ABSTRACT

Skin cancer has been gradually increasing among the people for decades. Every year the number of new cases of melanoma, and the death rate is increasing. In 2020 325,00 cases of melanoma were found among which 57,000 people died. Classifying these melanoma from images is a difficult task because of their minute variation from non cancerous skin lesions. In this project we are going to build a computer-aided diagnosis system for classifying skin lesions. In the preprocessing steps hair and other artifacts from the image are removed using morphological filtering. And to extract the foreground or lesion region from the image we used grab-cut segmentation. Melanoma and benign lesions are detected according to the image processing method using CNN's. Pre trained CNN's like Resnet50, MobileNet, VGG16 were used in this project for the image classification task. And also to improve the efficiency Data Augmentation techniques like Rotation are also employed.

KEYWORDS: Computer Aided Diagnosis, HSV, Melanoma.

Table of Contents

Title	PageNo
Bonafide Certificate	ii
Acknowledgements	iii
List of Figures	iv
List of Tables	V
Abbreviations	vi
Abstract	vii
1. Summary of Base Paper	1
1.1 Introduction & Literature survey	1
1.2 Novelty 1.3 Proposed Work	3 3
1.4 Acquired Dataset	4
2. Merits and Demerits	5
2.1 Merits	5
2.2 Demerits	5
3. Source Code and Snapshots	6
3.1 Code for Hair Removal	6
3.2 Code for Image Sharpening	7
3.3 Code for Image Segmentation	7
3.4 Code for Image Augmentation	10
3.5 Code for ABCD Feature Extraction	11
3.5.1 Asymmetry	11
3.5.2 Border	12
3.5.3 Color	13
3.5.4 Dermoscopic Structures	14
3.6 Code for MobileNet Model	17
3.7 Code for VGG16 Model	18
3.8 Code for ResNet50 Mode	20
4. Conclusion and Future plans	23
4.1 Conclusion	23
4.2 Future plans	23
5. References	24
5.1 Base Paper	24
5.2 Other References	24
6. Plagiarism Report	25

CHAPTER-1

SUMMARY OF BASE PAPER

1.1 Introduction

Title	Automated deep learning approach for classification of malignant melanoma and benign skin lesions
Journal Name	Multimedia Tools and Applications
Publisher	Springer
Year	2022
Indexed in	Science Citation Index Expanded

Table 1.1 Base Paper Info

• In recent decades, the incidence of skin cancer has increased, making it a major health problem worldwide. Although the dermatological diagnosis of skin cancer is very effective, it is very difficult for an experienced dermatologist to accurately classify malignant melanoma and benign skin lesions from many dermatological images. Therefore, the development of a non-invasive CAD (Computer Aided Diagnostic) system for the classification of skin lesions is very important. Image preprocessing, segmentation, feature extraction and classification are the four major steps in CAD. The consecrated neural network (CNN) and the deep learning methods have increased due to the diagnosis of cancer. There are a series of data, such as data sets and medical images transmission. This is a useful tool. Simple adjustments for architectures and use require complete data and expensive calculations compared to CNN training to increase operational speed. Initially, the process called "data expansion data " by creating new data in the original data can increase the amount of income data. The diagnostic system is a result of a reasonable classification to discriminate malignant damage to cancer to cope with skin damage diagnostic systems.

Literature Survey

S.NO	TITLE	YEAR	TECHNIQUE
1	Skin Lesion Classification Using	2019	A novel regularizer technique
	Convolutional Neural Network With		to classify skin lesions into
	Novel Regularizer		benign or malignant
2	Classification of skin lesions using	2019	Using the theory of transfer
	transfer learning and augmentation		learning and the pre-trained
	with Alex-net. PLoS One		deep neural network
3	Classification of malignant	2016	The ABCD rule of
	melanoma and benign skin lesions:		Dermoscopy is a scoring
	implementation of automatic ABCD		method used by
	rule		dermatologists to quantify
			dermoscopy findings
4	Data augmentation for skin lesion	2018	investigated the impact
	analysis		Of data augmentation
			scenarios for melanoma
			classification trained on three
			CNNs (Inception-v4, ResNet,
			and DenseNet)
5.	Automatic detection of malignant	2014	New methods to weaken the
	melanoma using macroscopic image		effect of nonuniform
			illumination, correction of the
			effect of thick hairs and large
			glows on the lesion and also, a
			new threshold-based\
			segmentation algorithm

