A PROJECT REPORT

on

"SKIN CANCER CLASSIFICATION USING DEEP LEARNING"

Submitted to

KIIT Deemed to be University

In Partial Fulfillment of the Requirement for the Award of

BACHELOR'S DEGREE IN

Computer Science and Communication Engineering

BY

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1. Introduction

Skin cancer is the uncontrolled growth of unnatural cells in the epidermis, the layer situated in the outermost layer of the skin, caused by dilapidation DNA damage that stimulates mutations. These mutations cause the snowball like effect and thus skin cells multiply rapidly and form malignant tumors. Skin cancer can be recognised as completely different from person to another person due to appearance of skin color, its size and type of skin cancer, and where it is situated on the body.

There are two primary types of skin cancer: melanoma and non-melanoma:-
Non-melanoma is a type of skin cancer that includes basal cell carcinomas along with squamous cell carcinomas. Although These prove to be rarely fatal, the surgical treatment that is done to treat them is often very painful and disfiguring. Time trends in the incidence of non-melanoma skin cancers are challenging to determine for the reason that reliable registration of these cancers has not been accomplished yet. The range of occurrence of non-melanoma skin cancers worldwide is 2 and 3 million each year.

Cancer, the maximum extreme kind of pores and skin for most cancers, develops in the cells (melanocytes) that produce melanin, the pigment that offers the skin its color. melanoma can also shape to your eyes and, rarely, within the body, such as in the nostril or throat. The exact purpose of all melanomas is unclear, but publicity to ultraviolet (UV) radiation from daylight or tanning lamps and beds will increase your risk of growing cancer. About 32,000 skin melanomas occur globally every year.

As per the World Health Organization (WHO), there is no reliable estimate of the global incidence of skin cancer deaths. However, they report melanoma, the deadliest skin cancer, caused an estimated 59,782 deaths worldwide in 2020. skin cancer is one of the most common varieties of most cancers, affecting millions of human beings globally. Early detection and correct type of pores and skin lesions are important for a successful treatment and management of the sickness. However, diagnosing skin cancer can be challenging, even for experienced dermatologists, because many skin lesions look similar.

Machine learning algorithms and intense learning models have shown great potential in improving the accuracy and speed of skin cancer diagnosis. In this project, we classify skin lesions into nine categories using the DenseNet121 neural network architecture and data augmentation techniques.
The nine categories we classify are benign keratosis pigmentosa, melanoma, vascular lesion, actinic keratosis, squamous cell carcinoma, basal mobile carcinoma, seborrheic keratosis, dermatofibroma, and nevus. those classes constitute the most commonplace varieties of pores and skin cancer and skin lesions dermatologists stumble upon.

1. Pigmented benign keratosis: This is a common type of skin lesion that is usually benign but can sometimes resemble melanoma. It is usually a small, dark-coloured spot or spot on the skin that is rough to the touch. Benign keratosis pigmentosa can be caused by several factors, including sun damage and genetics.

2. Melanoma: Melanoma is a type of skin cancer that starts in melanocytes, which produce pigment in the skin. It is usually a dark, irregularly shaped spot or mole that may be asymmetrical and have an uneven edge. Melanoma is a serious and potentially fatal disease if not detected and treated early.

3. Vascular lesions are abnormal growths in blood vessels or lymphatic vessels. They can appear as red or purple spots on the skin and are usually benign. However, some vascular lesions, such as angiosarcomas, can be malignant.

4. Actinic keratosis: Actinic keratosis is a common skin condition caused by prolonged sun exposure. It appears as a scaly, rough patch on the skin, usually pink or red. Although actinic keratosis is usually benign, it can sometimes develop into squamous cell carcinoma if left untreated.

5. Squamous cell carcinoma: Squamous cell carcinoma is a type of skin cancer that begins in the squamous cells found in the outer layer of the skin. It usually appears as a scaly, red, or flesh-coloured bump or patch on the skin that may bleed or become crusted. Squamous cell carcinoma can be a serious and potentially life-threatening disease if not detected and treated early.

6. Basal cell carcinoma: Basal cell carcinoma is the most common type of skin cancer and usually appears as a small waxy bump on the skin that may have a pearly appearance. It can also appear as a red or pink spot on the skin. Basal cell carcinomas usually grow slowly and rarely spread to other body parts but can cause disfigurement if left untreated.

7. Seborrheic keratosis: Seborrheic keratosis is a common skin condition that usually affects older adults. It appears as a raised, waxy or scaly growth on the typically brown or black skin. Seborrheic keratosis is usually benign but can sometimes be difficult to distinguish from melanoma.

8. Dermatofibroma: Dermatofibroma is a common benign skin growth that usually appears as a small, hard bump. It may be brown or reddish and may be tender to the touch. Although dermatofibroma is mostly benign, it can sometimes look like melanoma, so a dermatologist must check it out.

9. Nevus: A nevus, also known as a mole, is a common type of skin growth that usually appears as a dark, raised spot on the skin. Most moles are benign and do not require treatment, but some can develop into melanoma. It's important to monitor moles for changes in size, shape, or colour changes and have them checked by a dermatologist if they look suspicious.

