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Classification of Skin Cancer using Deep Learning

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ABSTRACT: Cancer is a deadly disease that occurs by multiplication of the cells in an uncontrolled manner and thereby occupying the peripheral tissues. Although, skin cancer is less frequent than many other cancer types, itsmortality rate is quite high. It is of different types such as Malignant Melanoma, Basal cell carcinoma and Squamous cell carcinoma. Melanoma incidence is described to increase more rapidly than the other forms of skin cancer. Melanoma is responsible for 4% of all the skin cancers but it is responsible for 75% of total deaths due to skin cancer. It is believed to be triggered by ultraviolet rays and occurs more commonly in areas have high exposure to sunlight. In Europe, more than 62.000 new cases are detected each year.
Various research works have been done using Computer vision and Image processing to classify skin cancer into seven types. There were limitations of earlier models as some used PH2 data sets [4][5], having fewdermoscopy images and some used images of lower resolution. Most of the model uses KNN model [1][4][6][7][9].
Compared to the previous researches we used HAM(Human Against Machine) data sets, which hasmore than 10,000 high resolution images. CNN model is used for classification of cancer.

I. INTRODUCTION

In the last 10 years, the number of Melanoma cases has increased by more than 50% due to increased sun exposure. Out of the many cancers of skin, Melanoma is the most lethal types causing death in most of the cases but a diagnosis at early stage can lead to high chances of survival. A correct diagnosis is of utmost importance yet difficult due to the similarities in the various lesions of the skin. Dermatologists have 65% to 80% accuracy rate in the diagnosis of Melanoma. However, in difficult cases visual inspection is followed by dermatoscopic images. Automated lesion classification involving machine learning therefore, comes into picture. Skin cancer classification can support dermatologists and provide fast access to life saving diagnosis.

In this paper, we have tried to propose a model for skin cancer classification using high resolution images.

Objectives

To propose a model for skin cancer classification using high resolution images.
To automate the detection approach using faster and more accurate image classification algorithms.
To decrease treatment time with increase in prediction accuracy.

II. LITERATURE REVIEW

NAY CHILYNNet. al. (2017) proposed classification and segmentation of skin Melanoma from images of skin lesions. Pre-processing was done like hair removal using Dull Razor tool, after that image segmentation is done by semi-supervised mean shift algorithm and feature extraction is done using ABCD rule (A representing Asymmetry B representing Border C indicating Colour variation and D showing Diameter), next step is classification, they used three classification algorithms - Decision Tree, KNN and SVM. The maximum accuracy was 78.2% using SVM algorithm. Suleiman et. al. (2017) presented model on Image processing & SVM classification for Melanoma Detection. In this, ABCD rule was used for detection and classification. In pre– processing, changing the contrast, which makes the patch, looks bright, then using HSV (Hue, Saturation and value). After that segmentation phase comes in which grab cut technique was used. Accuracy of this model was 80.00%. For improving the accuracy SVM (Support Vector Machine) was used. Nabinet. al. (2016) detected Melanoma in Dermoscopy Images using Image Processing and machine Learning. The work was divided intoFeature segmentation, Lesion segmentation, Feature Generation and classification. In Lesion segmentation infected skin was taken for processing. Next was feature segmentation after this step the last step was feature generation and classification in which lesion was classified into the appropriate category of cancer.

ILKER ALI et. al. (2017) presented classification of Skin lesion using machine learning algorithms and PH2 data sets which has 200 768x560 resolutiondermoscopy images with each image having RGB channel. Four classifying techniques were applied on the data sets which were Artificial Neural Network(ANN), SVM, K-Nearest Neighbor(KNN) and Decision Tree(DT). Zahra Waheedet. al. (2017) proposed Detection of Melanoma with Dermoscopic Images and Machine Learning Approach using two techniques on PH2 datasets - feature extraction and classification. In feature extraction,colour feature and texture feature were used. 13-D feature vector was formed with four texture features and nine color features. 13-D feature vector was obtained for each of the dermoscopic images and saved in the the database with respective class labels. In the proposed method, SVM classifier was chosen to classify melanoma images from all the given dermoscopic images contingent on texture features and extracted colors.

