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R. Gomathi, S. Gnanavel, K.E. Narayana & B. Dhiyanesh

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# ACGAN: adaptive conditional generative adversarial network architecture predicting skin lesion using collaboration of transfer learning models

R. Gomathi[a], S. Gnanavel[b], K.E. Narayana[c] and B. Dhiyanesh[d]

[a]Department of Computer Science and Engineering, Bannari Amman Institute of Technology, Sathyamangalam, India; [b]Department of Computing Technologies, Faculty of Engineering and Technology, SRM Institute of Science and Technology, Kattankulathur, India; [c]Department of Computer Science and Engineering, Rajalakshmi Engineering College, Chennai, India; [d]Department of Computer Science and Engineering - ETech, SRM Institute of Science and Technology, Chennai, India

**ABSTRACT**

Skin cancer has become a serious disease which has the potential to scale up if it is not identified earlier. It is imperative to detect and give treatment to skin cancer promptly. Diagnosing skin cancer manually takes a lot of time and it is costly, and the probability of false diagnosis has increased due to the outstanding resemblances among various skin lesions. Enhancing the classification of multi-class lesions of skin needs the development of investigative systems which should be automated. Data augmentation with GANs and Adaptive Conditional Generative Adversarial Network strategies improves performance. The performance is tested using balanced and unbalanced datasets. Using a proper process of augmentation of data, the suggested system attains a 94% accuracy for the VGG16, 93% for the ResNet50 and 94.25% for ResNet101. The process of collaboration of all such methods improves accuracy further to 95%. In summary, the novelty of the work lies in its holistic approach to automated skin lesion classification, incorporating advanced deep learning models, novel data augmentation techniques and comprehensive performance evaluation on real-world datasets. These contributions collectively advance the field of computer-aided diagnosis for the detection of skin cancer and treatment.

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**KEYWORDS**
Skin cancer; deep learning; healthcare; neural networks; generative adversarial networks; data augmentation

## Abbreviations

| | |
|---|---|
| BCC | basal cell carcinoma |
| MEL | melanoma |
| SCC | squamous cell carcinoma |
| KS | Kaposi sarcoma |
| GAN | Generative Adversarial Networks |
| DL | Deep learning |
| ML | Machine Learning |
| CNN | convolutional neural networks |
| AK | actinic keratosis |
| SVM | support vector machine |
| ROC | receiver operating characteristic |
| FRCNN | Faster Region Convolutional Neural Networks |
| AGTO | African Gorilla Troops Optimizer |
| M-SVM | multi-class support vector machine |

### *Actinic keratosis*

| | |
|---|---|
| BKL | benign keratosis |
| DF | dermatofibroma |
| MEL | melanoma |
| NV | nevus |
| VASC | vascular lesion |

## 1. Introduction

Diseases like Skin cancer occur because of the process in which the DNA of healthy skin is mutated which leads to unwanted division and malignancy [1,2]. Certain factors, which contribute to the development of such disease, involve overexposure to ultraviolet (UV) radiation, exposure to the sun for a long time and the use of tanning beds [3]. In history, the disease skin cancer originates as irregular cell structures with different chromatin, nucleus and cytoplasm features [4]. It was found globally that this kind of disease ranks first which, in turn, is the reason for mortality [5]. Skin cancer poses a major public health challenge globally, with detecting earlier is crucial for efficient treatment and management. Manual diagnosing skin lesions is not just time-consuming and expensive but also subject to errors because of the subtle visual similarities among various types of lesions. To address these challenges, there has been a growing interest in developing automated systems for the classification of lesions of skin using the models of deep learning.

Many types of skin cancer diseases are available. Among them, some of the common types include BCC, MEL, non-melanoma skin cancer and squamous

**CONTACT** R. Gomathi rgomathi364@gmail.com Department of Computer Science and Engineering, Bannari Amman Institute of Technology, Sathyamangalam, 638401, India

cell carcinoma (SCC). Skin cancer types KS and AK encompass solar keratosis, lymphoma and keratoacanthoma less frequently occur. Some forms of skin cancer can lead to fatal problems and not all skin lesions indicate malignant tumours. The outermost layer of the skin called the epidermis is where the skin lesions originate. The type of skin lesion as a cancerous lesion or non-cancerous is determined according to a visual examination done after biopsy [6].

Skin lesion classification is a critical task in dermatology for early detection and treatment of various skin conditions, including skin cancer. Traditional models rely heavily on manual inspection by dermatologists, which are subjective and take more time. With advancements in AI and ML, automated systems are increasingly designed to assist in this diagnostic process. One promising approach is the use of Generative Adversarial Networks (GANs), a class of neural networks known for their ability to generate synthetic data that closely resemble real data. GANs have shown promise in various domains, including computer vision and medical imaging. GANs can be employed to generate realistic images of skin lesions, augmenting limited datasets and improving the generalization ability of machine-learning models.

In overcoming these challenges, computer vision, notably deep learning (DL) methods, emerges as a valuable solution. Unlike traditional machine-learning techniques that depend on domain expertise for specifying features, DL models – specifically convolutional neural networks (CNNs) – can be trained on a diverse dataset comprising benign and cancerous images. The DL model learns nonlinear correlations, empowering it to discern whether an image is malign or benign without the need for explicit feature extraction expertise. This study specifically concentrates on the utilization of CNNs in deep learning for the diagnosis of cancer of the skin.

The goal of this work was to create a novel and cost-effective diagnostic solution for skin cancer, highlighting the significance of early cancer detection for better treatment and potential cure. To attain this objective, we implemented an ensemble-based architecture crafted to improve the accuracy of the individual methods.

This research focuses on enhancing the classification accuracy of multi-class skin lesions through the application of current deep learning architectures, specifically Inception V3, ResNet50 and ResNet101. The motivation behind this study stems from the need to leverage computational methods to improve diagnostic accuracy, reduce diagnostic variability and expedite patient care in dermatological practice. The reason for choosing Inception V3 is the ability to automatically extract essential features from images and the concept of transfer learning. Also, Inception V3 Improves training stability and reduces the need for manual hyper-parameter tuning. ResNet50 & ResNet101 address the problem of vanishing gradient, allowing the network to learn deeper representations for more complex patterns.