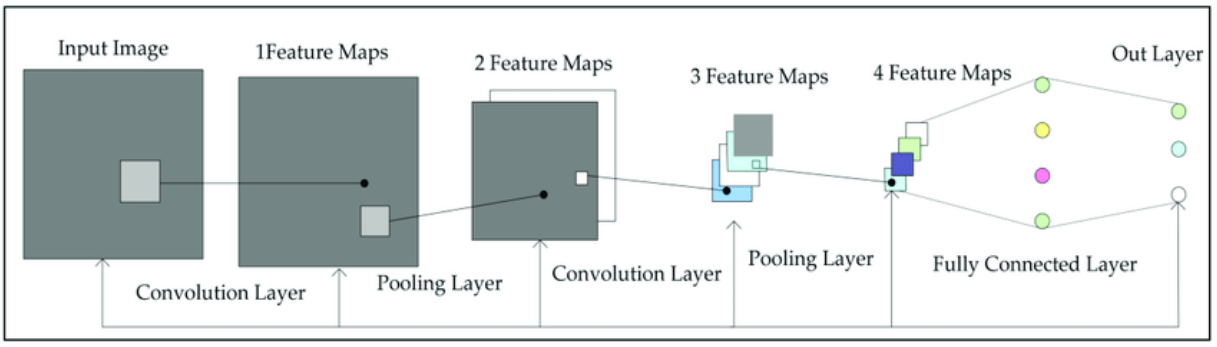
We chose to use the DenseNet121 architecture because it is a powerful and popular deep-learning model that has been shown to achieve superior performance in image classification tasks. DenseNet121 is a neural network variant of the DenseNet family with 121 layers and achieves high accuracy by repeatedly using feature maps from previous layers.

Our ultimate goal is to develop a highly accurate and efficient skin cancer classification model to help dermatologists diagnose and treat skin cancer. This model can be used as a screening tool to identify suspicious lesions that require further examination by a dermatologist or as a second opinion for dermatologists to improve the accuracy of their diagnoses. By improving the speed and accuracy of skin cancer diagnosis, we can improve patient outcomes and save lives.

2. Methodology / Proposal

2.1. Design model

In a conventional feedforward convolutional neural network (CNN), every convolutional layer except the primary (which enters) gets the output of the previous convolutional layer and produces an output function map that is then exceeded to the next. Convolutional layer. Therefore, for layers 'L', there are direct connections 'L', one between each layer and the following. However, because the quantity of layers in a CNN will increase, i.e., the "vanishing gradient" problem arises as they get deeper.



DenseNets resolve this problem through editing the usual CNN architecture and simplifying the connectivity pattern between layers. In a DenseNet architecture, each layer is connected directly with each different layer, as a result of the Densely connected Convolutional community. There are L(L+1)/2 direct connections for the' L' layers.
DenseNet121 architecture is based on the idea of densely connected layers. In a traditional CNN, each layer inputs the previous layer's output. In contrast, in a dense block, each layer takes a concatenation of element maps of all earlier layers in the block as input. This enables feature reuse and propagation across the network, leading to better feature representation.

Components of DenseNet

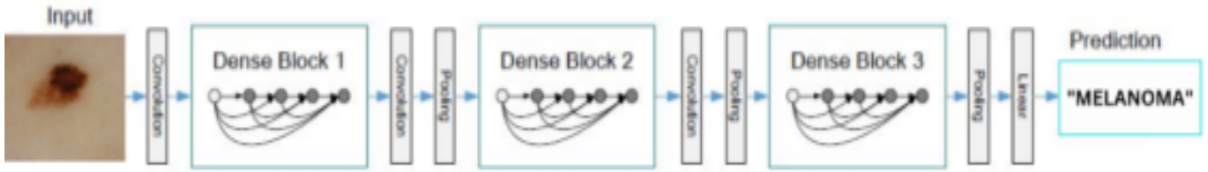
- **Connectivity**

In every layer, the characteristic maps of all previous layers are not summed but concatenated and used as inputs. As a end result, DenseNets require fewer parameters than equivalent conventional CNNs, permitting function reuse as redundant feature maps are discarded. So the 1st layer receives as input the characteristic maps of all previous layers, x0,...,xl-1:

$$\mathbf{x}_\ell = H_\ell([\mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_{\ell-1}]),$$

- **DenseBlock**

To try this, DenseNets are split into DenseBlocks, where the size of the function maps continues to be constant within a block, but the quantity of filters between them varies. The layers among the blocks are known as transition layers, which lessen the wide variety of channels to half the range of current channels. For each layer, from the above equation, Hl is described as a compound function that applies three consecutive operations: batch normalization (BN), rectified linear unit (ReLU), and convolution (Conv).

