proposed technique improves the early detection and management of skin cancer, leading to better patient results and potentially saving lives.

## 2. Proposed Methodology

To effectively classify a skin cancer and enhance patient outcomes, early detection and correct diagnosis are essential. Artificial intelligence approaches hold considerable potential for automating the diagnosis and detection process, especially with the advances in computer vision and DL. Conventional techniques may struggle to capture the diverse and intricate features present in skin cancer lesions. They may have limited capacity to learn and represent complex patterns associated with different kinds of skin cancer. Henceforth, the proposed work developed a novel multi-module CNN for accurate classification, which leverages the depth and hierarchical structure of its network to learn more discriminative features and leading to improved feature representation and better detection performance. Fig. 1 exhibits the flow diagram for the implemented work.

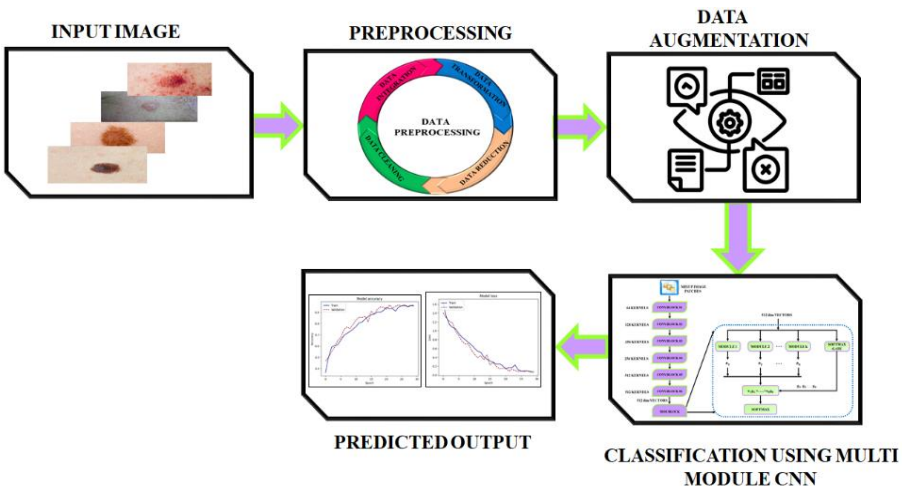



**Fig. 1:** Proposed Block Diagram of Skin Cancer Prediction Model.

The SIIM-ISIC 2019 dataset, a well-known benchmark dataset for the diagnosis of skin cancer, provides a vast number of dermoscopic pictures of skin lesions that are used as input for an algorithm. To improve their quality for further analysis, the input images from the SIIM-ISIC 2019 dataset go through preprocessing procedures. It includes data cleaning, data reduction, data transformation, and data integration. To augment the SIIM-ISIC 2019 dataset and increase its diversity, data augmentation techniques are applied. These techniques involve random transformations like scaling, flipping, rotation, and adding noise to skin lesion images. Preprocessed and augmented images are applied to a multi-module CNN architecture. The multi-module CNN consists of interconnected CNN modules, each designed to learn specific features or patterns relevant to skin cancer detection with high classification accuracy. The predicted output provides probability or confidence scores for different classes of skin cancer, indicating the probability of multiple skin cancer classifications. The predicted output is assessed utilizing performance metrics.

### 2.1. Dataset

This dataset consists of 33,569 images. 25,331 images are employed for training, and 8,238 images are taken for testing. In addition to ground truth data for the training set, it also provides ground truth data for various classes. The eight classes from the training set are also

included in the testing set, along with one unidentified class. The training and testing sets both have access to patient metadata. Details like the patient's gender, anatomical place, lesion ID, and approximate age are provided by the training metadata. Among the training images, 23,247 have specified lesion IDs, while 2,084 images have unspecified lesion IDs. The specified lesion IDs belong to a total of 11,848 unique IDs out of the 25,331 training images, as in Table 2.