A critical issue in designing effective models of deep learning for the analysis of medical images, including skin lesion classification, is the availability of high-quality and diverse training data. Moreover, class imbalance within these datasets can lead to biased models that fail to generalize well to new data. To mitigate such challenges, the research employs advanced data augmentation techniques, including traditional image transformations and the novel use of Adaptive Conditional Generative Adversarial Networks (ACGANs) to generate synthetic dermoscopic images. This approach aims to enrich the training dataset, enhance model robustness and prevent overfitting.

Furthermore, the study evaluates the performance of proposed methods using the balanced and unbalanced datasets, providing insights into the models' adaptability to real-world data scenarios. The results demonstrate significant advancements, with accuracies of up to 95% achieved through model ensemble, underscoring the effectiveness of integrating multiple deep learning architectures and augmentation strategies.

The key contributions of this work include:

- Implementation of image augmentation models to balance dataset.
- Research into the conditional architecture of Generative Adversarial Networks (GAN) and making modifications in the architecture to be adaptive for detecting images of skin lesions.
- Analysis of the performance of fine-tuned pre-trained models – specifically Inception V3, ResNet50 and ResNet101 – on balanced and unbalanced datasets.
- Implementation of a collaborative algorithm, by combining predictions from the above 3 models to enhance performance

The article is organized into following sections: Section 2 focuses on previous research available on the topic, which, in turn, provides the context for the current research. Section 3 explains the data set used and the data augmentation process in the proposed methodology and its implementation. Section 4 explains the ACGAN model and its architecture. Section 5 details the process of classification using collaborative architectures. Section 6 discusses the experimental results, findings and comparisons. Finally, Section 7 concludes the investigation.

## 2. Related work

Several studies have utilized dermoscopic skin lesion databases to improve lesion diagnosis. Early research in

skin cancer predominantly concentrated on employing various algorithms to categorize skin lesions through traditional Artificial Intelligence (AI) approaches. These methods typically involved manual extraction of features, followed by different phases of training of the classifier. Initial efforts to distinguish between MEL (melanoma) and non-melanoma lesions relied on a low-level manually crafted nature [7]. However, features that are handcrafted for images of dermoscopy often demonstrate limited generalization power because of a lack of biological principles, understanding and human intuition. These low-level features struggled to differentiate the complex lesions of the skin, encountering challenges such as visual similarity, high intraclass disparity and the presence of artefacts in dermoscopic images, leading to suboptimal performance [8].

Recognizing these limitations, deep learning and Convolutional Neural Networks (CNNs) have emerged as preferred strategies in various applications of computer vision [6,9–11]. In one study, a dataset comprising over 100,000 images, was utilized to train a deep CNN employing the Inception-v3. This deep CNN effectively addressed 2 binary classification tasks: distinguishing keratinocyte carcinomas from benign seborrheic keratoses and identifying malignant melanomas vs benign nevi. The latter achieved an accuracy of $72.1 \pm 0.9\%$, surpassing dermatologist discrimination rates [6].

In another study, Alex Net was employed to classify 3 different using the PH2 dataset [12]. The suggested method exhibited exceptional performance, achieving high accuracy, sensitivity, specificity and precision measures of 98%, 98%, 98% and 97%,

A proposed ensemble technique for CNNs, as outlined by [13], integrated the intra-architecture and inter-architecture network into a fusion. This approach captured levels of abstraction of features through the utilization of various CNN architectures, with in-depth features from each network utilized to train distinct SVM classifications. The algorithm demonstrated notable performance, achieving an area under the ROC curve of 87% for melanoma and 95% for seborrheic keratosis classification when evaluated on 600 images from the ISIC 2017.

Explainable methods of DL for multi-class classification of skin lesions were emphasized in the literature. Explaining ability is crucial in medical applications to ensure transparency and trust in automated diagnostic systems. Contributions were made to the interpretability of deep learning models in dermatology research. Robust metrics of evaluation are important for determining the effectiveness of the suggested approach and its practical applicability. While explainable AI is emphasized, the actual methods used for explainability may not be straightforward or may add complexity to the model. If the explanation methods are not clearly articulated or are overly complex, it could hinder adoption by healthcare professionals who require clear and actionable insights from the model [14]. "Skin-Net" presents a novel architecture of a deep residual network tailored for skin lesion classification, incorporating advanced techniques like multilevel feature extraction, cross-channel correlation and outlier detection. Its contributions lie in improving accuracy and robustness in classifying skin lesions, which is crucial for early and accurate diagnosis in dermatology [15]. The challenge of accurately classifying skin lesions from medical images, which is crucial for detecting skin diseases early was addressed in the literature [16]. The refinement of the residual deep convolutional network suggests improvements in terms of model architecture and performance compared to previous methods of DL for the classification of skin lesions.

A study, focussing on using a combination of DL architectures and a new optimization algorithm to enhance the detection and classification of multiple types of skin lesions, was done in the literature [17]. In this study, they developed a system for automatic multiclass skin lesion localization and classification. A new contrast enhancement technique using image luminance information was proposed in the research [18]. It then leverages transfer learning to fine-tune pre-trained models of deep learning (DarkNet-53 and DensNet-201) with an altered residual block at the end. The two-step serial-harmonic mean fusion improves classification accuracy; it may introduce irrelevant information. This work [19] suggests a novel computer-aided approach to diagnose melanoma by fusing deep learning models like Faster R-CNN with the AGTO Algorithm. Faster R-CNN handles the classification, and the AGTO approach is utilized to choose important features. With a 98.55% accuracy rate, the suggested model outperforms other models when applied to the ISIC-2020 skin cancer dataset. A computer vision-based approach for diagnosing and detecting monkeypox is presented in this article [20], which makes use of twelve CNN-based models, such as VGG16, ResNet152 and DenseNet201. To overcome the problem of small sample sizes, the models are tested using a fewer skin images. According to the results, DenseNet201 has the highest classification accuracy, achieving classification rates of 100% for four classes, 98.89% for binary classes and 99.94% for six classes. By preprocessing pictures using a fusion-based contrast enhancement technique, this work [21] proposes an AI-based early detection tool for monkeypox. To extract deep feature vectors, transfer learning is used to modify and train two pre-trained DCNN models, NASNet-Large and Inception-ResNet-V2. These characteristics are categorized by M-SVM and merged using a convolutional sparse image decomposition fusion technique.