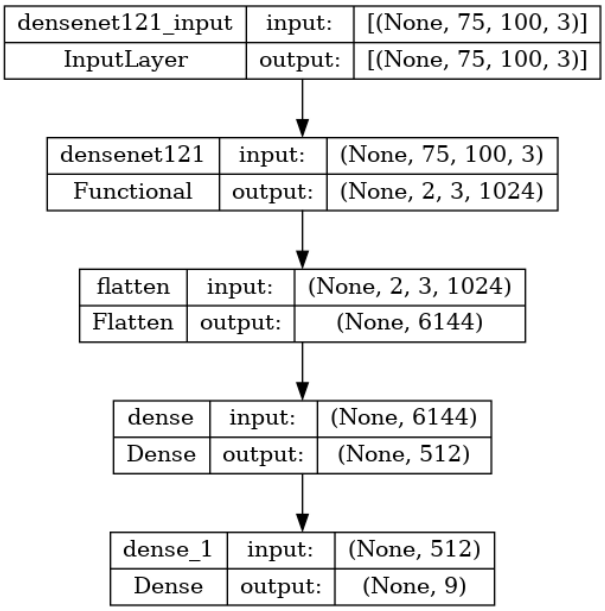


The photograph above shows a deep DenseNet with three dense blocks. The layers among adjacent blocks are transition layers that had been downsampling (i.e., converting the dimensions of the characteristic maps) via convolution and pooling operations. In a dense block, the scale of the characteristic maps is the identical to permit the concatenation of features.

DenseNet121 additionally consists of a international average pooling layer that averages function maps throughout spatial dimensions to provide one feature vector consistent with channel. this selection vector is then fed into a totally related layer accompanied through a softmax function that produces elegance chances for the enter photo.

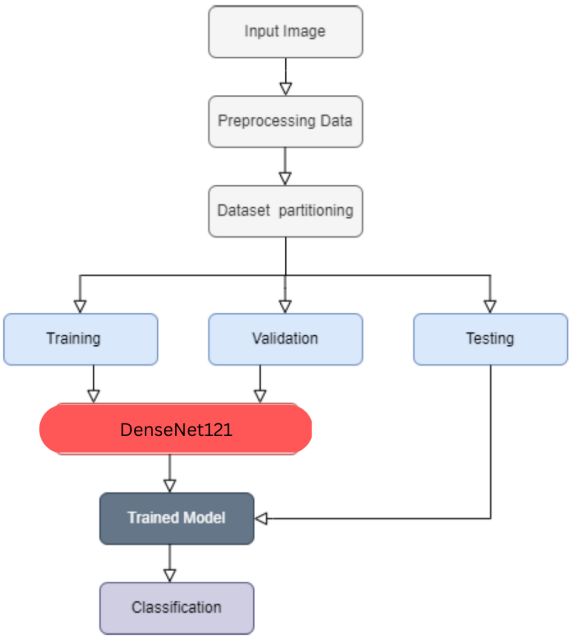
Each transition layer has a 1x1 convolutional layer and a 2x2 common pooling layer with a stride of 2. for that reason, the layers are as follows:

basic convolution layer with 1024 filters of size 2X3 and a stride of two. Dense Block 1 with 2 convolutions repeated 6 times. Dense Block 2 with 2 convolutions repeated 12 instances.



One of the advantages of DenseNet121 is the relatively small number of parameters compared to other CNN architectures with similar performance. This is due to function reuse and propagation over dense blocks, allowing efficient use of available parameters. Additionally, DenseNet121 has been shown to perform well even with limited training data, which benefits many real-world applications.

DenseNet121 is a robust CNN structure widely utilized in numerous computer vision responsibilities, consisting of picture type, object detection, and segmentation. Its capability to research effective capabilities and green use of parameters make it a famous choice for lots of deep-getting to know packages.



2.2. Implementation Platform

This test was conducted on an online compiler called Kaggle, using an Intel Core i7-8550U CPU @ 1.99 GHz, with an AMD Radeon 530 graphics card and 13GB of memory. During the implementation process, you found that training a model with a large amount of data for high accuracy could take significant execution time on a regular CPU. To overcome this, you used a GPU accelerator to speed up the model-building process. Your deep learning approach was built using the PyTorch framework.

2.3. Libraries

The libraries that we have used in our model are used for different tasks in the machine learning pipeline. The NumPy library is used for numeric operations and arrays, while pandas are used for data manipulation and analysis. The matplotlib library is used for data visualization and plotting. The os library provides a way to interact with the operating system, and the Keras library is used to build and train deep learning models. The library of TensorFlow is also used for building and training deep learning models, and the sci-kit-learn library is used for evaluating model performance. The Seaborn library creates visualizations, specifically heatmaps, for confusion matrices.

Several specific modules and functions are imported within Keras. A sequential model is used to build a sequential neural network. Dense, Dropout, Flatten, Conv2D, and MaxPool2D layers define the model layers. to_categorical is used to convert categorical labels to one-time encoding. The ImageDataGenerator class is used for data augmentation. The ReduceLROnPlateau class is used to reduce the learning rate of the model during training. The DenseNet121 model is used for transfer learning, and Flatten, and Dense layers are added for classification. The SGD optimiser is used to optimize the model weights during training.

These libraries and modules are essential for building, training, and evaluating deep learning models for image classification.

2.4. Data set Description

The dataset contains 2357 images in Total with 9 different classes. The number of pictures in each of the class is as follows: pigmented benign keratosis - 478, melanoma - 454, vascular lesion - 142, actinic keratosis - 130, squamous cell carcinoma - 197, basal cell carcinoma - 392, seborrheic keratosis - fibroma - 80, 111 and nevus - 373.

