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Research Article

Improving Skin Lesion Classification Accuracy Using VGG19 Combined with Optimized Random Forest of Uncorrelated High-Performing Trees

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ABSTRACT

Accurate and early prediction of skin cancer is essential for improving survival rates and minimizing the burden of treatment, as timely diagnosis greatly enhances patient outcomes. Automated classification methods have become invaluable tools for dermatologists, offering consistent, rapid, and objective analysis of skin lesions. Given the prevalence and potentially fatal nature of skin cancer, developing accurate and efficient classification systems is crucial for effective early detection and treatment. This study proposes an optimized Random Forest (RF) framework combined with VGG19-based feature extraction to enhance classification performance and computational efficiency. Features extracted from VGG19 were used to train N decision trees, and the top P high-performing trees were selected based on their accuracy. To ensure diversity and reduce redundancy, Jaccard distances were computed, and Q uncorrelated trees were identified using K-Means clustering. These optimized trees formed an ensemble, and predictions were aggregated through majority voting. The proposed framework achieved 88.21% accuracy, 81% precision, 93% recall, and 87% F1-score, significantly outperforming other state-of-the-art models.

Keywords: VGG19, Random Forest, Jaccard distance, K-Means, Skin cancer, classification.

1. INTRODUCTION

Skin cancer is a significant global health concern, contributing to substantial mortality rates. According to the World Health Organization (WHO), up to 10 million individuals succumb to skin cancer annually. Without timely and effective diagnostic measures, the prevalence of skin cancer is projected to increase considerably over the next two decades [1]. Ranked as the fifth most commonly diagnosed cancer type worldwide [2], skin cancer results from the abnormal growth of skin cells, leading to the formation of tumors. These tumors can be classified as either benign, characterized by orderly cell division without disrupting adjacent tissues, or malignant, where uncontrolled cell growth invades surrounding tissues and spreads to other body parts.

Among the various types of skin cancer, melanoma stands out as the deadliest. It accounts for approximately 5% of all skin cancer cases but is responsible for around 80% of related fatalities, with more than 55,500 deaths reported globally each year [3][4]. The prognosis for advanced melanoma is grim, with a five-year survival rate of less than 20% in incurable cases [5]. However, early detection can drastically improve outcomes, with survival rates reaching up to 95% when melanoma is diagnosed in its early stages [6].

Historically, the diagnosis of skin cancer relied heavily on the visual evaluation of lesions by expert dermatologists, supplemented by histopathological analysis. While effective, this approach has significant limitations, including subjectivity, variability in interpretation, and the labour-intensive nature of the process, which can delay both diagnosis and treatment [7]. However, the complex morphological patterns in dermoscopic images make manual diagnosis challenging, leading to increased reliance on computational tools for skin lesion analysis.

Recent advancements in deep learning, particularly Convolutional Neural Networks (CNNs), have significantly enhanced the capabilities of automated systems in medical imaging. VGG19, a deep CNN architecture pre-trained on ImageNet, has been widely adopted for its robust feature extraction capabilities, allowing it to effectively capture hierarchical representations in image data [8]. By leveraging transfer learning, researchers have successfully applied VGG19 to medical image classification tasks, including skin lesion analysis [9].

While CNNs like VGG19 excel at feature extraction, traditional machine learning classifiers such as Random Forests provide robust and interpretable frameworks for classification. Random Forests are ensemble learning methods that aggregate predictions from multiple decision trees, offering resilience against overfitting and the ability to handle high-dimensional data [10]. A study implemented watershed segmentation for lesion segmentation, followed by feature extraction using shape descriptors, the ABCD rule, and GLCM. Among the classifiers tested (kNN, Random Forest, and SVM), SVM demonstrated superior performance in classifying skin lesions [11].

This research integrates VGG19-based feature extraction with an optimized Random Forest classifier for skin lesion classification. The optimization involves selecting a subset of decision trees based on accuracy and diversity using Jaccard distances and clustering techniques. The hybrid framework aims to leverage the strengths of VGG19's feature extraction capabilities and Random Forest's robustness while addressing the limitations of tree redundancy. This approach demonstrates improved classification accuracy and reduced computational overhead, making it a promising solution for skin lesion analysis in clinical settings.

