PROJECT REPORT

1. Introduction

1.1 Project Overview

Now a day's people are suffering from skin diseases, more than 125 million people suffering from Psoriasis also skin cancer rate is rapidly increasing over the last few decades especially Melanoma is most diversifying skin cancer. If skin diseases are not treated at an earlier stage, then it may lead to complications in the body including spreading of the infection from one individual to the other. To overcome the above problem, we are building a model which is used for the prevention and early detection of skin cancer, psoriasis. Basically, skin disease diagnosis depends on the different characteristics like color, shape, texture etc. Here the person can capture the images of skin and then the image will be sent the trained model. The model analyses the image and detect whether the person is having skin disease or not.

1.2 Purpose

The diseases are not considered skin diseases, and skin tone is majorlysuffered from the ultraviolet rays from the sun. However, dermatologists perform the majority of non-invasive screening tests simply with the naked eye, even though skin illness is a frequent disease for which early detection and classification are essentialfor patient successand recovery. The characteristic of the skin images is diversified so thatit is a challenging job to devise an efficient and robust algorithm for automatic detection of skin diseaseand its severity. Automaticprocessing of such images for skin analysis requires quantitative discriminator to differentiate the diseases.

2. Literature survey

2.1 Existing problem

A neglected public health problem Skin diseases are among the most common health problems in humans. Considering their significant impact on the individual, the family, the social life of patients, and their heavy economic burden, the public health importance of these diseases is underappreciated.

2.2 References

[1] J. Kawahara and G. Hamarneh,“Multi-resolution-tract CNN with hybrid pretrainedand skin-lesion trainedlayers,” in International Workshop on Machine Learning in Medical Imaging, pp. 164–171,Springer, New York, NY, USA, 2016.

[2] S. Verma, M. A. Razzaque, U. Sangtongdee, C. Arpnikanondt, B. Tassaneetrithep, and A. Hossain, “Digital diagnosis of Hand, Foot, and mouth disease using hybrid deep neural networks,”IEEE Access, vol. 9, pp. 143481–143494, 2021.

[3] P. P. RebouçasFilho, S. A. Peixoto, R. V. Medeirosda Nobrega´ et al., “Automatichistologically-closerclassification of skin lesions,”Computerized Medical Imaging and Graphics,vol. 68, pp. 40–54, 2**018.**

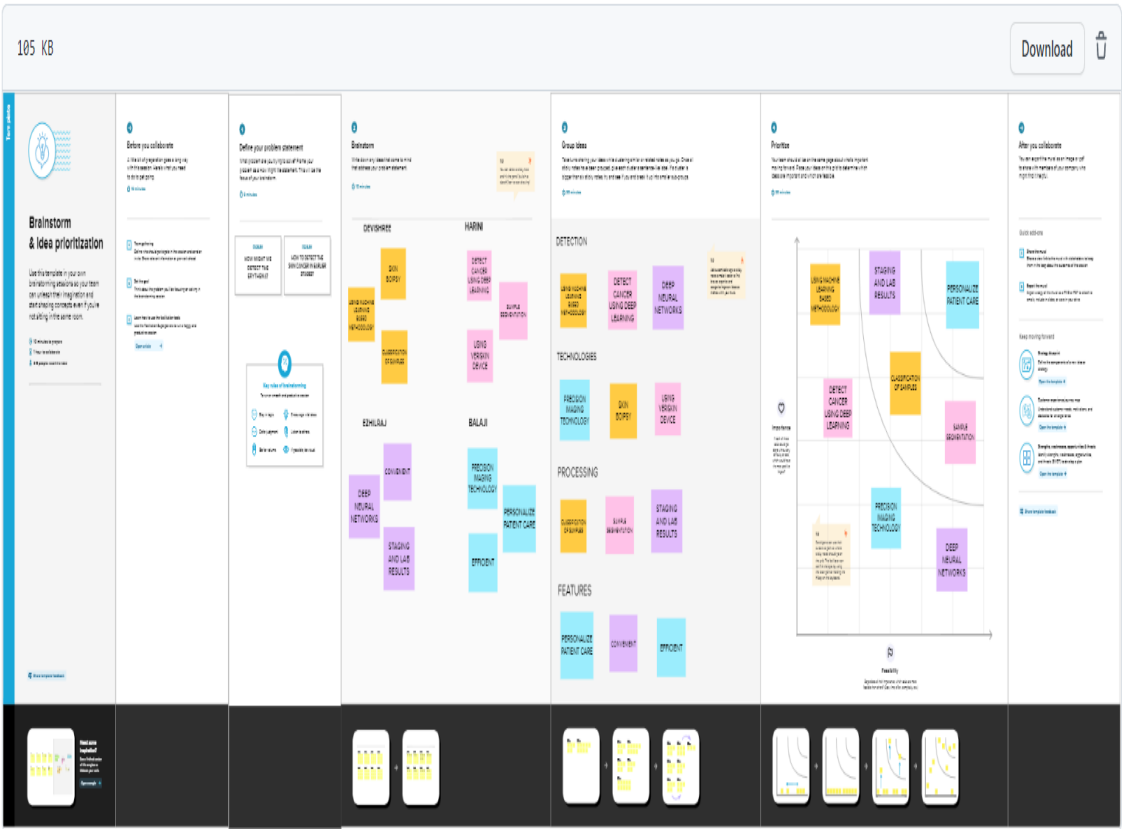
2.3 Problem Statement Definition

We're tryingto find a solution to identify Skin Disease but Developed modelis under trainingbecause given an image of skin, we can decompose, segment, and classify in a sequential manner whichtakes to Early detection of skin cancer,psoriasis.