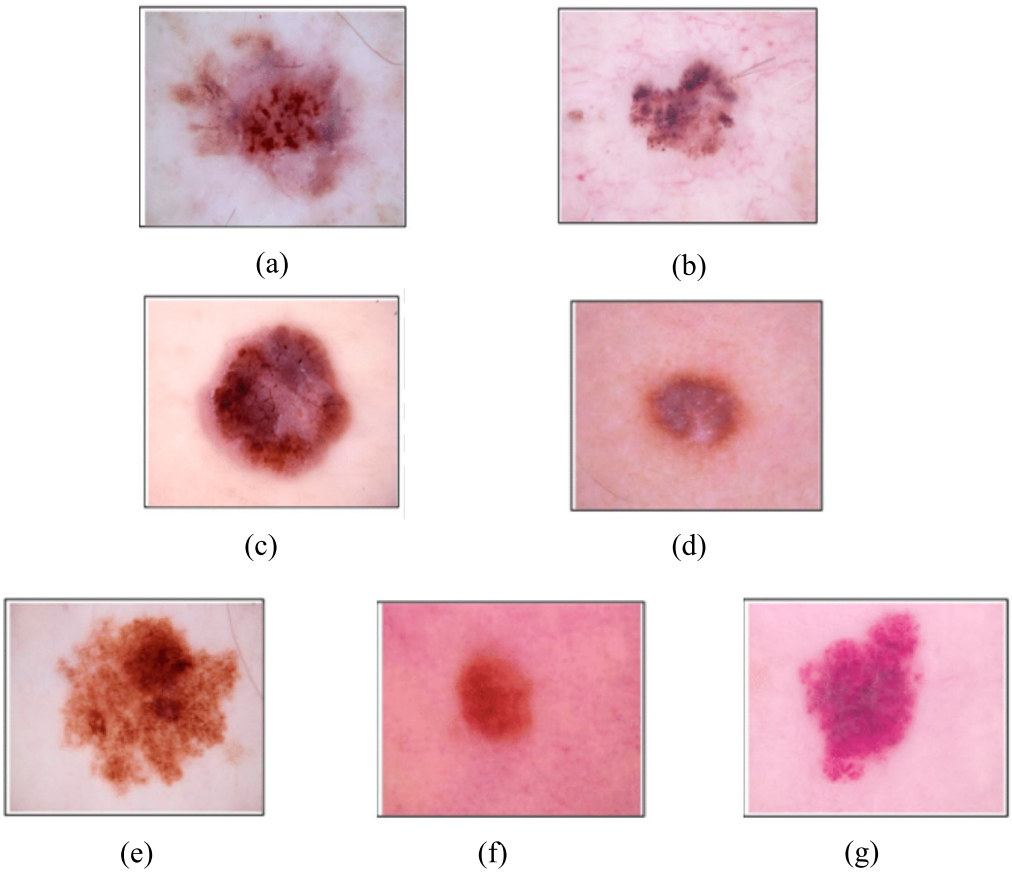


**Figure 1.** Sample images of skin lesions from the HAM10000 dataset: (a) AKIEC (b) BCC (c) BKL (d) DF (e) MEL (f) NV and (g) VASC.

## 3. Proposed methodology

### 3.1. Dataset

The dataset used for this work is HAM10000 [22], which is an acronym for "Human Against Machine with 10,000 images for training"[23]. The dataset is made by combining dermatoscopic image sources from a variety of people around the world. The data for this research are collected such that they contain a variety of categories of images which include the following skin lesions: AKIEC, BCC, BKL, DF, MEL, NV and VASC. The dataset used for this research consists of 8,017 images. Figure 1 displays some sample images of all categories of skin lesions mentioned above from the HAM10000 dataset used for this research.

In this research, to restructure the method developed, the original images in the dataset were rescaled to 256 × 256 pixels. Among the total images, taken for research, 75% of data were used for training, 15% of data for testing and 10% for validation. Based on this split-up, Table 1 provides information about the split-up statistics of the dataset for the different kinds of skin lesions.

**Table 1.** Statistical breakdown of skin lesions.

| Type of skin lesion | Training samples | Validation samples | Testing samples |
|---|---|---|---|
| AKIEC | 241 | 26 | 60 |
| BCC | 376 | 41 | 97 |
| BKL | 797 | 88 | 214 |
| DF | 88 | 9 | 18 |
| MEL | 807 | 89 | 217 |
| NV | 4833 | 536 | 1337 |
| VASC | 108 | 11 | 23 |

### 3.2. Data augmentation

The dataset in Table 1 is imbalanced which has a risk of overfitting when we perform training of the model [24]. To resolve this issue, the data augmentation process was introduced. This process applies random image transformations which in turn increases the number of images in underrepresented classes [25]. The operations like rotation, translation and flipping were performed during data augmentation. The augmentation operations were performed using the Python libraries[26]. A sample output of the augmented images of different skin lesions is shown in Figure 2.

This limitation can cause overfitting, in which the model learns robust features that apply to new samples but becomes overly sensitive to the artificially manipulated data. It is critical to strike a balance between augmentation and realistic transformations to reduce this risk and to assess model performance on a variety of relevant test sets. Assessing the actual impact of these strategies can also be aided by tracking performance indicators across original and augmented data.