SHALU et. al. (2018) proposed a model for the purpose of segmentation, using fusion strategy with basic algorithm. Then K-Nearest Neighbor classification was applied to classify the skin lesions - dysplastic, benign and malignant melanoma. For accuracy, measures like amount of lesions, age, sunburnsetc. reflecting the general risk were also acquired. Suggested methodology predominantly consists of four steps - Preprocessing (for enhancement of the images and removal of the artifacts), Segmentation (to find the region of interest), feature extraction (system accuracy was affected by the features used), and Classification (3 Classifiers were used namely Naive Bayes, Decision Tree, K-Nearest Neighbor). MED-NODE dataset was applied for evaluation of the system performance forskin cancer (Melanoma) detection system. Accuracy is 82.35.

MASOOD et. al. (2016) proposed different methods using computer aided classification. To mange the problem of availability of limited labeled data, they presented a semi-advised model for learning of automated recognition of cancer of skin using histopathological images. Deep belief architecture was made, utilizing unlabeled data by making use of limited labeled data for calibrating. Alongside, SVM algorithm was used to improve classification results.For effective generalization capacity of the model, Deep belief network andadvised SVM were trained laterally. The results were compiled using least square estimation weighing. The classification performance is correlated with some popular methods and the designed model surpassed popular techniques including ANN, KNN, semi supervised algorithms such as transductiveSVM based classification model and Expectation maximization algorithm.

SUNDAR et al. (2016) devised a novel model for detection of melanoma using Multiclass support vector machine (MSVM), where the queried images were organized and matched with higher probability type. In MSVM classifier algorithm, the test samples were charted with training samples and the probability value was adjusted for the highest match obtained from the group of training samples. They proposed a system containing an image database with all the five types of melanoma for classification and testing.The simulation results have shown the superior performance and accuracy of One-Against-All MCSVM. The reliability of the proposed support vector machine model is relatively high. Inaccuracy is avoided with the use of segmentation algorithm named K- means Clustering algorithm.

MASOOD et al. (2015) presented a semi supervised, learning scheme for automated recognition of melanoma with dermoscopicimages. Laterally, a self-advised SVM algorithm was used for the accuracy of classification results to counterbalance the effect of mis-classified data. They tested the model by making the use of 100 dermoscopic imagesand compared the performance with some popular classification methods. After going through the experimental results they computed the accuracy as 89%.

MUSTAFA et. al.(2018) suggested an automated system for detecting melanoma skin cancer with plain photographs of affected skin regions . They applied the ABCDEs rule for detecting melanoma as it is used in most of the cases. They used the GrabCut algorithm to segment an input image into lesions that resembled melanoma. They extracted features such as shape, geometry and color by using image processing techniques. They used Gaussian radial basis kernel (SVM·RBF) to categorize the extracted features as cancerous "malignant" or non-cancerous mole "benign". They found that only six features are sufficient to detect melanoma. The accuracy after the statistical analysis was computed as 86.67%.

III. TOOLS AND TECHNIQUES

Neural Network

Neural networks are a set of algorithms, mimicking human brain and are modeled to identify patterns. They decipher sensory data using a type of machine intelligence, clustering or labeling raw input. The patterns, identified are vectors, in which all real-world data, like sound,

images, text or time series, must be converted. Neural networks assist in classifying and clustering data once they have a labeled dataset to work upon. (Neural networks can also pull out features that are entered to other alogarithms for classification and clustering.

Convolutional Neural Network

CNNs are influenced by biological visual cortex. The cortex has small regions of cells, sensitive to the distinct areas of the visual field. Hubel and Wiesel in 1962, completed an experiment showing some individual having neurons in the brain that get activated only in the presence of edges of a particular orientation like vertical or horizontal edges. For example, some neurons fired when exposed to horizontal sides and vice-versa. Hubel and Wiesel established that all of these neurons were well ordered in a columnar fashion and they together were able to bring out visual perception. This design of particular elements inside of a system having specific tasks is similar to machines and CNNs.

VGG16

Proposed by K. Simonyan and A. Zisserman from the University of Oxford in research paper "Very Deep Convolutional Networks for Large-Scale Image Recognition", VGG16 is a convolutional neural network model and is among one of the top models submitted to ILSVRC-2014. The model attains top-5 test accuracy of 92.7% in ImageNet, which is a dataset of over 14 million images belonging to 1000 classes.