3. Ideation and Proposed Solution

3.1 Empathy Map Canvas

3.2. Ideation and brainstorming



3.3 Proposed Solution

Two-phase analysismodel. The originalimage primarily enters a pre-processing stage, where normalization and decomposition occur. Afterwards, the first step is segmentation, where cluster of abnormal skin are segmented and cropped. The second step is classification, where each cluster is classified into its corresponding class. Developed Model is Stillunder training.

3.4 Problem Solution fit

Skin disease can appear in virtually any part of body and there is a lack of data required to form probability of a skin disease based on the body part. A Solution model used for the prevention and early psoriasis by image analyses to detect whether the personis having skin disease or not. The location of t image and improvedperformance by CNN model to focus on particular subsections of the images.

4. Requirement Analysis

4.1 Functional requirements

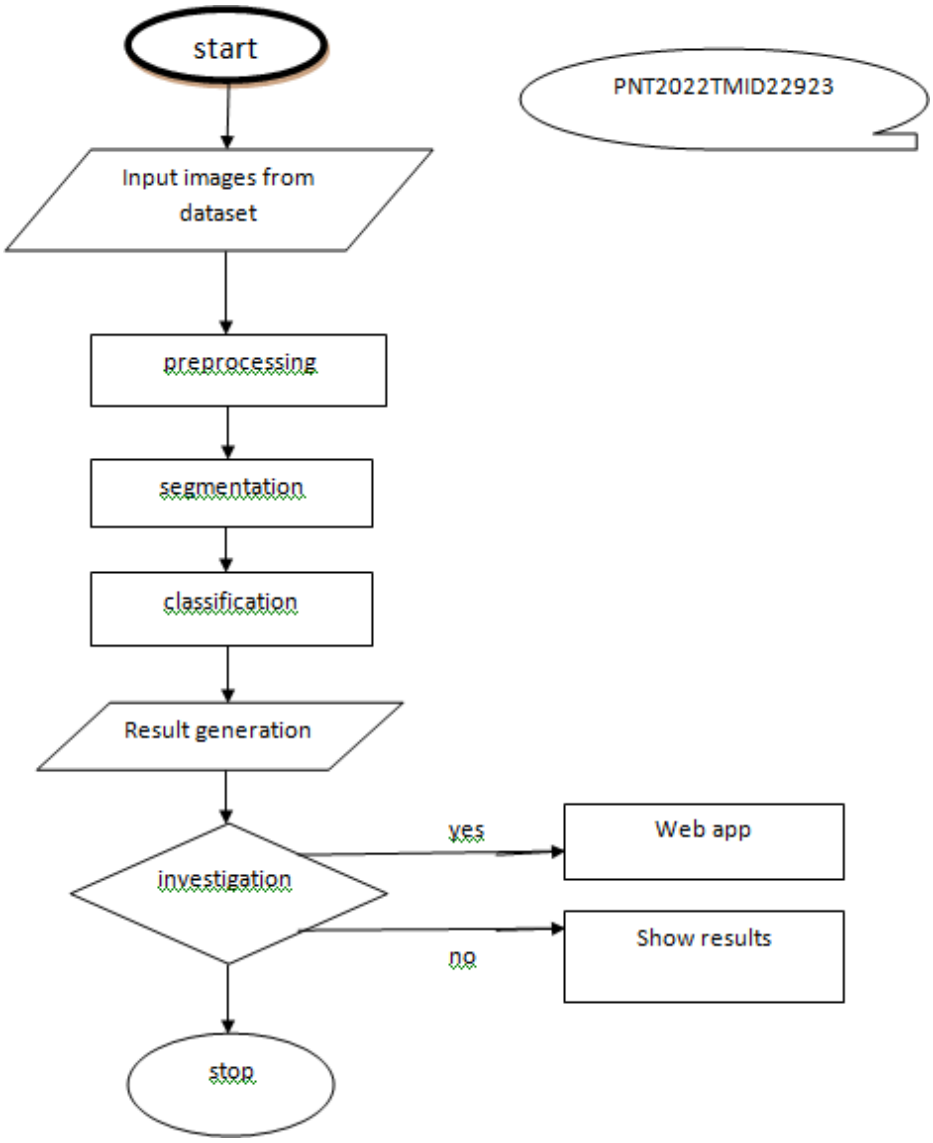
Image Acquisition, Pre-processing Steps such as Colour gradient generator on an image , Cropping and isolating region of interest and Thresholding and Clustering on image, Visual feature extraction, System Training YOLO Model for Skin disease classification with deep learning and CNN, Separate access of application for admin, Diagnosis of Skin diseaseand Data retrievaland Data manipulation.