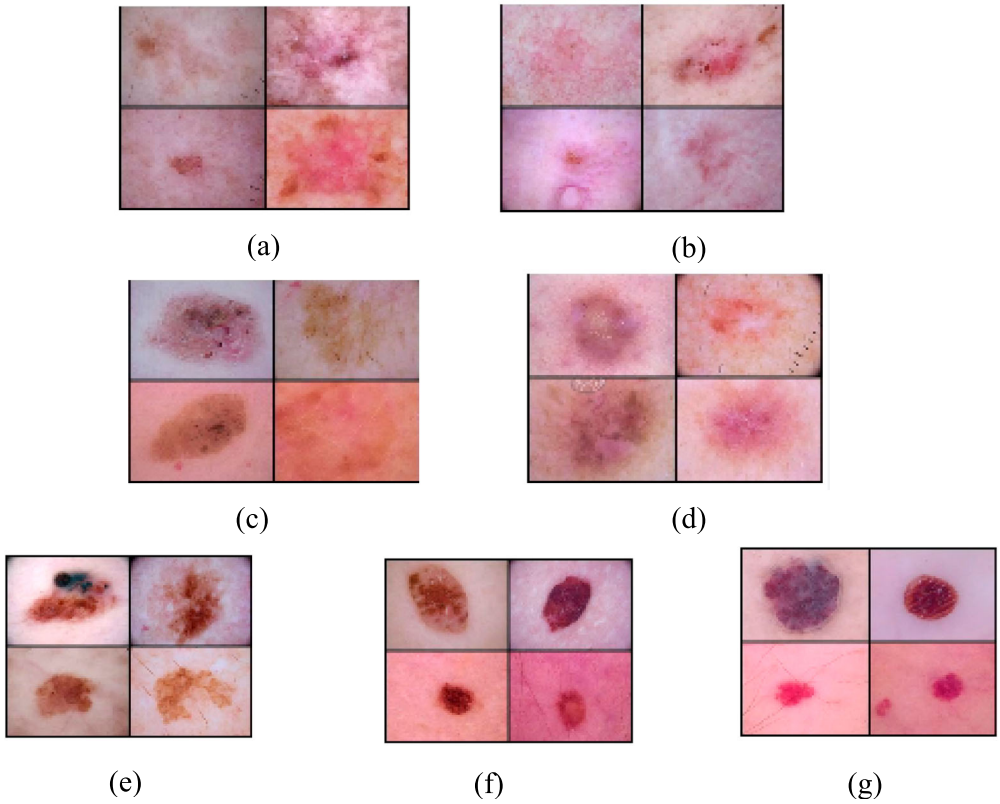


**Figure 2.** Sample images after augmentation: (a) AKIEC (b) BCC (c) BKL (d) DF (e) MEL (f) NV and (g) VASC.

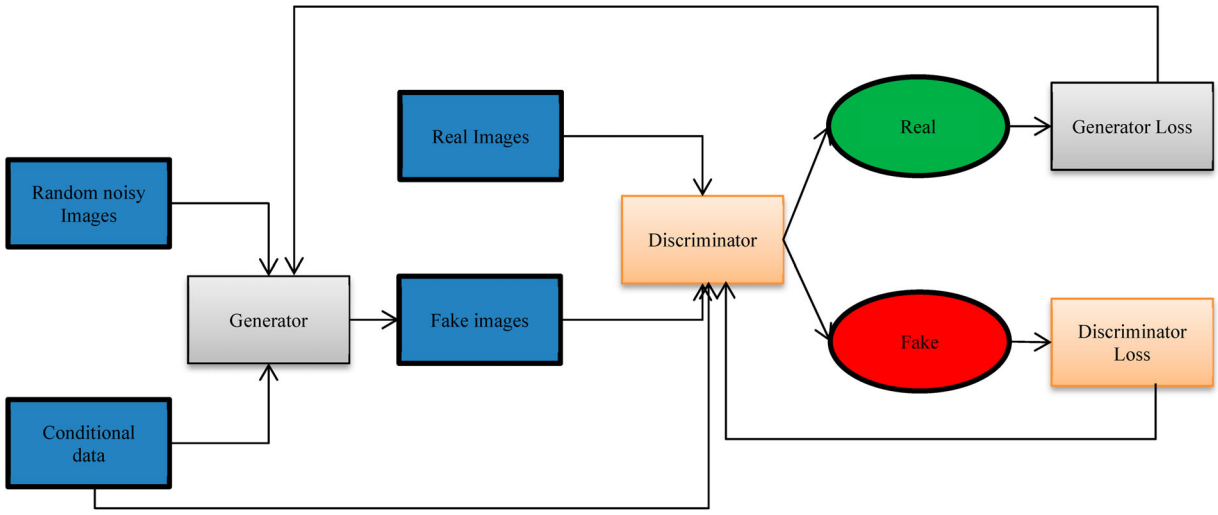


**Figure 3.** Adaptive Cconditional Ggenerative Aadversarial Nnetwork (ACGAN) architecture.

### *3.3. Adaptive conditional generative adversarial networks (ACGAN)*

In this research, to address the class imbalance issue, focal loss is implemented which down-weights well-classified examples, placing more emphasis on hard-to-classify examples. This can be beneficial for addressing the imbalance issue. The well-known Conditional Generative Adversarial Network (CGAN) architecture [27] was employed for image generation in which a few modifications were implemented in the manuscript in different sections.

Figure 3 illustrates the design of Adaptive Conditional Generative Adversarial Network (ACGAN) architecture with skip connections.

GANs [28] use a generator to study the creation of new images and a discriminator to study the discrimination between fake and real images [29]. The problem with traditional GANs is the lack of control over the generation of multi-class data.

Conditional Generative Adversarial Networks (CGANs) announce a conditional setting for training the generator and discriminator. Discrimination decisions are taken based on both generated images

and labels, with a higher importance on the former for the discriminator. By exposing the model to multiple inputs during training, the ideal CGAN model can study multimodal mapping of input-to-output.

In the proposed model ACGAN, skip connections were introduced both in the generator and discriminator. Introducing skip connections in a Conditional Generative Adversarial Network (CGAN) involves creating direct connections between layers in the generator or discriminator network. Skip connections, also known as residual connections, are paths that allow the network to bypass one or more layers, facilitating the flow of information during training. Here's how you can introduce skip connections in a CGAN.

#### 3.3.1. Modifications in the generator

Concatenate the conditional input with the input to each layer in the generator. This can be done at each layer or specific points within the network. Add skip connections by directly connecting the output of one layer to a deeper layer. This can be achieved by adding output tensors or using the Keras Add layer [30].