**Table 2:** Class Distribution of ISIC 2019 Dataset

| Class | ISIC 2019 dataset |
|---|---|
| Melanoma | 4522 |
| Melanocytic nevus | 12,875 |
| Basal cell carcinoma | 3223 |
| Actinic keratosis | 867 |
| Benign keratosis | 2624 |
| Dermatofibroma | 239 |
| Vascular lesion | 253 |
| Squamous cell carcinoma | 628 |
| Total | 25,331 |

## 2.2. Preprocessing stage

To ensure enhanced feature quality and consistency in classification outcomes, preprocessing is applied to all input images in the ISIC-2019 dataset. Given the Multi-Module CNN's reliance on extensive training iterations, a substantial image dataset was necessary to mitigate the risk of overfitting. The preprocessing stages are specified in Fig. 2, which is discussed as follows.

Data cleaning: The data cleaning process includes identifying and correcting errors or variations in the data. For skin cancer datasets, it could involve removing duplicates, correcting mislabeled images, or addressing any artifacts present in the images that could affect classification accuracy.

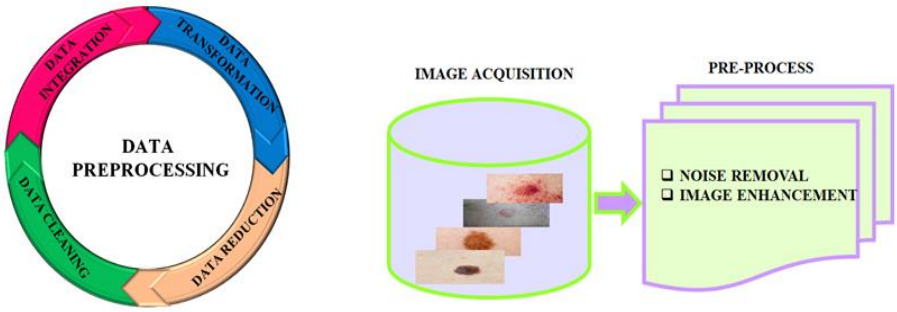



**Fig. 2:** Schematic Diagram of Data Preprocessing.

Data integration: Data integration as part of the preprocessing stage involves combining and harmonizing data from different sources to make a unified dataset that effectively used for analysis and modeling. To identify the relevant data sources for skin cancer analysis, these sources may include electronic health records, medical imaging databases, clinical trial data, genetic data repositories, or any other relevant sources containing information related to skin cancer.

Data reduction: Data reduction, as part of the preprocessing stage in skin cancer prediction, refers to techniques that aim to lessen the dimensionality or size of the dataset while preserving relevant information. It involves selecting a subset of features or instances to improve computational efficiency and mitigate the risk of overfitting.

Data transformation: It involves applying various mathematical or statistical techniques to modify the original dataset to improve the quality of the image or improve the skin cancer prediction model performance.

By applying the preprocessing stage, noise from the image is efficiently removed by enhancing the quality of the input image. The data augmentation process is utilized to augment a SIIM-ISIC 2019 dataset and increase its diversity, which is explained as follows.

## 2.3. Data augmentation model

To address overfitting and improve dataset diversity, a variety of data augmentation approaches are fed into the training set using the picture data generator function from the Python Keras package. Scaling pixel values to a range of 0 to 1 lowers the computational cost (achieved through a scaling factor of 1.0/255). Rotation transformations are employed, rotating images by 25 degrees. Width and height shift ranges of 0.1 were utilized to shift images horizontally and vertically, respectively. Shear transformation was applied with a shear angle of 0.2. Random zoom transformation is introduced with a zoom range of 0.2, magnifying images. Horizontal flipping was performed. Table 3 lists image augmentation systems.

**Table 3:** Image Augmentation Systems

| Transformations | Setting | |
|---|---|---|
| Zoom transformation | | 0.2 |
| Shear transformation | | 20° |
| Scale transformation | Ranged from 0 to 1 | |
| Horizontal transformation | True | |
| Rotational transformation | | 25° |

Brightness transformation is applied within a range of 0.5 to 1.0, where 0.0 signifies no change and 1.0 denotes extreme brightness. Channel shift transformation involved randomly shifting channel values within a range of 0.05, with the fill mode set to 'closest'. Moreover, a multi-module CNN architecture is employed, which consists of interconnected modules designed to capture diverse features crucial for accurate classification, as discussed as follows.