4.2 Non-Functionalrequirements

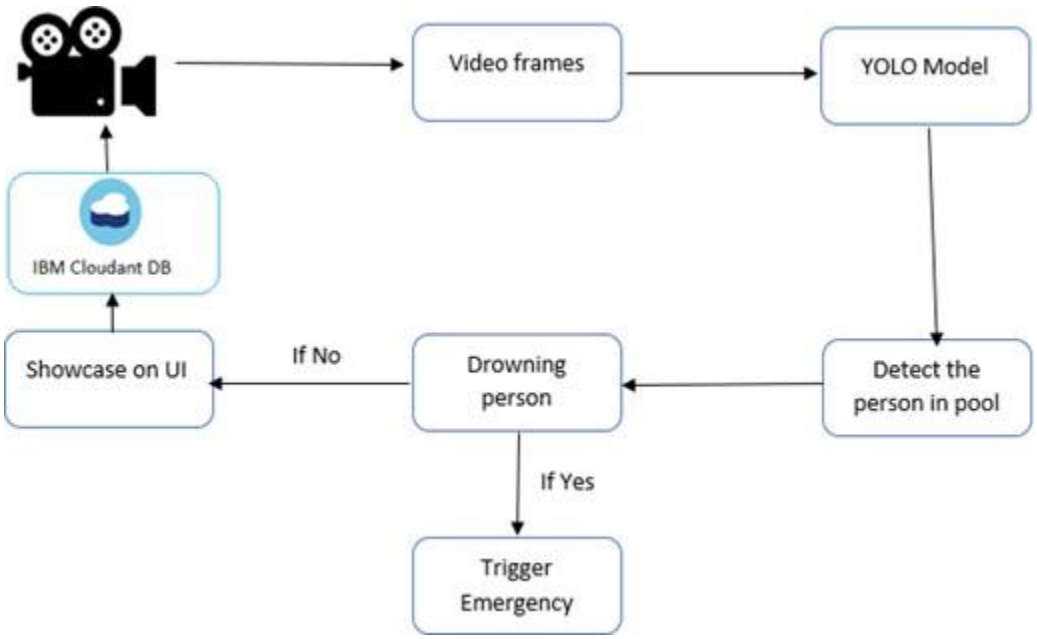
Software Quality Attributes, Prediction, Accuracy.

5. Project Design

5.1 Data Flow Diagram



5.2 Solution and Technical Architecture



5.3 User stories

FunctionalRequirement(Epic)	**User Story Number**	**User Story/ Task**	**Story Points**	**Priority**
Prerequisites	USN-1	Install Python IDE, Python packages, Microsoft VisualObject Tagging Tool,YoloStructure	3	High
Data Collection	USN-2	Dataset should be collected from google or using a Chromeextension such as Fatkun Batch Downloader	3	High
AnnotateImages	USN-3	Create A Projectin VOTT (Microsoft's VisualObject Tagging Tool)	2	Medium
TrainingYOLO	USN-4	train our modelusing YOLO weights	2	Medium

	USN-5	To Download and Convert Pre-TrainedWeights	3	High
	USN-6	To Train YOLOv3 Detector	3	High
Cloudant DB	USN-7	Register & Loginto IBM Cloud	3	High
	USN-8	Create Service Instant and Credentials	2	Medium
	USN-9	Launch DB and Createdatabase	3	High
DevelopmentPhase	USN-10	To build a web application	3	High
	USN-11	Building HTMLpages with pythoncode	2	Medium
	USN-12	To run the application	3	High
Testing Phase	USN-13	As a user loginto dashboard	2	Medium
	USN-14	As a user import the images with skindiseases to the software application	2	Medium
	USN-15	YOLO processes the image and give thenecessary details	3	High

6. Project Planning and Scheduling

6.1 Sprint Planning and Estimation

Sprint	Functional Requirement (Epic)	User Story Number	User Story / Task	Story Points	Priority	Team Members
Sprint-1	Prerequisites	USN-1	Install Python IDE, Python packages, Microsoft Visual Object Tagging Tool, YoloStructure	3	High	DEVISHR EEHARINI EZHILRAJ BALAJI

Sprint-1	Data Collection	USN-2	Dataset should be collected from google or using a Chrome extension such as FatkunBatch Downloader	3	High	DEVISHR EEHARINI EZHILR AJBALAJI
Sprint-1	Annotate Images	USN-3	Create A Projectin VOTT (Microsoft's Visual Object TaggingTool)	2	Medium	DEVISHR EEHARINI EZHILRAJ BALAJI
Sprint-2	Training YOLO	USN-4	train our modelusing YOLO weights	2	Medium	DEVISHR EEHARINI EZHILRAJ BALAJI
Sprint-2		USN-5	To Download and Convert Pre-Trained Weights	3	High	DEVISHR EEHARINI EZHILRAJ BALAJI

Sprint	Functional Requirement (Epic)	User Story Number	User Story / Task	Story Points	Priority	Team Members
Sprint-2		USN-6	To Train YOLOv3 Detector	3	High	DEVISHR EEHARINI EZHILRAJ BALAJI
Sprint-3	Cloudant DB	USN-7	Register & Login to IBM Cloud	3	High	DEVISHR EEHARINI EZHILR AJBALAJI
Sprint-3		USN-8	Create Service Instant and Credentials	2	Medium	DEVISHR EEHARINI EZHILR AJBALAJI
Sprint-3		USN-9	Launch DB and Createdatabase	3	High	DEVISHR EEHARINI EZHILRAJ BALAJI
Sprint-3	Development Phase	USN-10	To build a web application	3	High	DEVISHR EEHARINI EZHILRAJ BALAJI
Sprint-3		USN-11	Building HTML pages with python code	2	Medium	DEVISHR EEHARINI EZHILRAJ BALAJI

