Original Article

Melanoma Skin Cancer Detection Using Ensemble of Machine Learning Models with ResNeXt101 and TinyViT

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Abstract - Although skin cancer is a deadly condition, it can be effectively treated with a quick test. Still, it might be challenging to diagnose skin conditions in a timely manner. While most of the earlier work may be covered by a single model system, integrating multiple models helps increase classification accuracy. Early research usually used Deep Convolutional Neural Networks (DCNN), which struggle to capture global properties. ResNeXt101 and TinyViT are the two learning models that make up this hybrid model. The model performs better overall as a result of this integration. More significantly, when applied to melanoma cancer data, the hybrid model performs as a weighted model and achieves an astounding 91.6% accuracy.

Keywords - Skin cancer melanoma, Convolutional Neural Networks (CNN), Ensemble Learning, Vision transformer, ResNeXt101, TinyViT.

1. Introduction

Biomedical imaging is vital for detecting and treating cancer (melanoma) on the skin, which typically manifests in areas of the body that are prone to the sun. The study [1] enhances the VGG19 model with max pooling and a dense layer, integrating Machine Learning (ML) techniques and sophisticated deep learning models previously built for skin cancer diagnosis, demonstrating superior accuracy in multiclass classification compared to traditional classifiers. The study [2] proposes a method for early skin cancer identification using medical imaging. It employs fuzzy C-means clustering, filters, and visual features from images and employs a CNN for classification.

The method outperforms conventional techniques with a 91% detection accuracy. The proposed work makes recommendations for possible uses of more effective and precise skin cancer detection technologies using the Ensemble Model with the aim of high accuracy, which could result in timely diagnosis and improved treatment outcomes.

This research [6] analyses the efficacy of neural networks of Convolutional and Artificial classes in identifying skin cancer. It highlights the necessity for automated methods for skin lesion recognition and shows their potential for early and effective diagnosis. The DenseNet model performed better than the existing CNN models in terms of accuracy and loss in the study [11-13].

The melanoma detection algorithm presented in this research [15] is a hybrid ELM and TLBO algorithm that combines TLBO for enhanced performance with ELM for fast and accurate training.

This article [17-19] examines Machine Learning (ML) techniques for diagnosing skin cancer and evaluates how well they work using reference datasets. It highlights the possibility for early detection while discussing the drawbacks and downsides of the support vector machine, convolutional neural network, and k-nearest neighbor techniques.

The article [20] proposes a high-resolution model based on CNN with hyper-parameter optimization for skin cancer diagnosis using Dermatoscopic images. It addresses the problems of under- and over-segmentation and improves performance through data augmentation. Deep learning improves a real-time analytical method for an autonomous skin cancer detection system by extracting hidden information from polarization speckles [13, 21, 22].

When gathering broad features, deep Convolutional Neural Networks (DCNNs), the main instrument utilized in previous studies for skin cancer prediction, have limitations. In order to ensure accurate predictions in later phases, the suggested strategy extracts hidden features from known features using the ResNeXt101-TinyViT ensemble method to improve accuracy. To maximize features and address data dimensionality issues, an upgraded ensemble model technique is utilized. Using benchmark datasets, the proposed approach is compared to state-of-the-art models for accuracy, specifically the Kaggle skin cancer dataset.

The article is structured in the following manner: Section 2 outlines the study's methodology. Section 3 centers on the experimental analysis and presents the findings. Finally, Section 4 encompasses the conclusion and offers future paths for this research.

2. Material & Methods

This work aims to explore both stand-alone and ensemble learning models (resnext101 and tinyvit) for skin cancer patients of different types. This work also included the evaluation of the performance of this model after it was trained. Automated classification and analysis enabled by medical imaging technology has revolutionized skin cancer detection and treatment by providing targeted information extraction and tailored treatment strategies.

2.1. Dataset

The HAM10000 dataset is an extensive collection of dermatoscopic imagery depicting prevalent pigmented skin lesions from many origins. The HAM10000 dataset consists of 10,015 dermatoscopic images of prevalent pigmented skin lesions. All digital images were normalized and scaled to a

uniform dimension in preparation for dataset training. Subsequently, the dataset will be split into a training set (5514) and a test set (938) to facilitate the learning process. This split has only those images that have no duplicates. The images are divided into seven primary classes, Melanocytic nevi(nv), melanomas(mel), basal cell carcinomas(bcc), actinic keratoses(akiec), benign keratoses(bkl), dermatofibromas(df), and vascular lesions(vasc)

Figure 1 contains the train-test split data of the input dataset. Designed to train the suggested Ensemble Model for automatic skin cancer diagnosis.