This is a simple model utilizing only 3×3 convolutional layers stacked one on each other in increasing depth. Reducing volume size is handled by max pooling. Two fully connected layers, with 4,096 nodes each are followed by a softmax classifier.VGG16 was using NVIDIA Titan Black GPU's and was drilled for weeks.

ResNet

Kaiminget al introduced novel architecture having "skip connections" featuring heavy batch normalization called ResNet, at the ILSVRC. These skip connections also known as gated units have a resemblance to recent successful elements applied in RNNs. Using the technique they were able to accomplish a NN with 152 layers with lower complexity than VGGNet. It achieved a top-5 error rate of 3.57%, which subdues human performance on the dataset.

Although ResNet is much deeper than VGG16 and VGG19, it has a substantial smaller model size due to the utilization of global average pooling rather than fully connected layers — reduceing the model size down to 102MB for ResNet50.

Dataset Description

There are 10015 dermatoscopic images in the dataset, delivered as 'training dataset' for machine learning in academics and are available through ISIC archive. This benchmark dataset can be used for comparisons with human experts. The dermatoscopic images have been collected from different populations and stored by different modalities. Due to this diversity different cleaning methods were applied and semi-automatic specifically trained neural networks were developed for cleaning. Cases include a representative collection of all-important diagnostic categories in the realm of pigmented lesions. More than 50% of lesions have been confirmed by pathology, while the rest of the cases were followed-up with expert consensus or confirmation by in-vivo confocal microscopy.
Dimensions of image 600 X 450
Total number of images in dataset 10015
Number of images used for training the classifier: 8012 (80%)
Number of images used for testing the classifier: 2003 (20%)

Proposed Approach

The Proposed model helps the dermatologist in classification of 7 major categories of skin cancers, Melanocytic nevi, Benign keratosis-like lesions, Dermatofibroma, Basal cell carcinoma, Melanoma,Actinic keratosis and Vascular lesions.

We tried to create a Convolutional Neural Networks (CNNs) model, which automates most of the diagnostic processes with identical or better accuracy than the current models.In this model, we tried to replicate a CNN by using 10,000 training images and comparing the results to human experts. The dataset We used dataset including 7 major categories of skin cancers, Melanocytic nevi, Benign keratosis-like lesions, Dermatofibroma, Basal cell carcinoma, Melanoma,Actinic keratosis and Vascular lesions. This scheme uses the HAM10000 dataset and is GPU processed.

1. Importing Essential Libraries
These libraries include Matplotlib, Pandas, Numpy, Keras and Sklearn.

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```
In [2]: import numpy as np
import pandas as pd
import imageio
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, precision_recall_fscore_support
import scipy.ndimage
from scipy import misc
import skimage
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
plt.style.use('fivethirtyeight')

from tqdm import tqdm
from glob import glob
from scipy import stats
from sklearn.preprocessing import LabelEncoder, StandardScaler
from imblearn.under_sampling import RandomUnderSampler
from os import listdir

import keras
import tensorflow as tf
from keras.utils import to_categorical
from keras.layers import Dense, Input, Flatten, Reshape, Conv2D, MaxPool2D, concatenate, Activation, Dropout
from keras.optimizers import Adam, RMSprop
from keras.models import Model, Sequential, load_model
from keras.losses import binary_crossentropy
from keras.metrics import binary_accuracy
from keras.callbacks import ModelCheckpoint
from keras.preprocessing.image import ImageDataGenerator
from keras.preprocessing import image

Using TensorFlow backend.
```

Fig 1: Importing Essential Libraries

2. Reading Data

```
In [3]: variable = pd.read_csv("C:/Users/shivansh tiwari/skin-cancer-mnist-ham10000/HAM10000_metadata.csv")
variable.head()
```

Out[3]:

	lesion_id	image_id	dx	dx_type	age	sex	localization
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear

Fig 2: Reading Data

3. Data Cleaning

The dataset is checked for missing data types or values for each field, and are completed with null values (for age, in this case).

```
In [5]: skin_df.isnull().sum()
```

Fig 3: Data Cleaning

4. Exploratory data analysis - EDA

This is a step to foresee and comprehend the data for analyzing the different features and distribution of dataset and actual numbers.

