

Enhancing Early-Stage Detection of Melanoma using a Hybrid BiTDense

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Abstract

Melanoma, accounting for just 1% of skin cancers, disproportionately contributes to the majority of skin cancer-related deaths in the United States, often originating in normal skin rather than preexisting moles, with nearly 70% of cases not commencing in a mole. Over the past three decades, its diagnosis has surged, outpacing most other cancer types in growth rates. Traditional melanoma recognition methods are cumbersome and costly, but the potential of computer-assisted techniques offers optimism for swift and efficient early-stage identification. Leveraging a standard phone camera for skin image capture and subsequent analysis using computer vision models emerges as a promising approach. In a groundbreaking study, researchers introduced a hybrid model, BiTDense, amalgamating DenseNet121 and Big Transfer R101x1 for early melanoma classification. DenseNet's distinctive dense connections between layers establish direct connections with matching feature-map sizes, while Big Transfer incorporates Group Normalization (GN), dividing channels into groups for mean and variance computation, ensuring computational independence of batch sizes and stability across diverse ranges. BiTDense, with its 93.07% accuracy, 99.43% precision, remarkable 98.87% recall rate, and exceptional F1 Score of 99.15%, not only enhances precise melanoma diagnosis but also signifies a noteworthy advancement in skin cancer detection, owing to its sophisticated architecture involving pre-trained models and custom adaptations.

Keywords

Melanoma, Skin Cancer, Benign, Malignant, DenseNet121, Big Transfer

INTRODUCTION

Skin cancer is a substantial issue within the domain of international health due to its pervasive prevalence and severe ramifications. As UV light exposure becomes more prevalent in the modern world, the incidence of skin cancer is increasing steadily (Saginala et al., 2021). UV light, originating from both natural sources like the sun and artificial sources like tanning booths, is a substantial contributor to the progression of this detrimental ailment. An estimated 2 to 3 million non-melanoma skin cancer cases and 132,000 melanoma skin cancer cases are documented annually, posing a substantial obstacle for healthcare systems worldwide (Laikova et al., 2019).

Despite advancements in medical science and increased emphasis on preventive measures, skin cancer continues to be a substantial concern within the realm of public health. It is of the utmost importance to develop effective strategies for early detection and intervention. Early detection of problems is critical for enhancing treatment outcomes, as it increases the probability of successful intervention and decreases the need for extensive surgical procedures (Wu et al., 2022). However, conventional methods of skin cancer diagnosis, which rely on dermatologists' visual assessments, are arbitrary and subject to error (Naqvi et al., 2023a).

Researchers are currently investigating the potential of artificial intelligence (AI) in the classification of skin cancer in order to improve early detection programs. The objective of the researchers is to furnish clinicians with unparalleled capabilities for precisely identifying and classifying skin lesions through the development of state-of-the-art AI models. The combination of deep learning algorithms and convolutional neural networks (CNNs) has caused a major shift in the field. These new technologies make it possible to quickly and accurately pull-out relevant features from very large datasets. Safeguard your epidermis.

The goal of the study is to build a strong system that can tell the difference between benign and malignant melanoma lesions so that treatment can be done quickly and effectively by concatenating Big Transfer (R101x1) and DenseNet121 along with a custom DNN head (Naqvi et al., 2023b). Through an exhaustive analysis of existing research and the introduction of our novel hybrid model, our objective is to propel the domain of skin cancer diagnosis and treatment forward by introducing more accurate and efficacious methodologies.

LITERATURE REVIEW

Melanoma

Melanoma, a form of skin cancer, has a historical record dating back to ancient times. The initial documentation of melanoma is credited to the Greek physician Rufus of Ephesus in the first century AD. Substantial advancements in the understanding and treatment of human malignant melanoma occurred in the 19th century (Kamińska et al., 2021). Notably, in 1858, there was advocacy and implementation of wide and deep radical excision as a treatment approach for melanoma (Radiation, n.d.).