### 2.4. Modelling of multi-module CNN

According to the analysis of the C-DNN architecture, the initial six convolutional blocks are employed to transform input image patches into condensed and discriminative embeddings, which are referred to as high-level features. In the next step, a dense block consisting of a fully connected layer and a Softmax layer is employed to classify features. To address a potential issue of the embedding containing more information than can be extracted by a single fully connected layer, this system substitutes a dense block with a mixture-of-Modules (MoM) block, as illustrated in Fig. 3.

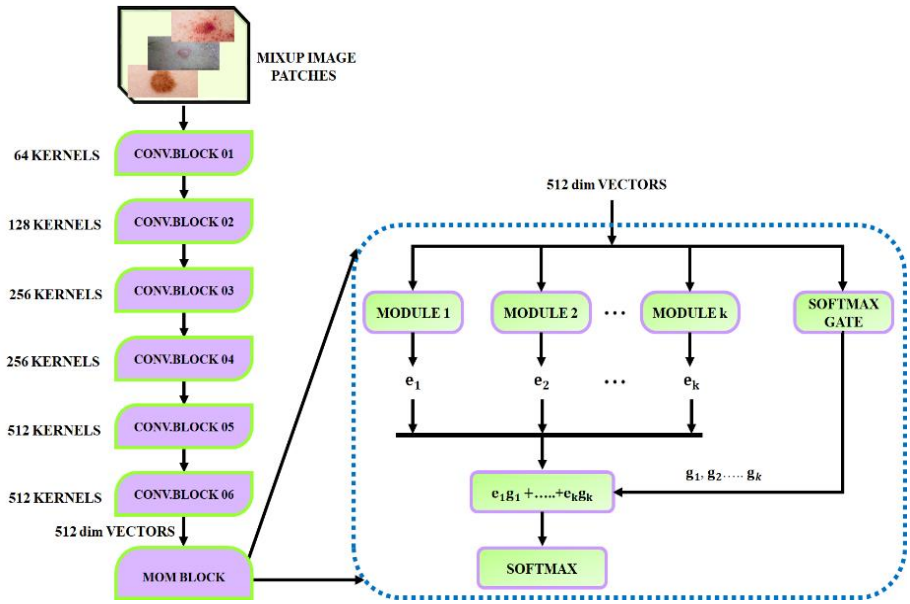



**Fig. 3:** Multi-Module CNN-Based Classification Model.

The structure of the Mom block consists of multiple modules as specified in Fig. 3, each connected to a gate network that determines which module is applied to a specific input region. As a result of our specific context, the final global average pooling layer (Gap) embedding is obtained concurrently with all modules. To create the final classification output, all module outputs are gated, which denotes that it is combined and weighted, and then passed through a Softmax layer. In, proposed system, each module is composed of a fully connected layer, followed by a Rectified Linear Unit (ReLU). Each module in an architecture has an input dimension of 512, meaning it receives a 512-dimensional input. The number of categories C that are undergoing classification determines the output dimension for each module. As an extra fully connected layer with a Softmax activation function, the gate network in this system is implemented as a Softmax Gate. An architecture's number of modules determines the Softmax Gate's gating dimension. The$g_1, g_2, \ldots, g_k$ indicates the output of the gate network, $e_1, e_2, \ldots, e_k \in R^C$ Specifies the output vectors from the K module. Here, $g_k \in R$ and$\sum g_k = 1$.
The forecast output is then found as,

$$\hat{y} = \text{softmax}\{\sum_{k=1}^{K} g_k e_k\} \quad (1)$$

The hyperparameters of the classification model are listed in Table 4.