2. REVIEW OF LITERATURE

The integration of deep learning models, particularly convolutional neural networks (CNNs) like VGG19, with machine learning classifiers such as Random Forests has been a focal point in advancing skin lesion classification. Recent studies have explored various methodologies to enhance the accuracy and efficiency of skin cancer detection systems.

Medhat et al. conducted a comparative analysis of various deep convolutional neural networks (CNNs), including AlexNet, MobileNet V2, and ResNet50, to assess their effectiveness in detecting skin cancer from dermatological images captured via smartphone. Among these models, AlexNet, enhanced with transfer learning (TL) and basic data augmentation, achieved the highest diagnostic accuracy, leveraging its pre-trained knowledge and enriched training dataset [12].

Faghihi et al. explored the use of VGG16 and VGG19 architectures with preserved ImageNet weights for skin cancer classification, integrating three initial layers from the pre-trained AlexNet model. However, this study did not incorporate data augmentation, highlighting an area for future research to enhance dataset diversity and comprehensiveness [13].

A hybrid approach combining DenseNet-201, InceptionV3, MobileNet, ResNet50, and VGG16 with machine learning algorithms such as Support Vector Machine (SVM), k-Nearest Neighbor (KNN), and Decision Tree demonstrated superior performance in skin cancer detection [14]. Random Forest (RF) was preferred over Decision Tree for its enhanced robustness and reliability [15]. These pre-trained models were consistently shown to be effective in identifying skin cancer [16].

MobileNet, introduced by Howard et al. [17], was particularly noted for its lightweight architecture, making it ideal for mobile and embedded applications while maintaining competitive accuracy. Similarly, InceptionV3, developed by Szegedy et al. [18], employed inception modules to extract multiscale features via parallel convolutions, thereby enhancing the model’s ability to capture intricate details in input data.

A study by Hasan et al. (2023) provided an extensive literature review on methodologies applied for skin lesion analysis, highlighting the prominence of VGG19 in extracting discriminative features for accurate classification. The review emphasized the model's capability in handling the complexities associated with dermoscopic images [19].

Random Forests, known for their robustness and ensemble learning capabilities, have been applied to skin lesion classification to enhance decision-making processes. A study discussed the combination of deep learning features with Random Forest classifiers, noting that such integration improves robustness and reduces overfitting, leading to more accurate classification outcomes [20].

The synergistic combination of VGG19 for feature extraction and Random Forests for classification has been explored to leverage the strengths of both methodologies. A recent study evaluated the performance of an enhanced VGG19 model (E-VGG19) integrated with traditional classifiers, including Random Forests, for real-time skin cancer detection. The findings indicated that this combination significantly improves overall classification accuracy, providing valuable insights into the effectiveness of hybrid models in medical diagnostics [21].

Recent studies highlight the effectiveness of combining VGG19-based feature extraction with ensemble classifiers to improve the accuracy of skin lesion classification. This hybrid approach harnesses the deep learning model's capability to extract complex features and the ensemble classifier's robustness, resulting in more reliable and efficient skin cancer detection. Continued research is vital to overcoming current challenges and optimizing these methodologies for clinical use.

3. METHODOLOGY

The proposed methodology integrates VGG19-based feature extraction with an optimized Random Forest classifier to improve the accuracy and efficiency of skin lesion classification. Figure 1 represents the proposed architecture diagram. The detailed steps, including necessary equations, are outlined as follows:

3.1 Dataset

The ISIC (International Skin Imaging Collaboration) dataset is a comprehensive collection of dermoscopic images aimed at advancing skin cancer research. It includes high-resolution images of various skin lesions, encompassing benign and malignant, annotated with metadata such as lesion type, diagnosis, and patient demographics. The dataset is widely usedfor training and validating machine learning models, particularly for classification, segmentation, and lesion detection. It is a benchmark resource in dermatological imaging and Al-based skin cancer diagnosis.