Sprint-3		USN-12	To run the application	3	High	DEVISHREEHARINIEZHILRAJBALAJI
Sprint-4	Testing Phase	USN-13	As a user loginto dashboard	2	Medium	DEVISHREEHARINIEZHILRAJBALAJI
Sprint-4		USN-14	As a user importthe images withskin diseases to the software application	2	Medium	DEVISHREEHARINIEZHILRAJBALAJI
Sprint-4		USN-15	YOLO processes the imageand give the necessary details	3	High	DEVISHREEHARINIEZHILRAJBALAJI

6.2 Sprint Delivery Schedule

Sprint	Total Story Points	Duration	Sprint Start Date	Sprint End Date (Planned)
Sprint-1	20	6 Days	24 Oct 2022	29 Oct 2022
Sprint-2	20	6 Days	31 Oct 2022	05 Nov 2022
Sprint-3	20	6 Days	07 Nov2022	12 Nov2022
Sprint-4	20	6 Days	14 Nov 2022	19 Nov 2022

7. Coding and Solutioning

pip3 install tensorflow tensorflow_hub matplotlib seaborn numpypandas sklearn imblearn

```
import tensorflow
as tf
importtensorflow_h
ub as hub
import
matplotlib.pyplot as
pltimport numpy as
np
import
pandas as
pd import
seabornas
sns
from tensorflow.keras.utils import get_file
from sklearn.metrics import roc_curve, auc, confusion_matrix


from imblearn.metrics importsensitivity_score, specificity_score

im
po
rt
os
im
po
rt
gl
ob
im
po
rt
zip
file
im
por
tra
nd
om

# to get consistent results after
multiplerunstf.random.set_seed(7)
np.random.seed(7)
random.seed(7)
```

```
# 0 for benign, 1 for
malignant class_names =
["benign", "malignant"]
```

Preparing the Dataset

```
def download_and_extract_dataset():
  # dataset from
  https://github.com/udacity/dermatologist-ai#
  5.3GB
  train_url =  "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-
  cancer/train.zip"# 824.5MB
  valid_url =  "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-
  cancer/valid.zip"# 5.1GB
  test_url = "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-
  cancer/test.zip"for i, download_link in enumerate([valid_url, train_url, test_url]):
  temp_file = f"temp{i}.zip"
    data_dir= get_file(origin=download_link, fname=os.path.join(os.getcwd(), temp_file))
    print("Extracting", download_link)
    with zipfile.ZipFile(data_dir, "r") as z:
      z.extractall("data")
    # remove
    the temp
    file
    os.remove(
    temp_file)

# commentthe below line if you already downloaded
the datasetdownload_and_extract_dataset()
# preparingdata
# generateCSV metadata file to read img pathsand labels
from itdef generate_csv(folder, label2int):
    folder_name =
    os.path.basename(folder)
    labels = list(label2int)
    # generateCSV file
    df =
    pd.DataFrame(columns=["filepath",
    "label"])i = 0
    for labelin labels:
        print("Reading", os.path.join(folder, label, "*"))
        for filepath in glob.glob(os.path.join(folder,
```

```
        label, "*")):df.loc[i] = [filepath,
            label2int[label]]
            i += 1
    output_file =
    f"{folder_name}.csv"print("Sa
    ving", output_file)
    df.to_csv(output_file)

# generateCSV files for all data portions, labelingnevus and seborrheic keratosis



# as 0 (benign), and melanoma as 1 (malignant)
# you should replace"data" path to your extracted dataset path
# don't replace if you used download_and_extract_dataset() function
generate_csv("data/train", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
generate_csv("data/valid", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
generate_csv("data/test", {"nevus": 0, "seborrheic_keratosis": 0,
"melanoma": 1})# loading data
train_metadata_filename
=                    "train.csv"
valid_metadata_filename
= "valid.csv" # load CSV
files as DataFrames
df_train =
pd.read_csv(train_metadata_filename)
df_valid =
pd.read_csv(valid_metadata_filename)
n_training_samples = len(df_train)
n_validation_samples = len(df_valid)
print("Number of training samples:",
n_training_samples) print("Number of validation
samples:", n_validation_samples)
train_ds = tf.data.Dataset.from_tensor_slices((df_train["filepath"],
df_train["label"])) valid_ds =
tf.data.Dataset.from_tensor_slices((df_valid["filepath"],
df_valid["label"]))
```

Output:

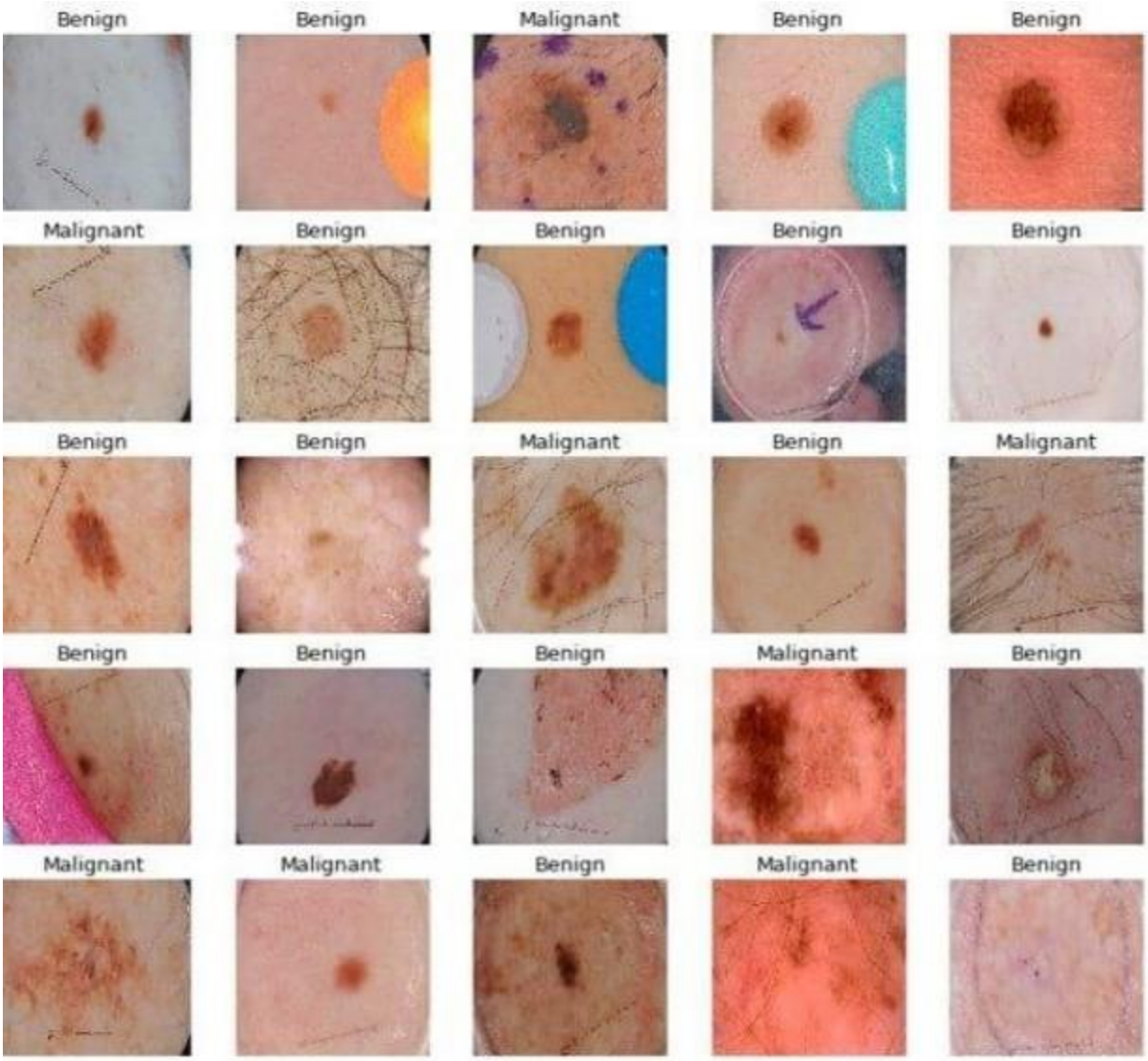
Number of training samples: 2000
Number of validation samples:150

```
#
preproce
ss  data
def
decode_im
g(img):

# convert the compressed stringto a 3D
  uint8 tensorimg =
  tf.image.decode_jpeg(img, channels=3)
  # Use `convert_image_dtype` to convert to floatsin the
  [0,1] range.img = tf.image.convert_image_dtype(img,
  tf.float32)
  # resize the image to the
  desired
  size.returntf.image.resize(i
  mg, [299, 299])


def process_path(filepath, label):
  # load the raw data from the file
  as a stringimg =
  tf.io.read_file(filepath)
  img =
  decode_img(
  img)return
  img, label


valid_ds                    =
valid_ds.map(process_path)
train_ds                    =
train_ds.map(process_path)
# test_ds = test_ds
for image, label in
    train_ds.take(1): print("Image
    shape:", image.shape)
```

```
print("Label:", label.numpy())
  Image shape: (299, 299, 3)
  Label: 0
  #
  trainingp
  arameters
  batch_size
  = 64
  optimizer
  =
  "rmspro
  p"


  def prepare_for_training(ds, cache=True, batch_size=64,
    shuffle_buffer_size=1000):if cache:
      if isinstance(cache, str):
        ds =
      ds.cache(ca
      che)else:
        ds = ds.cache()
    # shufflethe dataset
    ds =
    ds.shuffle(buffer_size=shuffle_buffer
    _size)# Repeatforever
    ds =
    ds.re
    peat
    () #
    split
    to
    batch
    es
    ds = ds.batch(batch_size)
    # `prefetch` lets the datasetfetch batches in the background while the
    model# is training.
    ds =
    ds.prefetch(buffer_size=tf.data.experimental.AUTOT
    UNE)return ds

  valid_ds = prepare_for_training(valid_ds, batch_size=batch_size, cache="valid-
```

```
cached-data") train_ds = prepare_for_training(train_ds, batch_size=batch_size,
cache="train-cached-data") batch = next(iter(valid_ds))

  def
    show_batch(b
    atch):
    plt.figure(figsi
    ze=(12,12))for
    n in
    range(25):
        ax =
        plt.subplot(5
        ,5,n+1)
        plt.imshow(
        batch[0][n])
        plt.title(class_names[batch[1][n].numpy()].title(
        )) plt.axis('off')

  show_batch(batch)
```