```
In [4]: fig,ax1 =plt.subplots(1,1, figsize =(10,5))
skin_df['cell_type'].value_counts().plot(kind='bar',ax=ax1)
```

Fig 4: Explotatory Data Analysis

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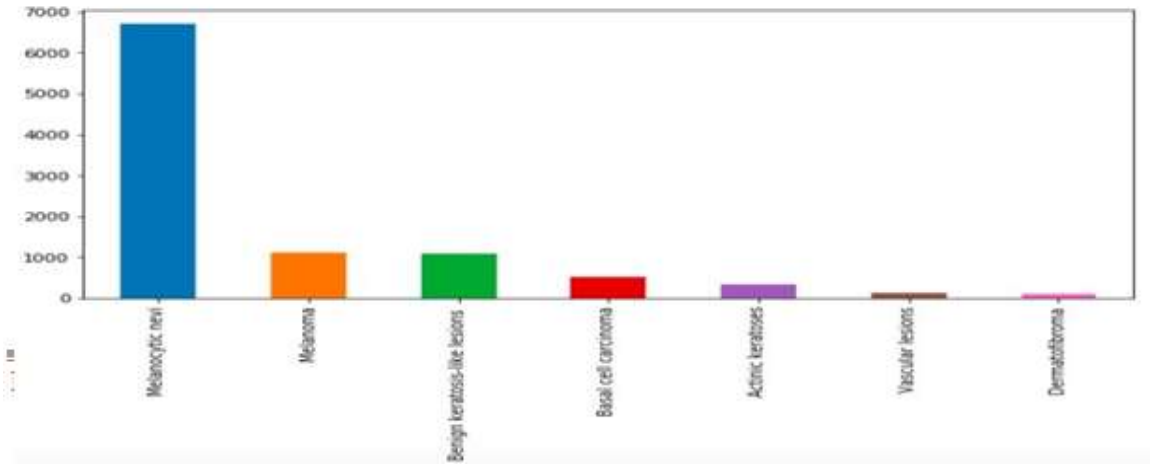
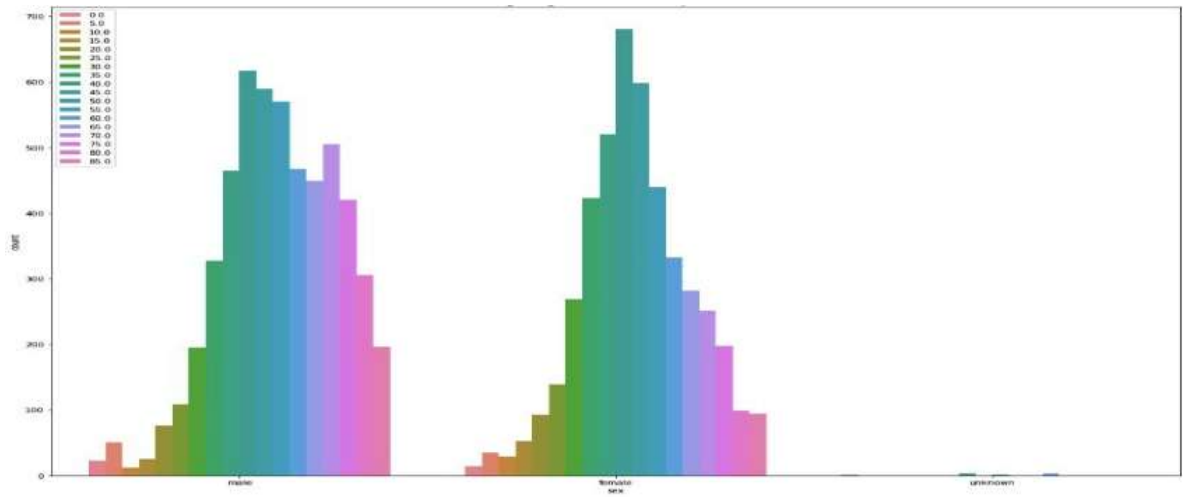


Fig 5: Exploratory Data Analysis

Age and Gender of cancer patients

```
In [15]: plt.figure(figsize=(20,15))
         sns.countplot(x='sex',hue='age',data=variable)
         plt.legend(loc='best')
         plt.title("Age & gender of cancer patient",size=15)
         plt.show()
```