#### 3.3.2. Modifications in the generator

Similar to the generator, concatenate the conditional input with the input to each layer in the discriminator. Introduce skip connections by connecting the output of one layer to a deeper layer. The key is to concatenate the conditional input with the regular input and introduce skip connections by directly connecting the output of one layer to another.

### 3.4. Addressing the imbalance challenge – implementing focal loss

To address the imbalance in datasets issue, the focal loss function is introduced to incorporate the focal loss term.

In this research, the first loss term is the focal loss applied to the generator output, and the second loss term is the standard binary cross-entropy loss for the discriminator.

The Focal Loss function for a Conditional Generative Adversarial Network (CGAN) can be defined as follows. Let's consider a binary classification scenario where $y_{\text{true}}$ is ground truth and $y_{\text{pred}}$ is the predicted probability output from the model. The focal loss function is given by

$$\begin{aligned}\text{Focal loss} = &-\alpha.(1-y_{\text{pred}})^{\gamma}.\log(y_{\text{pred}}).y_{\text{true}} \\ &-(1-\alpha).{y_{\text{pred}}}^{\gamma}.\log(1-y_{\text{pred}}) \\ &.(1-y_{\text{true}}) \qquad (1)\end{aligned}$$

where

$y_{\text{true}}$– indicates the ground truth label which may be 0 or 1; $y_{\text{pred}}$– is the predicted probability output by the model; $\alpha$ – balancing parameter; $\gamma$ – focusing parameter.

The gamma and alpha parameters were adjusted in the focal loss function according to our specific requirements and experimented with different values to find the optimal configuration for the dataset used.

### 3.5. Classification using the collaboration of high-speed transfer learning models

Managing large datasets can lead to processing competence challenges. The concept of the transfer learning method has addressed these challenges [31]. Transfer learning is one of the most popular employed methods for classification purposes in deep learning. Instead of starting from scratch, pre-trained models were used in this kind of architecture [32]. Most commonly, deep models like Inception V3 and ResNet, pre-trained on huge and compound image classification tasks like ImageNet's 1000 classes, are used for this purpose. The feature extractors of such deep models help in capturing essential features for classification [33]. In this research, three pre-trained deep learning models were used for ensembling: Inception V3 [34], ResNet50 and ResNet101 [29], which were pre-trained on the dataset of ImageNet. The architectures of developed models are explained below.

#### 3.5.1. Inception V3

Inception V3 is a CNN architecture characterized by 48 layers. Inception V3 is a model of image recognition which is proven to attain greater than 78.1% accuracy on the dataset of ImageNet. The model is the conclusion of numerous ideas developed by many researchers over the years.

#### 3.5.2. RESNET architecture and its variants

The residual network was an architecture introduced in research for addressing the challenge of the vanishing/exploding gradient problem. The issue happens due to the use of several layers in CNN architectures to enhance performance. The process of using skip connections was also present in the residual network architecture [35]. In any skip connection process, some of the successive connections were skipped and connected directly to the output layer. In a residual network (ResNet), the idea of "skip connections" is utilized. These skip connections enable the network to skip some subsequent connections, directly connecting the output to the input.

There are two variants of ResNet architecture:

(1) ResNet 50 which uses 50 layers.
(2) ResNet 101 which uses 101 layers and is more complex than ResNet 50.

### 3.6. Collaborating the high-speed transfer models

Because of the challenges faced in training individual deep learning algorithms for skin lesion identification,

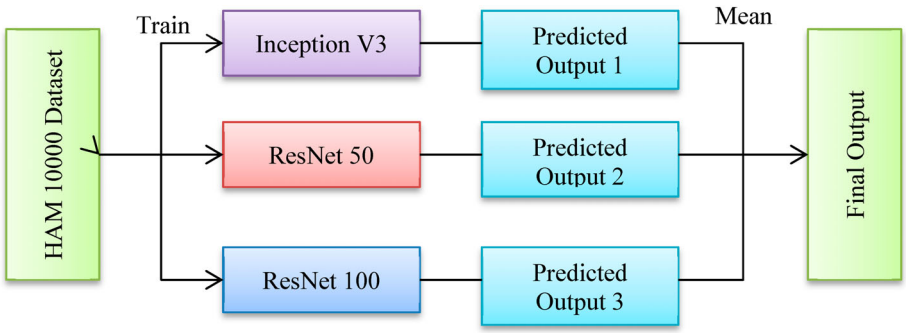


**Figure 4.** Ensembling process.

the research proposed here ensembles three different algorithms to achieve accuracy in predicting skin lesions. Combining several models offers the possibility to improve accuracy by averaging the yield of each model. In this ensemble algorithm, the mean of predictions of the individual models was considered to minimize the error in the model and also it aims to preserve generalizability. The architecture for the ensemble of the three algorithms is depicted in Figure 4.

### 3.7. Performance metrics

The performance indicators that are listed below were used for evaluating the performance of the proposed ensemble algorithm. The metrics considered were Precision, Recall, F1-Score and Accuracy.

#### 3.7.1. Precision

It is used to assess the accuracy of positive predictions made by the model.

Consider the following descriptions:

True Positives (TPV): Count of positive occurrences correctly predicted by the model.

False Negatives (FNV): Count of positive occurrences incorrectly predicted as negative.

False Positives (FPV): Count of negative occurrences incorrectly predicted as positive.

True Negatives (TNV): Count of negative occurrences correctly predicted by the model.

The formula to calculate precision is as shown [31] in Equation (2):

$$\text{Precision} = \frac{TPV}{TPV + FPV} \tag{2}$$

#### 3.7.2. Recall

It is used to measure all the applicable cases.

The formula to calculate precision is as shown in Equation (3):

$$\text{Recall} = \frac{TPV}{TPV + FNV} \tag{3}$$

*F*1-Score

It is computed by performing the harmonic mean of precision and recall. The formula to calculate F1-Score is as shown in Equation (4):

$$F1 - \text{Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision Recall}} \tag{4}$$

#### 3.7.3. Accuracy

It represents the overall prediction correctness and is calculated as the ratio of samples that are predicted correctly to the total number of samples as shown in Equation (5).

$$\text{Accuracy} = \frac{TPV + TNV}{TPV + TNV + FPV + FNV} \tag{5}$$

## 4. Experimental results

In continuation with the training for Inception V3, ResNet 50 and ResNet 101 architectures, skin lesion predictions were made on the test dataset for assessing performance. The final layer of the design was mainly responsible for making the prediction likelihood for each of the 7 classes. It's critical to evaluate the performance of each of these models in deciding about the suitable model for skin lesion prediction. Experimental analysis was performed on data obtained from executing Inception V3, ResNet50 and ResNet 101.