**Table 4:** Hyperparameters of Classification Model

| Parameters | Value/description |
|---|---|
| Number of convolutional blocks | 6 |
| Vector embedding dimension | 512 |
| Loss function | Categorical cross entropy |
| Optimizer | Adam |
| Initial learning rate | 0.001 |
| Batch size | 32 |
| Number of epochs | 30 |
| Regularization | dropout |
| Input dimension | 512 |
| Output dimension | 8 |
| Number of modules | 4 |

## 3. Results and Discussion

In this proposed study, preprocessing, data augmentation, and a novel multi-module CNN design are proposed for skin cancer detection. This proposed work is executed in Python software for validating the effectiveness of the proposed system. Moreover, a comparison analysis is made in the subsequent section to prove the importance of the developed work. This robust performance underlines the efficacy of our approach in accurately identifying skin cancer lesions, showcasing its potential for clinical application, and the results for the proposed work are given below.

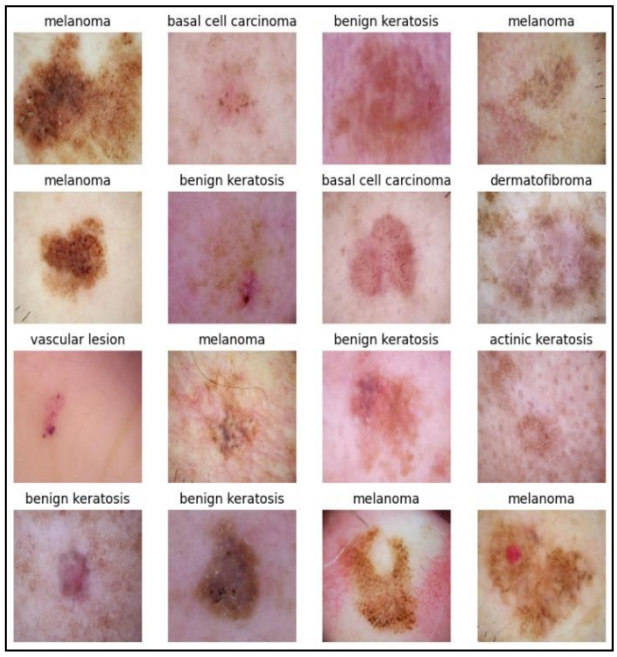



**Fig. 4:** Sample Skin Cancer Images Taken from the ISIC 2019 Dataset.

Fig. 4 indicates the Sample skin cancer images, taken from the ISIC 2019 dataset10,015 photos of skin lesions from seven types are included in the dataset: vascular lesions (142 images), actinic keratosis (327 images), basal cell carcinoma (514 images), melanocytic nevi (6705 images), Dermatofibroma (115 images), and melanoma (1113 images). All images are captured using a dermoscopy instrument, which is a type of magnifier specifically designed for photographing skin lesions.

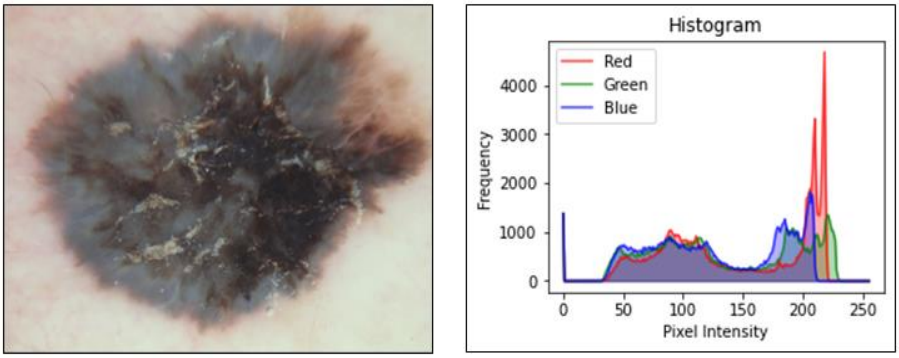



**Fig. 5:** Dermoscopic Image of A Skin Lesion with A Corresponding Histogram.

Fig. 5 presents a dermoscopic image of a skin lesion with a corresponding histogram of pixel intensity. A dermoscopic image showcases a melanocytic lesion with various shades of brown and black, indicative of potential malignancy. The histogram provides a distribution of pixel intensity values across Red, Green, and Blue (RGB) channels of the image, which is used to analyze the color characteristics and variations within the lesion. Peaks in the red channel suggest a dominance of red tones, which is a significant feature in the analysis of skin cancer images. Such detailed visual and statistical analyses assist in an accurate classification and diagnosis of skin conditions through image processing techniques.