```
In [32]: labels=variable.localization.value_counts().index
         sizes=variable.localization.value_counts().values
         plt.figure(figsize=(12,12))
         plt.pie(sizes,labels=labels,autopct="%1.f%%")
         plt.title("cancer location",size=25)
         plt.show()
```

Fig 6: Age and Gender of cancer patients

4. Label Encoding

Labels 7 different types and classes of skin cancer from numbers 0 to 6.

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```
In [4]: le = LabelEncoder()
        le.fit(metadata['dx'])
        LabelEncoder()
        print(list(le.classes_))

        metadata['label'] = le.transform(metadata["dx"])
        metadata.sample(10)

        ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']
```

Out[4]:

	lesion_id	image_id	dx	dx_type	age	sex	localization	label
2609	HAM_0000263	ISIC_0034058	bcc	histo	70.0	male	back	1
4894	HAM_0003399	ISIC_0028398	nv	follow_up	40.0	male	ear	5
2440	HAM_0001372	ISIC_0031103	vasc	consensus	35.0	female	trunk	6
5317	HAM_0006106	ISIC_0032295	nv	follow_up	45.0	female	neck	5
4969	HAM_0003249	ISIC_0025114	nv	follow_up	35.0	male	back	5
3415	HAM_0004134	ISIC_0026075	nv	follow_up	30.0	male	back	5
5039	HAM_0005793	ISIC_0024629	nv	follow_up	65.0	male	trunk	5
9387	HAM_0000698	ISIC_0027431	nv	consensus	NaN	male	foot	5
8763	HAM_0007263	ISIC_0028130	nv	histo	50.0	female	lower extremity	5
6558	HAM_0000584	ISIC_0025888	nv	follow_up	35.0	female	lower extremity	5

Fig 7: Label Encoding

5. Loading & Resizing of Images

```
In [6]: train_data = pd.DataFrame()
        train_image = []
        for i in tqdm(range(len(metadata))) :
            dire = base_dir  + '/' + metadata['image_id'][i] + '.jpg'
            img = image.load_img(dire)
            img = img.resize((128,128))
            img = image.img_to_array(img)
            img = img/255
            train_image.append(img)
        print(len(train_image))
        100%|██████████| 10015/10015 [05:23<00:00, 30.92it/s]
        10015
```

Fig 8: Loading & Resizing of Images

6. Train Test Split

Data is split into training and testing sets with 80 and 20 divisions respectively

```
In [7]: x = np.array(train_image)
        y = to_categorical(metadata['label'])
        del train_image

In [8]: X_train,X_test,Y_train,Y_test = train_test_split(x, y, test_size = 0.2)
        del x
        del y
```

Fig 9: Train Test Split

7. Model Building

Keras is utilized in sequential API and adding one layer at a time starting with input.

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```
[ ] model = Sequential()

    model.add(Conv2D(32, (3, 3),strides=(3,3), activation='relu', input_shape=(256,256,3)))
    model.add(Conv2D(32, (3, 3), activation='relu'))
    model.add(MaxPool2D((2, 2)))
    model.add(Conv2D(64, (3, 3), activation='relu'))
    model.add(MaxPool2D((2, 2)))
    model.add(Conv2D(128, (3, 3), activation='relu'))
    model.add(MaxPool2D((2, 2)))
    model.add(Conv2D(256, (3, 3), activation='relu'))
    model.add(MaxPool2D((2, 2)))
    model.add(Dropout(0.2))
    model.add(Flatten())

    model.add(Dense(256, activation='relu'))
    model.add(Dropout(0.4))
    model.add(Dense(7, activation='softmax'))
```

Fig 10: Model building

8. Setting Optimizer

```
[ ] model.compile(loss='categorical_crossentropy',
    optimizer='adam',
    metrics=['accuracy'])
```

9. Fitting the model

```
[ ] history = model.fit(X_train, Y_train, epochs=30, validation_data=(X_test, Y_test))
```