1.2 Novelty

- The dataset was having less malicious images that caused the imbalance. I fixed this and removed the imbalance.
- The quality of the image deteriorated after the image was preprocessed according to the paper. So I Enhanced using techniques like Gaussian Blur.
- Stopping early helped reduce computation time by building a CNN model using the Model checkpoint method.

1.3 Proposed Work

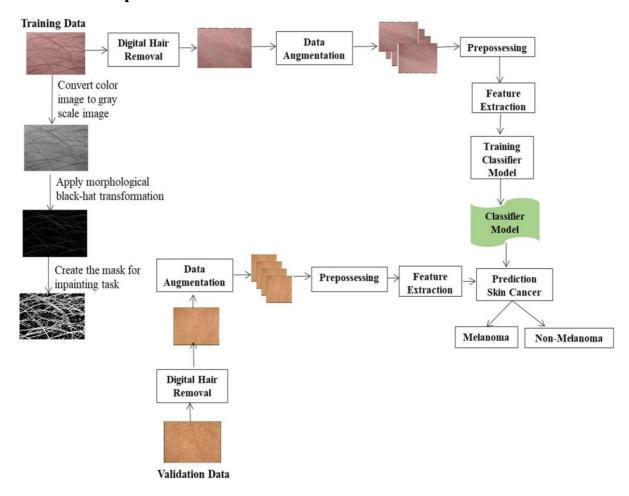


Fig.1.1

1.4 Acquired Dataset

The dataset contains 930 dermoscopic skin images , including Benign skin tumors(nevus, seborrheic keratosis) and Malignant Melanoma.





Fig.1.2

we acquired our images from ISIC 2017 database and then to scale up this dataset we had used data augmentation techniques like image rotation in which a single image is roasted by 4 angles(0,90,180,270) thus we finally get 930*4 im

CHAPTER-2

MERITS AND DEMERITS

2.1 Merits

- 1. Utilizing hybrid CNN (VGG16 and ResNet50 with SVM classifier) models had helped to increase the precision in classification.
- 2. This learning models have been shown to be highly accurate in a variety of image classification tasks, when we have modified with pre-trained models. This systems can use these patterns to provide reliable and accurate classification results, helping to detect potential cases of skin cancer early. Early detection of disease improves the patient's condition with good treatment.

2.2 Demerits

- 1. Automated systems may not incorporate human intuition, judgment and domain knowledge, which can be valuable in some cases. Because it is limited to the patterns and rules found in the training data, it may not be able to account for contextual or subtle factors.
- 2.Deep learning models for training are often based on large, diverse and well-defined datasets. These datasets are difficult and time-consuming to acquire, especially for medical imaging. Before using an automated system in a clinical setting, it must be thoroughly tested to prove its ability to work.

CHAPTER-3

Source Code and Snapshots

3.1 Code For Hair Removal:-

import cv2

import numpy as np import os from google.colab import drive

inDirectory = '/content/drive/MyDrive/Benign' outDirectory = '/content/drive/MyDrive/outBenign' kernel_size = 10 for filename1 in os.listdir(inDirectory):

img = cv2.imread(os.path.join(inDirectory, filename1)) gray = cv2.cvtColor(img, cv2.COLOR_BGR2GRAY) gray = cv2.addWeighted(gray, 0.3, gray, 0.59, 0) gray = cv2.addWeighted(gray, 1, gray, 0.11, 0)

kernel = cv2.getStructuringElement(cv2.MORPH_ELLIPSE, (kernel_size, kernel_size))
blackhat = cv2.morphologyEx(gray, cv2.MORPH_BLACKHAT, kernel)
_, mask = cv2.threshold(blackhat, 10, 255, cv2.THRESH_BINARY) mask =
cv2.inpaint(img, mask, 3, cv2.INPAINT_TELEA) cv2.imwrite(os.path.join(outDirectory, filename1), mask)