Class Label	Class Name	Count
0	pigmented benign keratosis	478
1	melanoma	454
2	vascular lesion	142
3	actinic keratosis	130
4	squamous cell carcinoma	197
5	cell basal carcinoma	392
6	seborrheic keratosis	80
7	dermatofibroma	111
8	nevus	373
Total		2357

2.4.1 Skin Cancer ISIC

This set consists of 2357 images of malignant and benign oncological diseases, which have been fashioned via The worldwide pores and skin Imaging Collaboration (ISIC). All snap shots had been looked after in line with the class excited about ISIC. All subsets have been divided into the same number of photos, besides for melanomas and moles, whose photographs are slightly dominant.

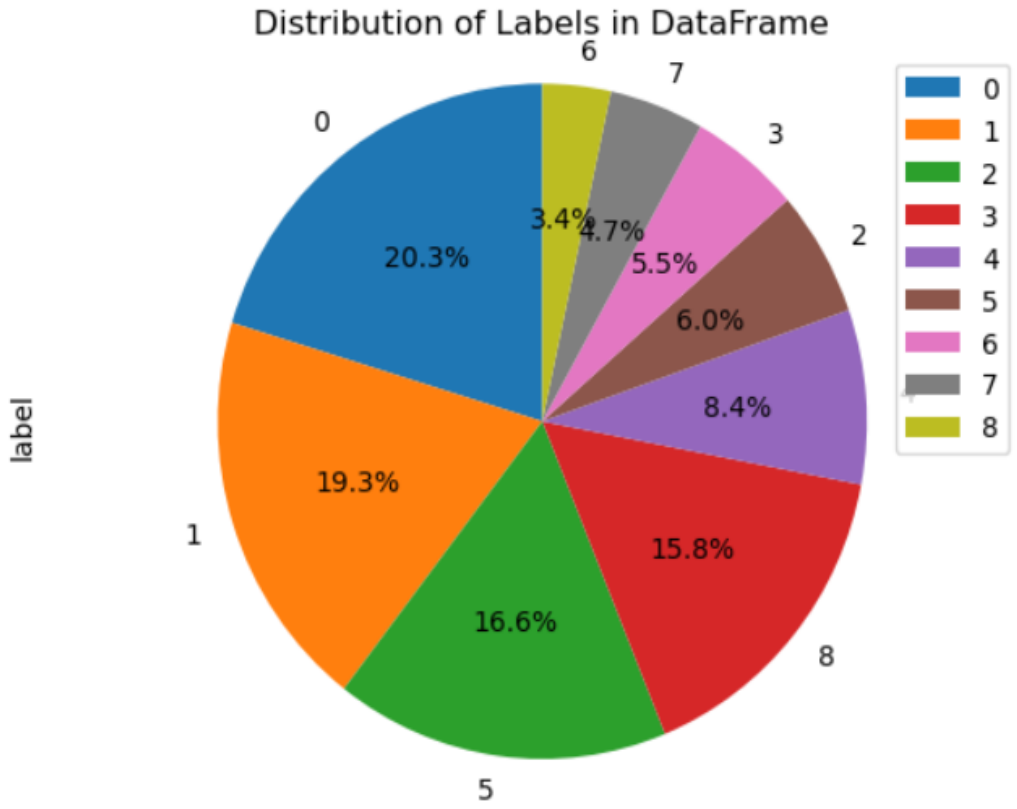
The data set contains the following diseases:

- actinic keratosis
- basal cell carcinoma
- dermatofibroma
- melanoma
- nevus
- pigmented benign keratosis
- seborrheic keratosis
- squamous cell carcinoma
- vascular lesion

2.4.2 Exploratory Data Analysis

The number of occurrences of each label in the data frame is counted, and a pie chart of the results is plotted as follows:-

pigmented benign keratosis(20.3%), melanoma(19.3), vascular lesion(6.0%), actinic keratosis(5.5%), squamous cell carcinoma(8.4%), basal cell carcinoma(16.6%), seborrheic keratosis(3.4%), dermatofibroma(4.7%) and nevus(15.8%)



2.5. Image Preprocessing

To get better distribution consequences and better features, all output photos of isic-2020 are inside the first place. The cnn technique needs plenty of repeated schooling for this motive. A huge-scale photo dataset changed into required to save you the hazard of over-fitting

2.5.1. Image Resizing,

The original images in the dataset are 600 pixels by 450 pixels, 600 pixels wide, and 450 pixels high. However, this size may not be optimal for processing with machine learning models. Larger images require more memory and processing power, leading to longer training times and an increased risk of overfitting.

To improve this, the image was changed to a smaller size of 100 x 75 pixels, 100 pixels wide and 75 pixels high this is done using the resize function from the pil python imaging library module, which resizes the to the desired size by shrinking the original images.

The pictures are scaled down by a factor of 6 which suggests that the width and height of the initial picture are isolated by 6 to get the new width and height of the resized picture. This comes about in 36 times fewer pixels within the resized picture than the first picture (600 x 450 = 270000) pixels vs (100 x 75 = 7500) pixels this smaller estimate permits faster processing and training of machine learning models while retaining enough information for accurate classification

2.5.2 Data Augmentation

It's far away used to artificially increase the scale of a data set with the aid of creating new data based on current records. This will help prevent overfitting and improve the accuracy of machine gaining knowledge of models.
The ImageDataGenerator object is a software magnificence in Keras that enables generating batches of picture statistics with actual-time data augmentation in the course of training. It lets us use numerous adjustments to the entered photographs, together with rotation, translation, shear, zoom, and flip, to artificially grow the scale of the dataset and enhance model overall performance. Each transformation has its own set of parameters that may be tuned to manipulate the diploma or depth of the transformation.