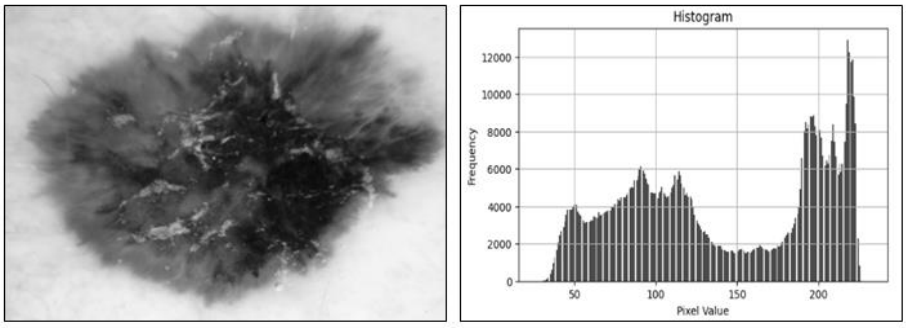



**Fig. 6:** Dermoscopic Image of Skin Lesion and Its Corresponding Grayscale Histogram.

Fig. 6 displays the monochrome (black and white) dermoscopic image of a skin lesion and its corresponding grayscale histogram. The dermoscopic image reveals the lesion with varied shades of gray, which provides important diagnostic cues when assessing for malignancy. The histogram quantifies the distribution of grayscale pixel values, offering insight into the texture and structural composition of the lesion.

High peaks in the histogram indicate a concentration of pixels with similar intensity values, which is integral to identifying patterns characteristic of certain types of skin lesions. This information is essential for automated analysis systems that rely on textural and color features to distinguish various malignant lesions in the early detection of skin cancer.

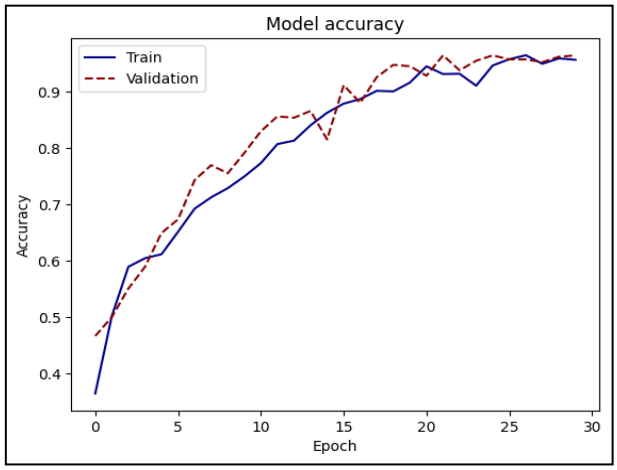



**Fig. 7:** Progress of Training and Validation Accuracy.

The skin cancer detection model is trained by utilizing categorical cross-entropy as the loss function and the Multi-Module CNN. The model is trained for 30 epochs with a batch size. An accuracy metric is employed to monitor the performance during training, by utilizing the proposed classification model, the superior accuracy is obtained by the value of 97%. After 30 epochs, both the training and validation accuracies reached a stable state. The learning curves depicting training and validation accuracies as presented in Fig. 7.