Output:




```
        # buildingthe model
# InceptionV3 model & pre-trained weights
module_url = "https://tfhub.dev/google/tf2-preview/inception_v3/feature_vector/4"

m = tf.keras.Sequential([
   hub.KerasLayer(module_url, output_shape=[2048],
   trainable=False), tf.keras.layers.Dense(1,
```

```
activation="sigmoid")
  ])

  m.build([None, 299, 299, 3])
  m.compile(loss="binary_crossentropy", optimizer=optimizer, metrics=["accuracy"])
  m.summary()
```

Output:

Model: "sequential"

Layer (type)	Output Shape	Param #
keras_layer(KerasLayer)	multiple	21802784
dense (Dense)	multiple	2049

Total params: 21,804,833
Trainable params: 2,049
Non-trainable params: 21,802,784

_____

Training the model

```
model_name = f"benign-vs-malignant_{batch_size}_{optimizer}"
tensorboard =  tf.keras.callbacks.TensorBoard(log_dir=os.path.join("logs",
model_name)) # saves model checkpoint whenevermwe reach better weights
modelcheckpoint = tf.keras.callbacks.ModelCheckpoint(model_name + "_{val_loss:.3f}.h5",
save_best_only=True, verbose=1)

history = m.fit(train_ds, validation_data=valid_ds,
            steps_per_epoch=n_training_samples //
            batch_size,
            validation_steps=n_validation_samples // batch_size, verbose=1, epochs=100,
            callbacks=[tensorboard, modelcheckpoint])
```

Output

Train for 31 steps,validate
for 2 stepsEpoch 1/100

30/31 [==============================>.] - ETA: 9s - loss: 0.4609 - accuracy: 0.7760
Epoch 00001: val_loss improvedfrom inf to 0.49703, saving model to benign-vs-malignant_64_rmsprop_0.497.h5
31/31 [==============================] - 282s 9s/step - loss: 0.4646 - accuracy: 0.7722 - val_loss:0.4970 - val_accuracy: 0.8125
<..SNIPED..>
Epoch 27/100
30/31 [==============================>.] - ETA: 0s - loss: 0.2982 - accuracy:0.8708
Epoch 00027: val_lossimproved from 0.40253 to 0.38991,saving model to benign-vs-malignant_64_rmsprop_0.390.h5
31/31 [==============================] - 21s 691ms/step - loss: 0.3025 - accuracy: 0.8684 - val_loss: 0.3899 - val_accuracy: 0.8359
<..SNIPED..>
Epoch 41/100
30/31 [==============================>.] - ETA: 0s -loss: 0.2800 - accuracy: 0.8802
Epoch 00041: val_loss did not improve from 0.38991
31/31 [==============================] - 21s 690ms/step - loss: 0.2829 - accuracy: 0.8790 - val_loss: 0.3948 - val_accuracy: 0.8281Epoch42/100
30/31 [==============================>.] - ETA: 0s - loss: 0.2680 - accuracy:0.8859
Epoch 00042: val_loss did not improve from 0.38991
31/31 [==============================] - 21s 693ms/step - loss: 0.2722 - accuracy: 0.8831 - val_loss: 0.4572 - val_accuracy: 0.8047

Model Evaluation

```
# evaluation

# load testing set

test_metadata_filename =

"test.csv"
```

```
df_test =
pd.read_csv(test_metadata_filename)
n_testing_samples = len(df_test)
  print("Number of testing samples:", n_testing_samples)
  test_ds = tf.data.Dataset.from_tensor_slices((df_test["filepath"],
  df_test["label"]))def prepare_for_testing(ds, cache=True,
  shuffle_buffer_size=1000):
    if cache:
      if isinstance(cache, str):
        ds =
      ds.cache(ca
      che)else:
        ds = ds.cache()
    ds =
    ds.shuffle(buffer_size=shuffle_buffer
    _size)return ds
  test_ds = test_ds.map(process_path)
  test_ds= prepare_for_testing(test_ds, cache="test-cached-data")
```

Number of testing samples

```
  600# evaluation
  # load testing set
  test_metadata_filename =
  "test.csv"
  df_test =
  pd.read_csv(test_metadata_filenam
  e)n_testing_samples = len(df_test)
  print("Numberof testing samples:", n_testing_samples)
```

```
test_ds = tf.data.Dataset.from_tensor_slices((df_test["filepath"], df_test["label"]))



def prepare_for_testing(ds, cache=True,
shuffle_buffer_size=1000):ifcache:
if
isinstance(c
ache, str):ds
=
ds.cache(cac
he) else:
ds = ds.cache()
ds =
ds.shuffle(buffer_size=shuffle_buffer_
size)return ds
test_ds = test_ds.map(process_path)
test_ds = prepare_for_testing(test_ds, cache="test-cached-data")


# load the weights with the least loss
m.load_weights("benign-vs-
malignant_64_rmsprop_0.390.h5")
print("Evaluating the model...")
loss, accuracy = m.evaluate(X_test, y_test,verbose=0)print("Loss:", loss, "  Accuracy:", accuracy)
```