The rotation transform determines the maximum number of degrees by which the image can be randomly rotated. The width-shift transform and the height-shift transform determine the maximum width-to-height ratio of an image that can be randomly translated horizontally or vertically. The shear transformation determines the maximum intensity of the shear transformation. The zoom transform determines the maximum ratio by which an image can be randomly zoomed in or out. The horizontal flip parameter determines whether images should be randomly flipped horizontally. The fill mode parameter specifies the method for filling newly created pixels after a rotation or displacement transformation.

By applying these transformations, we can generate additional similar images but not identical to the original images, effectively expanding the training dataset and allowing the model to learn from more diverse examples. Augmented images can help the model become more robust to changes in input data and improve its accuracy on unseen test data.

we generate augmented images for each class in a given dataset. then go through each class label and calculate the number of additional images needed for the current class. If additional images are needed, we apply the transformation to a random subset of the

original images and generate new images. we then add the original and new images for the current class to the data frame. we repeat this process for each class in the dataset. Finally, we group the extended data frame by the 'label' column, filter out additional images, and sample the data frame to shuffle the order of the images. The resulting data frame can be used for further processing.

Transformation	Value
Rotation transformation	20°
Width shift transformation	0.2
Height shift transformation	0.2
Shear transformation	0.2
Zoom transformation	0.2
Horizontal flip	True
Fill mode	'nearest'

2.1.6. Training, Validation and Testing

The data of different classes are divided into three portions: training, validation and testing. The percentage of the training , validating and Testing in pigmented benign keratosis are 11.32%, 11.11%, 10.44% respectively. The training , validating and Testing in melanoma are 11.01%, 11.42%, 11.2% respectively. The training , validating and Testing in vascular lesion are 11.21%, 10.97%, 10.91% respectively. The training , validating and Testing in actinic keratosis are 11.37%, 10.94%, 10.42% respectively. The training , validating and Testing in squamous cell carcinoma are 11.05%, 11.16%, 11.26% respectively. The training , validating and Testing in basal cell carcinoma are 11.26%, 10.5%, 11.11% respectively. The training , validating and Testing in seborrheic keratosis are 10.84%, 11.47%, 11.66% respectively. The training , validating and Testing in dermatofibroma are 10.99%, 11.27%, 11.35% respectively. The training , validating and Testing in nevus are 10.94%, 11.14%, 11.62% respectively.

Class Label	Train	Validation	Test
pigmented benign keratosis	1630	400	470
melanoma	1585	411	504
vascular lesion	1614	395	491
actinic keratosis	1637	394	469
squamous cell carcinoma	1591	402	507
basal cell carcinoma	1622	378	500
seborrheic keratosis	1562	413	525
dermatofibroma	1583	406	511
nevus	1576	401	523
Total	14400	3600	4500

2.1.7. Parameters used in the Experiment

Parameters	Values
Architecture Used	DenseNet 121
Type of Transfer	From scratch transfer knowledge
Train layers	All
Learning Algorithm	SGD
Learning Rate	0.001
Activation Function	Relu & Softmax
Loss Function	categorical_crossentropy
Batch Size	32
Epochs	100

3. Result Analysis

3.1.1 Classification Accuracy

Classification accuracy is measured as the proportion of accurate predictions to all accurate predictions used

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

The accuracy of our model is 0.9082

3.1.2 Precision

Several instances show that classification accuracy is not necessarily a reliable indicator of model performance as a whole. One of these situations is when there is an uneven distribution of classes. It makes no sense to attain a high accuracy rate if we treat all samples as being of the highest calibre. Contrarily, accuracy implies that consistency can be established when using the same instrument again, such as when measuring the same part. One of these metrics is precision, which is defined as

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

The precision of our model is 0.9091

3.1.3. Recall

Another crucial metric is recall, which is the division of input samples into classes that the algorithm accurately predicted. The calculation for the recall is

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

The recall score of our model is 0.9092

3.1.4. F1 Score

A popular statistic that combines recall and precision measurements is the f1 score.
The f1 score is determined by :

$$\text{F1 Score} = \frac{2 * (\text{Precision} * \text{Recall}}{(\text{Precision} + \text{Recall})}$$