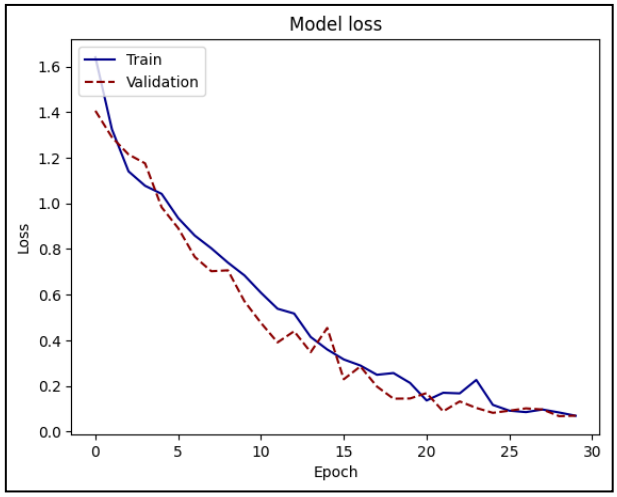



**Fig. 8:** Process of Training and Validation Loss.

The model employs the DL with a cross-entropy loss function and tracks performance using accuracy as a metric. Training lasts for 30 epochs with a batch size of 16, during which both training and validation accuracies stabilize. The learning curves are represented in Fig.8respectively.

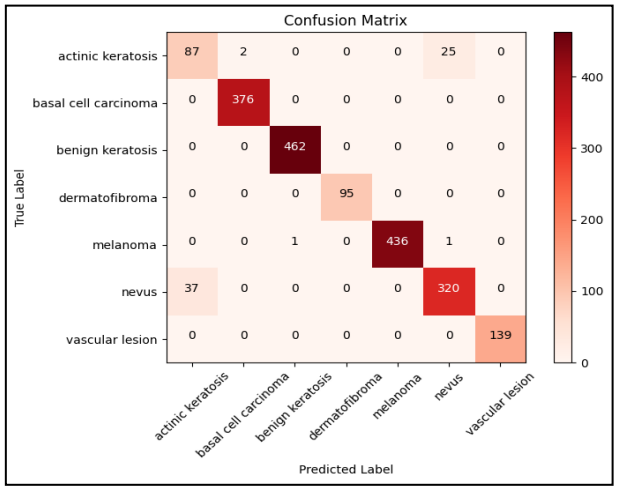



**Fig. 9:** Confusion Matrix Using the Multi-Module CNN for Skin Lesion Classes.

The confusion matrix for the Multi-Module CNN displays the counts of true positives and false negatives forecast by the developed model, as specified in Fig. 9, which illustrates the confusion matrix for categorizing the labels using Multi-Module CNN models and balanced data following the suggested method. The figure demonstrates that the overall accuracy has reached 97%, surpassing the performance achieved when using imbalanced data, as anticipated.

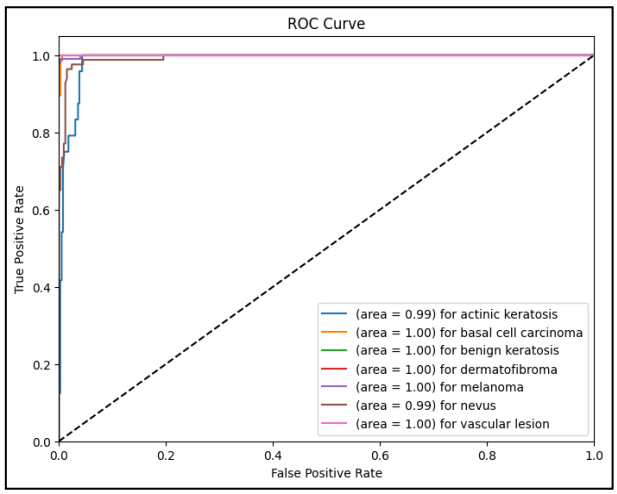



**Fig. 10:** ROC Curve for Each Class Obtained in the Proposed Multi-Module CNN.

The ROC plots in Fig. 10 confirm the superiority of the Multi-Module CNN-based DL over the existing model, which exhibits a better AUC. Additionally, both the micro-average and macro-average areas are higher in the proposed model, although it incurs reduced computational complexity and requires minimal computation. However, in the domain of medical diagnosis, precision outweighs lower computational cost compared to other ML and DL models.