Benign melanoma denotes non-malignant proliferation of pigment-forming cells, specifically melanocytes (Vanka & Chakravarty, 2022). These formations typically exhibit well-defined boundaries, exhibit gradual growth, and remain confined without infiltrating surrounding tissues or metastasizing to distant locations (Szumera-Ciećkiewicz & Massi, 2021). While they generally do not pose significant issues, surgical removal may be necessary if they induce discomfort or give rise to medical concerns (Scarano et al., 2020).

On the other hand, malignant melanoma is a form of cancer originating from melanocytes, marked by unregulated proliferation and the capacity to infiltrate adjacent tissues and metastasize to distant regions (Matias et al., 2021). Early diagnosis and treatment are crucial in cases of malignant melanoma, as it can pose a life-threatening risk. Distinguishing between benign and malignant melanocytic lesions is essential to guiding appropriate management strategies and establishing prognosis (Ward et al., 2017).

Deep learning and Melanoma

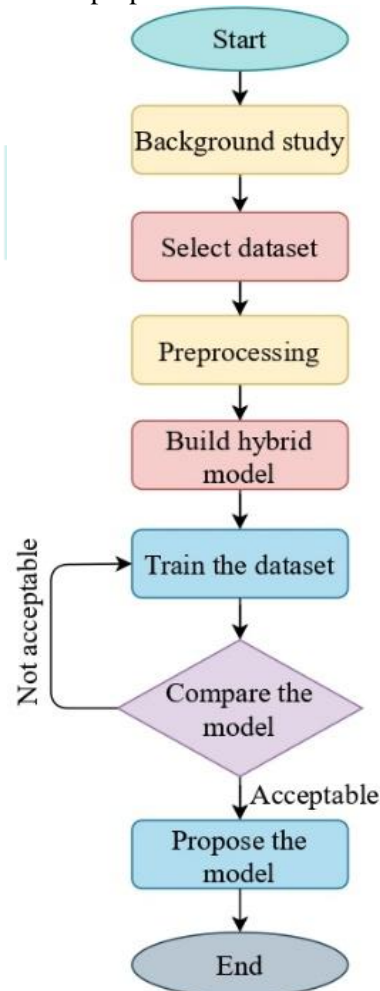
Deep learning has played a pivotal role in the categorization of benign and malignant melanoma, presenting noteworthy progress in the automated detection of skin cancer (Reis et al., 2022). Introduced the InSiNet framework, a deep-learning approach that has demonstrated remarkable efficacy in classifying skin cancer images. It achieved impressive accuracy rates, with performance reaching up to 94.59% for melanoma identification. The effectiveness of this approach has been rigorously assessed using diverse datasets, including the HAM1000 images sourced from the ISIC database (Pham et al., 2021). (Kushimo et al., 2023) conducted research proposing a methodology to enhance the accuracy of melanoma prediction in an imbalanced dataset. This involves modifying the Convolutional Neural Network (CNN) architecture and optimizing algorithms. The adaptations include the integration of a custom loss function, custom mini-batch logic, and a restructured configuration of fully connected layers. Our proposed method is better than 157 dermatologists' best efforts and the latest cutting-edge methods (Pham et al., 2021). It does this by using a large training dataset of 17,302 images that include both melanoma and nevus cases. It achieves notable metrics with an area under the curve of 94.4%, a sensitivity of 85.0%, and a specificity of 95.0%. Demonstrating the potential for medical diagnosis, the approach exhibits well-balanced evaluation metrics with a sensitivity of 90.0% and a specificity of 93.8% (Pham et al., 2021). Various techniques and datasets were examined for skin cancer classifiers and training at Table 1.