Output

```
Evaluating the model...
Loss: 0.4476394319534302  Accuracy: 0.8
```

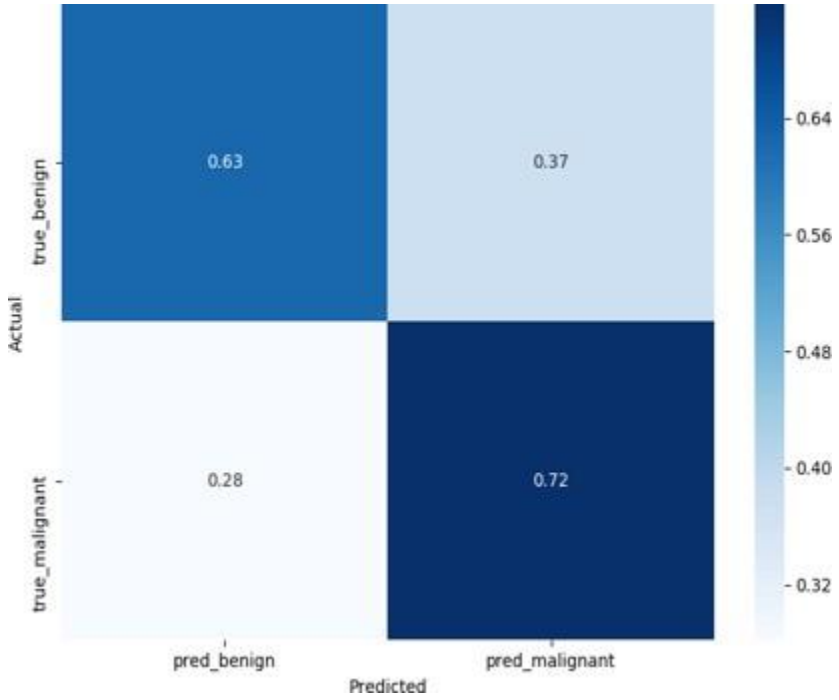
```
def get_predictions(threshold=None):
"""
Returns predictions for binary classification given `threshold`
For instance, if threshold is 0.3, then it'll output 1 (malignant) for
that sample ifthe probability of 1 is 30% or more (instead of 50%)
```

```
    """
    y_pred =
    m.predict(X_te
    st)if not
    threshold:
    threshold = 0.5
    result =
    np.zeros((n_testing_samples
    ,))for i in
    range(n_testing_samples):
      # test melanoma
      probabilityif
      y_pred[i][0] >=
      threshold:
      result[i] = 1
      # else, it's
    0
    (benign)retu
    rn result

  threshold = 0.23
  # get predictions with 23% threshold
  # which means if the model is 23% sure or more that is
  malignant,# it's assignedas malignant, otherwiseit's
  benign
  y_pred = get_predictions(threshold)
  def plot_confusion_matrix(y_test, y_pred):
    cmn =
    confusion_matrix(y_test,
    y_pred)# Normalise
    cmn = cmn.astype('float') / cmn.sum(axis=1)[:,
    np.newaxis]# print it
    print(cmn)
    fig, ax =
    plt.subplots(figsize=(10,10))
    sns.heatmap(cmn, annot=True,
    fmt='.2f',
xticklabels=[f"pred_{c}" for c in class_names],yticklabels=[f"true_{c}" for c in class_names],
            cmap="Blues"
            )
    plt.ylabel('Actual
    ')
    plt.xlabel('Predic
```

ted')
 # plot the resulting
confusion
matrixplt.show()

plot_confusion_matrix(y_test, y_pred

Output



sensitivity =
sensitivity_score(y_test, y_pred)
specificity =
specificity_score(y_test, y_pred)

print("Melanoma Sensitivity:",
sensitivity)print("Melanoma
Specificity:", specificity)

Output

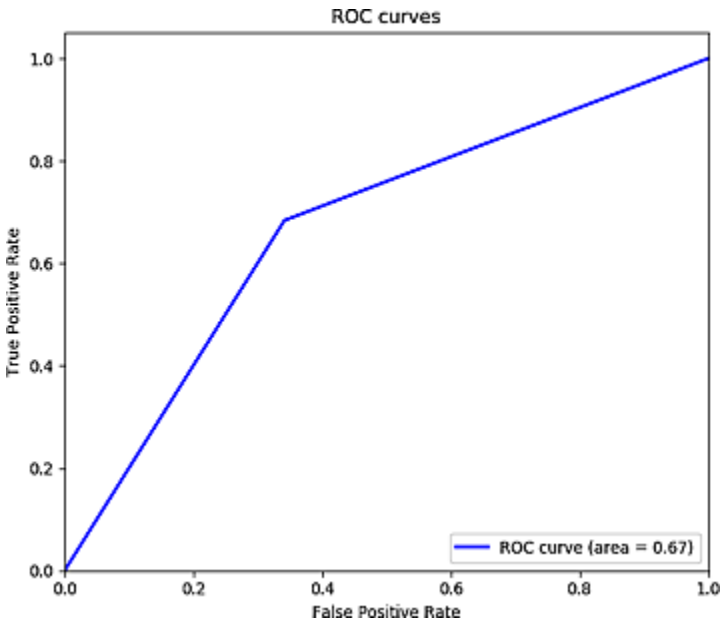
Melanoma Sensitivity: 0.717948717948718

Melanoma Specificity: 0.6252587991718427

```
def plot_roc_auc(y_true, y_pred):
    """
    This functionplots the ROC curves and provides the
    scores."""
    #
    prepare
    for
    figure
    plt.figu
    re()
    fpr, tpr, _ = roc_curve(y_true, y_pred)


    # obtain
    ROC
    AUC
    roc_auc =
    auc(fpr,
    tpr)# print
    score
    print(f"ROC AUC:
    {roc_auc:.3f}")# plot
    ROC curve
    plt.plot(fpr, tpr, color="blue", lw=2,
             label='ROC curve (area = {f:.2f})'.format(d=1,
    f=roc_auc))plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False
    Positive
    Rate')plt.ylabel('Tr
    ue Positive Rate')
    plt.title('ROC
    curves')
    plt.legend(loc="lo
    wer right")
    plt.show()
```

plot_roc_auc(y_test, y_pred)