Fig. 1 Train and test data of the HAM10000 dataset

2.2. Data Preprocessing and Data Augmentation

The data should be ready for more processing and analysis that describes the preprocessing well, especially in the domain of ML and data analysis. This is especially crucial in the case of skin cancers, as the type and standard of the input data can greatly influence the overall metrics and performance of the prediction models. In order to ensure consistency and enhance the diagnosis performance, data augmentation methods, such as translation, rotation, and scaling, have been utilized to grow the dataset's effective dimension. Figure 2 displays images of several classes present in the dataset.



Fig. 2 Images taken in original form from the HAM10000 dataset

The number of training epochs, the image size, and the learning rate were among the hyperparameters of the training process that were optimized to improve the efficacy of skin cancer prediction. Figure 3 indicates the comparison between the original image and the augmented image.



Fig. 3 Comparing Images of the original image from the dataset, preprocessed image and augmented image

2.3. ResNeXt101

This work investigates how the resNeXt101 model can be used over the Skin Cancer HAM10000 Dataset, which contains dermatoscopic images of different types of skin lesions. With a few modifications over ResNet architecture, the resNeXt101 model has demonstrated encouraging results in image classification. Combining the advantages of different convolutional blocks improves the performance of feature extraction and classification. As a result, the model can achieve a more parameter-efficient and cardinality approach that will be used for the dataset so that it can be trained on easier datasets like HAM10000. Results display the model's capability to detect and classify skin cancer autonomously, confirming its performance of correctly detecting different skin lesions.

2.4. TinyViT

Vision Transformers, especially TinyViT, demonstrate significant accuracy and computational efficiency attributes, making it a suitable candidate for our use case of resourceconstrained devices.

The other novelty of TinyViT is its efficiency at gathering long-range associations in visual input through the built-in self-attention mechanism of the Transformer, unlike traditional CNNs that rely on fixed receptive fields and local connectivity, where the input from the dataset is divided into a grid of patches, which are then independently encoded and merged through a stack of transformer layers. Because of its numerous functionalities and the possibility for adaptive inference of relationships among image regions, TinyViT can represent features more accurately and perform a lot better overall.

Moreover, TinyViT combines a series of plug-and-play design choices that reduce its size and computational costs without affecting accuracy, like dynamic sequence length and efficient tokenization.

2.5. Ensemble Model

Ensemble modeling is an approach in machine learning that enhances model accuracy by combining predictions across multiple models. Indirect techniques have been developed for the classifier, thus outperforming single-based classifiers and showing benchmark studies, where the average of the classifier output is calculated by pooling together the outputs of many modelers and considering their advantages and disadvantages.

Regarding image classification, this method is very helpful because several models cannot capture all the subtleties. Hardware restrictions, such as a big model size or a sluggish training speed, can be problematic, though. Even with these difficulties, ensemble methods frequently outperform individual models in terms of classification and prediction accuracy.

The mathematical representation of the Ensemble Model is,

 $E_{M}(S_{M}, D_{T}, M_{D}, R_{A}, C_{A}) = S_{M}(\sum_{1}^{n} I_{L}(D_{T}, M_{D}, R_{A}, C_{A})) \quad (1)$ Where, E_M - Ensemble Model S_M - Integration Model Strategy D_T - The input dataset M_D - Models considered for the study R_A - Result Analysis C_A - Computational Analysis I_L - Individual Learning Models

2.6. Benefits of the Proposed Ensemble Model

ResNeXt101 and TinyViT coupled models can improve performance, robustness, and generalization, making an ensemble model more resistant to overfitting. Additionally, it provides a fair trade-off between processing power and computational efficiency, enabling high-performing results without unduly straining computer resources.

Algorithm 1: Ensemble Learning Model Approach for the Skin Cancer Classification

1 Begin: There are L labels in the dataset with n number of images

	i.e. $\{\alpha_i^k\}_{i=1}^n \in \{\beta_j\}_{j=1}^C$ Here, (i,j,k) are indices of (vector, label, model) α_i^k and β_j : elements of corresponding sets	;
2	α_s^k : s th data as the test sample $D_T \subset D_S (D_s - Dataset D_{TR} - Train_Dataset D_T - Test_Dataset)$	
3	E: Ensemble Model Constituents	
4	I: The Number of Individual Models in Ensemble Model	
5	for $s = 1$ to m do	
6	for $t = 1$ to I do	
7	Train E_t with Train Dataset D_{TR} ;	
8	Predict $\beta_s^{k^t}$ with E_t for the input images α_s^k ;	
9	Save $\beta_s^{k^t}$ for every image in a feature matrix Z (with m×I) as $\mathbb{Z}^{m\times I}$ that belongs D_{TR}	
10	Find the average class label $\beta_s^{k^f}$ - represent the test data sample's final predicted class	
	$\alpha_{s}^{k};$	
11	end	
12	end	
13	End	