OUTPUT OF HAIR REMOVAL

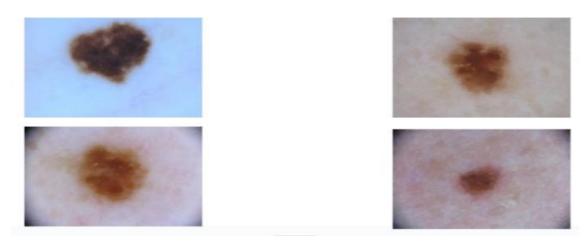


Fig.3.1

3.2 Code For Image Sharpening:-

import cv2 import os

inDirectory = '/content/drive/MyDrive/outBenign' outDirectory =

'/content/drive/MyDrive/blurremovedBenign' kernel size = (5,5)

 $unsharp_weight = 1.5$

blur weight = -0.5

for filename1 in os.listdir(inDirectory):

img = cv2.imread(os.path.join(inDirectory, filename1)) blur = cv2.GaussianBlur(img, kernel size, 0)

unsharp_mask = cv2.addWeighted(img, unsharp_weight, blur, blur_weight, 0) cv2.imwrite(os.path.join(outDirectory, filename1), unsharp_mask)

OUTPUT OF IMAGE SHARPENING:



Fig.3.2

3.3 Code For Image Segmentation:-

import cv2 as c import os import numpy as np

from google.colab.patches import cv2_imshow image = c.imread('ISIC_0000020.JPG')

```
hsv = c.cvtColor(image, cv2.COLOR BGR2HSV)
clahe = c.createCLAHE(clipLimit=2.0, tileGridSize=(8,8)) hsv[:::,2] =
clahe.apply(hsv[:,:,2])
bgr = c.cvtColor(hsv, cv2.COLOR HSV2BGR) image mask = np.zeros(image.shape[:2],
np.uint8) background = np.zeros((1,65), np.float64) foreground = np.zeros((1,65),
np.float64)
rect = (10, 12, 250, 270)
c.grabCut(bgr, image mask, rect, background,foreground,30, c.GC INIT WITH RECT)
mask2 = np.where((image mask==2)|(image mask==0), 0, 1).astype('uint8') segmented =
bgr*mask2[:,:,np.newaxis]
mask2[mask2 == 1] = 255
mask2[mask2 == 0] = 0
ground truth = c.imread('ISIC 0000020 segmentation.png', c.IMREAD GRAYSCALE)
ground truth = c.resize(ground truth, (300, 300))
intersection = np.logical and(ground truth, mask2) union = np.logical or(ground truth,
mask2)
jc = np.sum(intersection) / np.sum(union) c imshow(segmented) c imshow(mask2)
print('Jaccard Coefficient:', jc)
c.waitKey(0) c.destroyAllWindows()
```

OUTPUT OF IMAGE SEGMENTATION:-

Based on this Jaccard coefficient value we can evaluate the correctness of our segmented images. Segmented images are compared with ground truth images which were present along with dataset and jaccard coefficient value is calculated for them.

Grab-Cut	Mask	Ground-Truth Image	Jaccard Goefficient Value
			0.855
			0.814

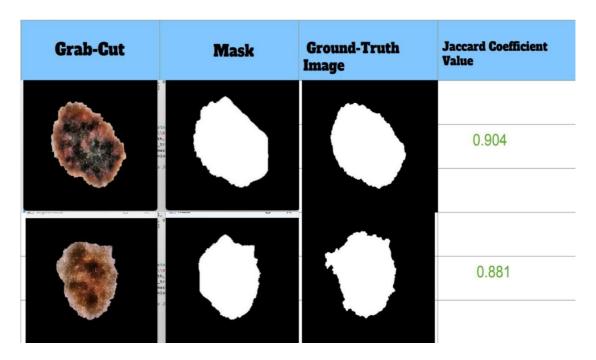


Fig 3.3

3.4 Code For Image Augmentation:-

from PIL import Image import os inDirectory = "/content/drive/MyDrive/blurremovedBenign" outDirectory = "/content/drive/MyDrive/augmentedBenign" angles = [0, 90, 180, 270] for filename1 in os.listdir(inDirectory):

lesion = Image.open(os.path.join(inDirectory, filename1)) for angle in angles: rotated_lesion = lesion.rotate(angle)

new_filename = filename[:-4] + "_" + str(angle) + ".jpg"
rotated_lesion.save(os.path.join(outDirectory, new_filename1))