Table 1 Skin Cancer Diagnoses Classifier and Training

Ref	Algorithm	Dataset	Description	Results
Gursoy et al., 2016	CNN	170 skin lesion images	2 convolving layers	Acc: 81%
Wu et al., 2022	SVM + deep CNN	3753 dermoscopic images	Pertained to deep CNN and AlexNet	Acc: BCC-95.1%
Esteva et al., 2017	Deep CNN	ISIC-Dermoscopic Archive	Expert-level performance	Acc: 72.1%
Hu et al., 2016	CNN ensemble	ISIC 2017 dataset	CNN ensemble of AlexNet, VGGNet, GoogleNet	Avg Acc: 83.8%
Kalouche, 2016	VGG-16 and CNN	ISIC dataset	Trained on three separate learning models	Acc: 78%
Hasan et al., 2019	CNN	ISIC database	ABCD symptomatic checklist for feature extraction	Acc: 89.5%

METHODOLOGY

A thorough review of the relevant subject and literature is done to understand the problem and potential forecasting methods. After extensive background investigation, a dataset is chosen for forecasting model training and testing. To assure modeling suitability, the dataset is preprocessed. Addressing missing numbers, outliers, and other data quality issues may be necessary. Different deep learning methods are used to develop categorization models. This hybridization takes advantage of diverse models to improve prediction accuracy. All hybrid models are then trained on the preprocessed dataset. The most accurate classification model was proposed.

**Fig. 1** Research Methodology Flowchart

Data Acquisition and Preprocessing

The dataset used in this study is the “Melanoma Skin Cancer Dataset of 10000 Images” which as provided by Muhammad Hasnain Javid (*Melanoma Skin Cancer Dataset of 10000 Images*, n.d.). The dataset contains 10000 images belonging to two classes: benign and malignant skin cancer illustrated in Table 2.

Table 2 Distribution of 10,000 Images across Two Classes

Class	Training	Validation	Test
Benign	5000	500	500
Malignant	4605	500	500
Total	9605	1000	1000

Models

Densenet121

DenseNet-121 is a Convolutional Neural Network (CNN) structure that is highly regarded for its comprehensive architecture, efficient instruction method, and noteworthy accomplishments in medical imaging tasks (Huang et al., 2018a). The DenseNet-121 model has been employed for the early stratification of Alzheimer's disease through the utilization of MRI scans, the categorization of COVID-19 by analyzing chest X-ray visuals, and the detection of myeloma cells in bone marrow smears (Solano-Rojas et al., 2020). The DenseNet-121 architecture comprises four dense blocks, each with a distinct number of layers: 6, 12, 24, and 16 (Huang et al., 2018b). These blocks exhibit intricate connections between each layer, and a 1x1 convolution layer is integrated to decrease the input's channel count. DenseNet121 has proven valuable in the classification of melanoma, a form of skin cancer (Girdhar et al., 2023). Functioning as a Convolutional Neural Network (CNN), DenseNet-121 has demonstrated effectiveness in numerous medical imaging applications, encompassing disease detection and classification. Renowned for its elegance and efficiency, this CNN stands out due to its unique architecture, making it a highly beneficial tool in the realm of medical imaging.

Big Transfer (BiT-M-R101x1)

Big Transfer (BiT) stands out as a sophisticated method for transfer learning in image classification, specifically designed to improve the efficiency of training deep neural networks for vision tasks. Its primary objectives include enhancing sample efficiency and simplifying the process of hyperparameter tuning (Team, n.d.). Among the various BiT models, BiT-M-R101x1 is notable, employing the ResNet-101x1 architecture and undergoing pre-training on the ImageNet-21k dataset (*Google-Research/Big_transfer*, 2020/2024). The architecture of BiT-M-R101x1 is rooted in ResNet-101x1, featuring convolutional layers, identity blocks, and shortcut connections (Singh & Singh, 2023). The BiT-M-R101x1 model has been utilized to perform binary classification on the DEAP dataset, specifically for the arousal, valence, and dominance affective states. Big Transfer (BiT) is an exemplary and effective technique for transferring knowledge in image classification. One prominent instance of BiT is BiT-M-R101x1. The architecture of the model is derived from ResNet-101x1 and has demonstrated effective applications in several medical imaging tasks, including BCI and signature verification (Kolesnikov et al., 2020).