### 4.1. The effect of collaborating the models

The ensemble model combines the mean of predictions by all 3 models Figure 5.

Figure 6 displays the class-wise performance of ensemble models for the unbalanced dataset. With a 94% recall rate, 90% precision rate and 90% F1-score, NV (nevus) performs the best across all measures, making it the most accurately classified class. However, MEL (melanoma) performs worse, with an *F*1-score of 73%, a recall of 64% and a precision of 86% indicating difficulties with precise identification. In general, the model has strong performance in most classes; nevertheless, MEL continues to be a difficult category. NV and VASC demonstrate exceptionally high scores.

Figure 6 displays the class-wise performance of the ensemble models for the balanced dataset. For the majority of classes, the model obtains high and balanced scores; DF (dermatofibroma) leads the pack with

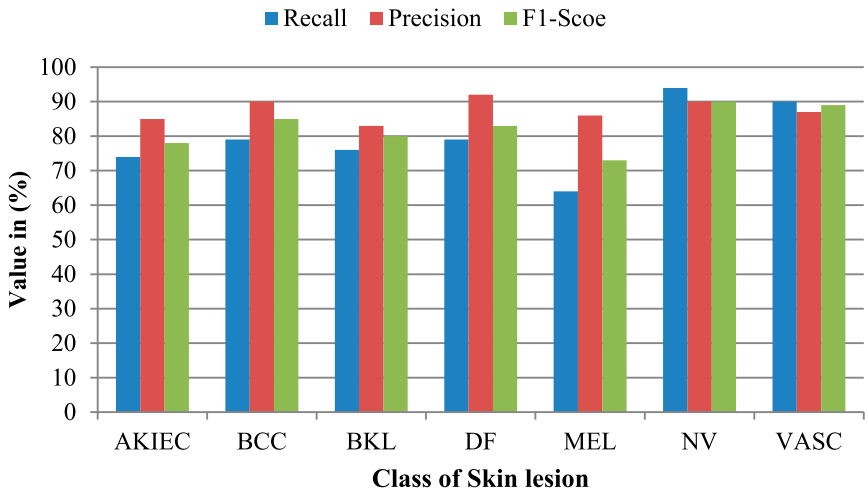


**Figure 5.** Class-wise performance of collaborative models for the unbalanced dataset.

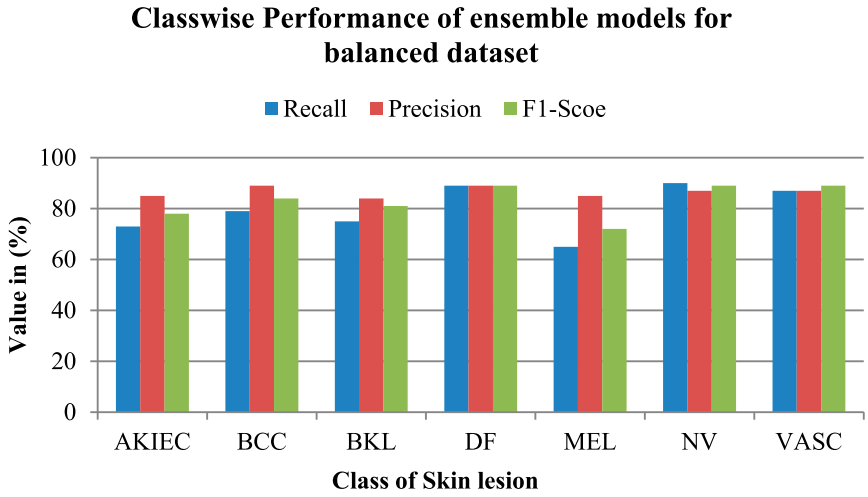


**Figure 6.** Class-wise performance of collaborative models for the balanced dataset.

an *F*1 score of 89% flawless recall and a precision of 89%. Vascular lesions (VASC) and nevus (NV) perform well, with high an *F*1 score of 89%. Melanoma, on the other hand, has the lowest *F*1 score of any disease (72%), indicating that recall is lower and precision is quite high, exposing regions where the model struggles to reliably detect cases of melanoma. Overall, there is very little performance variation in the model's robust performance across the classes.

### 4.2. Comparison of evaluation metrics

Figure 7 compares the evaluation metrics of the proposed ensemble model with the Inception V3, ResNet 50 and ResNet 101 models.

A comparison of the introduced ensemble model's performance metrics with those of Inception V3, ResNet 50 and ResNet 101 is shown in Figure 7. The ensemble model achieves 95% accuracy compared to ResNet 101's maximum of 92.25%, outperforming the individual models in accuracy. With considerable gains in each measure, it also leads to recall, precision and *F*1 score. The ensemble model exhibits a superior capacity to identify reliably and consistently across several measures, as evidenced by its recall of 89.93%, a precision of 94.26% and a F1 score of 91.85%. This shows that compared to standalone designs, the suggested ensemble model provides a more reliable performance.

### 4.3. Comparison of accuracy

Figure 8 compares the prediction accuracy of the proposed model with that of previous research works .

Figure 8 presents the enhanced prediction precision of the suggested ensemble model in contrast to earlier models. The CNN model accuracy was 90.67%, the MobileNet model was 83.1% and the ResNet 50 and ResNet 100 models were 89.8%. The suggested ensemble model, on the other hand, attains a noticeably greater accuracy of 95%. This improvement is ascribed to the integration of high-speed transfer models, the use of focal loss to address the issues of class imbalance and the inclusion of skip connections in the discriminator and generator. Together, these novel components enhance the suggested system's exceptional performance.