OUTPUT OF AUGMENTATION:

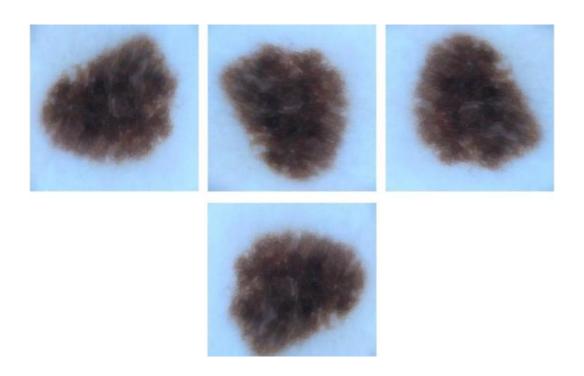


Fig.3.4

3.5 Code For ABCD Feature Extraction:-

3.5.1Asymmetry:

```
import cv2
import numpy as np
import glob
a=[]
b=[]
c=[]
d=[]
ABCD = []
for fil in glob.glob('/content/drive/MyDrive/sample/*.JPG'):
  # Load the image
  img1 = cv2.imread(fil)
  img = cv2.cvtColor(img1, cv2.COLOR BGR2GRAY)
  # Calculate the center of gravity
  M = cv2.moments(img)
  cg x = int(M['m10']/M['m00'])
  cg_y = int(M['m01']/M['m00'])
  # Draw two orthogonal axes
  cv2.line(img, (cg x - 100, cg y), (cg x + 100, cg y), (0, 0, 255), 2)
  cv2.line(img, (cg_x, cg_y - 100), (cg_x, cg_y + 100), (0, 0, 255), 2)
  # Divide the lesion into four quadrants
  quadrants = [
    img[0:cg_y, 0:cg_x],
    img[0:cg y, cg x:],
    img[cg_y:, 0:cg_x],
    img[cg_y:, cg_x:]
  # Calculate the mean and standard deviation for each quadrant
  mean bright = []
  mean color = []
  std bright = []
  std color = []
```

```
for quadrant in quadrants:
    if quadrant.ndim == 2:
        # Quadrant is grayscale, with only one channel
        mean_bright.append(np.mean(quadrant))
        mean_color.append(0)
        std_bright.append(np.std(quadrant))
        std_color.append(0)
    else:
        # Quadrant is color, with three channels
        mean_bright.append(np.mean(quadrant[:,:,0]))
        mean_color.append(np.mean(quadrant[:,:,1:], axis=(0,1)))
        std_bright.append(np.std(quadrant[:,:,0]))
        std_color.append(np.std(quadrant[:,:,1:], axis=(0,1)))
```

```
# Calculate the asymmetry score for each axis
axis1_score = abs(mean_bright[0]-mean_bright[2])/max(std_bright[0], std_bright[2])
axis2_score = abs(mean_bright[1]-mean_bright[3])/max(std_bright[1], std_bright[3])
if(axis1_score>0.2 and axis2_score >0.2):
    asymmetry_score=2;
elif(axis1_score>0.2 or axis2_score>0.2):
    asymmetry_score=1;
else:
    asymmetry_score=0;
print("Asymmetry score:", asymmetry_score)
a.append(asymmetry_score)
```