BiTDense (Proposed Model)

The name of the proposed model is BiTDense which is made by concatenating the DenseNet121 and Big Transfer with ResNet101x1 backbone.

The presented architecture in Fig. 2 establishes a hybrid deep learning model designed for image classification using TensorFlow and Keras. This model combines two pre-trained neural networks, namely DenseNet121 and Big Transfer (ResNet101x1), integrated with a tailored classification head for a specific classification task. DenseNet121, a convolutional neural network pre-trained on ImageNet, is incorporated with its upper layers excluded and weights set to be non-trainable. Similarly, Big Transfer is sourced from the TensorFlow Hub, with its parameters configured as non-trainable. The model's architecture consists of two branches, each dedicated to one of the pre-trained models. These branches generate outputs that are concatenated using a concatenate layer, effectively combining distinctive features. Subsequently, a custom head is introduced, incorporating densely connected layers with linear activation functions and a gradual reduction in units. The final layer utilizes softmax activation with two output units, aligning with the binary nature of the classification task. The compiled model, utilizing the Adam optimizer and categorical crossentropy loss, is configured for training and evaluation on pertinent datasets. This hybrid approach strategically leverages the inherent strengths of both pre-trained models, optimizing overall predictive performance.

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Hyperparameters

In the realm of deep learning, a hyperparameter is a predetermined parameter established prior to the initiation of the learning process, serving to govern and regulate the learning dynamics. Distinguished from model parameters, which are iteratively adjusted during training, hyperparameters exist externally to the model and are not inferred from the data but rather set based on domain knowledge and empirical considerations.

Utilizing the Adam optimizer incorporating a learning rate of 0.0001 and categorical crossentropy loss function, a convolutional neural network model is trained over 100 epochs with a batch size of 64, operating on input data of

dimensions 224x224x3. This experimental setup adheres to established standards in deep learning methodology, aiming to optimize model performance and convergence through meticulous parameter tuning and data preprocessing techniques.

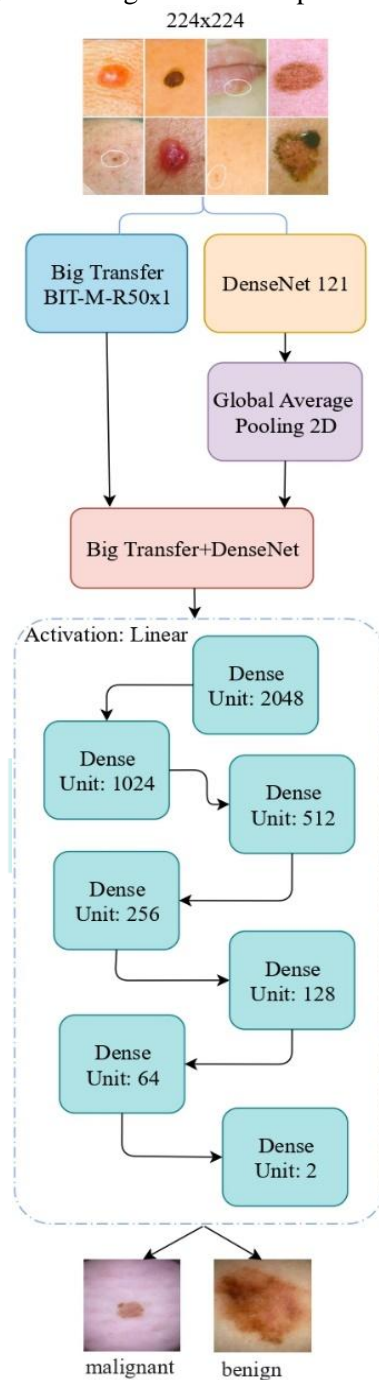


Fig.2: BitDense Structure

RESULTS AND ANALYSIS

After running 100 epochs on Google Colaboratory and using 4.3 Gb of system RAM and 8.1 GB of system GPU (T4 GPU).