3. Results and Discussion

This section displays the experimental results for the prediction of melanoma skin cancer. We implemented the proposed method with Python. The averaged outcomes of multiple experiments indicate a noteworthy enhancement of the proposed model compared to the existing state-of-the-art models. The new model significantly improves the outcomes across a wide range of metrics.

The results of two training models (ResNeXt101 and TintViT) and the Ensemble Model with ResNeXt101 and TintViT are described.

- i. The model was trained using ResNeXt101 and TintViT as individual models
- ii. The model was trained using ResNeXt101 and TintViT as Ensemble models with average as a strategy.

The hybrid neural network integration procedure improves the evaluation and classification processes, and it also improves the system results and consequences in terms of the assessment metrics. We evaluated and compared the ensemble model's performance to the ResNeXt101 and TintViT models.

The assessment indicators of this model simulation were evaluated and compared. The hybrid neural network ensemble model produces better results with fewer errors than other models. Current models such as ResNeXt101 and TintViT are compared with the ensemble model. The hybrid ResNeXt101 and TintViT ensemble model enhances the features of the training and analysis processes for extraction and classification.





(b) Accuracy vs Val_Accuracy of ResNext101



Fig. 4 Result analysis (a) and (b) ResNeXt101, (c) and (d) TinyViT, (e) and (f) Proposed ensemble model.

3.1. ResNeXt101

The loss metrics during training of the ResNeXt101 model are shown in Figure 4(a). The training_accuracy and val_accuracy of the ResNeXt101 model are shown in Figure 4(b). The observations based on the results about loss and accuracy are

- The model has a 7% loss.
- The model's accuracy is 88.2%.
- The Best_3 loss of the model is 2%
- The Best_3 accuracy of the model is 98.4%

3.2. TinyViT

The loss metrics during training of the TintViT model are shown in Figure 4(c). The training_accuracy and val_accuracy of the TintViT model are shown in Figure 4(d). The observations based on the results about loss and accuracy are

- The model has a 4% loss.
- The model's accuracy is 90.76%.
- The Best_3 loss of the model is 0.4%
- The Best_3 accuracy of the model is 99.9%

3.3. Proposed Ensemble Model

The Training_loss and val_loss of the proposed ensemble model with ResNeXt101 and TinyViT are shown in Figure 4(e). The accuracy values during training of the proposed ensemble model with ResNeXt101 and TinyViT model are shown in Figure 4(f). The observations based on the results about loss and accuracy are

- The model has a 6% loss
- The mode's accuracy is 92%
- The Best_3 loss of the model is 0.2%
- The Best_3 accuracy of the model is 99.9%

3.4. Comparative Analysis

A comparison of the suggested model and the current conventional system is shown in this section. The performance of these models on diverse data sets, computational effectiveness, and task generalization will all be compared. When this model is compared to the previous way, the performance of this tool is superior.

Figure 5 compares the three models' performance in multi-class classification, ResNeXt101, TinyViT and Proposed Ensemble Model. ResNeXt101 reaches 88.2% accuracy but makes it confused with similar categories, such as the pair of vasc and df. TinyViT, which achieves an accuracy of 90.76%, performs better than ResNeXt101 regarding the classification of skin cancer; for example, the former performs better than the latter in both melanoma and basal cell carcinoma classes. However, some misclassifications remain, suggesting room for further improvement.



Fig. 5 Confusion matrices of ResNeXt101, TinyViT, proposed ensemble model

	Pr	recision		Recall			f1-score		
	Ι	II	III	Ι	Π	III	Ι	Π	III
nv	0.88	0.90	0.92	1.00	1.00	0.99	0.93	0.95	0.96
mel	0.85	0.92	0.87	0.60	0.74	0.81	0.70	0.82	0.84
bkl	0.91	0.91	0.96	0.76	0.81	0.89	0.82	0.86	0.92
bcc	0.90	0.97	0.87	0.69	0.66	0.68	0.78	0.78	0.76
akiec	0.88	0.85	0.92	0.53	0.66	0.62	0.67	0.65	0.74
vasc	1.00	1.00	0.82	0.38	0.50	0.31	0.55	0.67	0.45
df	0.83	0.83	0.83	0.24	0.31	0.33	0.37	0.45	0.48