3.5.2 Border:

```
for fil in glob.glob('/content/drive/MyDrive/output_directory3/*.png'):

# Load the image
img = cv2.imread(fil)
```

```
# Divide the image into eight equal parts (slices)
 slices = []
 for i in range(8):
  y1 = i * img.shape[0] // 8
  y2 = (i+1) * img.shape[0] // 8
  slice = img[y1:y2, :]
  slices.append(slice)
 # Initialize the border score
 border score = 0
 # Loop over each slice and calculate the border score
 for slice in slices:
  # Convert the slice to grayscale
  gray = cv2.cvtColor(slice, cv2.COLOR BGR2GRAY)
  # Apply a Canny edge detector to the slice
  edges = cv2.Canny(gray, 100, 200)
  # Calculate the number of contours in the slice
  contours, = cv2.findContours(edges, cv2.RETR TREE,
cv2.CHAIN APPROX_SIMPLE)
  num contours = len(contours)
  # Calculate the border score for this slice
  slice border score = 1 if num contours > 1 else 0
  # Add the slice border score to the overall border score
  border score += slice border score
 # Print the overall border score
 print('Border score:', border score)
 b.append(border score)
```

3.5.3 Color:

```
import cv2
import numpy as np
import glob

# Define the suspicious colors
suspicious_colors = {
```

```
"white": (255, 255, 255),
  "red": (0, 0, 255),
  "black": (0, 0, 0),
  "light brown": (165, 123, 63),
  "dark brown": (60, 20, 20),
  "blue gray": (100, 149, 237)
# Load all the images in the directory
for fil in glob.glob('/content/drive/MyDrive/sample/*.JPG'):
  # Load the image
  img = cv2.imread(fil)
  # Convert the image to HSV color space
  hsv img = cv2.cvtColor(img, cv2.COLOR BGR2HSV)
  # Initialize the color score to 0
  color score = 0
  # Calculate the total number of pixels in the image
  num pixels = img.shape[0] * img.shape[1]
  # Check for each suspicious color
  for color name, color value in suspicious colors.items():
    # Create a mask for the color
    lower range = np.array([color value[0]-10, 100, 100])
    upper range = np.array([color value[0]+10, 255, 255])
    mask = cv2.inRange(hsv img, lower range, upper range)
    # Calculate the number of pixels of the color
    num_color_pixels = cv2.countNonZero(mask)
    # Check if the color is present in the image
    if num color pixels >= num pixels * 0.05:
       color score += 1
  print("Color score:", color_score)
   c.append(color score)
```

3.5.4 Dermoscopic Structures:

```
-- DERMOSCOPIC STRUCTURES-
for fil in glob.glob('/content/drive/MyDrive/output directory3/*.png'):
  img = cv2.imread(fil)
  gray = cv2.cvtColor(img, cv2.COLOR BGR2GRAY)
  blur = cv2.GaussianBlur(gray, (5, 5), 0)
  ret, thresh = cv2.threshold(blur, 0, 255,
cv2.THRESH BINARY INV+cv2.THRESH OTSU)
  contours, hierarchy = cv2.findContours(thresh, cv2.RETR TREE,
cv2.CHAIN APPROX SIMPLE)
  network = False
  structureless = False
  branched streaks = False
  dots = False
  globules = False
  for contour in contours:
    area = cv2.contourArea(contour)
    if area < 20:
       continue
    x, y, w, h = cv2.boundingRect(contour)
    aspect ratio = float(w) / h
    if aspect ratio > 5:
       network = True
    elif aspect ratio < 1.5:
       if area > 50:
         structureless = True
       elif area > 20:
         dots = True
    elif aspect ratio < 2.5:
       if area > 70:
         branched streaks = True
    elif aspect ratio < 5:
       if area > 70:
         globules = True
  score = 0
  if network:
    score += 1
  if structureless:
    score += 1
  if branched streaks:
```

```
score += 1
  if dots:
     score += 1
  if globules:
     score += 1
  print(f"Dermoscopic score: {score}")
  d.append(score)
import os
output dir1 = '/content/drive/MyDrive/total1/benign'
output dir2 = '/content/drive/MyDrive/total1/Melanoma'
if not os.path.exists(output dir1):
os.makedirs(output dir1)
if not os.path.exists(output dir2):
os.makedirs(output_dir2)
input_dir = '/content/drive/MyDrive/output_directory3'
i=0;
for filename in os.listdir(input_dir):
 img = cv2.imread(os.path.join(input dir, filename))
 ABCD[i] = float(a[i])*1.3 + float(b[i])*0.1 + float(c[i])*0.5 + float(d[i])*0.5
 print(ABCD[i])
 if(ABCD[i]>4.45):
  cv2.imwrite(os.path.join(output dir1, filename), img)
  else:
   cv2.imwrite(os.path.join(output_dir2, filename), img)
 i=i+1
```