### 3.1. Evaluation metrics

Assessing model performance is essential for understanding its effectiveness in predicting outcomes accurately. This evaluation varies based on the type of model employed, including classification or regression. For classification tasks like identifying cancerous cells in skin lesion images, evaluation metrics are crucial, which is as discussed below. These metrics collectively gauge the model's capacity to classify lesions correctly, providing insights into its efficacy in clinical settings.

Precision: When evaluating a model's performance, precision is an essential parameter, especially when dealing with situations where False Positives could have serious repercussions. When it comes to the skin cancer classification, precision is referred to as the probability of correctly predicting malignant occurrences among all cases; then the model is anticipated to be positive. A low precision suggests a higher likelihood of false alarms, where non-cancerous images are incorrectly classified as cancerous.

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \tag{2}$$

In this context, TP denotes True Positive occurrences, while FP signifies instances of False Positives.

Recall: In addition to precision, recall refers to a sensitivity, which precisely identifies every positive case. In the context of aggressive detection classification problems like identifying cancerous cells, recall specifies the proportion of correctly identified cancerous cases between all actual positive cases. A low recall suggests a higher rate of false negatives, where cancerous cells are erroneously classified as non-cancerous. On the other hand, a high recall specifies that the model is successful in reducing false negatives, meaning that most malignant cells are correctly recognized.

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FP}} \tag{3}$$

F1 Score: It delivers a detailed evaluation of a model's performance, which ranges from 1 to 0, and shows how recall and precision are balanced. When the predicted values perfectly align with the expected ones, the F1 score reaches its maximum value of 1. Conversely, if expected ones are not matched with predicted values, the F1-score drops to 0, which classifies both positive and negative events by combining precision and recall.

$$\text{F1} - \text{Score} = \frac{\text{2.precision.Recall}}{\text{Precision+Recall}} \tag{4}$$

Accuracy: Accuracy assesses the proximity of the forecast output to the actual value.

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \tag{5}$$

In this instance, TN stands for True Negatives, while FN Indicates occurrences of False Negatives.

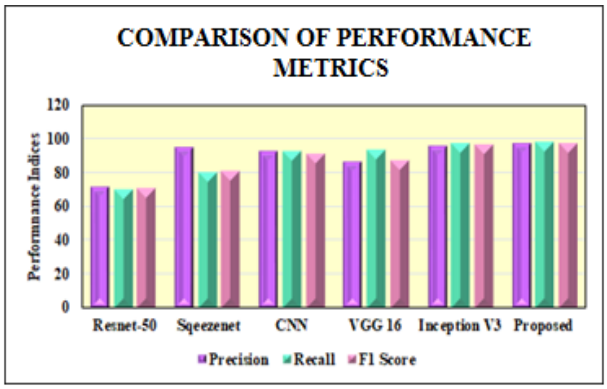



**Fig. 11:** Comparison Graph of Performance Indices.

The Multi-Module deep learning model has attained greater performance than the existing models as indicated by a comparative assessment in Fig. 11. Across all three performance metrics, including precision, Recall, and F-score model outperforms the proposed topology as represented in Table 5.

**Table 5:** Comparison of Performance Indices

| DL topologies | Precision (%) | Recall (%) | F1 Score (%) |
|---|---|---|---|
| Resnet-50[25] | 72 | 70 | 71 |
| SqueezeNet[26] | 95.1 | 80.77 | 80.84 |
| CNN[27] | 93 | 93 | 91.7 |
| VGG 16 [28] | 87 | 94 | 87.5 |
| Inception V3 [29] | 96.32 | 97.25 | 96.85 |
| Proposed | 97.34 | 97.98 | 97.34 |

