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Deep Learning Model for Accurate Classification of Skin Cancer using Dermoscopic Images

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Abstract: *Cancer is a group of diseases that damage tissues by the uncontrolled proliferation of cells. The difficulty of distinguishing skin cancer, which is a common type of cancer, without technical support necessitates studies that can help specialists in the diagnosis phase. In this study, a deep learning model with 7 convolution layers and 3 neural layers was designed to classify the HAM10000 dataset, which consists of 7 classes and includes dermoscopic images. The accuracy rate for the test data of the proposed model was calculated as 99.01%. This result shows that the proposed model can help experts in diagnosing skin cancer.*

Keywords: Skin Cancer, Deep Learning, Classification

I. INTRODUCTION

Skin malignant growth is quite possibly of the most overall infection that cause passing [1]. Melanoma and non-melanoma skin cancer are the two types. Early location of these injuries might expand the restoring rate to 90% [2]. The high degree of similarity that exists between various types of skin lesions makes visual examination challenging and may result in an incorrect investigation [3]. Therefore, skin lesion classification necessitates the use of an automated system [4]. Image processing and artificial intelligence were used in this classification system.

II. LITERATURE SURVEY

Attempts to create commercially viable automated screening machines have increased in recent years, following more than four decades of research into the automation of the screening process for Papanicolaou (Pap) smears. Price-to-performance ratios in computers and other electronic devices are improving, making these advancements possible in part. False-negative cases, their effects on patients, and the associated legal liability have been the subject of concern, particularly in the United States, despite the fact that the Pap smear has significantly reduced cervical cancer mortality over the past forty years. Concern about managing the workload has also been raised as a result of a shortage of cytotechnologists, which has been exacerbated by new regulations limiting the number of slides that can be examined each day. This workload is likely to grow as more people gain access to preventive health care. Although automated screening machines may substantially increase the cost of Pap smears, they may also make it possible to detect abnormal cases that are missed by conventional screening. The way cervical cytology specimens are processed by automated screening machines has changed, and with some machines, the way the cytology laboratory works has changed significantly. Over the past four decades, there has been little change in the methods used to process and evaluate Pap smear results. Some of the operating principles and practical aspects of automated screening machines are discussed in this review.

Echocardiography is an important diagnostic tool for evaluating the functions of the heart. Notwithstanding, physically naming the left ventricle district on echocardiography pictures is tedious and dependent upon spectator inclination. As a result, it is essential to develop an automated assessment tool that is both high-performing and effective. Enlivened by the progress of the transformer structure in vision undertakings, we foster a lightweight model named 'TransBridge' for division errands. A transformer structure and an encoder-decoder structure of a convolutional neural network (CNN) are combined in this hybrid framework. The transformer layers span the CNN encoder and decoder to meld the

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staggered highlights separated by the CNN encoder, to construct worldwide and between level conditions. The dense patch division method and shuffled group convolution have been used to create a new patch embedding layer that reduces the number of parameters in the layer and the size of the token sequence. The left ventricle segmentation task uses the EchoNet-Dynamic dataset to evaluate the model. The Dice coefficient rises to 91.4% and the total number of parameters is reduced by 78.7% in comparison to CoTr [22], demonstrating the structure's effectiveness.

Cervical disease is one of the most destructive and normal types of malignant growth among ladies on the off chance that no move is made to forestall it, yet it is preventable through a basic screening test, the purported PAP-smear. This is the most effective method for preventing cancer that has been created thus far. Yet, the visual assessment of the smears is tedious and costly and there have been various efforts to robotize the examination since the test was presented over a long time back. Around the turn of the millennium, the first commercial systems for automated cell sample analysis appeared, but they have had little effect on screening costs. In this paper, we look at the most important problems that need to be fixed when creating an automated analysis system and how these problems have been solved over time. The lessons learned may be useful in the development of a screening system that is both affordable and effective. This could make screening for cervical cancer available to all women around the world at a price that is affordable, thereby preventing most of the quarter million annual deaths that are still caused by this disease.