The dataset consists of 3,297 samples, divided into two classes: malignant and benign. 2,637 samples are used for training, while 660 are allocated for testing. The malignant class includes 1,497 cases, with 1,197 used for training and 300 for testing. Similarly, the benign class consists of 1,800 cases, with 1,440 designated for training and 360 for testing.

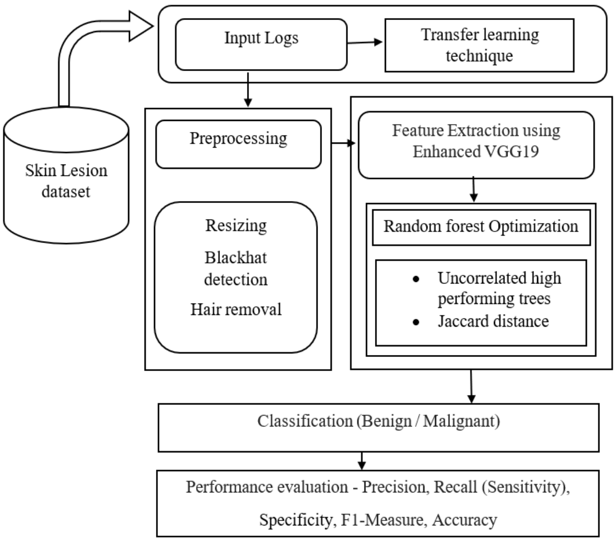

Figure 1. The proposed Architecture Diagram

3.2 Preprocessing Steps

Preprocessing medical images is essential to remove noise and artifacts, ensuring higher quality data for accurate analysis. The following steps are involved:

- Resize the images to standardized dimensions (e.g., 1024x1024 pixels) to ensure consistency.
- Denoising: Apply Gaussian and median filters to remove noise while preserving critical details. Gaussian filtering smooths the image, while the median filter removes impulsive noise.

- Hair Removal: Use Blackhat filtering to highlight hair contours and inpainting techniques to remove hair, ensuring that important skin features are visible.
- Inpaint: Enhance image quality by reconstructing lost details which improves the visibility of subtle features that may be critical for diagnosis.

The final pre-processed image provides a clean and quality enhanced representation of skin lesions, ready for feature extraction.

3.3 Feature Extraction Using VGG19

VGG19, a deep convolutional neural network pre-trained on the ImageNet dataset, was employed for feature extraction. The fully connected layers of VGG19 were removed, retaining the convolutional layers to extract hierarchical feature representations. Images were pre-processed and the pixel values are normalized. Feature maps were extracted from the final convolutional layer and flattened into a two-dimensional array, providing high-dimensional input features for the subsequent Random Forest classifier. Each image is normalized using:

$$I' = \frac{I-\mu}{\sigma} \qquad (1)$$

where I is the input image, μ is the mean, and σ is the standard deviation of the ImageNet dataset.

The convolutional layers of VGG19 output a feature map $F \in R^{h\times w\times}$ *where h, w, d* represent the height, width, and depth of the feature map. The feature map is reshaped into a two-dimensional array for compatibility with machine learning classifiers:

$$X = \text{Flatten}(F)$$

Here, $X \in R^{n\times m}$, where n is the number of images and $m = h\cdot w\cdot d$.

Global average pooling ensures effective feature selection for classification. It reduces the spatial dimensions of a feature map by averaging the values in feature channel and helps to reduce the number of parameters that overfit deep learning models.

3.4 Random Forest Training

A Random Forest classifier, initialized with N decision trees, was trained using the features extracted by VGG19. Each decision tree was independently evaluated for accuracy on the training data. To enhance the classifier's efficiency, the top P high-performing trees were selected based on their individual accuracies.

3.5 Optimization of Random Forest Using Clustering

To address redundancy among the selected decision trees, a clustering-based optimization strategy was implemented. Jaccard distances were calculated between tree predictions to measure their dissimilarity. K-Means clustering was applied to group the trees into Q clusters. Within each cluster, the tree with the highest accuracy was chosen as a representative, forming an optimized Random Forest ensemble with reduced redundancy and improved diversity.