The F1 score of our model is 0.9087

3.1.5. Kappa Score

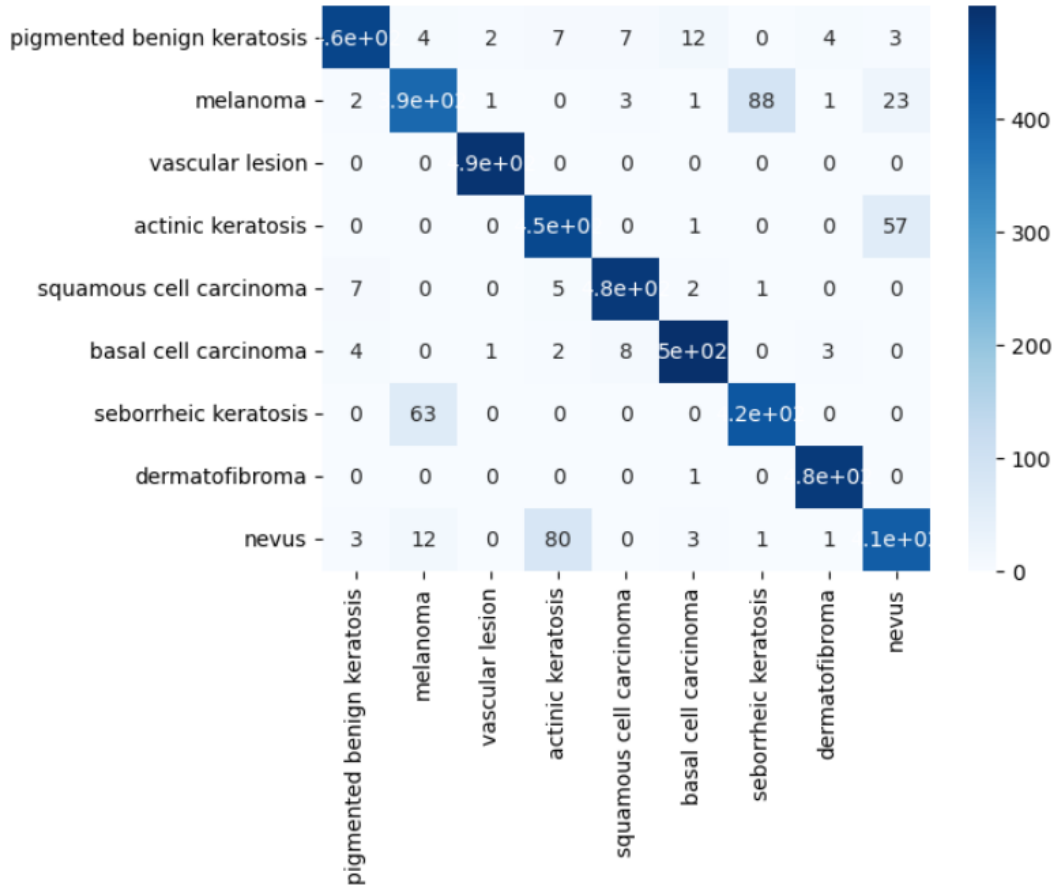
Kappa is a statistical measure that assesses the degree of agreement between a classification model's anticipated and actual classes while accounting for the likelihood that the agreement could have happened by chance. A value of 1 means that the anticipated and actual classes perfectly match each other. Kappa has a range of -1 to 1.

$$\kappa = \frac{p_o - p_e}{1 - p_e} = 1 - \frac{1 - p_o}{1 - p_e},$$

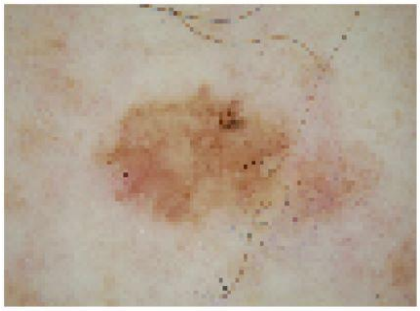
The kappa score of our model is 0.8967

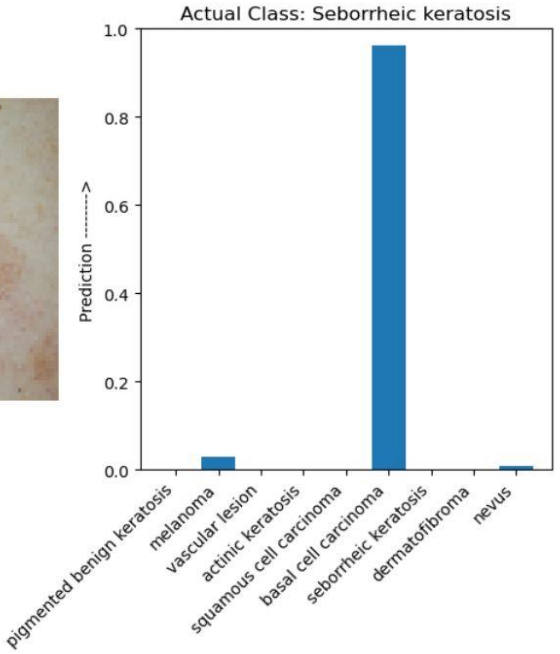
3.2.Confusion Matrix

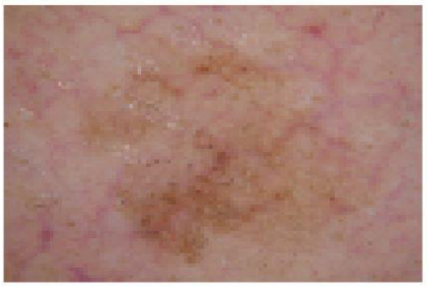
It serves as a performance indicator for classification problems using machine learning where the output can include two or more classes. There are four possible anticipated and actual value combinations in the table. Recall, precision, specificity, accuracy, and—most importantly—AUC-ROC curves may all be measured with great success with this tool.