The most lethal type of skin cancer is melanoma. While reparable with early identification, just profoundly prepared experts are able to do precisely perceiving the sickness. Automated systems that are able to identify diseases have the potential to save lives, reduce the number of unnecessary biopsies, and cut costs due to the limited supply of expertise. We propose a system that accomplishes this by combining recent advances in machine learning with ensembles of methods that are capable of segmenting skin lesions and analyzing the detected area and the tissue surrounding it for melanoma detection. The largest dermoscopic image benchmark dataset, which includes 900 training and 379 testing images, is used to evaluate the system. An improvement in the area under the receiver operating characteristic curve of 7.5% (0.843 vs. 0.783), an increase in average precision of 4% (0.649 vs. 0.624), and a specificity measured at the clinically relevant 95% sensitivity operating point that is 2.9 times higher than the previous state-of-the-art are all examples of new state-of-the-art performance levels. Contrasted with the normal of 8 master dermatologists on a subset of 100 test pictures, the proposed framework creates a higher precision (76% versus 70.5%), and explicitness (62% versus 59%) assessed at an identical responsiveness (82%). Introduction With over 5 million new cases diagnosed annually [1], skin cancer is the most common type of cancer in the United States. Melanoma, the deadliest type of skin cancer, accounts for approximately 100,000 new cases and over 9,000 deaths annually in the United States [2]. The expense for the U.S. medical services framework surpasses $8 billion [3]. Skin cancer also poses a significant threat to public health worldwide. In Australia, there are more than 13,000 new occasions of melanoma yearly, prompting north of 1,200 passings [4]. Melanoma is responsible for over 20,000 deaths annually in Europe [5]. Melanoma mortality is on the rise, so early detection is essential. For melanoma to be detected accurately and early, highly trained professionals and professional equipment are currently required. Dermoscopy is a particular strategy for high-goal imaging of the skin that decreases skin surface reflectance, permitting clinicians to picture further basic designs. Specially trained clinicians have demonstrated diagnostic accuracy of up to 75-84% with this device [7]. However, when clinicians lack adequate training, recognition performance significantly deteriorates [8, 9]. There are over 10,000 dermatologists in the United States, but there are only a few in other parts of the world. In 2004, there were approximately 340 registered dermatologists in Australia [10], and there were 16 in New Zealand [11]. Providing adequate levels of care to populations at risk presents additional challenges when access to expert consultation is restricted. To address the restricted stock of specialists, there has been exertion in the examination local area to foster computerized picture examination frameworks to identify illness from dermoscopy pictures. Such 1 The final version of this paper will be published in the IBM Journal of Research and Development, volume 61, no. 4/5, 2017, as a component of a unique issue on "Profound Learning." Please cite the official paper version of the IBM Journal. For more data on the diary, see: IBM's website is http://www.research.ibm.com/journal/. 2 technology has the potential to serve as a diagnostic tool for routine screening by primary care physicians and staff, as well as clinicians who are not otherwise trained to interpret dermoscopy images. Survey articles covering a range of distributions have been as of late introduced [7, 12-15]. Although there is a wide range of automated image analysis methods discussed, the majority of them fall under the purview of traditional computer vision approaches. These methods typically make use of