Jaccard Distance: The dissimilarity between two trees t_i and t_j is computed using Jaccard distance on their predictions:

$$d_{ij} = 1 - \frac{|P_i \cap P_j|}{|P_i \cup P_j|} \qquad (2)$$

where P_i and P_j represent the sets of samples classified as positive by t_i and t_j, respectively.

Constructing the Distance Matrix: The pairwise Jaccard distances are used to construct a distance matrix $D \in R^{N\times N}$, where N is the number of trees in the ensemble. The element D_{ij} represents the dissimilarity between the predictions of trees t_i and t_j. This distance matrix forms the input for the K-Means clustering algorithm.

K-Means Algorithm: The K-Means algorithm assigns each tree to one of K clusters by minimizing the intra-cluster variance (the sum of squared distances between trees in the same cluster). The result of this process is a set of K clusters, where each cluster contains trees that are more similar to each other than to trees in other clusters. The goal is to select trees that provide complementary predictions by focusing on trees with high dissimilarity.

Cluster Representative Selection

Once the decision trees are grouped into clusters through K-Means clustering, the next step is to select a representative tree from each cluster. The representative tree is typically the one that performs the best in terms of classification accuracy, as it is likely to contribute the most useful information from that cluster.

Selection Criteria: The criteria for selecting the best representative tree from each cluster is based on its individual performance on the training data. Specifically, the accuracy of each tree is evaluated:

$$\mathrm{Acc}_i = \frac{\text{Correct Predictions}}{Total\ samples} \tag{3}$$

Selecting the Best Tree in Each Cluster: For each cluster, the tree that yields the highest accuracy is selected as the representative. This selection is based on the assumption that the more accurate trees are better at generalizing and therefore contribute more reliable and diverse information to the ensemble.

Optimized Ensemble: The set of representative trees from each cluster forms the final optimized Random Forest ensemble. This ensemble is smaller in size compared to the original ensemble but is expected to exhibit improved performance due to the diversity and high accuracy of the selected trees. The optimized ensemble is then used for classification tasks, where predictions are made by aggregating the results of the selected trees.

The proposed methodology integrates VGG19 for feature extraction with an optimized Random Forest classifier, employing clustering to reduce redundancy and enhance diversity among decision trees. This approach improves classification accuracy and efficiency, demonstrating its potential for reliable skin lesion diagnosis and advancing computer-aided diagnostics.

4. PROPOSED METHOD

A deep convolutional neural network, VGG19, was utilized for feature extraction, followed by training a Random Forest classifier with N decision trees. From these, P high-performing trees were selected based on accuracy. To optimize further, Q uncorrelated trees were chosen using a clustering approach, forming an ensemble of diverse, high-performing trees for classification. The method to build an optimized random forest follows the following steps.

Step 1: Feature extraction: Use VGG19 convolutional neural network to extract features from skin lesion images.

Step 2: Tree classifier building (Random Forest): use the extracted features to build a tree and then give the evaluation value to the tree. Continue this step until all trees are generated;

Step 3: Tree ordering: sort all these K trees in their $Accuracy$ descending order;

Step 4: Selection of high performing trees: select the top P trees with high $Accuracy$ values.

Step 5: Tree Dissimilarity Matrix (d): find the dissimilarities among the top p trees is computed using Jaccard distance based on their predictions.

Step 6: Tree Clustering: use the observed d as input for the K-Means clustering and obtain Q correlated clusters of trees.

Step 7: In each cluster sort the trees in their $Accuracy$ descending order. Select a tree from each cluster with high $Accuracy$ values which gives Q uncorrelated high performing trees

Step 8: Optimized random forest building: use the majority vote of these uncorrelated high performing trees to make an ensemble classification decision.

The optimized random forest method has two more key parameters, *i.e.*, the number of P top performing trees from which Q uncorrelated high performing trees are selected to form an optimized random forest.