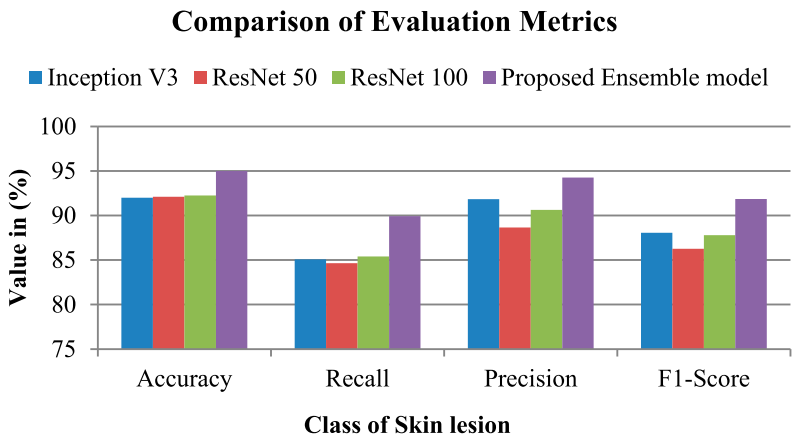


**Figure 7.** Comparison of evaluation metrics.

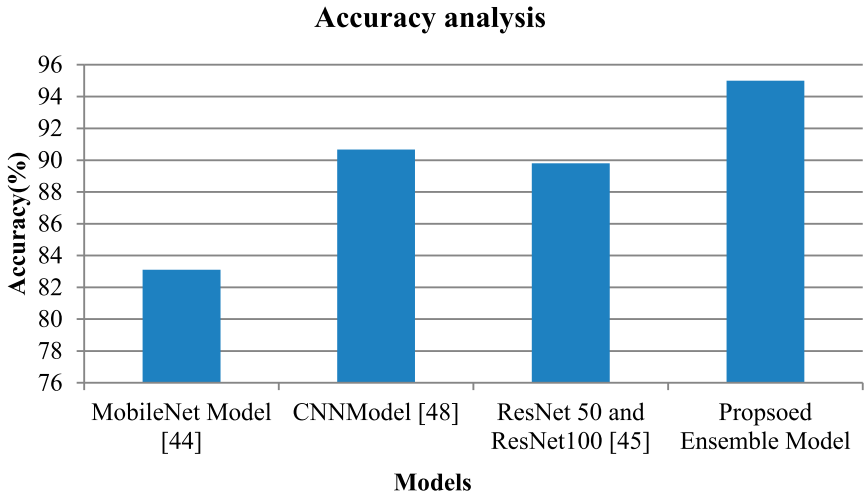


**Figure 8.** Comparison of accuracy.

## 5. Discussion

While using transfer learning models in conjunction with the architecture of Adaptive Conditional Generative Adversarial Networks (ACGAN) for skin lesion prediction, there are several advantages and limitations to consider. Positively, the system may provide a variety of synthetic samples that can raise the model's resilience and greatly boost data augmentation capabilities. Pre-trained models are used in transfer learning to increase predictive accuracy and speed training, while the conditional generation aspect allows for more individualized and precise predictions by conditioning on certain attributes. Besides, dataset imbalance is another major problem in skin lesion prediction that ACGANs effectively handle.

These benefits are not without noteworthy drawbacks, though. Training ACGANs can be computationally demanding and complex, requiring a large investment of time and resources. Another worry is training instability because GANs can have problems like mode collapse and convergence difficulties. The generated synthetic images can differ in quality, which could affect the model's overall performance. Finally, interpretability is still a problem because it might be challenging to comprehend and believe the model's predictions due to the complexity of GAN-generated data.

In conclusion, integrating ACGANs with transfer learning models presents many challenges about system complexity, computational demands, training stability, image quality and interpretability, but it also greatly improves data augmentation and predictive accuracy and addresses dataset imbalance. To optimize these strategies' efficacy in clinical applications, these problems must be addressed via careful planning, rigorous experimentation and comprehensive validation.

## 6. Conclusion

a DL model was developed to improve the early prediction of skin lesions, a critical need given the life-threatening nature of skin cancer. Detecting skin cancer early is a significant research challenge that offers substantial benefits to medical practitioners for planning effective treatments. Early prediction also plays an important role in preventing the progression of skin diseases to more severe stages. This study effectively addressed the imbalance issue present in the HAM10000 dataset, thereby enhancing the models of deep learning performance. Augmentation methods

and translations proved pivotal in balancing the dataset. Furthermore, a collaborative model was devised by integrating architectures like Inception V3, ResNet 50 and ResNet 101. This model underwent evaluation using balanced and unbalanced datasets. The experimental results demonstrate that the collaborative approach achieved an impressive accuracy of 95%, surpassing previously developed algorithms.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

## Ethics approval and consent to participate

No participation of humans takes place in this implementation process.

## Human and animal rights

No violation of Human and Animal Rights is involved.

## Data availability statement

Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

## References


[1] Armstrong BK,Kricker A. Skin cancer. Dermatol Clin. 1995;13(3):583–594. doi:10.1016/S0733-8635(18)30064-0

[2] Simões MCF, Sousa JJS, Pais AACC. Skin cancer and new treatment perspectives: a review. Cancer Lett. 2015;357(1):8–42. doi:10.1016/j.canlet.2014.11.001

[3] Cassano R, Cuconato M, Calviello G, et al. Recent advances in nanotechnology for the treatment of melanoma. Molecules. 2021;26(4):785. doi:10.3390/molecules26040785

[4] Buljan M, Bulat V, Šitum M, et al. Variations in clinical presentation of basal cell carcinoma. Acta ClinicaCroatica. 2008;47(1):25.