3.6 Code For MobileNet Model:-

```
import numpy as np
import pandas as pd
import tensorflow as tf
from tensorflow.keras.applications.resnet50 import ResNet50
from tensorflow.keras.applications.resnet import ResNet101
from tensorflow.keras.applications.inception v3 import InceptionV3
from tensorflow.keras.applications.mobilenet import MobileNet
from tensorflow.keras.layers import Dense, Flatten
from tensorflow.keras.models import Model
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from google.colab import drive
drive.mount('/content/gdrive')
# Load the dataset
data dir = '/content/gdrive/MyDrive/total1'
batch size = 16
train datagen = ImageDataGenerator(rescale=1./255, validation split=0.2)
train generator = train datagen.flow from directory(
  data dir,
  target size=(224, 224),
  batch size=batch size,
  class mode='binary',
  subset='training'
)
val generator = train datagen.flow from directory(
  data dir,
  target size=(224, 224),
  batch size=batch size,
  class mode='binary',
  subset='validation'
)
# Define the model
base model = MobileNet(include top=False, input shape=(224, 224, 3), pooling='avg')
x = Dense(1, activation='sigmoid')(base model.output)
model = Model(inputs=base model.input, outputs=x)
model.compile(
  optimizer=tf.keras.optimizers.Adam(learning rate=1e-3),
  loss='binary crossentropy',
  metrics=['accuracy']
)
```

```
# Train the model
history = model.fit(
  train generator,
  epochs=10,
  validation data=val generator,
  verbose=1,
  validation steps=len(val generator),
  steps per epoch=len(train generator)
)
# Evaluate the model
test loss, test acc = model.evaluate(val generator, verbose=1)
print('Test accuracy:', test acc)
3.7 Code For VGG16 Model:-
import matplotlib.pyplot as plt
import numpy as np
import os
import PIL
import cv2
import pandas as pd
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras.models import Sequential
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.applications.vgg16 import VGG16
from keras.callbacks import EarlyStopping, ModelCheckpoint, ReduceLROnPlateau
from sklearn.model selection import train test split
from sklearn.metrics import accuracy score
from keras import models
from keras.optimizers import Adam
from keras.optimizers import SGD
from google.colab import drive
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.regularizers import 12
drive.mount('/content/gdrive')
```

```
# Load the image data and labels
images = np.load('/content/gdrive/MyDrive/images.npy')
labels = np.load('/content/gdrive/MyDrive/labels.npy')
```