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combinations of low-level visual feature representations (such as color, edge, and texture descriptors, quantification of melanin based on color, etc.), k-nearest neighbor (kNN) and support vector machine (SVM) algorithms, as well as rule-based image processing or segmentation algorithms Algorithms that include segmentation of the lesion have been presented in some publications [16-21]. Based on color, edge, and texture descriptors, a group from Portugal's Pedro Hispano Hospital wanted to see how different machine learning classifiers, such as SVM and kNN, performed [22,23]. Ensemble learning methods were utilized by other teams [24-26]. Neural network machine learning methods were used in some previous work, which is interesting [27-31]. However, hand-coded low-level features served as the foundation for these. In the dermatology and dermoscopy application domain, more recent research has begun to examine the effectiveness of the most recent deep learning approaches to image recognition [32,33]. In a dataset consisting of more than 2,000 dermoscopy images, state-of-the-art performance was achieved by utilizing representations learned from the natural photo domain in conjunction with unsupervised and hand-coded features [32]. Notwithstanding, the work was restricted to sore pictures that had been physically pre-sectioned: Images had already been cropped to include the relevant lesion. For the purpose of developing and evaluating clinical and automated methods for the diagnosis of melanoma, the International Skin Imaging Collaboration (ISIC) organized a global effort in 2016 to aggregate a dataset of dermoscopic images from multiple institutions [34]. At the 2016 International Symposium on Biomedical Imaging (ISBI 2016), a melanoma recognition challenge was held using a snapshot of the dataset that contained the most comprehensive annotation set. "Skin Lesion Analysis toward Melanoma Detection" was the challenge's title [35]. Over the course of the three image analysis tasks, 38 individual participants contributed 79 submissions, 43 of which were for the purpose of disease classification. This was the main openly coordinated huge scope normalized assessment of calculations for the identification of melanoma. Deep learning techniques, such as fully convolutional networks for segmentation and Deep Residual Networks for classification [36, 38], were the most effective. For the purpose of melanoma recognition and segmentation in dermoscopy images, we combine hand-coded feature extractors, sparse-coding techniques, and SVMs with more recent machine learning methods like fully convolutional neural networks and deep residual networks. For the purpose of evaluation, we have decided to make use of the ISBI 2016 dataset, which gives us the chance to compare our results to those of dozens of previous algorithms right away and to others in the future. Across a variety of evaluation metrics, new, cutting-edge performance levels are demonstrated, including a nearly tripling of specificity at 95% sensitivity. These outcomes underline that joining a large number of AI approaches can yield better execution than depending on any a single technique, particularly with respect to acknowledgment of melanoma in dermoscopic pictures.

Deep learning, sparse coding, and support vector machine (SVM) learning algorithms are combined in this method for melanoma detection in dermoscopy images. One of the useful parts of the proposed approach is that solo advancing inside the space, and component move from the area of regular photos, disposes of the need of clarified information in the objective assignment to learn great elements. The system can also draw analogies between observations in dermoscopic images and observations in the natural world using the applied feature transfer, mimicking the method that medical professionals use to describe patterns in skin lesions. Performance is measured on a dataset from the International Skin Imaging Collaboration that contains 2624 clinical cases of melanoma (334), atypical nevi (144), and benign lesions (2146) in order to evaluate the methodology. On this dataset, the method and the prior standard are compared. Twenty times (20 total experiments) of two-fold cross-validation are used for evaluation, and two discrimination tasks are examined: 1) Melanoma against all non-melanoma lesions and 2) Melanoma against only atypical lesions. For the first task, the proposed method achieves an accuracy of 93.1 percent (94.9% sensitivity, and 92.8% specificity), while for the second task, it achieves an accuracy of 73.9 percent (73.8% sensitivity, and 74.3% specificity). In examination, earlier condition of-craftsmanship group displaying approaches alone yield 91.2% precision (93.0% responsiveness, and 91.0% explicitness) first the main undertaking, and 71.5% exactness (72.7% awareness, and 68.9% particularity) for the second. Performance differences were statistically significant (p 0.05), indicating that the proposed strategy is an effective advancement over previous state-of-the-art methods.

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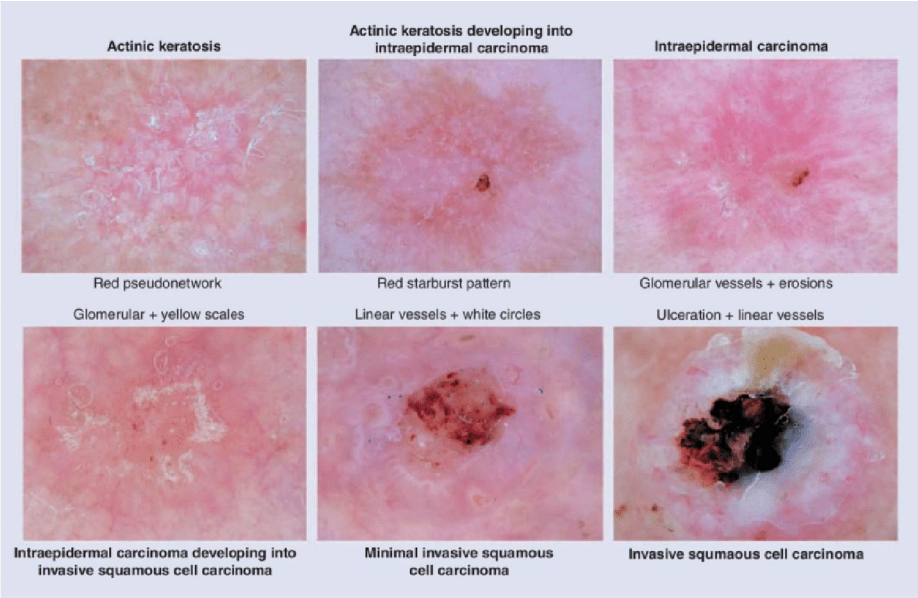
III. TECHNOLOGICAL INNOVATION THEORY