[5] Kanavy HE, Gerstenblith MR. Ultraviolet radiation and melanoma. Semin Cutaneous Med Surg. 2011;30(4):222–228. doi:10.1016/j.sder.2011.08.003

[6] Esteva A, Kuprel B, Novoa RA, et al. Dermatologist-level classification of skin cancer with deep neural networks. Nature. 2017;542(7639):115–118. doi:10.1038/nature21056

[7] Barata C, Celebi ME, Marques JS. A survey of feature extraction in dermoscopy image analysis of skin cancer. IEEE J Biomed Health Inform. 2019;23(3):1096–1109. doi:10.1109/JBHI.2018.2845939

[8] Celebi ME, Kingravi HA, Uddin B, et al. A methodological approach to the classification of dermoscopy images. Comput Med Imaging Graph. 2007;31(6):362–373. doi:10.1016/j.compmedimag.2007.01.003

[9] Yu L, Chen H, Dou Q, et al. Automated melanoma recognition in dermoscopy images via very deep residual networks. IEEE Trans Med Imaging. 2017;36(4):994–1004. doi:10.1109/TMI.2016.2642839

[10] Havaei M, Davy A, Warde-Farley D, et al. Brain tumor segmentation with deep neural networks. Med Image Anal. 2017;35:18–31. doi:10.1016/j.media.2016.05.004

[11] Osman FM, Marti R, Zwiggelaar R, et al. "End-to-end breast ultrasound lesions recognition with a deep learning approach," medical imaging 2018: G. Ian, "generative adversarial nets,". Advances in Neural Information Processing Systems; San Francisco; CA, USA. Morgan Kaufmann Publishers Inc, 2014.

[12] Lisa T, Jude S. Transfer learning handbook of research on machine learning applications. IGI Glob. 2009.

[13] Simonyan K, Zisserman A. "Very deep convolutional networks for large-scale image recognition," 2014, arXivPrepr. arXiv1409.1556.

[14] Hosny KM, Said W, Elmezain M, et al. Explainable deep inherent learning for multi-classes skin lesion classification. Appl Soft Comput. 2024;159:111624. doi:10.1016/j.asoc.2024.111624

[15] Alsahafi YS, Kassem MA, Hosny KM. Skin-net: a novel deep residual network for skin lesions classification using multilevel feature extraction and cross-channel correlation with detection of outlier. J Big Data. 2023;10(1):105. doi:10.1186/s40537-023-00769-6

[16] Hosny KM, Kassem MA. Refined residual deep convolutional network for skin lesion classification. J Digit Imaging. 2022;35(2):258–280. doi:10.1007/s10278-021-00552-0

[17] Bibi S, Khan MA, Shah JH, et al. MSRNet: multiclass skin lesion recognition using additional residual block based fine-tuned deep models information fusion and best feature selection. Diagnostics. 2023;13(19):3063. doi:10.3390/diagnostics13193063

[18] Hussain M, Khan MA, Damaševičius R, et al. SkinNet-INIO: multiclass skin lesion localization and classification using fusion-assisted deep neural networks and improved nature-inspired optimization algorithm. Diagnostics. 2023;13(18):2869. doi:10.3390/diagnostics13182869

[19] Nivedha S, Shankar S. Melanoma diagnosis using enhanced faster region convolutional neural networks optimized by artificial gorilla troops algorithm. Inf Technol Control . 2023;52(4):819–832. doi:10.5755/j01.itc.52.4.33503

[20] Ren G. Monkeypox disease detection with pretrained deep learning models. Inf Technol Control . 2023;52(2):288–296. doi:10.5755/j01.itc.52.2.32803

[21] Maqsood S, Damaševičius R. Monkeypox detection and classification using deep learning based features selection and fusion approach. 2023 IEEE International Systems Conference (SysCon). p. 1–8. IEEE; 2023.

[22] He K, Zhang X, Ren S, et al. Deep residual learning for image recognition. Compu Vis pattern Recognit. 2016;2016:90.

[23] Biomedical applications in molecular, structural, and functional imaging. 2018;10578:1057819.

[24] Mendonça T, Ferreira PM, Marques JS, et al. PH2-A dermoscopic image database for research and benchmarking. Proceedings of the 2013 35th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC); Osaka, Japan. 5437–5440, IEEE, July 2013.

[25] Mahbod A, Schaefer G, Ellinger I, et al. Fusing fine-tuned deep features for skin lesion classification. Comput Med Imaging Graph. 2019;71:19–29. doi:10.1016/j.compmedimag.2018.10.007

[26] Tschandl P, Rosendahl C, Kittler H. Data descriptor: the HAM10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions. Sci Data. 2018;5(1):180161. doi:10.1038/sdata.2018.161

[27] Codella NCF. Proceedings of the skin lesion analysis Toward melanoma detection: a Challenge at the 2017 international symposium on biomedical imaging (ISBI), hosted by the international skin imaging collaboration (ISIC); Washington, DC, USA. 2018.
[28] Iqbal I, Younus M, Walayat K, et al. Automated multiclass classification of skin lesions through deep convolutional neural network with dermoscopic images. Comput Med Imaging Graph. 2021;88:101843. doi:10.1016/j.compmedimag.2020.101843
[29] Syamala M, Chandrasekaran R, Balamurali R, et al. Evaluating generative adversarial networks for virtual contrast-enhanced kidney segmentation using ResUNet in non-contrast CT images. Multimed Tools Appl. 2024: 1–24.
[30] Babu PA, Rai AK, Ramesh JVN, et al. An explainable deep learning approach for oral cancer detection. J Electr Eng Technol. 2024;19(3):1837–1848. doi:10.1007/s42835-023-01654-1
[31] Ali MS, Miah MS, Haque J, et al. An enhanced technique of skin cancer classification using deep convolutional neural network with transfer learning models. Mach Learn Appl. 2021;5:100036. doi:10.1016/j.mlwa.2021.100036
[32] Chiranjeevi P, Rajaram A. A lightweight deep learning model based recommender system by sentiment analysis. J Intell Fuzzy Syst. 2023;44(6):10537–10550. doi:10.3233/JIFS-223871
[33] Tamilarasi K, Maheswari K, Ramesh S, et al. "A decentralized smart healthcare monitoring system using deep federated learning technique for IoMT," 2023.
[34] Mirza M, Osindero S. "Conditional generative adversarial nets," arXivPrepr. arXiv1411.1784. 2014.
[35] Sucharitha G, Sankardass V, Rani R, et al. Deep learning aided prostate cancer detection for early diagnosis & treatment using MR with TRUS images. J Intell Fuzzy Syst. 2024;46(2):3395–3409. doi:10.3233/JIFS-235744