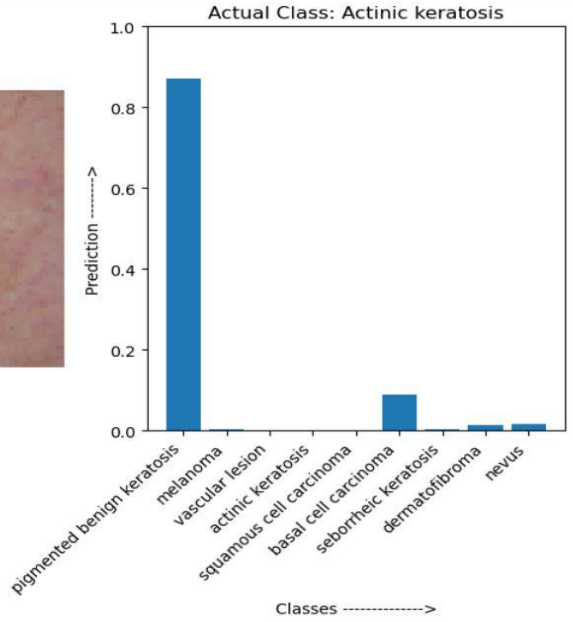


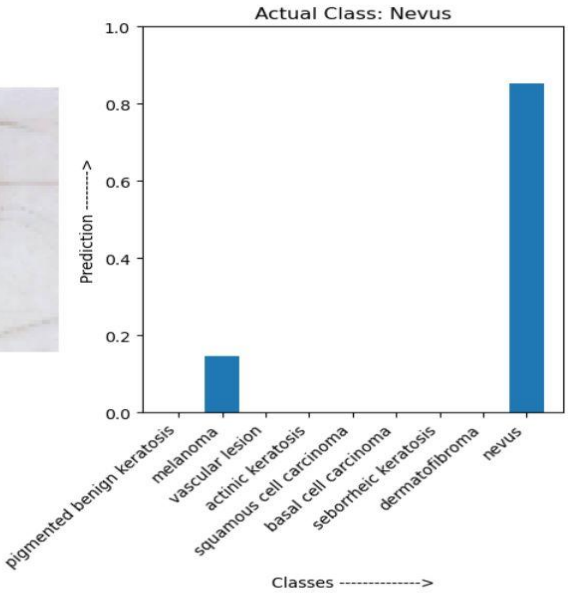
3.3. Resultant Outcomes











4. Conclusions and Future Scope

4.1 Conclusion

The most dangerous skin cancer is melanoma, but it is not fatal if caught earlerefore, it is very important to use remediation methods that are useful in diagnosis, and the use of CNNs can be used to evaluate skin images, reduce the need for human interpretation, and increase efficiency. This method can also help break the limits of traditional methods, which can be imaginative and rely on the dermatologist's knowledge.

These techniques are based on techniques doctors use to find melanoma at an early stage before the cancer has spread to nearby cancer cells. In this study, we present a DenseNet121-based transformation learning model to identify benign and malignant skin lesions, which can be used to identify suspicious lesions.

Proposed method to classify disease as benign or malignant using cancer images from the ISIC2020 database. Data augmentation makes the dataset large and increases DenseNet's accuracy. The design performed well with a detection accuracy of 98.2%. Finally, the proposed method is used to compare the accuracy of various state-of-the-art models.It has been established that the suggested design offers the best categorization without the need to change the model to enhance the outcomes. In the future, this project will produce a series of skin cancer photos from patients in India after gathering a significant number of high-resolution images.

The proposed architecture has been proven to provide the best classification without reintroducing the model to improve its results. In the future, after collecting a large number of high-resolution images, this study will generate a series of skin cancer images from patients in India.

4.2 Future Scope

The proposed model is designed for the efficient use of lighting equipment. The model uses the DenseNet121 architecture, which requires significant parameters for better accuracy. However, due to residual interference in the architecture, the model achieves high accuracy with least effort. To further improve the model, it can include self-learning and learning from previous experiences, which will reduce the effort required to train the model. It is important to mechanize the model to evaluate the impact of extracted features on each strategy and use random components to improve performance.

In future studies, it is important to investigate biomarker-based feature extraction techniques. Biomarkers can efficiently identify diseases from multiple data sources, including genomics, protein sequences, and pathological and imaging data. When transmitting physiological and biological data in the healthcare system, it is necessary to consider the security of light to protect the privacy of the patient. In addition, it would be beneficial to develop user-friendly smart device applications that can display alerts and facilitate communication between patients and doctors in eHealth and telehealth environments, and share and share information securely.

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INDIVIDUAL CONTRIBUTION REPORT:

Skin Disease Classification Using Deep Learning

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Abstract: Melanoma is a deadly type of skin cancer with high fatality rates if not detected and treated in the early stages. Computer-assisted diagnostic support systems can aid in the early detection of skin cancer and potentially increase patient survival rates. In this study, we propose a novel deep transfer learning model for Skin Disease classification using DenseNet121. To address this issue, we apply various data augmentation techniques to increase diversity in the dataset. Our experimental results show that our proposed deep learning technique outperforms state-of-the-art deep learning techniques in terms of accuracy and computational cost. The findings of this study suggest that our proposed model can be a useful tool for accurate melanoma classification and early detection, potentially leading to improved patient outcomes.

Individual contribution and findings: As a member of the project group, my role was to develop the code for the project using transfer-based learning models. I experimented with different models and hyperparameters to find the best-performing model. I also switched the optimizer from Adam to SGD for better accuracy.