3.1 Existing Analysis

Using the International Skin Imaging Collaboration (ISIC-ISBI) 2018 test dataset, various deep learning-based neural networks, such as PNASNet-5-Large, InceptionResNetV2, SENet154, and InceptionV4, have been proposed in the literature. With an accuracy of 76%, the PNASNet-5-Large model produced the best results [7]. Ten distinct skin lesions were classified using a linear classifier in another study [8]. An AlexNet with a convolutional layer as the last fully connected layer was used to extract features from 10 distinct skin lesions from a generic dermophyte image library containing 1300 clinical images, with an accuracy of 81.8% [8]. Random forest and support vector machine classifiers were used to categorize the public dataset of ISIC-ISBI 2016 in another study. The proposed system's classification accuracy was 93.89% when tested on ISIC-ISBI 2016 with a random forest classifier [9].

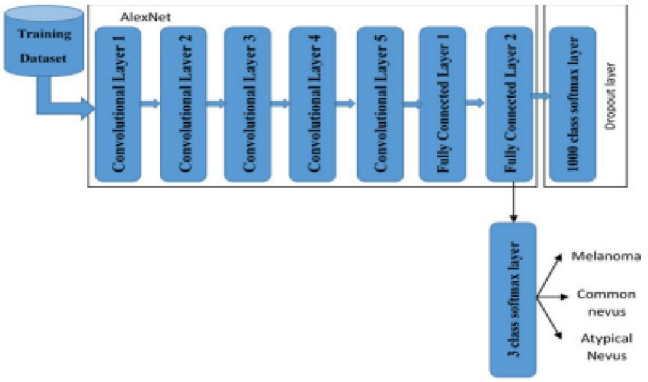
3.2 Proposed Analysis

In order to classify the HAM10000 dataset, which contains dermoscopic images and is divided into seven classes, a deep learning model with seven convolution layers and three neural layers was created for this study. The proposed model's test data were found to have an accuracy rate of 99.01%. Experts can use the proposed model to aid in the diagnosis of skin cancer, as demonstrated by this result



Progression model of keratinocytes skin cancer

3.3 Application Architecture



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```
##################IMPORTANT INFORMATION###################################
# the model is built with 20 epochs which gives only 43% of validation accurcay
# which will predict 50/50 accurately try to build the model with 200 epochs for
# better accuracy for detection and classification
from __future__ import division, print_function
# coding=utf-8
import sys
import os
import glob
import re
import numpy as np

# Keras
from keras.applications.imagenet_utils import preprocess_input, decode_predictions
from keras.models import load_model
from keras.preprocessing import image

# Flask utils
from flask import Flask, redirect, url_for, request, render_template
from werkzeug.utils import secure_filename
import sqlite3

app = Flask(__name__)

UPLOAD_FOLDER = 'static/uploads/'

# allow files of a specific type
ALLOWED_EXTENSIONS = set(['png', 'jpg', 'jpeg'])

# function to check the file extension
def allowed_file(filename):
 return '.' in filename and \
filename.rsplit('.', 1)[1].lower() in ALLOWED_EXTENSIONS

model_path2 = 'model/model.h5' # load .h5 Model
classes2 = {0:"ACTINIC KERATOSIS",1:"BASAL CELL
CARCINOMA",2:"DERMATOFIBROMA",3:"MELANOMA",4:"NEVUS",5:"PIGMENTED BENIGN
KERATOSIS",6:"SEBORRHEIC KERATOSIS",7:"SQUAMOUS CELL CARCINOMA",8:"VASCULAR LESION"}
CTS = load_model(model_path2)
from keras.preprocessing.image import load_img, img_to_array