5. RESULTS AND DISCUSSION

The proposed hybrid approach, combining VGG19-based feature extraction with an optimized Random Forest classifier, significantly improves skin lesion classification accuracy. DenseNet, MobileNetV2, ResNet50V2, Xception, VGG16, and traditional VGG19. The proposed method achieved an accuracy of 88.21%, precession of 81%, recall of 93%, and F1-score of 87%. The Table 1 represents the comparison and result of the proposed model. And Figure 2 represents the of the pictorial representation of the above result. These results highlight the robustness and effectiveness of the optimization strategies employed.

Architectures in paper [34]	Accuracy (%)	Precision (%)	Recall (%)	F1_Score (%)
DenseNet	74.68	78	85	81
MobileNetV2	73.98	76	83	80
ResNet50V2	73.42	78	86	82
Xception	70.62	75	88	81
VGG16	71.46	74	87	80
VGG19	68.67	72	89	79
Proposed EVGG19 with Optimized RF	**88.21**	**81**	**93**	**87**

Table 1: Result of Proposed Model and Comparison with Other State-of-Art

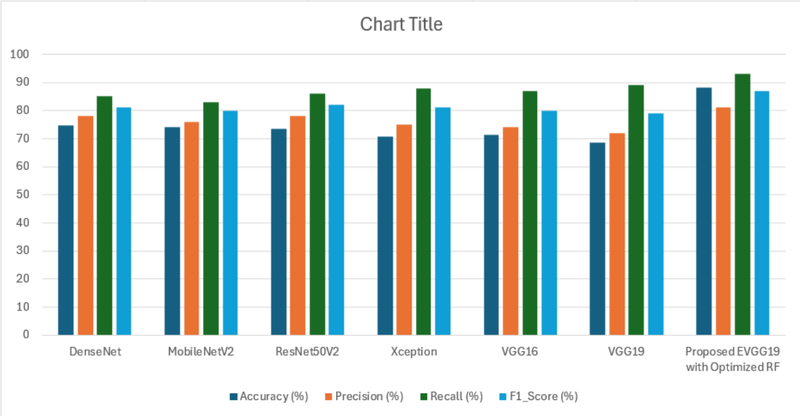

Figure 2. Result of Proposed Model and Comparison with Other State-of-Art

The use of transfer learning in VGG19 ensures robust feature extraction, while the clustering-based tree selection in Random Forest enhances model diversity and reduces redundancy. High recall indicates excellent sensitivity in detecting melanoma cases, which is critical for early diagnosis and treatment in medical applications. Overall, the proposed methodology successfully integrates the strengths of deep learning and ensemble learning, offering a powerful tool for accurate and efficient skin cancer classification.

6. CONCLUSION

This research presents a novel hybrid framework that combines VGG19-based feature extraction with an optimized Random Forest classifier to improve skin lesion classification. The study addresses key limitations of traditional Random Forest models, such as redundancy and inefficiency, by leveraging clustering techniques to select diverse and high-performing trees. The proposed EVGG19-Optimized RF method achieved state-of-the-art performance with an accuracy of 88.21%, precession of 81%, recall of 93%, and F1-score of 87%. These results demonstrate the potential of this hybrid approach in enhancing classification accuracy and computational efficiency, making it a promising solution for real-world clinical applications in skin lesion analysis.

Future work will focus on expanding the dataset to include multi-class skin lesion categories, improving model interpretability, and exploring advanced optimization techniques to further enhance performance. The integration of this framework into clinical workflows can significantly contribute to early detection and diagnosis of skin cancer, ultimately improving patient outcomes.

REFERENCES

[1] Hasan N, Abdel-Galil H, Saleh H. Skin cancer: understanding the journey of transformation from conventional to advanced treatment approaches. Mol Cancer. 2023;22(1). doi:10.1186/s12943-023-01854-3.

[2] Deshpande A, Estrela VV, R N. Computational intelligence methods for super-resolution in image processing applications. Cham: Springer International Publishing; 2021. doi:10.1007/978-3-030-67921-7.