```
[ ] 8012/8012 [==============================] - 12s 2ms/step - loss: 0.5287 - acc: 0.7958 - val_loss: 0.6688
    Epoch 19/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.5103 - acc: 0.8055 - val_loss: 0.6606
    Epoch 20/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.4933 - acc: 0.8143 - val_loss: 0.6566
    Epoch 21/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.4532 - acc: 0.8268 - val_loss: 0.6902
    Epoch 22/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.4262 - acc: 0.8360 - val_loss: 0.7250
    Epoch 23/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.4176 - acc: 0.8411 - val_loss: 0.6899
    Epoch 24/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.3646 - acc: 0.8606 - val_loss: 0.7050
    Epoch 25/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.3492 - acc: 0.8709 - val_loss: 0.7407
    Epoch 26/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.3369 - acc: 0.8732 - val_loss: 0.7747
    Epoch 27/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.2965 - acc: 0.8897 - val_loss: 0.7628
    Epoch 28/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.2967 - acc: 0.8868 - val_loss: 0.7726
    Epoch 29/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.2792 - acc: 0.8952 - val_loss: 0.8450
    Epoch 30/30
    8012/8012 [==============================] - 12s 2ms/step - loss: 0.2543 - acc: 0.9051 - val_loss: 0.8903

[ ]
```

Fig 11: Fitting the Model

IV. RESULTS AND OBSERVATIONS

After comparing results, we can see that CNN model have best results having accuracy Validation accuracy of 0.7688

S. No.	Model Used	Resolution	Validation Accuracy
1.	CNN	128 x 128	0.7354
2.	CNN	256 x 256	0.7688

3.	VGGNet16	256 x 256	0.7269
4.	VGGNet16	256 x 256	0.7452
5.	RESNet50	128 x 128	0.7579
6.	RESNet50	256 x 256	0.7139

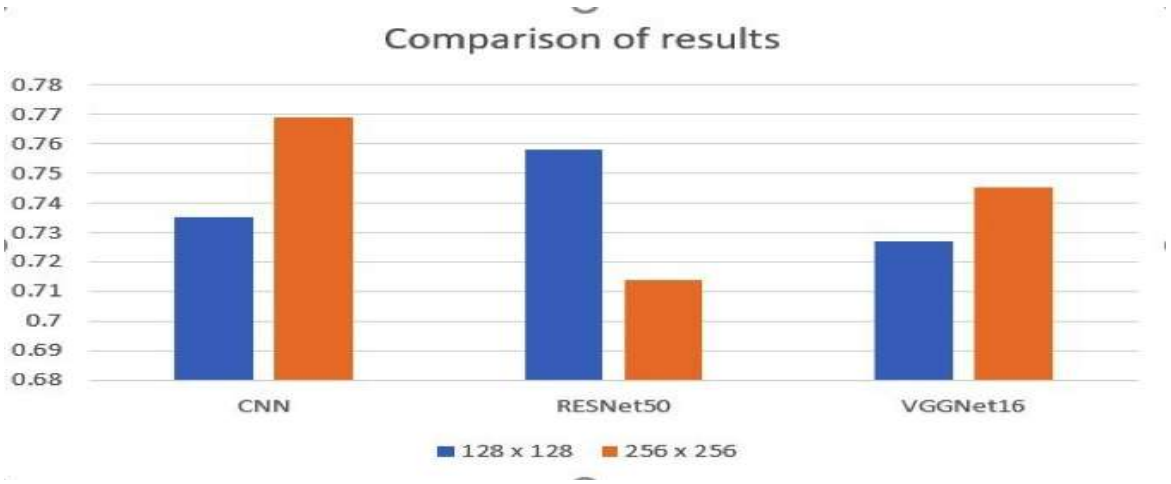

Fig 12: Comparision of Results

V. CONCLUSION

In this work, different types of neural networks were used to classify skin cancer. The results achieved are not impressive when compared to the accuracy obtained by previous researchers. This is due to a few reasons and one of the reason is unbalanced dataset due to this neural networks faced primary challenge on this dataset is to accurately classify all the seven types of skin lesion. Even though we used HAM10000 dataset because it is the most recent and complete dataset of this kind. Apart from these things we can increase its accuracy by tuning or by adding some new samples to the dataset. We can also do experiments with different pooling, architectures and optimizers because these things can make a big difference in our model behavior. In this work, we used RESNet50, CNN and VGGNet16 neural networks for classification of skin cancer and with CNN we have achieved highest accuracy of 76.88%

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