Table 1. Classwise metrics of the ResNeXt101(I), TinyViT(II) and proposed ensemble model (III)

Meanwhile, The Proposed Ensemble Model achieves 91.76% of the best accuracy and delivers more uniform classification performance. Here, the confusion matrix reveals this model with fewer misclassified errors than those of ResNeXt101 and TinyViT, with 72 correctly identified instances for bkl vs 68 and 69(ResNext101 and TinyVit). The proposed ensemble model as trained with both ResNeXt101 and TinyViT, and the combination shows better classification performance than them, which leads to reduced classification errors.

This comparison analysis compares and contrasts the proposed ensemble model with the two machine learning approaches existing currently, ResNeXt101 and TinyViT, as seen in Figures 6(a) and 6(b). Compared to the ResNeXt101's 0.88 and TinyViT's 0.91 accuracy, the research results showed a high accuracy of 0.92. The ensemble model exhibits higher precision compared to the existing model. The proposed strategies surpass the existing ones in effectiveness.

Table 1 shows classification metrics for the three models ResNeXt101, TinyViT, and the Proposed Ensemble Model for multi-class skin lesions. Precision calculates how many actual positive cases were correctly predicted versus all positive cases predicted; a higher precision means fewer false positives, which is very important in medical diagnosis. For example, for akiec, the ensemble model has the highest score in akiec identification with negligible false positives(0.92>0.88 and 0.85 for ResNeXt101 and TinyViT).

Recall is the ratio of actual positive cases correctly identified by the model, thus yielding fewer false negatives, which is important in skin cancer detection. For example, in the case of mel class, Recall improves from 0.60 (ResNeXt101) to 0.74 (TinyViT) and finally to 0.81 (Proposed Ensemble Model), which indicates that the ensemble model can detect many cases of melanoma.

The F1-Score integrates Precision and Recall into a singular statistic that represents the equilibrium between the two. It is especially useful when there is a trade-off between Precision and Recall. In a sense, the F1-score is slightly improved, from 0.93 in ResNeXt101 \rightarrow 0.95 in TinyViT \rightarrow 0.96 in the Proposed Ensemble Model, which shows continuous improvement of overall performance in the nv class.

Employing ensemble methods has been investigated as a way to take use multiple models' advantages and improve accuracy. Furthermore, practitioners and academics will be better able to select the appropriate architecture for the specific use cases they are working on, owing to the knowledge gained from this study. When comparing performance measures, we found that the TinyViT model outperformed ResNeXt101. The proposed Ensemble model fared better on performance metrics than both TinyViT and ResNeXt101. An array of evidence from earlier research demonstrates the benefits of adopting ensemble techniques. Notably, even a simple ensemble of identical structures can outperform a single massive model. This can be explained by reducing the impact of noisy contributions by averaging the predictions from different models. Furthermore, it has been shown that testing accuracy grows monotonically with data size. Table 2 contrasts the accuracy of the proposed model with that of the existing models.



Accuracy Best 3 Accuracy

(a) Accuracy vs Best_3 Accuracy of ResNeXT101(A), TinyVIT(B) and Proposed Ensemble Model (C)





(b) Loss vs Best_3 Loss of ResNeXT101(A), TinyVIT(B) and Proposed Ensemble Model (C) Fig. 6 Comparison of three models

Model Used in Earlier Work	Year	Accuracy
CNN-Fuzzy C-Means [2]	2024	91%
Ensemble of Machine Learning Models [5]	2024	89.6%
Deep CNN [12]	2019	86%
Enhanced Deep Learning Method [13]	2021	78%
ResNet [13]	2021	82%
Proposed Ensemble Model	2024	92%

Table 2. Comparison of accuracy of previous work with the proposed ensemble model

4. Conclusion

Using ResNeXt101 and TinyViT, an ensemble model is introduced in this work. The suggested average-based ensemble method integrates the TinyViT and ResNeXt101 models for the task of melanoma skin cancer detection. Initially, A dataset of melanoma skin cancer is obtained with extensive pattern embeddings from a deep learning framework. Next, this dataset is used to train each ML model separately. With an accuracy of 90.7%, TinyViT outperforms ResNeXt101, which has an accuracy of 88.21%. The suggested model performs 92% more accurately than the other two when compared to it. Additionally, the proposed model performs better than existing research studies.

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