Individual contribution to project report preparation: I contributed to several chapters. Specifically, I provided the graphs and hyperparameters from the model and conducted a thorough analysis of the results. I also contributed to the image section of the report by providing relevant images for the project. I contributed to several chapters. Specifically, I provided the graphs and hyperparameters from the model and conducted a thorough analysis of the results. I also contributed to the image section of the report by providing relevant images for the project.

Individual contribution to project presentation and demonstration: During the presentation, I played a significant role in its preparation. Specifically, I referenced several sources of information and contributed to the results section of the presentation. I included the formulas and values created during the testing phase of the model, and I added a confusion matrix to the presentation.

Full signature of the student

INDIVIDUAL CONTRIBUTION REPORT:

Skin Disease Classification Using Deep Learning

SHIVENDRA SINGH

2029197

Abstract: Melanoma is a deadly type of skin cancer with high fatality rates if not detected and treated in the early stages. Computer-assisted diagnostic support systems can aid in the early detection of skin cancer and potentially increase patient survival rates. In this study, we propose a novel deep transfer learning model for Skin Disease classification using DenseNet121. To address this issue, we apply various data augmentation techniques to increase diversity in the dataset. Our experimental results show that our proposed deep learning technique outperforms state-of-the-art deep learning techniques in terms of accuracy and computational cost. The findings of this study suggest that our proposed model can be a useful tool for accurate melanoma classification and early detection, potentially leading to improved patient outcomes.

Individual contribution and findings: My work in the project was to analyze different models and find the best suitable one for our project I tried different models like inception, exception,mobilenet,resnet, etc, and worked tirelessly on them to finally decide the best model and increased the results significantly doing the same I also tried different architectures and concluded the best possible one for the project. I found out at DENSENET 121 gave the best results for our particular model.

Individual contribution to project report preparation: Helped in setting up the index to properly demonstrate and present the report, also helped in going through different reports and books to make the report more effective and readable.

Individual contribution to project presentation and demonstration: Presented and explained the current challenges and constraints of the project and how we overcame them and made our project effective also explained in detail what current practices were lacking and what we did better to overcome them.

Full signature of the student

INDIVIDUAL CONTRIBUTION REPORT:

Skin Disease Classification Using Deep Learning

ANSUHKA AMAR

2029048

Abstract: Melanoma is a deadly type of skin cancer with high fatality rates if not detected and treated in the early stages. Computer-assisted diagnostic support systems can aid in the early detection of skin cancer and potentially increase patient survival rates. In this study, we propose a novel deep transfer learning model for Skin Disease classification using DenseNet121. To address this issue, we apply various data augmentation techniques to increase diversity in the dataset. Our experimental results show that our proposed deep learning technique outperforms state-of-the-art deep learning techniques in terms of accuracy and computational cost. The findings of this study suggest that our proposed model can be a useful tool for accurate melanoma classification and early detection, potentially leading to improved patient outcomes.

Individual contribution and findings: I made sure that we are using the best possible dataset available as finding a good dataset is the core for the project. I analyzed and went through different dataset available and picked the latest and best issued by ISIC and I wrote the report by going through the code.

Individual contribution to project report preparation: I wrote the report from scratch by taking little help from my group members and made sure that the report is as per the format and has all the required elements and data.

Individual contribution to project presentation and demonstration: Presented and explained what skin cancer is and why we choose this project and what classification we have done. Also, explained the need for making this project and explained the classifications of the different skin cancers and how we have classified them.

Full signature of the student

INDIVIDUAL CONTRIBUTION REPORT:

Skin Disease Classification Using Deep Learning

SWAMITA SACCHAN

2029038

Abstract: Melanoma is a deadly type of skin cancer with high fatality rates if not detected and treated in the early stages. Computer-assisted diagnostic support systems can aid in the early detection of skin cancer and potentially increase patient survival rates. In this study, we propose a novel deep transfer learning model for Skin Disease classification using DenseNet121. To address this issue, we apply various data augmentation techniques to increase diversity in the dataset. Our experimental results show that our proposed deep learning technique outperforms state-of-the-art deep learning techniques in terms of accuracy and computational cost. The findings of this study suggest that our proposed model can be a useful tool for accurate melanoma classification and early detection, potentially leading to improved patient outcomes.

Individual contribution and findings: I helped in finding the Dataset that was best suitable for our Problem set of ours. To balance the data I suggested some methods so that we can balance the data and also helped in creating a readable code.

Individual contribution to project report preparation: As a member of the group I helped in writing about the model Architecture and the related images and created some of the images on my own to visualize the model in a better way. Finally, I help in the Result part where we did the result analysis and added the relevant images from the Code.

Individual contribution to project presentation and demonstration: I helped in the creation of the presentation from scratch and add all the necessary information related to the Topic that we are working on and edited all the necessary parts that are required for a better analysis/explanation of the code. Lastly, I concluded the presentation of the project in detail.

Full signature of the student:

TURNITIN PLAGIARISM REPORT

SKIN CANCER CLASSIFICATION USING DEEP LEARNING

ORIGINALITY REPORT

22%	19%	9%	11%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	iq.opengenus.org Internet Source	4%
2	maryadewunmi.medium.com Internet Source	2%
3	affderm.com Internet Source	2%
4	books.byui.edu Internet Source	2%
5	www.healthcarepro.co.uk Internet Source	2%