[3] Abd-Allah GM, Medhat S, Abdel-Galil H, Saleh H. miRNAs as potential game-changers in melanoma: A comprehensive review. Pathol Res Pract. 2023;244:154424. doi:10.1016/j.prp.2023.154424.
[4] Urban K, Mehrmal S, Uppal P, Giesey RL, Delost GR. The global burden of skin cancer: A longitudinal analysis from the global burden of disease study, 1990–2017. JAAD Int. 2021;2:98–108. doi:10.1016/j.jdin.2020.10.013.
[5] Shi K, Jiang Y, Zhang Y, Liu X. Clinical characteristics of malignant melanoma in central China and predictors of metastasis. Oncol Lett. 2019. doi:10.3892/ol.2019.11219.
[6] Singh RK, Gorantla R, Allada SGR, Narra P. SkiNet: A deep learning framework for skin lesion diagnosis with uncertainty estimation and explainability. PLoS One. 2022;17(10):e0276836. doi:10.1371/journal.pone.0276836.
[7] Ali K, Shaikh ZA, Khan AA, Laghari AA. Multiclass skin cancer classification using EfficientNets – a first step towards preventing skin cancer. Neurosci Inform. 2022;2(4):100034. doi:10.1016/j.neuri.2021.100034.
[8] Simonyan K, Zisserman A. Very deep convolutional networks for large-scale image recognition. Int Conf Learn Represent. 2015.
[9] Aburaed N, Aburaed F, Al-Ahdal M, et al. Skin cancer classification model based on VGG19 and transfer learning. Int Conf Signal Process Inform Secur (ICSPIS). 2021.
[10] Breiman L. Random forests. Mach Learn. 2001;45(1):5–32.
[11] Murugan A, Nair SAH, Kumar KP. Detection of skin cancer using SVM, random forest and kNN classifiers. J Med Syst. 2019;43:1–9.
[12] Medhat S, Abdel-Galil H, Aboutabl AE, Saleh H. Skin cancer diagnosis using convolutional neural networks for smartphone images: A comparative study. J Radiat Res Appl Sci. 2022;15(1):262–7. doi:10.1016/j.jrras.2022.03.008.
[13] Faghihi A, Fathollahi M, Rajabi R. Diagnosis of skin cancer using VGG16 and VGG19 based transfer learning models. Multimed Tools Appl. 2023. doi:10.1007/s11042-023-17735-2.
[14] Keerthana D, Venugopal V, Nath MK, Mishra M. Hybrid convolutional neural networks with SVM classifier for classification of skin cancer. Biomed Eng Adv. 2023;5:100069. doi:10.1016/j.bea.2022.100069.
[15] Ma X, Shan J, Ning F, Li W, Li H. EFFNet: A skin cancer classification model based on feature fusion and random forests. PLoS One. 2023;18(10):e0293266. doi:10.1371/journal.pone.0293266.
[16] Venugopal V, Raj NI, Nath MK, Stephen N. A deep neural network using modified EfficientNet for skin cancer detection in dermoscopic images. Decis Anal J. 2023;8:100278. doi:10.1016/j.dajour.2023.100278.
[17] Howard AG, Zhu M, Chen B, et al. MobileNets: Efficient convolutional neural networks for mobile vision applications. 2017.
[18] Szegedy C, Vanhoucke V, Ioffe S, Shlens J, Wojna Z. Rethinking the inception architecture for computer vision. IEEE Conf Comput Vis Pattern Recognit (CVPR). 2016;2818–26. doi:10.1109/CVPR.2016.308.
[19] Hasan MK, Akhtar Z, Rehman H, et al. Skin lesion analysis and cancer detection based on machine learning and image processing techniques: A comprehensive survey. Life. 2023;13(1):146.
[20] Mustafa S, Jaffar A, Rashid M, Akram S, Bhatti SM. Deep learning-based skin lesion analysis using hybrid ResUNet++ and modified AlexNet-Random Forest for enhanced segmentation and classification. PLoS One. 2025;20(1):e0315120.
[21] Kandhro IA, Manickam S, Fatima K, Uddin M, Malik U, Naz A, et al. Performance evaluation of E-VGG19 model: Enhancing real-time skin cancer detection and classification. Heliyon. 2024;10(10).