def model_predict2(image_path,model):
 print("Predicted")
 image = load_img(image_path,target_size=(224,224))
 image = img_to_array(image)
 image = image/255
 image = np.expand_dims(image,axis=0)

 result = np.argmax(model.predict(image))
```

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```
 prediction = classes2[result]

 if result == 0:
 return "ACTINIC KERATOSIS","after.html"
elif result == 1:
 return "BASAL CELL CARCINOMA","after.html"
elif result == 2:
 return "DERMATOFIBROMA","after.html"
elif result == 3:
 return "MELANOMA","after.html"
elif result == 4:
 return "NEVUS","after.html"
elif result == 5:
 return "PIGMENTED BENIGN KERATOSIS","after.html"
elif result == 6:
 return "SEBORRHEIC KERATOSIS","after.html"
elif result == 7:
 return "SQUAMOUS CELL CARCINOMA","after.html"
elif result == 8:
 return "VASCULAR LESION","after.html"
@app.route("/")
def index():
 return render_template("index.html")
@app.route('/logon')
def logon():
        return render_template('signup.html')
@app.route('/login')
def login():
        return render_template('signin.html')
@app.route("/signup")
def signup():
 username = request.args.get('user','')
 name = request.args.get('name','')
 email = request.args.get('email','')
 number = request.args.get('mobile','')
 password = request.args.get('password','')
 con = sqlite3.connect('signup.db')
 cur = con.cursor()
cur.execute("insert into `info` (`user`,`email`, `password`,`mobile`,`name`) VALUES (?, ?, ?, ?,
?)",(username,email,password,number,name))
con.commit()
con.close()
 return render_template("signin.html")
@app.route("/signin")
def signin():
 mail1 = request.args.get('user','')
 password1 = request.args.get('password','')
 con = sqlite3.connect('signup.db')
 cur = con.cursor()
```

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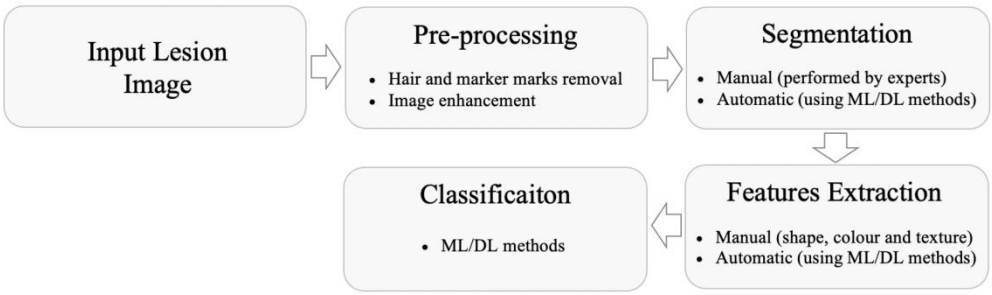
```
cur.execute("select `user`, `password` from info where `user` = ? AND `password` = ?",(mail1,password1,))
 data = cur.fetchone()
 if data == None:
 return render_template("signin.html")
elif mail1 == 'admin' and password1 == 'admin':
 return render_template("home.html")
elif mail1 == str(data[0]) and password1 == str(data[1]):
 return render_template("home.html")
 else:
 return render_template("signup.html")
@app.route('/home')
def home():
        return render_template('home.html')
@app.route('/predict2',methods=['GET','POST'])
def predict2():
 print("Entered")
 print("Entered here")
 file = request.files['files'] # fet input
 filename = file.filename
 print("@@ Input posted = ", filename)
file_path = os.path.join(UPLOAD_FOLDER, filename)
file.save(file_path)
 print("@@ Predicting class.....")
 pred, output_page = model_predict2(file_path,CTS)
 return render_template(output_page, pred_output = pred, img_src=UPLOAD_FOLDER + file.filename)
if __name__ == '__main__':
app.run(debug=False)
```



This subsection presents the results attained using the DenseNet201 and the proposed Modified DenseNet201. The detailed results are presented, which is based on several evaluation parameters.shows that DenseNet201 attained an accuracy of 94.09% on the used dataset. In addition, the sensitivity, specificity, precision, and F1 score were recorded as 92.16%, 96.05%, 95.96%, and 94.02%, respectively. The proposed Modified DenseNet201 shows superiority over the pre-trained DenseNet201 by attaining an accuracy of 95.50%. To further ensure the authenticity of the obtained results, several other parameters were also considered. The sensitivity and specificity obtained by the Modified DenseNet201 model are 96.96% and 97.06%, respectively. Whereas precision and F1 score were recorded as 97.02% and 95.46%, respectively. The results shown in Table 4 are also verified using the confusion matrix.