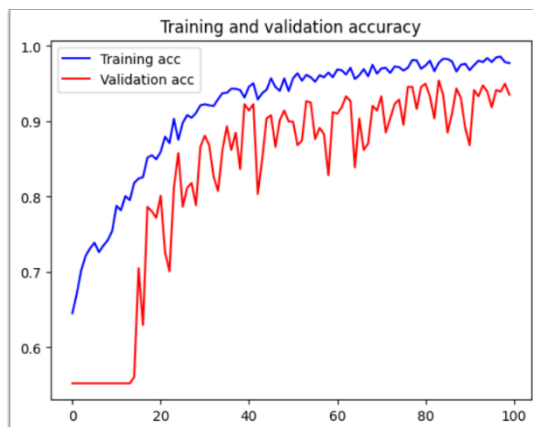


Fig.3 Training Validation Accuracy

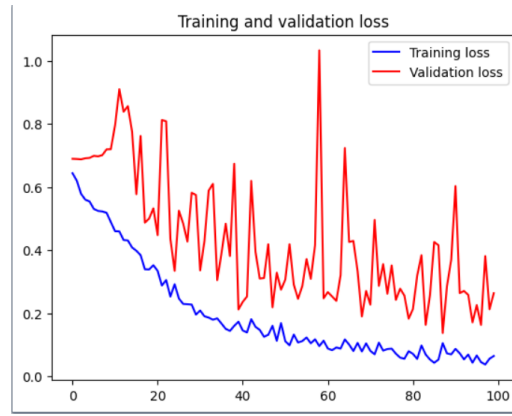


Fig.4 Training Validation Loss

Table 3 Performance Comparison of Skin Cancer Diagnosis Classifiers with Pre-trained Models

Model	Precision (%)	Recall (%)	F1-score (%)	Accuracy (%)
ResNet 121	83.3	81.6	79.5	82.3
InceptionV3 1	94.2	94.5	93.8	94.1
Attention CNN 2	95.1	93.9	94.6	95.3
Efficientnet-B1	93.8	95.2	94.4	93.9
Proposed model	99.43	98.87	99.15	93.07

Metrics Evaluation

A confusion matrix evaluates a classification model's performance, comprising true positive (TP), true negative (TN), false positive (FP), and false negative (FN) segments. From this matrix, metrics like accuracy, precision, recall, and F1 score are derived. Precision measures accurate positive predictions, recall detects true positives, and the F1 score balances both. These metrics collectively gauge the model's effectiveness in classification tasks (Narkhede, 2021).