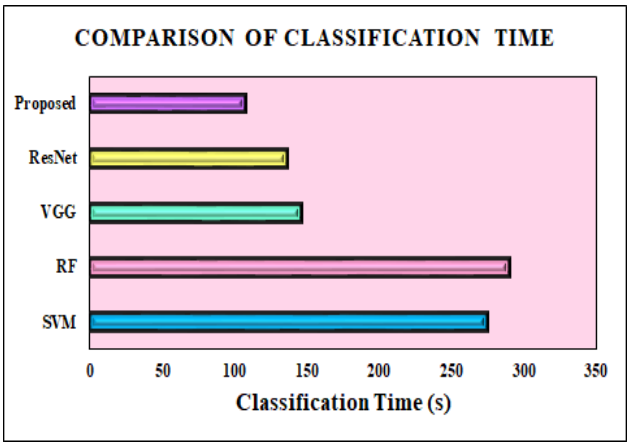



**Fig. 12:** Comparison of Classification Time (S).

The proposed Multi-Module CNN is compared with other existing topologies like ResNet, VGG, RF, and SVM for the classification time. From the graph indicated in Fig.12 obvious that the developed Multi-Module DL technique outperforms better than the conventional topologies by a time of 107s.

**Table 6:** Comparison of Accuracy

| DL approaches | Accuracy (%) | Sensitivity (%) | Specificity (%) |
|---|---|---|---|
| Resnet-50 | 70 | 68.5 | 71.2 |
| SqueezeNet | 92.18 | 90.4 | 93.1 |
| CNN | 91.2 | 89.7 | 92.0 |
| VGG 16 | 93.5 | 92.3 | 94.1 |
| Inception V3 | 96.87 | 95.6 | 96.9 |
| Proposed | 97 | 96.8 | 97.4 |

Compared to previous studies outlined in Table 6, the model presented in this work has demonstrated notably high accuracy of 97%, sensitivity of 96.8% and specificity of 97.4% for detecting skin cancer in early stages. The proposed approach performs efficiently in identifying true positive cases, thereby reducing the risk of false negatives. This underscores the effectiveness of the developed approach for classifying melanoma in its initial stages. Partnering with clinical experts ensures that the model's outputs are clinically relevant, interpretable, and aligned with diagnostic protocols. Dermatologists can provide valuable insights during model development, such as annotating ambiguous lesions, validating predictions, and identifying clinically meaningful patterns that may be overlooked by purely data-driven approaches. Moreover, integrating the proposed multi-module CNN model into clinical diagnostic workflows enhances diagnostic accuracy, reduces workload, and assists in triaging high-risk patients. By embedding this model into smartphone-based diagnostic tools or web platforms, users, especially those in remote or underserved areas capture images of suspected skin lesions and get instant early-stage evaluations. This capability can greatly enhance early detection and triaging, reducing the burden on dermatologists and facilitating faster access to care.

## 4. Conclusion

The current work presented a novel multi-module CNN approach based on classification for efficient early diagnosis of skin cancer. The Preprocessing, data augmentation, and classification topologies are used to show that the suggested strategy is effective in appropriately categorizing different classes of skin cancer. The integration of preprocessing steps enhances the quality of the original skin image, optimizing it with the multi-module CNN for further analysis. The classification mechanism makes reliable and precise predictions by utilizing this CNN technique, which helps with early identification and better patient outcomes. The proposed framework showed better performance indices, indicating that it could be a helpful tool for supporting dermatologists in promoting early skin cancer diagnoses. Performance of the proposed system is validated by implementing it in Python software, and a comparative analysis is made to show the significance of the developed work. As a consequence, the outcomes demonstrate that the proposed Multi-Module CNN achieves better performance metrics, which accomplishes a high accuracy of 97% and takes less classification time than the other DL models. Thereby, this research provides a foundation for developing advanced systems for early skin cancer prediction and ensuring advanced treatment for patients. The lack of clinical validation is one major issue; while the model demonstrates high accuracy on benchmark datasets like ISIC 2019, its performance is not directly translated to clinical settings due to variations in imaging devices, patient demographics, and lesion presentations. Addressing this limitation in the future is crucial before widespread adoption in dermatological practice can be achieved.

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