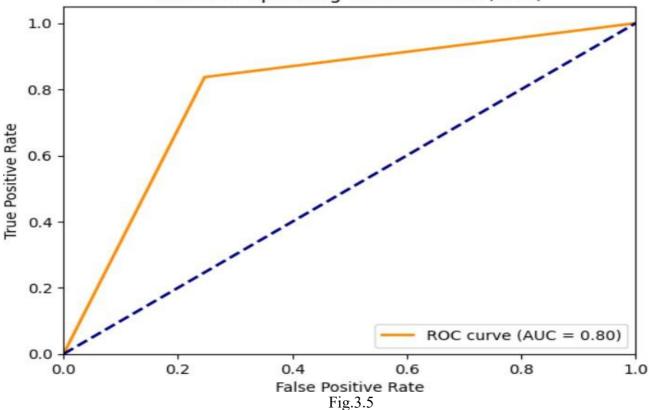
```
# Set the image dimensions and batch size img_height, img_width = 224, 224 batch_size = 16
```

```
# Split the data into training, validation, and testing sets
X train, X test, Y train, Y test = train test split(images, labels, test size=0.2,
random state=42)
X train, X val, Y train, Y val = train test split(X_train, Y_train, test_size=0.2,
random state=42)
# Define the VGG16 model and add additional layers
vgg model = Sequential()
pretrained model = VGG16(include top=False,
           input shape=(224, 224, 3),
           pooling='avg', classes=2,
           weights='imagenet')
# Unfreeze the layers in the pre-trained model
for layer in pretrained model.layers[:-10]:
  layer.trainable = False
vgg model.add(pretrained model)
vgg model.add(layers.Flatten())
vgg model.add(layers.Dense(1024, activation='relu'))
vgg model.add(layers.Dropout(0.5))
vgg model.add(layers.Dense(1024, activation='relu'))
vgg model.add(layers.Dropout(0.5))
vgg model.add(layers.Dense(1, kernel regularizer=12(0.01), activation='linear'))
# Compile the model
opt = SGD(learning rate=0.0001,momentum=0.9)
vgg model.compile(optimizer=opt, loss='hinge', metrics=['accuracy'])
# Set the path to save the model in your Google Drive
model path = '/content/gdrive/MyDrive/Models/vggfinetune.h5'
os.makedirs(os.path.dirname(model path), exist ok=True)
model checkpoint = ModelCheckpoint(model path, monitor='val accuracy',
save best only=True)
# Train the model with data augmentation
history=vgg model.fit(X train, Y train, batch size=batch size, validation data=(X test,
Y test), epochs=100, callbacks=[model checkpoint])
```

RESULTS FOR VGG16 MODEL:-

	precision	recall	f1-score	support
mel	0.84	0.75	0.80	361
ben	0.75	0.84	0.79	313
accuracy			0.79	674
macro avg	0.79	0.80	0.79	674
weighted avg	0.80	0.79	0.79	674
[[272 89] [51 262]]				





3.8 Code For ResNet50 Model:-

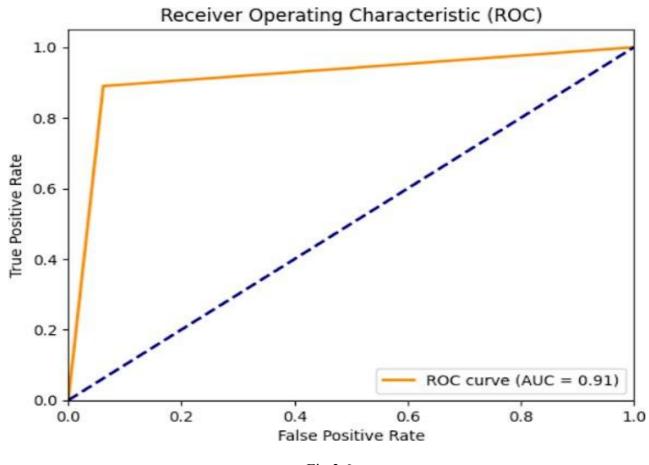
```
import matplotlib.pyplot as plt
import numpy as np
import os
import PIL
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.python.keras.layers import Dense, Flatten
from tensorflow.keras.models import Sequential
from tensorflow.keras.optimizers import Adam
import numpy as np
import os
import cv2
import pandas as pd
import tensorflow as tf
from sklearn.model selection import train test split, KFold
from keras.models import Sequential, Model
from keras.layers import Dense, Flatten, Dropout
from tensorflow.keras.applications.resnet50 import ResNet50
from keras.callbacks import EarlyStopping, ModelCheckpoint, ReduceLROnPlateau
from sklearn.svm import SVC
from sklearn.metrics import accuracy score
from keras import models
```

```
from keras.optimizers import Adam
from google.colab import drive
from tensorflow.keras.regularizers import 12
from keras import models
drive.mount('/content/drive')
images = np.load('/content/drive/MyDrive/images.npy')
labels = np.load('/content/drive/MyDrive/labels.npy')
img height, img width = 224,224
batch size=40
kfold = Kfold(n splits=5, shuffle=True, random state=42)
for fold, (train idx, val idx) in enumerate(kfold.split(images, labels)):
  print(f"Fold: {fold}")
  X train, X val = images[train idx], images[val idx]
  Y train, Y val = labels[train idx], labels[val idx]
  resnet model = Sequential()
  pretrained model= tf.keras.applications.ResNet50(include top=False,
           input shape=(224,224,3),
           pooling='avg',classes=2,
           weights='imagenet')
  resnet model.add(pretrained model)
  resnet model.add(Flatten())
  resnet model.add(Dense(512,activation='relu'))
  resnet model.add(Dense(1,
kernel regularizer=tf.keras.regularizers.12(0.01),activation='linear'))
  for layer in pretrained model.layers[:-16]:
    layer.trainable = False
  opt = Adam(learning rate=0.001)
  resnet model.compile(optimizer = 'adam', loss = 'hinge', metrics = ['accuracy'])
  # Set the path to save the model in your Google Drive
  model path = f'/content/drive/MyDrive/Models/new fold{fold}.h5'
  os.makedirs(os.path.dirname(model path), exist ok=True)
  model checkpoint = ModelCheckpoint(model path, monitor='val accuracy',
save best only=True)
  history = resnet model.fit(X train, Y train, batch size=batch size,
validation data=(X val, Y val), epochs=100, callbacks=[model checkpoint])
```