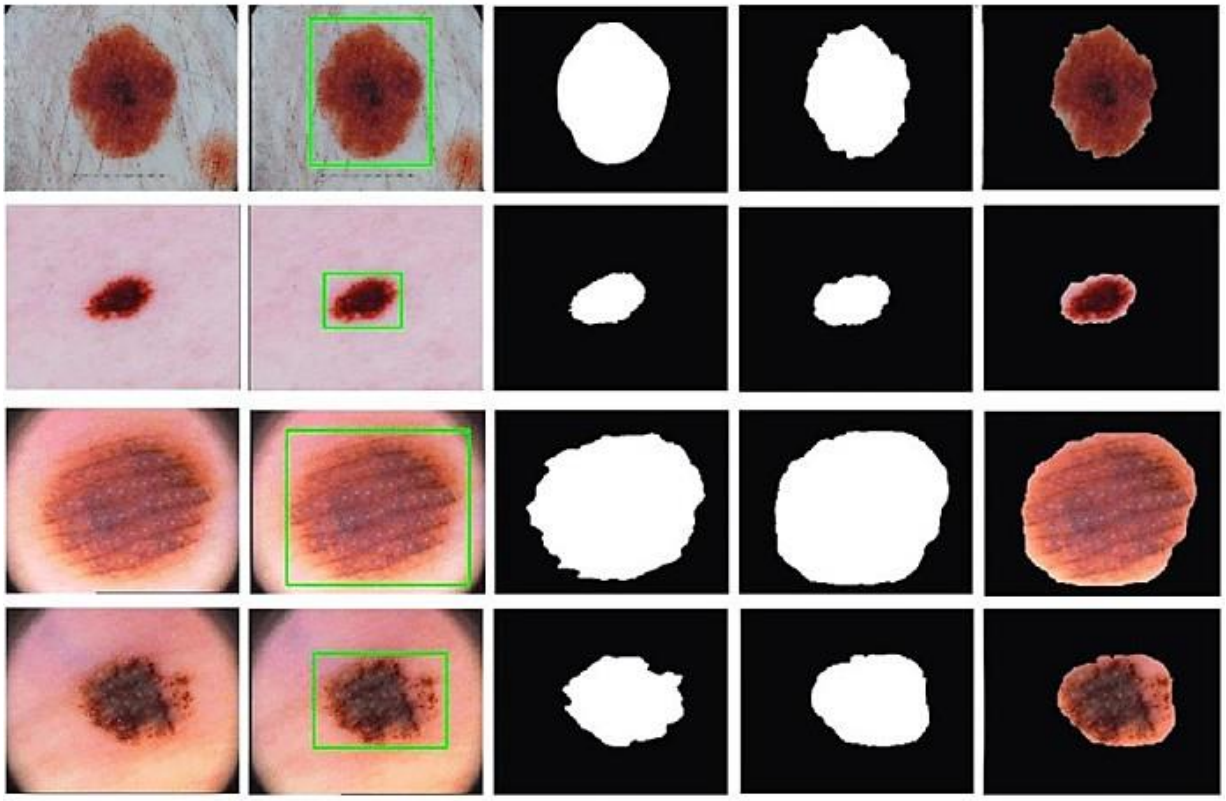
Output



ROC AUC: 0.671

8.Results

The finalresults are based on the accuracy resultsin the form of the melanoma and the non-melanomaskin diseases classifications.



9. Advantages and Disadvantages

9.1 Advantages

Instant Response, improvesprediction of Skin Disease, no referral needed, Saves Money and Time, and Confidential Advice.

9.2 Disadvantages

Network Connectivity and Accuracy

10.Conclusion

We have shown that even without a large dataset and high-quality images, it is possible to achieve sufficient accuracy rates. In addition, we have shown that current state-of-the-art CNN models can outperform models created by previous research, through proper data pre-processing, self-supervised learning, transfer learning, and special CNN architecture techniques. Furthermore, with accurate segmentation, we gain knowledge of the location of the disease, which is useful in the pre-processing of data used in classification, as it allows the CNN model to focus on the area of interest. Lastly, unlike previous studies, our method provides a solution to classify multiple diseases within a single image. With higher quality and a larger quantity of data, it will be viable to use state-of-the-art models to enable the use of CAD in the field of dermatology.

11. Future Scope

This implementation of the Structural Co-Occurrence matrices for featureextraction in the skin diseasesclassification and the pre-processing techniques are handled by using the Median filter, this filter helps toremove the salt and pepper noise in the image processing; thus, it enhances the quality of the images, and normally, the skin diseasesare considered as the risk factor in all over the world.Our proposed approach provides97% of the classification of the accuracyresults while anotherexisting model such asFFT + SCM gives 80%, SVM + SCM gives 83%, KNN + SCM gives 85%, and SCM + CNN gives 82%. Future work is dependent on the increasedsupport vector machine'saccuracy in classifying skin illnesses, and SCM is used to manage the featureextraction technique.

12. Appendix

Github link:

https://github.com/IBM-EPBL/IBM-Project-36112-1660292850