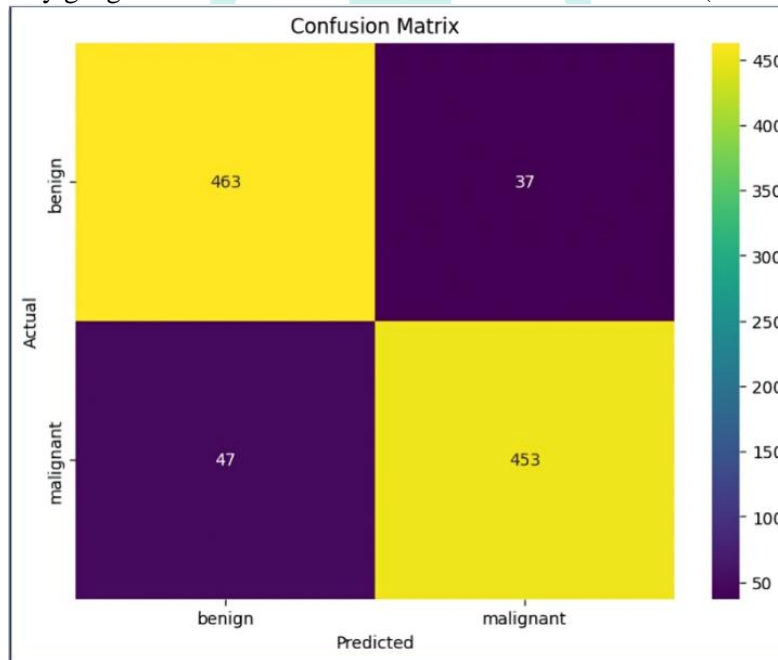


Fig. 5 Confusion Matrix Based on the Testing Dataset

$$\text{Precision} = \frac{TP}{TP+FP} \quad (1)$$

$$\text{Recall} = \frac{TP}{TP+FN} \quad (2)$$

$$\text{F1 - score} = \frac{2 \times \text{Recall} \times \text{Precision}}{\text{Recall} + \text{Precision}} \quad (3)$$

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (4)$$

Precision, a measure of exactness in positive predictions, is represented by a value of 0.994318, indicating the model's 99.43% accuracy in correct identifications, emphasizing its proficiency in minimizing false positives. Meanwhile, Recall, measuring the completeness of positive predictions, stands at 0.9887005, reflecting the model's capacity to accurately identify 98.87% of actual positive instances and underscoring its effectiveness in reducing false negatives. The F1 Score,

harmonizing precision and recall, is calculated as 0.991501416, demonstrating an excellent overall balance between accuracy and completeness in positive predictions, with high scores across all metrics affirming the model's robust classification capabilities.

In Table 3, the comparison of skin cancer diagnosis classifiers utilizing pre-trained models reveals distinct performance metrics for ResNet 121, InceptionV3, Attention CNN, Efficientnet-B1, and the proposed model. ResNet 121 demonstrates precision, recall, and F1-score ranging from 80-83%, accompanied by an 82.3% accuracy. InceptionV3 showcases robust performance, achieving precision, recall, and F1-score in the 93-94% range, coupled with an accuracy of 94.1%. Attention CNN attains notable precision (95.1%) and accuracy (95.3%), striking a balanced recall and F1-score. Efficientnet-B1 performs well, exhibiting precision, recall, and F1-score within the 93-95% range and an accuracy of 93.9%. The proposed model distinguishes itself with remarkably high precision (99.43%), recall (98.87%), and F1-score (99.15%), albeit at an accuracy of 93.07%. In summary, the proposed model displays superior precision and recall in skin cancer diagnosis, emphasizing the importance of considering specific requirements and trade-offs among precision, recall, and accuracy when selecting a model.

CONCLUSION AND FUTURE WORK

The flexible hybrid deep learning architecture BiTDense classifies benign and malignant melanoma, a huge breakthrough in the area. A bespoke classification head with DenseNet121 and Big Transfer (ResNet101x1) neural networks provides the BiTDense model with exceptional predictive power. After extensive training and evaluation of relevant datasets, the model achieved outstanding accuracy rates of 93.07%, 94.21%, and 93.07% on training, validation, and test sets. The model's precision, recall, and F1 Score metrics show it reduces and addresses false positives and negatives. Pre-trained models and the BiTDense model's remarkable classification performance make it a promising melanoma classification tool. In addition to its impressive metrics, the BiTDense model can improve diagnostic procedures and patient outcomes. The high accuracy and precision offer hope for improved and faster diagnosis, which could lead to early therapies and better melanoma outcomes. Training the BiTDense model on more datasets and using interpretability techniques would improve it. Enhancing the model's interpretability can improve prediction confidence and clinical adoption. Enhancing the model to encompass more skin cancer sub-types and darker skin-toned images could boost its dermatological diagnosis value.

The maize leaf disease detection investigation conducted by DenseViT has the potential for further refinement and future application. DenseViT has the capability to detect and categorize diseases in many crops, enhancing its flexibility to accommodate diverse environmental conditions and crop differences. The incorporation of precision farming technology has the potential to enable real-time disease monitoring. Additionally, the utilization of multi-scale characteristics and transfer learning can enhance the performance and adaptability of the model. The utilization of DenseViT in practical field scenarios, with a specific emphasis on interpretability and explainability, has the potential to enhance its acceptance among agricultural stakeholders.

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