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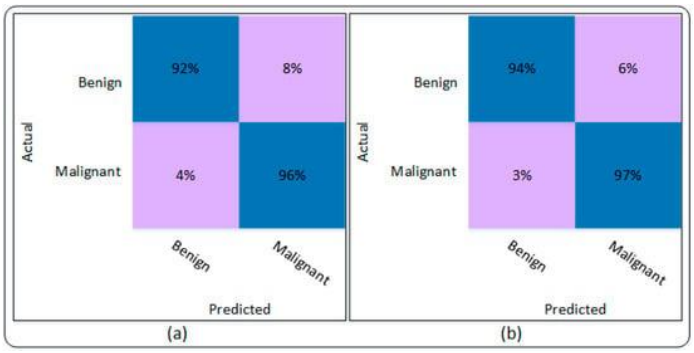
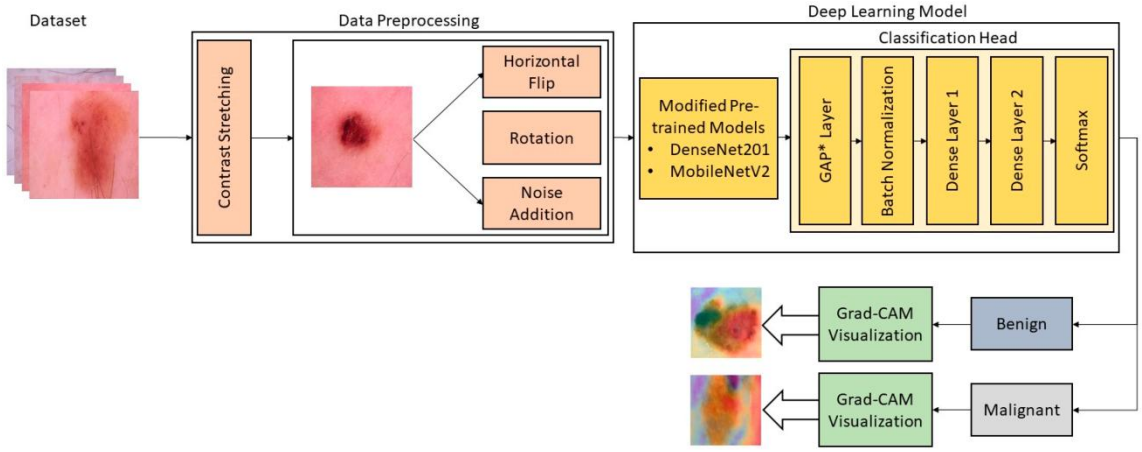


A new framework for the classification of skin lesions is presented in this section. The proposed framework can differentiate cancerous and non-cancerous lesions using deep learning models. The proposed framework requires a series of steps for the efficient classification of lesions. It starts by augmenting the available dataset and subsequently follows steps to retrain the deep learning model that includes transfer learning, fine-tuning of the model along with hyperparameter tuning. The fine-tuned model is able to extract desired features for the classification of skin cancer lesions. Two different deep learning techniques are used in this work. The augmented dataset is used for the fine-tuned deep learning model according to the requirements of this work. The general workflow of the proposed framework is presented in Figure 1. Each step of the workflow is discussed in the following subsections.



IV. CONCLUSION

A huge number of labeled images is needed to build a successful deep neural network. The transfer learning and image augmentation are applied to a pre-trained AlexNet to overcome this major challenge. The proposed method has the ability to classify three different lesions by replacing the last layer to softmax with three classes only. According to the transfer learning, the weights of the modified model have been fine-tuned in addition to the augmentation of the dataset images. Four performance measures have been computed for the proposed to compare with existing methods where the obtained results prove that the proposed method outperformed the existing methods

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