RESULTS OF ResNet50 Model:-

	precision	recall	f1-score	support
mel	0.91	0.94	0.92	712
ben	0.93	0.89	0.91	636
accuracy			0.92	1348
macro avg	0.92	0.91	0.91	1348
weighted avg	0.92	0.92	0.92	1348
FF1				

[[668 44] [70 566]]



CHAPTER-4

CONCLUSION AND FUTURE PLANS

4.1 Conclusion

we can conclude that we have designed a model that helps to classify the skin cancer as melanoma or benign.we have used the Hybrid models like VGG-16,ResNet50 with SVM classifier to improve the correctness of classification.we have learned to extract the features from the images. These features are used to train the SVM classifier. These model can take a input image and classify the image as benign or melanoma. Finally we checked our results with the help of metrics like accuracy, precision, F1-Score and got accuracy around 91% using ResNet50 model. This can help the patients and doctors to classify the skin cancer as early as possible.

4.2 Future Plans

- 1.We can explore other advanced pre-built models and integrate them into your system. Other CNN models like InceptionV3, DenseNet or EfficientNet gave good results in image classification problems.
- 2.working with university and doctors(or)researchers to know the working of the model and checking the accuracy of the model with the help of real images
- 3. Developing a web app to upload the images and categorize the skin cancer

CHAPTER 5

REFERENCES

5.1 Base Paper

https://link.springer.com/article/10.1007/s11042-022-13081-x

5.2 Other References

- 1. Abbas Q, SadafM, Akram A (2016) Prediction of dermoscopy patterns for recognition of both melanocytic and non-melanocytic skin lesions. *Computers* 5(3):13.
- 2.Brinker TJ, Hekler A, Utikal JS, Grabe N, Schadendorf D, Klode J, Berking C, Steeb T, Enk AH (2018) and C. Von Kalle: Skin cancer classification using convolutional neural networks: systematic review. *JMed Internet Res* 20(10):e11936.
- 3.Dalila F, Zohra A, Reda K, Hocine C (2017) Segmentation and classification of melanoma and benign skin lesions. *Optik* 140:749–761.
- 4.Garnavi R, Aldeen M, Bailey J (2012) Computer-aided diagnosis of melanoma using border-and wavelet based texture analysis. *IEEE Trans Inf Technol Biomed* 16(6):1239–1252.
- 5.Hardie R, Ali R, Silva D, Kebede TM (2018) Skin lesion segmentation and classification for ISIC 2018using traditional classifiers with hand-crafted features. *arXiv* preprint *arXiv*:1807.07001.
- 6.Kasmi R, Mokrani K (2016) Classification of malignant and benign skin lesions: implementation of ofautomatic ABCD rule. *IET Image Proc* 10(6):448–455.
- 7.Telea A (2004) An image inpainting technique based on the fast marching method. *J* Graph Tools 9(1):23–34.